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RESEARCH ARTICLE

Genetic Characterization of Local Adaptable Rice Landraces of Nagaland, India

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Nagaland is one of the parts of the center of origin of rice, and has diversified rice landraces with unique cooking quality, taste, aroma and stress tolerance. In current study, landraces were evaluated for grain quality, yield and stress tolerance. Landraces Aongsho, Semmeki, Goyo Tsük and Moya Tsük showed higher yield as compared to Bhalum-3 check variety in the upland ecosystem. Whereas, Mehourü was the smallest landraces with a height of 65 cm. Among all the landraces under study, Yunghah, Goyo Tsük, Rükhatang and Vepvu Tsük were found strongly aromatic. While, Teke, Aongsho and Semmeki landrace showed moisture stress tolerance. Cluster and principal component analysis grouped the landraces into six distinct clusters. These landraces harbor the genes for various grain quality traits, drought tolerance and brown spot disease (*Cochliobolus miyabeanus*) tolerance. Superior landraces identified for grain quality, drought tolerance and brown spot can be utilized in future breeding programmes. This study may help in pre-breeding activities for development of improved varieties/hybrids for this agro-climatic zone.

Key Words: Diversity analysis, Genetic variation, Grain quality, Rice landraces, Yield and stress tolerance

Introduction

Rice is the major staple food grain crop of the world and its demand is continuously increasing for this staple food crop. Around, 2 billion population (25.9%) of the world population did not have regular access to nutritious and sufficient food in 2019 (FAO, IFAD, UNICEF, WFP and WHO, 2020). Globally, rice productivity has to be increased at the rate of 1.0–1.2% annually beyond 2020 to feed the ever-growing population and keep prices affordable (IRRI, Africa rice and CIAT, 2013). Considering the immediate need for addressing food problem, replacement of poor yielder landraces is required by high yielding improved varieties for greater interest of food security and wellbeing of all nations' peoples. New improved rice varieties have high yield potential and tolerance for biotic and abiotic stresses as compared to landraces. This necessitates development of improved rice varieties by efficient utilization of landraces/germplasm to feed the ever-growing population.

Nagaland lies in the hills and mountains of northeastern part of East Himalayas region of India. This region is deeply dissected by the Doyang and Dikhu in the north, the Barak in the southwest, and the tributaries of the Chindwin River of Myanmar in the southeast. Agro-climatic conditions vary from tropical to sub-temperate. Farmers of Nagaland cultivate rice in diverse ecosystem ranging from upland rice in rainfed *jhum* fields to wetland terrace rice cultivation (WTRC) with varied altitudinal ranges of hills having varied temperature regimes. WTRC is practiced in hilly as well plain areas of Nagaland. About 43 % (91,250 ha) of the total rice cropped area in the state is under rainfed *jhum* cultivation (upland rice) with a production of 1,81,570 tonnes, whereas remaining 57% (1,20,750 ha) is under wetland terrace rice cultivation with a production of 342870 tonnes (Directorate of Economics and Statistics, Nagaland, 2018). In north eastern India, majority of farmers have been cultivating and conserved so many diverse rice landraces since time immemorial. In Nagaland alone, a total of 867 traditional 'landraces' of rice has been identified by the State Agriculture Research Station (SARS), Nagaland (Sharma, 2017). Nagaland is a rich source of rice genetic resources and these landraces were studied by researchers for grain

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quality and yield attributes only (Roy *et al.,* 2014;, Roy *et al.,* 2015; Zeliang *et al.,* 2020). Here, these landraceevolved after long years of acclimatization in local environments. These landracehave unique taste and texture after cooking, early maturity, highly adaptable to local climate and have significant tolerance to biotic and abiotic stress. The traditional landraces can serve as an important gene pool for valuable traits, for example, the upland landraces of rice present in northeast India are drought tolerance, photoperiod insensitivity, disease and insect tolerance, better root system, etc. (Travis *et al.,* 2015; Umakanth *et al.,* 2017; Verma *et al.,* 2019; Verma *et al.,* 2020). So, these landraces have different donor genes which can not only increase genetic diversity and genetic variability in pipelines varieties and hybrids while also lead to food security and sustainability.

Improvement in the grain yield is the prime objective of plant breeders for several decades, however grain and cooking quality attributes preference in a particular region determines the acceptance of a variety at larger scale. Under the regime of climate change climate resilient varieties are preferred by the farming community for cultivation. So, the best strategy is the improvement of limiting traits without compromising the farmers' preferred traits. In this regard, morphological characterization and clustering of traditional landraces on the basis of useful traits can helps in improvement of these local cultivars for limiting traits through different breeding methods (Kapoor *et al.,* 2019). Therefore, considering these points current study evaluated major landrace of Nagaland in local agro-climatic zones to measure the extent of genetic variation and genetic relationships between genotypes for grain quality, yield and stress tolerance for development of improved cultivars. If these are not conserved and characterized, they might be lost in time.

Material and Methods

Experimental Materials

A total of 38 rice landraces were collected along with passport data containing location, geographic coordinates from Longleng, Kohima, Wokha and Mokokchung districts of Nagaland during 2017-18 (Table 1 and Fig. 1). Seeds of these landraces along with two check varieties were directly sown at a spacing of 30 x 10 cm in Randomized Complete Block Design (RCBD) with three replications during *kharif* season (First fortnight of June to October) of 2018-19 at ICAR Research complex Nagaland Centre, research farm, Medziphema, Nagaland (25^{o}45'24"N, longitude of 93^{o}50'26"E, and altitude of 295 m above MSL). The soil of experimental field was sandy loam and acidic in reaction (pH 5.6). The landraces were cultivated under recommended agronomic practices including nutrient, pest and disease management practices. Recommended dose of N, P and K @ of 80, 60, 40 was applied. Half dose of N, full dose of P and K were applied basal through urea, Single Super Phosphate and Muriate of potash, respectively. Remaining half dose of nitrogen was applied as top dressing 45 days after sowing (DAS). This region received total rainfall of 1408 mm during 2018 of which maximum rainfall occurs during May to October month and experiences mean annual daily minimum and maximum temperature of 24°C and 36°C, respectively during the rice season.

Data Recording

These 38 landraces along with Bhalum-3 as yield check and Pusa Sughandha-5 as aroma check variety were evaluated for yield traits such as tillers per plant (TP), plant height (cm) (PH), panicle length (cm) (PL), Grains per panicle (GPP), Spikelet Fertility (%) (SF), maturity duration (MD) and yield and grain quality traits such as grain length (mm) (GL), grain width (mm) (GW), grain shape (GS), grain colour, amylose content (AC), gel consistency (GC), gelatinization temperature (GT) and aroma and moisture stress and reaction to brown spot disease (*Cochliobolus miyabeanus*). Ten plants were randomly selected in each plot to record plant height, tillers per plant and grain quality traits. The seed yield (tonnes/ha) and duration were recorded on a plot basis of size 15×6m^2.

AC was determined as per Kaur *et al*. (2014) method. GT was assessed indirectly as the alkali spreading value of hulled kernels, as per the procedure of Zhang *et al.* (2020). Similarly, gel consistency was measured by the procedure of Zhang *et al.* (2020). GC was assessed as very hard (< 25 mm), hard (26–40 mm), medium (41–60 mm) or soft (61–100 mm) based on the length of the gel. The aroma of rice was determined as per the method described by Mishra *et al.* (2019) and scored as strongly scented (SS), mild scented (MS) and non-scented. Length and breadth of 10 milled rice kernels were measured using vernier caliper in replication and the average was calculated based on 3 replications. Grain shape was determined following the guidelines of the PPV&FRA (2007) classification.

Table 1. Passport data with location of rice landraces collected from Nagaland

Name of landrace	Date of collection	Place of collection	Location (Geographic coordinate)	Type of seed	Grain Type	Grain color	Awn (Absent/ Present)	Flowering Duration
Dzükunya	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Indica	LB	White	Present	Early
Rosholha	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Indica	SB	Brown	Absent	Medium
Kemenya	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Indica	LS	White	Absent	Early
Mekrilha kecha	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Indica	LB	White	Absent	Early
Mekrilha ketei	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Indica	LB	White	Absent	Medium
Khezharhi	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Indica	LB	Brown	Present	Late
Nyari	10/1/2017	Khonoma Village (Kohima)	25.650 N 94.033 E	Japonica	LB	White	Absent	Medium
Keteiu	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Japonica	SB	White	Absent	Late
Tsorenyü	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Indica	MS	Red	Present	Medium
Mehourü	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Indica	LB	Brown	Absent	Medium
Kemese-u	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Japonica	SB	White	Absent	Late
Kemeluo-ü	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Indica	SB	White	Absent	Late
Khenulha	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Indica	LB	White	Absent	Early
Thevürü	10/1/2017	Chedema Village (Kohima)	25.6792 N 94.1424 E	Indica	SB	Brown	Absent	Medium
Boyoh	10/14/2017	Dungkhao Village (Longleng)	26.5145 N 94.8347 E	Indica	SB	White	Absent	Early
Doulong	10/14/2017	Hukpang Village (Longleng)	26.4692 N 94.8049 E	Indica	SB	White	Absent	Early
Shangha	10/14/2017	Hukpang Village (Longleng)	26.4692 N 94.8049 E	Indica	SB	Brown	Absent	Early
Hahhak	10/13/2017	Nian Village (Longleng)	26.5934 N 94.8614 E	Indica	SB	Brown	Absent	Medium
Shuphok	10/13/2017	Nian Village (Longleng)	26.5934 N 94.8614 E	Indica	SB	White	Absent	Early
Angja	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Indica	SB	Brown	Absent	Early
Aongsho	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Indica	SB	White	Absent	Early
Maibo	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Indica	SB	Red	Absent	Early
Nukjau Nyakla	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Indica	SB	Brown	Absent	Early
Nukjau Shola	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Indica	MS	White	Absent	Early
Vam	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Japonica	SB	Brown	Absent	Early
Yunghah	10/13/2017	Tangha Village (Longleng)	26.4902 N 94.8197 E	Indica	LB	White	Absent	Early

Name of landrace	Date of collection	Place of collection	Location (Geographic coordinate)	Type of seed	Grain Type	Grain color	Awn (Absent/ Present)	Flowering Duration
Mepongchuket Masu	10/16/2017	Khensa Village (Mokokchung)	26.3478 N 94.4889 E	Japonica	SB	Brown	Absent	Medium
Semmeki	10/16/2017	Khensa Village (Mokokchung)	26.3478 N 94.4889 E	Indica	LB	White	Absent	Medium
Mapok Tanakla	10/16/2017	Longjang Village (Mokokchung)	26.4519 N 94.5483 E	Japonica	LB	Brown	Present	
Goyo Tsük	10/16/2017	Longkhum Village (Mokokchung)	26.2611 N 94.4124 E	Indica	LB	White	Absent	Early
Moya Maso	10/16/2017	Longkhum Village (Mokokchung)	26.2611 N 94.4124 E	Indica	LB	Red	Present	Early
Moya Tsük	10/16/2017	Longkhum Village (Mokokchung)	26.2611 N 94.4124 E	Indica	LB	White	Absent	Medium
Teke	10/16/2017	Longkhum Village (Mokokchung)	26.2611 N 94.4124 E	Indica	SB	Brown	Absent	Early
Motso Tsuk Wokha	9/30/2017	Wokha Town	26.0915 N 94.2592 E	Indica	LB	White	Absent	Early
Rukhatang	10/30/2017	Wokha Town	26.0915N 94.2592E	Indica	SB	White	Absent	Medium
Vapvu Tsük	10/30/2017	Sanis Village, Wokha	26.1972N 94.1931E	Indica	SB	White	Absent	Early
Tsuktsa	1/20/2017	Dibuia Village (Mokokchung)	26.526 N 94.500 E	Indica	SB	White	Absent	Early
Zu Tsük	10/30/2017	Wokha Town	26.091N 94.259E	Indica	LS	White	Present	Medium

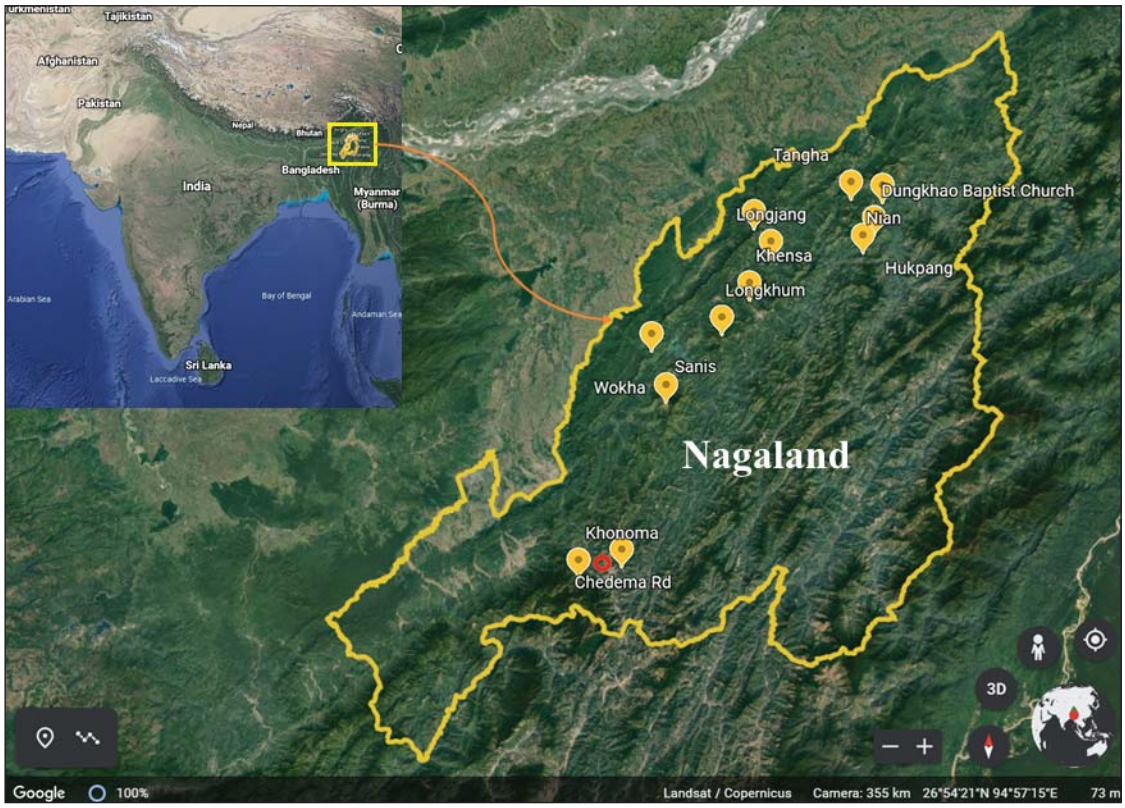

Fig. 1. Areas surveyed during rice germplasm collection in Nagaland

Reproductive drought tolerance was recorded based on leaf rolling score and drought recovery rate at 60 days after withdrawal of life-saving irrigation when the soil moisture content was around 6-8% (W/V) using standard evaluation system for rice (Verma *et al.*, 2019). Bhalum-3 was used as an upland check variety. Soil moisture content was determined at three days interval by the gravimetric method (Pask and Reynolds, 2013). The 38 landraces were evaluated for disease reactions against the brown spot of rice using a standard disease rating scale of IRRI (2002). The percentage disease index (PDI) was calculated using the formula given by Khan *et al.* (2014).

Statistical Analysis

The agronomic yield data were subjected to analysis of variance and the genetic parameters such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad-sense (h2), and genetic advance as 5 percent of mean (genetic gain) were worked out as suggested by Falconer (1981). Correlation coefficients were calculated to assess relationship among traits. The mean data were used to determine the phenotypic diversity among the genotypes using principal component analysis by the R package FactoMineR (Le *et al.*, 2008) factoextra (Kassambara and Mundt, 2017) and clustering based on the algorithm of Ward's method (Galili, 2015).

Results & Discussion

Presently, global focus is to develop climate-resilient improved varieties having high yield potential, good cooking quality. In the present study 40 genotypes were evaluated for grain quality, yield and stress tolerant traits. Analysis of variance revealed significant differences among the genotypes for all traits measured in the study (Table 2). Roy *et al.* (2014) also reported considerable variation in agronomic and grain characteristics of Nagaland rice germplasm.

Descriptive statistics for different agro-morphological, grain quality along with stress tolerance traits are presented in Supplementary Table S1. Results revealed that Mehourü was the shortest landrace (65 cm) and Nukjau Shola was the tallest (180 cm). The negative skewness of plant height indicated that most of the landraces were tall. In the present study majority of landraces were tall, as farmers have selected tall landraces for the upland ecosystem to avoid competition with weeds. The tiller numbers per plant varied from 3 to 8 with a mean value of 4.88. The maximum number of tillers was observed in Mekrilhakecha (8 tillers) followed by Suphok (7). Upland rice usually has low numbers of tillers per plant (IRRI, 1975), in the present study also the majority of landraces have 3-4 numbers of tillers per plant. Landraces Aongsho (4.5 t/ha), Semmeki (4.2 t/ha), Goyo Tsük (4.3 t/ha) Moya Tsük (4.2 t/ha) and Moya Maso (3.9 t/ha) also showed significantly high yield compared to check variety Bhalum-3 (3.8 t/ha). Yield per plant was higher as compared to other studies (Rao *et al.*, 2018) this might be attributed to genotypic, cultivation management practices and adaptability (Mellidou *et al.*, 2020).

Grain quality in rice is determined by physical appearance, cooking and eating quality and nutritional quality (Fitzerald *et al.*, 2009; Verma *et al.*, 2015a; Sharma & Khanna 2019). In the present study, four distinct types of grain shape were observed. The maximum number of genotypes were short bold followed by long bold. It indicates that for daily consumptions Nagas prefer to eat bold rice grains and occasionally they use long slender and medium slender. Roy *et al.* (2015) also reported short and long bold grain shapes in the landraces of Nagaland. Pathak *et al.* (2016) reported the

Table 2. Analysis of variance for yield and yield attributes

Source of Variation	df	Mean square						
		Tiller/plant	Plant Height	Panicle length	Grains/panicle	Spikelet fertility	Duration	Yield
Genotypes	39	5.17*	2977.60*	25.61*	13842.14*	309.93*	451.46*	231.34*
Replication	2	0.13	11.80	1.38	63.60	10.67	4.18	5.63
Error	78	0.77	10.82	2.67	17.02	5.67	8.16	3.75
CV		18.02	2.47	6.72	3.09	2.79	2.37	6.32

*Significant at 1%

**Supplementary Information: Supplementary table or figure mentioned in the article are available in the online version.*

majority of *sali* rice of Assam has long bold grain shape. Among the landraces, 11 brown and 4 red rice kernels were observed. Brown rice is consumed as piping hot and served during special festivals. Red rice is a good source of iron (Fe) and magnesium (Mg), therefore it is good food for pregnant women and the populace suffering from iron deficiency and heart patients (Raghuvanshi *et al.,* 2017; Priya *et al.,* 2019).

The cooking and organoleptic properties of rice grain are determined by AC, GC and GT (Rani *et al.,* 2011; Sharma and Khanna, 2019). AC is the major determinant of rice eating and cooking quality (Juliano, 1993). AC determines the hardiness, cohesiveness, tenderness and texture of cooked rice (Kumar & Kush, 1986; Sabouri, 2009; Verma *et al.,* 2015b). Rice varieties with very low AC (3-9%) become very sticky, moist and tender on cooking, whereas varieties with intermediate AC (20-25%) become fluffy, soft, moist and tender and those with high AC (>25%) becomes fluffy, dry and harden on cooling (Kumar & Kush, 1986). The AC varied from 0.64% in 'MepongchuketMasu' to 16% in Shuphok and Zu Tsuk. Among the 38 landraces, majority of the landraces (23) were in low amylose class (10-19%) followed by 13 landraces with very low amylose class (3-9%), whereas, Mepongchuket Masu and Vam genotypes have very low AC (< 3%). Thongbam *et al.* (2012) evaluated 18 traditional landraces of Tripura and revealed that the majority of them have low amylose content (<20%) and few of them have intermediate amylose content (20-25%). In the *Sali* rice of Assam, AC varied from very low to very high and the majority of them have low amylose content (Verma *et al.,* 2015b; Pathak *et al.,* 2016). The famous 'Chakhao' aromatic rice of Manipur has low amylose content (2-8%) (Shijagurumayum *et al.,* 2018). Amylose content of Sikkim rice landraces varied from 15 to 26%, and the majority of them have intermediate amylose content (Kapoor *et al.,* 2019).

Gel consistency of rice varied from-soft to hard (Tang *et al.,* 1991). Cooked rice with soft gel consistency cooks tender and remain soft upon cooling for long hours as compared to rice with hard gel consistency (Tang *et al.,* 1991). Gel consistency varied from 23.0 mm (hard) in Shuphok to 110 mm (soft) in 'Mekrilhakecha'. Kapoor *et al.* (2020) reported the presence of soft to hard GC in Sikkim rice and the majority of Sikkim rice has medium-soft GC, whereas the majority of Assam rice has soft GC (Verma *et al.,* 2015b; Pathak *et al.,* 2016). Based on alkaline spreading value, six distinct classes of GT were recorded among the landraces. Intermediate GT (69-74^{o}C) was present in 10 landraces. Rice with soft to medium gel consistency (GC), intermediate amylose content (AC) and intermediate gelatinization temperature (GT) are preferred by most consumers (Rohilla *et al.,* 2000; Pang *et al.,* 2016).

Among all the landraces, Yunghah, Goyo Tsük, Rükhatang and Vepvu Tsük have strong aroma and 9 of them have mild aroma. Genotypes Goyo Tsük, Yunghah, Kemenya, Zu Tsuk, Rukhatang and Vapvu Tsuk are popular aromatic rice of Nagaland.These aromatic rices are used staple food and served as special rice items such as deserts, during the festive occasion and religious and marriage ceremonies. Aromatic landraces of Nagaland have short bold, long bold and the long slender grain shape. Whereas the aromatic rice of Bangladesh generally has short bold and medium bold grain shape (Islam *et al.,* 2016). The basmati rice of north-western Indo-Gangetic region of India has extra-long slender grains, pleasant aroma, highlinear grain elongation on cooking (Kaur *et al.,* 2011; Singh *et al.,* 2018).

Based on leaf rolling and drought score Teke, Aongsho and Semmeki genotypes were reproductive moisture stress-tolerant. The *Ahu* rice of Assam, north-eastern India cultivated from March to June are also drought tolerant. Most of the moisture stress-tolerant genotypes were identified from the north-eastern rice germplasm (Torres *et al.,* 2013; Rahman *et al.,* 2016; Verma *et al.,* 2019).

Brown spot is the major disease of upland rice and severely reduces productivity. The result of screened genotypes against brown spot disease is presented in supplementary Table S1. The occurrence of brown spot severity among the genotypes ranged from 5.50 to 76.10%. The maximum brown spot disease index of 63.5% was observed in 'Maibo', whereas the least disease index was observed in Nyari (4.5%). Based on the disease reaction, again evaluated genotypes were categorized into different classes (online supplementary Table S2). Out of 40 genotypes, none of the genotypes were immune, whereas only one genotype Nyari showed resistance against the brown spot. It was observed that under field conditions, the severity of brown spot disease was fairly significant. Similarly, the 15 genotypes showed moderate resistance, whereas 8 genotypes showed high susceptibility to brown spot disease. In other studies, also variation for the brown spot was reported and resistant

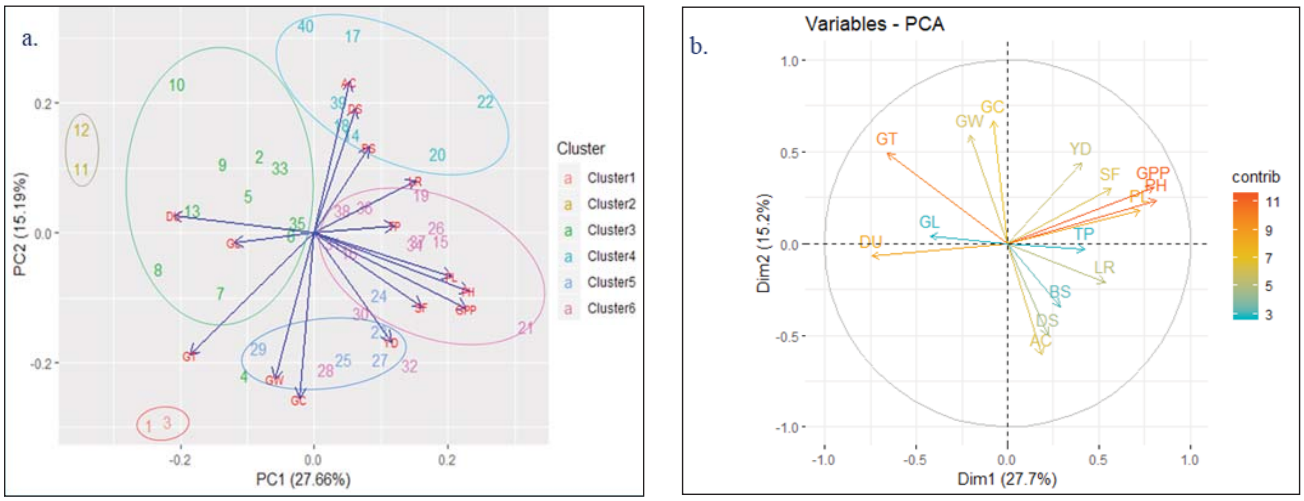

Fig. 2 a. Grouping of landraces based on first two principal components. b. Biplot of 40 rice landraces for PC1 and PC2, arrows show the magnitude and direction of the trait in PC1and PC2

genotypes have been identified (Chauhan *et al.*, 2000; Alam *et al.*, 2016). In the present study, brown spot disease severity ranged from 6 to 76%. Whereas, Liu *et al*. (2007) reported 0-80 % of the brown spot severity in rice. These differences in disease severity might be attributed to differences in genotypes' capacity to resist and weather conditions. The level of disease severity in the host plant mainly depends on the interaction between the R genes in the host and pathogenicity factors of a pathogen.

Various variability parameters studied are presented in the Table 3. The maximum variation among all the traits was observed in grains per panicle, ranging from 34 in Nyari to 293 in Mepongchuket Masu. Whereas The low degree of variation among the landraces was observed for maturity duration ranging from 95 days in Maibo to 150 days in Kemeluo-u with a mean of 121 days. The difference between GCV and PCV was less which indicate the high correspondence between phenotype and genotype. Large variation, high heritability coupled with high genetic advance as per cent of mean was recorded for grains per panicle which indicates preponderance of additive gene action and can be improved through simple selection. Heritability in combination with genetic advance would give a more reliable index of selection value (Pathak *et al.*, 2016). The high heritability estimates along with low genetic advance indicates that non-additive type of gene action and genotype-environment interaction plays a significant role in the expression of the traits. Thus, the characters showing high heritability along with moderate or low genetic advance could be improved by intermating the superior genotypes of segregating population developed from combination breeding (Samadia, 2005; Pathak *et al.*, 2016).

In the present study, genotypic correlation coefficients between all pairs of combinations for grain quality, yield attributes and stress-tolerant parameters are presented in Table 4. A positive correlation between plant height and panicle length suggests that the selection of tall landraces might result in increased panicle length and a high number of grains per panicle. Similar associations were reported by Sohrabi *et al*. (2012). A negative correlation between maturity duration and spikelet fertility indicates that a long duration of maturity in upland landraces results in poor yields. Over a period of time, it has been observed that monsoon withdraws by the end of September or first fortnight of October, therefore late-maturing landraces faces moisture stress problem and results in chaffy grains and poor yields.

PCA Analysis

The PCA biplot diagram (Fig. 2a) between PC 1 and PC2 explained the distribution and the nature of diversity for both variables and the genotypes. The loadings depicts that almost all the genotypes and variables have high degree of variation. PCA analysis revealed that the first principle component contributed to 27.66% of variation to the total variation in the present germplasm set with an eigenvalue of 4.2 and the second principal component accounted for additional 15.19% of contribution to total variation with an eigenvalue of 2.3 (Fig. 2b). These two principle components indicated that grain number per

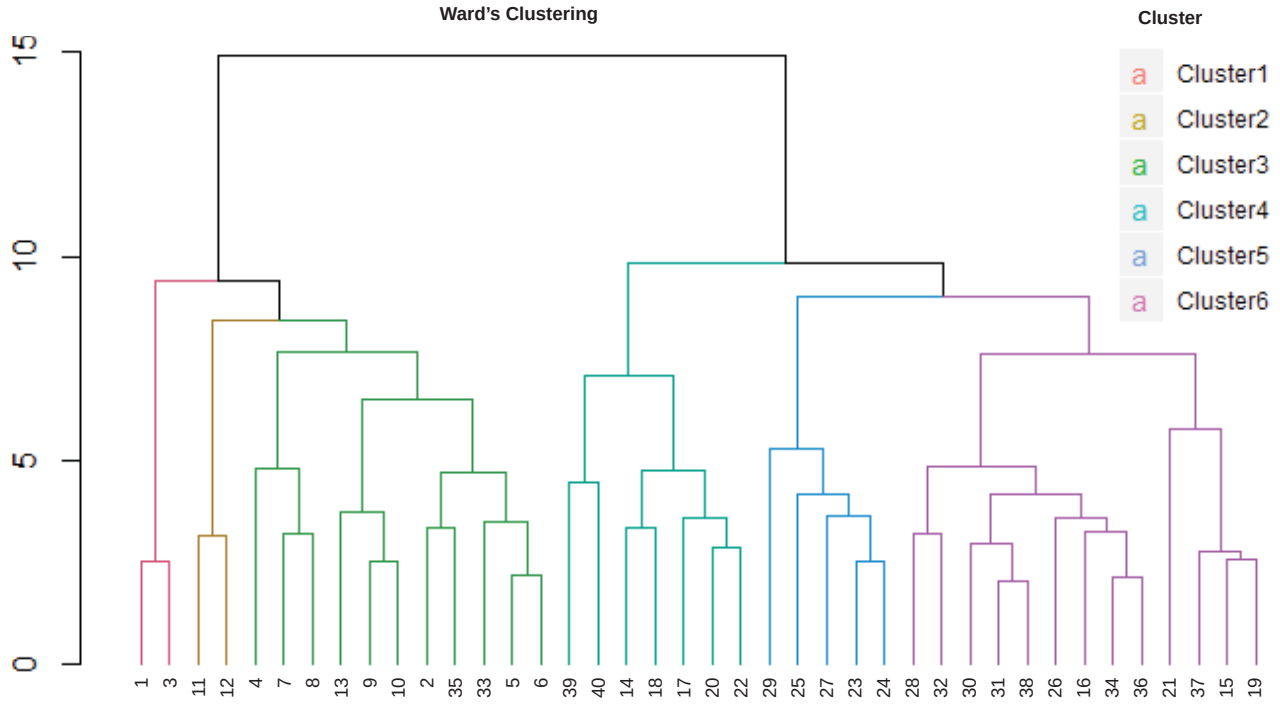

Fig. 3. Grouping of landraces for yield attributes, grain quality and stress tolerance characteristics using Ward's clustering method

Table 3. Genetic variability of grain quality, yield attributes and stress tolerance in rice

Trait	Range		Mean±SEm	GCV	PCV	Heritability in broad sense	GA as 5 % of mean
	Min.	Max.					
TP	3.0	8.0	4.9±0.50	24.8	30.6	0.65	41.3
PH	65.2	179.6	133.1±1.89	23.6	23.7	0.98	48.4
PL	19.2	29.4	24.3±0.94	11.4	11.4	0.74	20.2
GPP	34.3	293.5	133.1±2.38	51.0	51.1	0.98	104.9
SF	55.2	98.6	85.1±1.37	11.8	12.2	0.94	23.7
MD	94.6	149.7	120.5±1.65	10.1	10.4	0.94	20.2
Yield	1.5	4.5	3.07±0.11	28.4	29.1	0.95	57.1
GL	4.1	9.0	5.92±0.11	16.7	17.0	0.96	33.8
GW	2.0	3.5	2.7±0.13	13.5	16.0	0.71	23.5
AC	0.6	22.0	10.9±0.89	40.8	43.1	0.89	79.5
GC	24.6	107.0	46.3±2.05	43.7	44.4	0.96	88.6
GT	1.0	6.0	2.7±0.15	54.0	54.8	0.97	109.6
DS	1.2	5.6	4.9±0.10	21.0	21.2	0.98	42.8
LR	1.3	11.0	6.9±0.03	29.3	30.2	0.94	58.6
BS (PDI)	5.5	76.1	33.2±1.54	51.6	52.2	0.97	104.9

TP: Tillers per plant, PH: Plant height (cm), PL: Panicle length (cm), GPP: Grains per panicle, SF: Spikelet fertility, MD: Maturity duration, GL: Grain length (mm), GW: Grain width (mm), AC: Amylose content (%), GC: Gel consistency (mm), GT: Gelatinization temperature, DS: Drought score, LR: leaf rolling score, BS (PDI): Brown spot (percent disease index)

Table 4. Correlation coefficient at genotypic (above diagonal) and phenotypic level (below diagonal) among various yield and grain quality traits

Traits	TP	PH	PL	GPP	SF	MD	Yield	GL	GW	AC	GC	GT
TP	1	0.374	0.214	0.167	0.257	-0.052	0.259	-0.255	-0.382	0.073	0.128	-0.224
PH	0.308	1	0.679**	0.626**	0.460	-0.568	0.338	-0.311	-0.194	-0.055	0.211	-0.340
PL	0.143	0.584**	1	0.566	0.393	-0.531	0.360	-0.294	-0.135	-0.065	0.107	-0.479
GPP	0.128	0.621**	0.484	1	0.674**	-0.564	0.438	-0.125	0.196	0.048	-0.044	-0.265
SF	0.214	0.444	0.323	0.656**	1	-0.605**	0.467	-0.098	0.214	0.054	-0.051	-0.286
MD	-0.052	-0.551	-0.429	-0.548	-0.578**	1	-0.144	0.234	-0.098	-0.174	0.133	0.465
Yield	0.211	0.330	0.298	0.427	0.441	-0.144	1	0.049	0.040	-0.094	0.149	-0.114
GL	-0.199	-0.303	-0.247	-0.123	-0.090	0.228	0.052	1	0.179	0.206	0.111	0.201
GW	-0.327	-0.160	-0.080	0.164	0.171	-0.064	0.047	0.1381	1	-0.172	0.202	0.318
AC	0.081	-0.050	-0.015	0.047	0.044	-0.152	-0.084	0.1980	-0.118	1	-0.540	-0.423
GC	0.101	0.204	0.081	-0.041	-0.044	0.131	0.141	0.1052	0.160	-0.506	1	0.384
GT	-0.166	-0.331	-0.417	-0.261	-0.272	0.445	-0.105	0.1986	0.251	-0.394	0.374	1

**Significant at 5%

TP: Tillers per plant, PH: Plant height (cm), PL: Panicle length (cm), GPP: Grains per panicle, SF: Spikelet fertility, MD: Maturity duration, GL: Grain length (mm), GW: Grain width (mm), AC: Amylose content (%), GC: Gel consistency (mm), GT: Gelatinization temperature

plant, plant height, maturity duration, panicle length, GT, GC, AC, spikelet fertility and yield traits were the main discriminatory traits (Fig 1).

In the present study, the first two PC contributed to 43% to the total variation whereas in other studies the first two PC contributed below 34% to the total variation (Gour *et al.,* 2017; Roy *et al.,* 2014). While Asante *et al.*, (2019) reported that the first two principal components explained 57 % of the total variation. In the present study, genetic variation and PCA analysis revealed that grain number per plant, plant height, maturity duration, panicle length, GT, GC, AC, spikelet fertility and yield govern the main diversity. Asante *et al*. (2019) reported Kernel length-to-width ratio, kernel length, days to flowering, and yield were the main principle discriminatory characteristics.

Cluster Analysis

The set of 40 rice landraces was grouped into six different clusters based on Ward's clustering and showed similar results as of PCA. Clusters I and II each comprised of two genotypes. Cluster III, IV, V and VI comprised 11, 7, 5 and 13 genotypes respectively (Fig. 3). Cluster I consist of Dzukunya and Kemenya which showed moisture stress-tolerance. Cluster II consists of Kemese-u and Kemeluo, these two genotypes are famous as Nagaland special rice among 'Angami' community because of their good taste and cooking qualities. Genotypes of cluster III were moderate to highly tolerant for the brown spot disease. Among cluster III landraces, the Nyari genotype showed a resistant reaction against brown spot pathogen. The cluster IV genotypes were poor yielder. Genotypes of cluster V were tall and also have low AC and soft GC. Genotypes of cluster VI showed a high number of grains per panicle, spikelet fertility, high tillering ability and high yield potential. The five genotypes of cluster VI Aongsho, Semmeki, Moya Tsük, Goyo Tsük and Yunghah were the best genotypes for yield and yield attributes. These genotypes were the best genotypes of *Phom, Ao* and *Lotha* tribes for yield. Cluster analysis revealed that traditional landraces of *Angami* tribe were distinct from *Ao*, *Phom* and *Lotha* tribes. Grouping patterns in cluster analysis was not according to their geographical origin. A similar trend was also reported in other studies (Roy *et al.,* 2014; Mbanjo *et al.,* 2019).

These multivariate analyses revealed that traditional landraces have wide genetic variation for grain quality, yield, yield attributes, drought tolerance and brown spot resistance traits. PCA as well Ward's cluster analysis were equally effective in revealing the relationship among the rice germplasm (Roy *et al.,* 2016; Mbanjo *et al.,* 2019).

All this analysis suggests that hybridization between Aongsho and Kemese-u would be effective for development of short duration high yielding and moderately drought tolerant cultivar with acceptable grain and cooking quality. Hybridization between Aongsho and Teke would results in trailing of early maturing, drought tolerant genotype with high yield. Crossing of Nyari with Aonsho may help in development of brown spot tolerant improved variety.

Conclusion

These diversified landraces are a reservoir of important genes/alleles for yield, quality traits such as taste, glutinous trait, aroma and grains shape; and abiotic and biotic stresses. These landraces can be used as principal foundation material in breeding programmes for the development of new improved varieties. These landraces must be collected and conserved using *in-situ* as well as *ex-situ* conservation methods for their effective use in future crop improvement programmes. Considering the uniqueness of such landraces, it is of paramount importance to conserve such resources wither in-situ or ex-situ. The utilization of such a rich gene pool in the breeding programmes will help in the development of suitable rice varieties.

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*Supplementary Table or Figure mentioned in the article are available in the online version.

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RESEARCH ARTICLE

Agro-Morphological Characterization, Genetic Variation and Heritability Analysis of Rice Landraces (*Oryza sativa* L.) of Arunachal Pradesh, Northeast India

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The present study describes characterization of 35 rice landraces collected from different parts of Arunachal Pradesh. High degree of variations was observed for morphological traits. Mean plant height of 127.39 cm, panicle length (25.7 cm), flag leaf length (40.54 cm), flag leaf width (2.10 cm), blade leaf length (58.66 cm), blade leaf width (1.82 cm), ligule length (2.14 cm), test weight (2.44 g) and mean grain yield per hectare of (18.65 q/ha) were recorded respectively. The cluster analysis grouped 35 landraces into 4 clusters (67% dissimilarity) in which *Jhum* and wetland landraces formed distinct clusters. The first three PCA extracted accounted for 81.64% of the total variation based on 12 phenotypic traits. A significant positive association was observed among the traits, and the genetic variability computation revealed higher PCV than GCV. Highest PCV (43.61%), GCV (43.3%), heritability (98.44%) and GAM (88.43%) were recorded for grain yield. The high variability with promising yield potential among the Arunachal Pradesh landraces is expected to be significance immense significance for rice breeding programmes.

Key Words: Agromorphology, Arunachal Pradesh, Characterization, Genetic Variation, Landraces, Rice

Introduction

The state Arunachal Pradesh is one of the world's biodiversity hotspots and the richest biogeographical province of the Himalayan zone (Hussain and Hore, 2008). Due to its remote location coupled with undulating topography, *jhuming* or shifting cultivation still prevails in the state as subsistence farming. The state is endowed with diverse rice germplasms and the cultivars vary from one district to another (Hore, 2005). The state is contiguous with the region from where ecogeographic races of Asian rice cultigens originated, diversified, and disseminated (Chang, 1985). Northeast India is one of the hot spots and important centers of origin of rice inhabited by thousands of indigenous rice landraces (Durai, 2015). These landraces have great genetic diversity and accounted for 60% of all rice grown in India (Longvah and Prasad, 2020). The region has extremely diverse rice-growing climatic conditions up to 2000 m above sea level when compared to other parts of the country. Such a diverse cultivation system is known to promote allelic variation and genetic diversity (Roy *et al.,* 2014a).

There has been interweaving of the rice-based agriculture system of the Indian subcontinent with its socio-cultural fabric, and thousands of landraces with poorly tapped agronomic traits have been nurtured in these bio-culturally diverse North-Eastern states of the country (Chakraborty and Ray, 2019). As the improvement of existing variety depends upon desirable genes that are possibly present in landraces and wild varieties, the importance of landraces can never be denied in the agriculture system (Holden *et al.,* 1993). They possess a valuable gene pool for the future breeding programme (Richharia, 1979; Patra, 2000). The efforts made to understand the existing landrace diversity as well as to improve them were so limited. There is a rich genetic diversity in rice germplasm from different parts of north-eastern India (Bhuyan *et al.,* 2007; Rathi and Sarma, 2012; Choudhury *et al.,* 2013). But the systemic characterization of rice landraces of Arunachal Pradesh is lacking and scanty. Characterization of germplasm is essential to identify desirable traits, effective utilization of genetic resources, and breeding programme. The valuable germplasms has little practical utility until a collection has been properly evaluated and its attributes become known to breeders. Therefore the collection, characterization, and conservation of these valuable rice landraces are important (Sharma *et al.,* 2007; Thomson *et al.,* 2009; Sanni *et al.,* 2012; Sinha *et al.,* 2013).

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Materials and Methods

Collection of germplasm and field experiment

The study comprised of 35 landraces (19 genotypes of *jhum/upland and 16 wetland rice cultivation (WRC)/* lowland) collected from different parts of the state Arunachal Pradesh (Table 1). Field experiment was conducted for two seasons *Kharif* 2015 and *Kharif* 2016 in Randomised Block design (RBD) with two replications using standard checks. Five competitive plants were randomly selected from each germplasm for recording field observations for all the traits. Data for different qualitative and quantitative traits were recorded at different growth stages based on five competitive plant samples following standard evaluation system for rice from the International Rice Research Institute (IRRI 2002).

Table 1. List of rice landraces of Arunachal Pradesh used in the study

Variety	Village/ Place	Latitude (N)	Longitude (E)
Mingpong	Seppa	27° 19' 59.1996"	93° 3' 47.6928"
Yali amo	Jomoh	28° 11' 20.724"	94° 37' 27.912"
Bali red	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Bali white	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Kimin white	Dali	$28^0$17'597"	$94^0$50'677"
Kimin red	Pagi	27° 55' 50.844"	94° 42' 54.036"
Ampu	Tai	28° 1' 7.356"	94° 34' 42.888"
Jarli	Sodo Doke	$28^0$02.224'	094^o37.939'
Pumik	Tai	28° 1' 7.356"	94° 34' 42.888"
Kecha	Boleng	28°18'25.5468"	94°57'11.7792"
Bamtare	Bam	27°58'56.776"	94°41'23.451"
Poore	Dumporijo	27° 59' 32.208"	94° 17' 25.44"
Chipu	Dake	28° 1' 7.356"	94° 34' 42.888"
Amchiriri	Tai	$28^0$00.034'	094^o31.715'
Angkear	Sago	27° 55' 50.844"	94° 42' 54.0432"
Takear	Yumlo Mongku	28° 9' 57.0564"	94° 38' 13.3728"
Mukte	Pushi Doke	28° 3' 2.2392"	94° 42' 38.9412"
Ambher	Tuting	28° 59' 42.648"	94° 53' 22.056"
Lemmuk	Pushi Doke	28° 3' 2.2392"	94° 42' 38.9412"
Deku amo	Pashighat	28°04'12.00"	94°19'48.00"
Bodong amo	Boleng	28°18'25.5468"	94°57'11.7792"
Amham	Yumlo Mongku	28° 9' 57.0564"	94° 38' 13.3728"
Amkeer	Boleng	28°18'25.5468"	94°57'11.7792"
Pumde	Tai	$28^0$00.060'	094^o31.722'
Gejang	Boleng	28°18'25.5468"	94°57'11.7792"
Tinin	Dake	28° 1' 7.356"	94° 34' 42.888"
Taok amo	Daporijo	$27^0$59'9.83"	$94^0$13'18.16"
Amtum	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Pumso	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Amlum	Gori	27° 58' 50.8836"	94° 41' 19.6692"
Deku oval	Pashighat	28°04'12.00"	94°19'48.00"
Riew amo	Boleng	28°18'25.5468"	94°57'11.7792"
Basmati	Pashighat	28°04'12.00"	94°19'48.00"
Mugme	Bam	27°58'56.776"	94°41'23.451"
Ame amli	Tato	28° 30' 29.34"	94° 27' 28.296"

Data Analysis

The statistical analysis was conducted by the pooling of two-year data. All descriptive statistics with test of significance, Principal Component Analysis (PCA) and Multidimensional scale analysis and Pearson's correlation coefficient (r) were performed by using SPSS version 20.0 (IBM Corp. Released 2011. IBM SPSS Statistics for Windows, Version 20.0. Armonk, NY: IBM Corp.). Unweighted Pair Group Method with Arithmetic Mean (UPGMA) hierarchical clustering based on dissimilarity matrix to assess the phenotypic diversity among the rice landrace was computed in the DARwin software version 6.0.12 (Perrier and Jacquemoud, 2006) DARwin software http://darwin.cirad.fr/). The phenotypic and genotypic variance was estimated according to Burton and Devane (1953), heritability as per Hanson *et al.* (1956), and genetic advance was estimated using the formula suggested by Johnson *et al.* (1955).

Results and Discussion

Traits Variability Among the Landraces

From the analysis of variance, it was observed that the landraces have a significant variation of agro-morphological traits. Among the 35 landraces, the traits under study showed significant variations (Table 2). Plant height (PH) ranges from 54.6 cm to 161.60 cm with a mean of 127.39 cm and 22.20 CV%. Panicle length (PnL) ranges from 10 to 32.20 cm with a mean of 25.70 cm (%CV=17.53). Girth diameter (GD) ranges from 0.42 cm to 0.83 cm with a mean of 0.64 cm (%CV=19.19). The number of primary branches per panicle (PBR) ranges from 8.70 to 15 with a mean of 11.49 (%CV=13.32). Flag leaf length (FLL) ranges from 24.84 to 52.60 cm with a mean of 40.54 (%CV=18.53) and Blade leaf (BLL) ranges from 34.84 cm to 70.00 cm with mean of 58.66 cm (%CV=14.25) respectively. Flag leaf width (FLW) recorded mean of 2.10 cm (%CV=20.46) and blade leaf width (BLW) recorded mean of 1.82 cm (%CV=23.82) respectively.

Table 2. Agromorphological variation of rice landraces (*Jhum* and WRC)

Trait	Range	Minimum	Maximum	Mean	SEM (±)	Std. Deviation	CV(%)	C.D. (5%)
PH	107.00	54.60	161.60	127.39*	5.93	28.28	22.20	16.45
PnL	22.20	10.00	32.20	25.70*	1.22	4.50	17.53	3.40
GD	4.2	4.2	8.4	6.4	0.4	1.2	181.9	1.1
PBR	6.30	8.70	15.00	11.49*	0.75	1.53	13.32	2.08
FLL	27.76	24.84	52.60	40.54*	3.55	7.51	18.53	9.84
FLW	1.56	1.14	2.70	2.10*	0.10	.42	20.46	0.27
BLL	35.16	34.84	70.00	58.66*	3.85	8.36	14.25	10.67
BLW	1.72	.88	2.60	1.82*	0.12	.43	23.82	0.33
LgL	2.48	1.40	3.88	2.14*	0.15	.58	27.51	0.42
FGP	206.80	70.60	277.40	172.47*	18.09	42.93	24.89	50.14
TW	1.10	1.95	3.05	2.44*	0.14	.31	13.07	0.40
YLH	30.30	5.00	35.30	18.65*	0.71	8.10	43.43	2.04

*significant at the 0.05 level SEM: Standard error of mean

Plant height (PH cm), Panicle length(PL cm), Girth diameter (GD mm), Primary branch number per panicle (PBR), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLLcm), Blade leaf width (BLWcm), Ligule length (LgLcm), Filled grain number per panicle (FGP), Test weight 100 seeds in gram (TW), Yield per hectare in quintal (YLH).

Although all the landraces under study have cleft type ligule, a significant variation in ligule length (LgL) was observed which ranges from 1.40 cm to 3.88 cm with a mean of 2.14 cm (%CV=27.51). The number of filled grain per panicle (FGP) recorded a mean of 172.47 per panicle which ranges from 70.60 to 277.40 per panicle (%CV=24.89). The highest variation was recorded in yield potential which ranges from as low as 5q per ha to 35.30 q/ha with a mean of 18.65 q/ha (%CV=43.43) respectively. Among the *jhum* landraces, six genotypes Bali Red (30.8 q/ha), Pumik (28.3 q/ha), Jarli (26 q/ha), Chipu (25.3 q/ha), Mingpong (24.3 q/ha and Yali amo (23.6 q/ha) respectively were identified as promising (Fig. 1). While among WRC, Amham (35.3 q/ha), Amlum (31 q/ha), Pumde (29 q/ha), Riew Ammo (28 q/ha), Tinin (27.6 q/ha) and Amtum (26.0 q/ha) respectively were found to be promising (Fig. 2). The agro-morphological characterization of germplasm variety is fundamental to provide information for plant breeding programmes (Lin, 1991). It is the basic foundation for crop improvement to facilitate the utilization of germplasm by breeders (Upadhyaya *et al.*, 2008) and the genetic analysis of quantitative traits is one of the prerequisite for planning a breeding programme (Khatun *et al.*, 2015). Rice is not

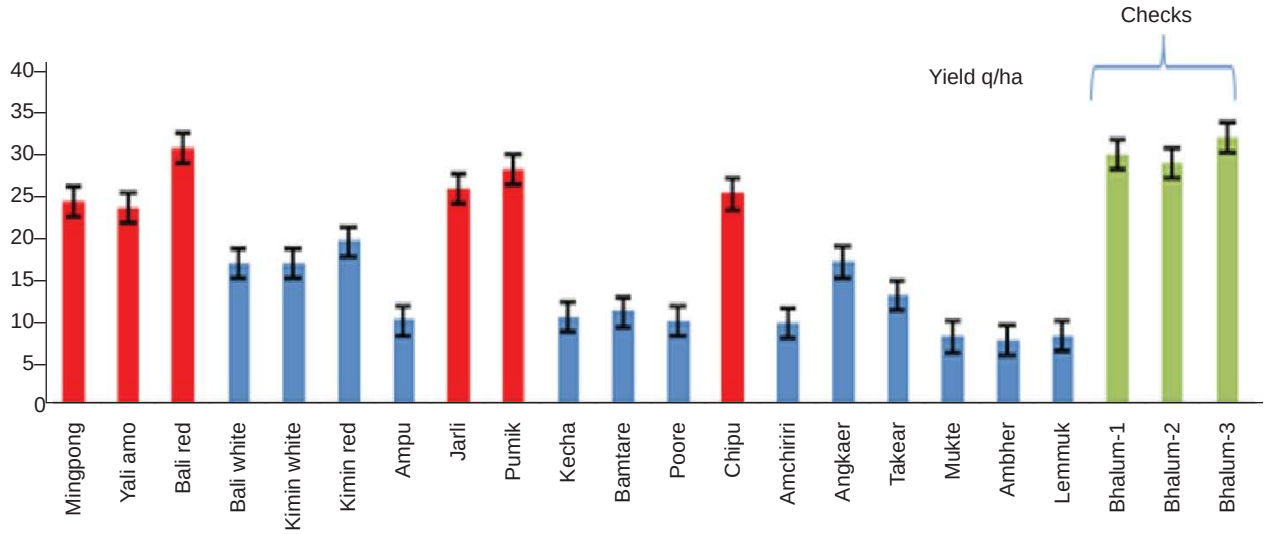

Fig. 1. Yield variation of *jhum* landraces

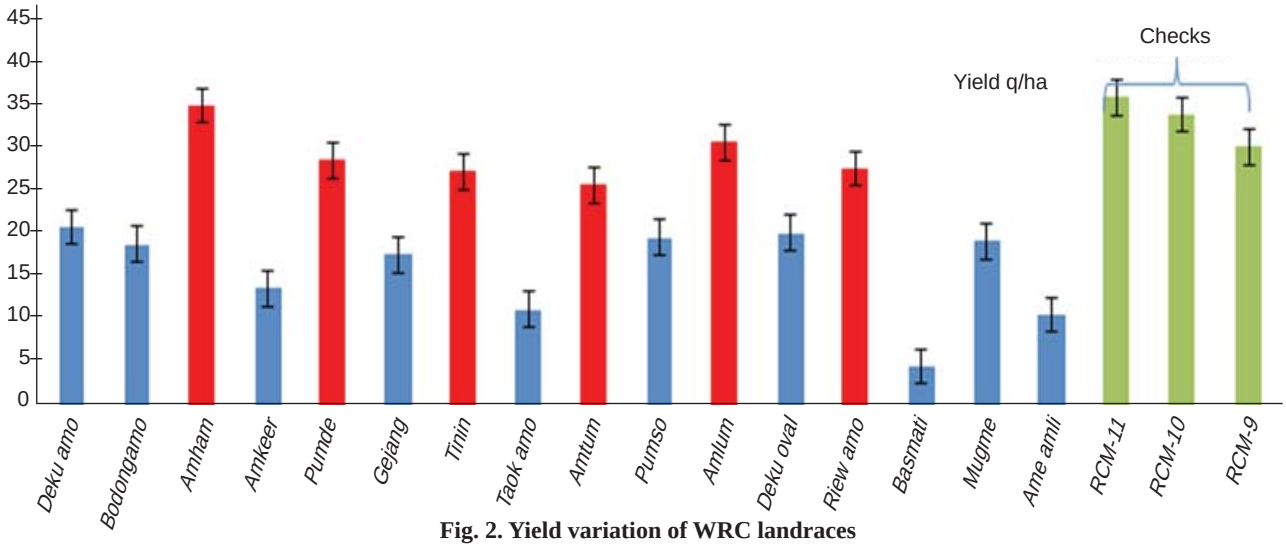

Fig. 2. Yield variation of WRC landraces

only stapled food to these hill dwellers. The tribal farming communities have selected and maintained numbers of landraces with deep-rooted socio-cultural attachment and many indigenous cultivars of rice are being conserved and cultivated by the resource-poor farmers. The farmers in the region usually classify hill rice cultivars based on agronomic traits (Roy *et al.*, 2016). Although the state Arunachal Pradesh is endowed with large varieties of rice germplasms which vary place to place (Hore, 2005), its systemic characterization informations are scanty and fragmented.

Similar to earlier reports (Subudhi *et al,*. 2012**;** Singh, 2013), the coefficient of variation of morphological traits ranges widely (5.4% to 23.45%) and little variation on qualitative traits. In general the *jhum* landraces were taller with lower average yield in compare to WRC genotypes. Tall stature, droopy or deflex flag leaf nature of *jhum* rice landraces as compare to erect flag leaf nature of lowland/WRC landraces could be one of the main variations in yield concerning efficiency and longevity of photosynthates accumulation during grain filling. In spite of low average yield as a whole, the study observed at par yield potential of identified promising landraces against check varieties. As the rice landraces maintained by farmers harbour wide genetic variability (Fukuoka *et al.*, 2006; Ram *et al,*. 2007; Rana *et al.*, 2007), these landraces with broad genetic base will be of immense help for future improvement breeding programme.

Diversity Pattern by Cluster Analysis

Based on 12 agro morphological traits, UPGMA Hierarchical clustering grouped the 35 rice landraces into four clusters with 67% dissimilarity (Fig. 3). Cluster-I comprised of 15 WRC genotypes with a characteristic of erect flag leaf with slender grain. Cluster-III comprised of 18 genotypes of *jhum* landraces with deflex or droopy flag leaf with bold and short-grain characteristics. These two clusters (I&II) were further grouped into four sub-clusters each with 66% and 65% dissimilarity respectively. The mean plant height, GD, FLL, and width, BLL, and width were lower in cluster-I as compare to cluster III. Bali red, a popular landaces of *jhum* formed distinct sub-cluster. While Takear constituted cluster-II and Amham constituted cluster-IV respectively. This revealed that Amham and Takear were distinct from the rest of the landraces and will be useful for future breeding programme. The highest PH of 146 cm, GD (7.27 mm), and grain number per panicle were recorded in cluster-III (Table 3). While highest PnL (29.2 cm), PBR (13), and yield (35.3 q/ha) were recorded in cluster-IV. The highest means of FLL, FLW, BLL, BLW, and TW were recorded in cluster-II. While the highest LgL was recorded in Cluster-I and have the lowest mean value of traits like BLL, BLW, FGP, and PH. The highest inter-cluster genetic dissimilarity of 98.1 was recorded in between Cluster-III and II (Table 4) and lowest in between Cluster-IV and III (32.3).

Similar to the present investigation, grouping of rice genotypes based on various phenotypic traits have been reported earlier by Kumar *et al.* (2013) on jhum rice germplasm of Northeast India, Sinha *et al.* (2013) in West Bengal rice, Ahmed *et al.* (2016) in Bangladesh rice genotypes and Roy *et al.* (2016) in hill rice landraces of Northeast India into *japonica* and *indica* types. Out

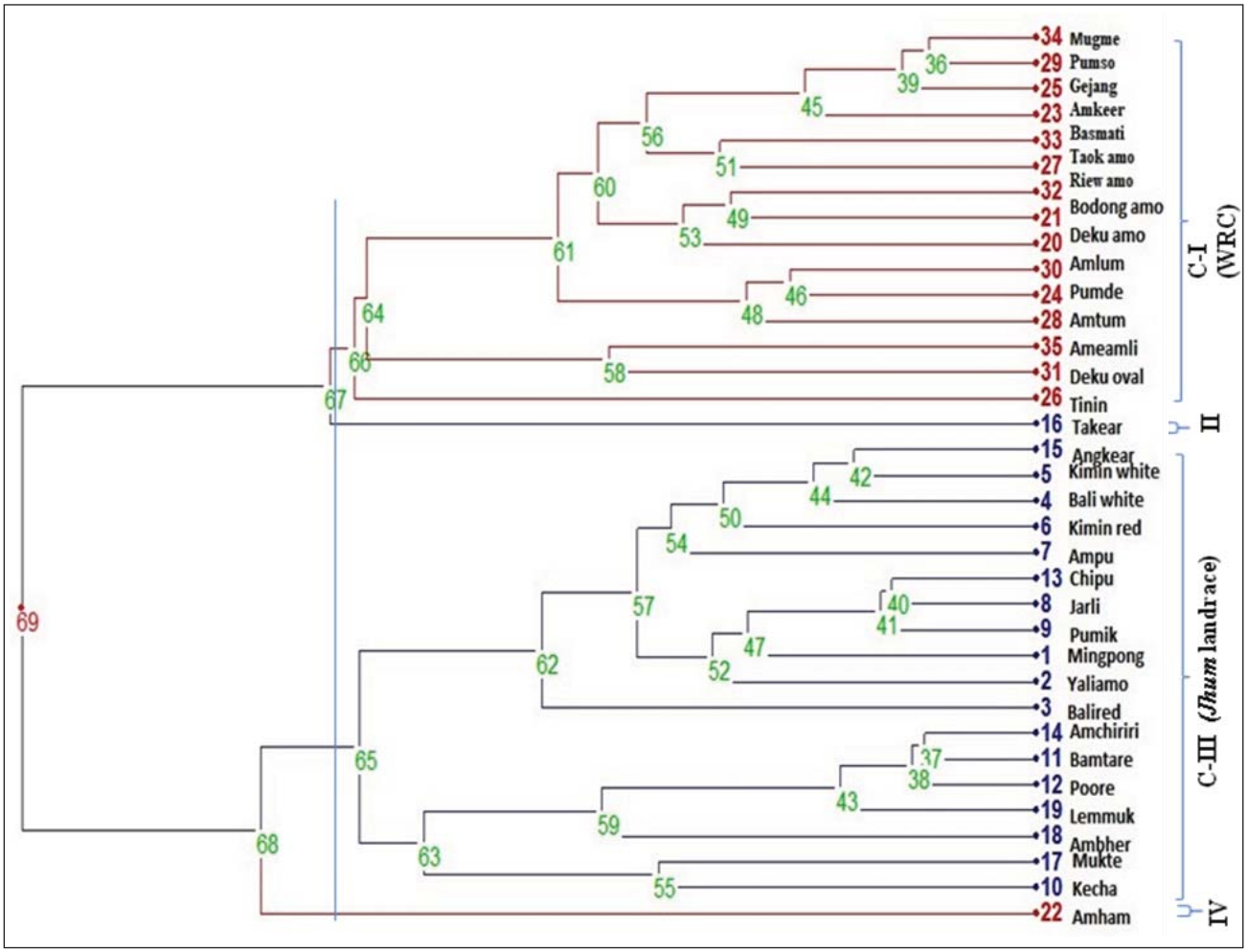

Fig. 3. Grouping of 35 rice landraces based on unweighted pair-group method with arithmetic means (UPGMA) hierarchical clustering method

Table 3. Inter cluster means of agromorphological traits

	PH	PnL	GD	PBR	FLL	FLW	BLL	BLW	LgL	FGP	TW	YLH	Genotypes
Cluster-I	110	22.7	5.48	12	36	1.7	52	1.4	2.54	142	2.42	20.1	15
Cluster-II	54.6	27.6	5.36	10	47	2.6	68	2.5	2.2	162	2.8	13	1
Cluster-III	146	28	7.27	11	44	2.4	63	2.1	1.78	197	2.44	16.8	18
Cluster-IV	122	29.2	5.97	13	39	2.1	61	1.7	2.6	205	2.67	35.3	1

Table 4. Genetic distance between groups and between cluster

	Dissimilarity matrix			
	Euclidean Distance			
	Cluster-I	Cluster-II	Cluster-III	Cluster-IV
Cluster-I	0.000			
Cluster-II	62.654	0.000		
Cluster-III	67.178	98.117	0.000	
Cluster-IV	66.761	83.791	32.318	0.000

of the 35 landraces, landraces like Amham (WRC), Takear (*jhum*) and Bali red (*Jhum*) which deviated distinctively from their respective group with promising yield potential would be useful for future breeding programme. *Jhum* landraces generally have bold seed, panicle well exerted, and droopy or deflex flag leaf with tall plant height. Whereas, the landraces of WRC generally have erect flag leaf with slender grain with shorter plant height characteristics.

Principal Component Analysis (PCA)

Principal component analysis (PCA) resolved three principal components (Eigenvalue >1) with cumulative total phenotypic variance of 81.64% (Table 5). The first principal component (PC1) explained 56.55% of the total variance and the traits like LgL, PH, BLL, FLL, FLW, BLW, PBR, and FGP have high positive loadings respectively. While traits like TW, PnL, Yield, and GD have negative loadings. The second component (PC2) accounted the additional variance of 16.70% in which traits like PBR, Yield, TW, LgL, FLL, BLL, and FLW have high positive loadings respectively. Whereas traits like FGP, PnL, PH, GD, and BLW have been negatively loaded. The third principal component (PC3) accounts additional variance of 8.38% with high positive loading of TW, GD, PnL, FGP, BLW, and Yield respectively. Whereas traits like LgL, PH, and PBR were negatively loaded in the third component. Similar to cluster analysis, the PCA biplot grouped the landraces (*Jhum*/upland and WRC) into different coordinates (Fig. 4.). The *Jhum* landraces with higher values for PH, PnL, GD, FLL, FLW, BLL, and BLW occupied the right half of biplot. While WRC landraces occupied the left half of biplot having a higher value for traits such as PBR, LgL, and Yield.

Table 5. Component Score Coefficient Matrix

Traits	Component		
	PC1	PC2	PC3
FGP	.003	–.006	.300
TW	–.235	.299	.599
PnL	–.020	–.045	.303
YLH	–.011	.362	.028
PH	.218	–.124	–.193
GD	–.036	–.262	.400
PBR	.032	.381	–.129
FLL	.198	.068	–.123
FLW	.174	.009	–.038
BLL	.199	.025	–.104
BLW	.108	–.052	.125
LgL	.229	.194	–.259
Eigen values	6.786	2.005	1.006
Variance (%)	56.554	16.706	8.383
Cumulative (%)	56.554	73.260	81.643

PCA discerns the important characters which have a greater impact on the total variables and the degree of contribution (Sanni *et al.*, 2008). The first three principal components are often the most important in reflecting the

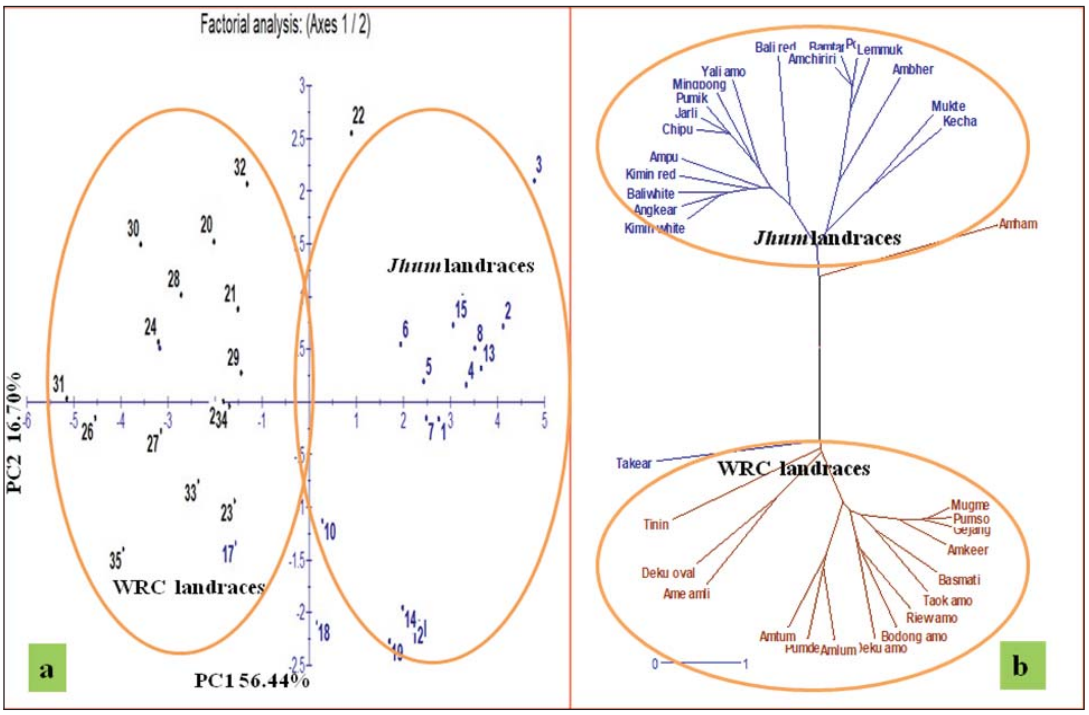

Fig. 4. a. A representation of 19 jhum landraces and 16 WRC landraces on the first two principal component scores, b. Representation of population structure of *jhum* and WRC landraces

variation patterns (Clifford and Stephenson, 1975; Guei *et al.*, 2005). The total cumulative variance revealed by the first three PCA (81.64%) in the present study was higher than the total variance of 79.05%, 56% and 76.4% reported by (Sinha *et al.*, 2013; Kumar *et al.* (2013; Roy *et al.*, 2016) respectively. High positive loading of traits like PH, PBR, FGP, LgL, flag leaf area, and blade leaf area in the first principal component followed by yield and test weight in the second component reflects the high variation of these traits among the landraces. Roy *et al.* (2014b) have also reported high positive loading of traits like leaf length, leaf breadth, plant height, and panicle length in the first principal component. A similar trend was reported by Ibrahim *et al.* (2019).

Correlation among the Traits (Pearson's co-efficient)

Pearson's correlation (r) measured the strength of the association between the two characters. The correlations among the traits in the present study showed a significant positive association among the traits. The grain yield showed positive correlation with TW, PnL, PBR, BLL, BLW, PH, FLL, FLW and LgL (Table 6). The number of primary branches per panicle positively correlates with FLL, FLW, BLL, and BLW. Similar significant positive associations were revealed between FLL with BLW, Grain number per panicle with test weight, PH with GD, TW with PBR etc. Negative correlations were found between PH with PBR, FLL, BLL, FLW, LgL, and TW. Panicle length with FLL, FLW, BLL, and LGL. Flag leaf area and BLL with FGP respectively. The significant positive correlation associations among yield contributing traits show an ample scope for genetic architecture enhancement of the landraces in the future breeding programme. The significant positive correlation of 100-grain weight with grain yield in the present study was in agreement with the earlier reports by (Efendi *et al.*, 2015; Ibrahim *et al.*, 2019). Thus the manipulation of these traits would have a high positive impact on yield enhancement. Except for girth diameter and the number of grain per panicle, all the traits show a positive correlation with yield. A significant positive correlation of yield with LgL observed in the study was also in agreement with Ibrahim *et al.* (2019). A similar finding of negative correlation of yield with the number of filled grain per panicles have also reported by Saha *et al.* (2019). The positive association of plant height with yield in the present study was in agreement with earlier reports (Mohaddesi *et al.*, 2010; Roy *et al.*, 2014b). But this was in contrast with negative associations reported by (Akinwale *et al.*, 2011; Sarawgi *et al.*, 2013). The positive association of plant height with yield in the present study may be due to its ecological needs of landraces to survive against harsh climatic conditions and to have high competitive growth with luxuriant weeds growth. But according to Karine *et al.* (2014),

Table 6. Correlation among agromorphological traits of 35 landraces

	PH	PnL	GD	PBR	FLL	FLW	BLL	BLW	LgL	FGP	TW	YLH
PH	1	.										
PnL	.507**	1										
GD	.718**	.564**	1									
PBR	-.070	.009	-.350*	1								
FLL	-.377*	-.318	-.730**	.474**	1	.						
FLW	-.508**	-.419*	-.932**	.452**	.844**	1						
BLL	-.113	-.130	-.618**	.498**	.851**	.859**	1					
BLW	.085	.079	-.380*	.523**	.812**	.665**	.928**	1				
LgL	-.321	-.271	-.780**	.524**	.936**	.943**	.964**	.866**	1			
FGP	.422*	.464**	.589**	.069	-.226	-.412*	-.056	.085	-.216	1		
TW	-.088	.203	.055	.342*	.168	.039	.170	.279	.152	.381*	1	.
YLH	.054	.131	-.150	.327	.306	.292	.416*	.565**	.392*	-.024	.460**	1

**. Correlation is significant at the 0.01 level (2-tailed). *. Correlation is significant at the 0.05 level (2-tailed).
Plant height (PH cm), Panicle length (PL cm), Girth diameter (GD mm), Primary branch number per panicle (PBR), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLWcm), Ligule length (LgLcm), Filled grain number per panicle (FGP), Test weight 100 seeds in gram (TW), Yield per hectare in quintal (YLH)

high yielding types of rice should be of short stature. Similarly, the tall stature of *jhum* landraces in the present study has low yield capacity than the shorter stature of WRC landraces. Plant height had a significant positive correlation with PnL and the number of filled grains per panicle reported in the present study was supported by (Roy *et al.,* 2014b; Srijan *et al.,* 2016 and Saha *et al.,* 2019). A significant positive correlation of filled grain per panicle with PnL was also reported by Roy *et al.* (2014b). Both the flag leaf and blade leaf area have a negative association with plant height. The negative correlation of the flag leaf area with plant height was also reported by Saha *et al.* (2019). As most of the landraces have droopy leaf characters, the photosynthetic efficiency would have been affected and become an unnecessary load to the culm could be one of the reasons. But both have a significant positive correlation between them and with the number of primary branches per panicle. The positive correlation of the flag leaf area and blade leaf area was in accordance with Roy *et al.* (2014b).

Genetic Variability, Heritability and Genetic Advance

The study revealed that the phenotypic variance of all traits was higher than the genotypic variance. Similarly, the phenotypic coefficient of variation (PCV) was also slightly higher than the genotypic coefficient of variation (GCV) in all the traits under study (Table 7). The highest PCV was recorded in Yield (43.60%) followed by FGP (32.55%), LgL (31.04%), BLW (27.21%), FLL (25.5%), PH (24.07%), FLW (22.59%) and GD (22.47%) respectively (Table 8). The lowest PCV of (14.31%) was recorded in test weight. Traits like PnL, BLL, and PBR recorded PCV<20% respectively. Similarly, the highest GCV was recorded in yield (43.26%) followed by LgL (26.55%), BLW (22.89%), FGP (22.57%), PH (21.7%) respectively. The lowest GCV of 11.61% was recorded in the number of primary branches per panicle. Traits like FLW, GD, PnL, FLL, BLL, and test weight have GCV>20% respectively. The traits under study were highly heritable in which heritability value under ranges from 38.8% (PBR) to 98.4% (Yield). Heritability values of 81.3%, 71.4%, and 48.1% were recorded in plant height, PnL, and the number of grain per panicle respectively. The genetic advance as percent of the mean (GAM) ranges from 14.9% (PBR) to 88.4% (Yield).

Variability of any trait is measured by the Genotypic coefficient of variation and the extent of the environmental influence on any traits are indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Existence of large differences reflect about the high influence of environment, while small differences reveal high genetic influence. High heritability coupled with high genetic advance is more helpful in forecasting genetic

Table 7. Components of variation for agronomic traits among 35 landraces

	G Mean	Fratio	PV	GV	PCV%	GCV%	h^2%	GA	GAM%
PH	127.394	22.7	941	765	24.08	21.7	81.27	51.35	40.31
PnL	25.7097	13.47	26.3	18.8	19.97	16.9	71.38	7.548	29.36
GD	6.4147	7.609	2.08	1.18	22.47	17	56.93	1.691	26.35
PBR	11.4966	4.168	4.6	1.78	18.66	11.6	38.78	1.714	14.9
FLL	40.5486	4.482	107	43.9	25.5	16.3	41.05	8.746	21.57
FLW	2.1006	18.18	0.23	0.17	22.6	19.9	77.45	0.758	36.06
BLL	58.6697	4.713	129	55.1	19.38	12.7	42.61	9.981	17.01
BLW	1.8234	13.11	0.25	0.17	27.22	22.9	70.77	0.724	39.68
LgL	2.1404	14.66	0.44	0.32	31.04	26.6	73.2	1.002	46.81
FGP	172.477	5.632	3152	1516	32.55	22.6	48.09	55.62	32.25
TW	2.4456	5.035	0.12	0.08	14.32	11.7	66.86	0.482	19.72
YLH	18.6543	127.3	66.2	65.1	43.61	43.3	98.44	16.5	88.43

*GAM: Genetic Advance as percent of mean

Plant height (PH cm), Panicle length (PL cm), Girth diameter (GD mm), Primary branch number per panicle (PBR), Flag leaf length (FLLcm), Flag leaf width (FLWcm), Blade leaf length (BLL cm), Blade leaf width (BLWcm), Ligule length (LgLcm), Filled grain number per panicle (FGP), Test weight 100 seeds in gram (TW), Yield per hectare in quintal (YLH)

gain (Johnson *et al.,* 1955). Selection based on the only yield is often unwise. So it is necessary to know the association between yield and its components (Akhtar *et al.,* 2011). Higher PCV than the corresponding GCV for all the traits in the present study revealed an influence of the environmental effects. However the PCV (43.6%) with GCV (43.3%) recorded in yield revealed that it is highly under genetics factor. Similar findings of higher PCV than GCV were reported earlier by (Bhadru *et al.,* 2012; Khatun *et al.,* 2015; Saha *et al.,* 2019).

The PCV, GCV, heritability, and GAM recorded in the present study were moderate to high among the traits. Traits like yield per hectare, FGP, plant height, FLL, and BLW have high PCV (>20%). Traits with PH, and BLW have high GCV (>20%). Traits with moderate GCV (10-20%) were FLW, GD, PnL, FLL, BLL, 100 seed weight, and PBR. Likewise, GAM was high (>20%) for all the traits except 100 seed weight, BLL, and PBR. Kumar at al. (2013) have reported a similar trend of high PCV, GCV, heritability, and GAM from the study of jhum rice germplasm of Northeast India, Khatun *et al.* (2015) on upland rice and Saha *et al.* (2019) on Bangladesh rice germplasm. However, PCV and GCV in the present study were higher than the earlier study of Akinwale *et al.* (2011) on African rice and Kumar *et al.* (2018) from 12 traits of improved lines. High heritability and high GAM on grain per plant, plant height, and yield were also reported by Khatun *et al.* (2015) and Kumar *et al.* (2018). The present study also observed a small difference in PCV and GCV which ranges from 0.34% (yield) to 9.9% (grain number per panicle). This represented some degree of environmental influence on the phenotypic expression of these characters. A similar small difference was reported earlier by Khatun *et al.* (2015). This suggests that traits like yield, PnL, PH, FLW, and test weight were highly genetic control, and selection based on these characters would be effective for future crossing programmes.

The high estimates of heritability and genetic advance observed for the above characters were closed in agreement with the earlier reports in rice by (Islam *et al.,* 2004; Manna *et al.,* 2006; Singh *et al.,* 2007; Sarangi *et al.,* 2009; Akinwale *et al.,* 2011; Kumar *et al.,* 2013). Neha and Verma. (2018) and Saha *et al.* (2019) also reported high heritability with high GAM in yield, plant height, number of grain per panicle, PnL, flag leaf, and blade leaf similar with the present study. The relatively high value of heritability and genetic advance observed in the present study indicated that superior genotype could be selected in the segregating population derived from hybridization between selective parents

Conclusion: As these valuable landraces from Arunachal Pradesh possess vast treasured huge genetic variability, most of the untapped landraces in the present study would be of great value to complement and broaden the gene pool in rice breeding. Promising landraces identified in the present study are expected immense help for their popularization.

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RESEARCH ARTICLE

Genetic Diversity of *Gora* Rice (*Oryza sativa* L.) Landraces of Chotanagpur Plateau Region in Eastern India

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The rice cultivars grown in the uplands of the state of Jharkhand, India are traditionally known as *gora* rice. These cultivars possess many important traits such as high seedling vigour, deeper roots and drought tolerance. In this study, a collection of *gora* landraces were assessed for morpho-genetic diversity using SSR markers. Morpho-agronomic analysis indicated that although seed morphological features are traditionally used for differentiating landraces, based on overall morpho-agronomic features also the cultivars could be differentiated as found in case of black gora. A genetic diversity analysis using 39 SSR markers detected considerable gene diversity (0.52) within *gora* cultivars. The white gora accessions were classified as *indica,* and rest including black gora, brown gora and other gora accessions belonged to *aus* group. This germplasm set provides scope for further genetic studies on multiple abiotic stress tolerance traits such as drought, submergenece and phosphorus starvation and traits for aerobic adaptation.

Key Words: Eastern India, genetic diversity, Gora rice, population structure

Introduction

The Chotanagpur plateau region in eastern India which covers much of Jharkhand state and adjacent parts of Chhattishgarh, Odisha and West Bengal (22.0-22.5^{o}N latitude; 83.95-88.0^{o}E longitude; 140-1200 m above msl). This region has a rich rice agroecological diversity due to variable soils and landscapes. The region is also endowed with diverse traditional cultivars and wild genetic resources of rice largely cultivated by the tribal communities inhabiting in the inaccessible areas (Chauhan *et al.,* 1995). In the state of Jharkhand, rice is grown in around 60% of total cropped area and approximately 33% of rice growing area in the state is upland. Jharkhand is the homeland of thirty two tribes including eight primitive tribes. These indigenous communities have selected diverse rice cultivars based on their food habits, suitability to environments and soil conditions, and tolerance to biotic and abiotic stresses. It is well documented that there is an inextricable link between cultural and biological diversity (Maffi, 2001; Gavin *et al.,* 2015). However, the harmonious link between biological and cultural diversity has become vulnerable due to homogenizing effects of climate change, urbanization and modern agriculture, among other influences (Liu *et al.,* 2002). Nevertheless, the tribal communities inhabiting remote areas still cultivate traditional cultivars because of cultural values, quality and individual preferences (Sinha & Xaxa, 2014).

As per revenue class, the land types in Jharkhand are classified in two broad classes: *tanr* (upland) and *don* (lowland). The uplands/ *tanr* is further classified based on fertility and slopes into *tanr*-I (homestead/ *bari* land), *tanr*-II (typical upland/ *gora* land) and *tanr*-III (sloppy and gravelly land). So, basically *gora* is a land type and any rice cultivars grown in *tanr*-II or *gora* land are popularly known as *gora* rice (Mandal *et al.,* 2011). Though the productivity is quite less, these rices provide sustenance to the poor and marginal farm families living in the most fragile environments. *Gora* rices are traditionally categorized based on husk colour (*karanga*/ black gora, *bhura*/brown gora, *charka*/white gora, etc.) and grain shape and sizes: *chhote*/*saria* (small-grained) gora, and *barka*/ *dani* (large-grained) gora (Sinha *et al.,* 1990).

Gora cultivars have evolved under marginal environments where the crop is challenged by a plethora of abiotic (such as drought and phosphorus starvation) and biotic stresses (such as high crop-weed competition, blast, brown spot and insect pests). Hence, these cultivars represent a valuable genetic resource for

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rice breeding. For example high seedling vigour and deep roots have been reported in black gora (Shrestha *et al.,* 2014; Redoña and Mackill, 1996). Earlier studies with molecular markers have classified *gora* cultivars within *aus* (Courtois *et al.,* 1997; Ali *et al.,* 2011) and *indica* (Garris *et al.,* 2005). However, these studies, conducted on a global-scale, are often limited by the relatively small number of accessions obtained from a specific geographic region. In contrast, studies with rice germplasm from a narrow geographical region, are also important to understand rice genetic diversity at micro level which is often shaped by intricate influences of the environment and cultural references of human communities. A study with 511 rice cultivars, including 5 *gora* accessions collected from Assam, Bangladesh and West Bengal reported two distinct groups within the *aus* sub-population (Travis *et al.,* 2015). Genetic diversity analysis of 69 imporved and traditional drought tolerant cultivars of India using SNP markers clasisifed accessions into *indica* and *aus* specific groups, and two *gora* aceessions identified as *aus* (Vikram *et al.,* 2016).

In this study, we assess the genetic diversity and population structure of a collection *gora* rice accessions grown in the upland ecologies of Chotanagpur Plateau in Eastern India using agro-morphological traits and SSR markers. The genetic relationship between the *gora* accessions is compared by cultivar groups and check varieties from *indica* and *aus* subpopulations. Overall, this study provides an exhaustive examination of the genetic diversity within *gora* rice accessions for further utilization.

Materials and Methods

Plant Materials

A set of 49 *gora* rice accessions was used in the study. The accessions were sampled from rice germplasm collection being maintained at Central Rainfed Upland Rice Research Station (CRURRS), ICAR-National Rice Research Institute, Hazaribag, Jharkhand, India. These genotypes were collected earlier from different parts of the states of Jharkhand and Bihar in the Chotanagpur plateau region of Eastern India (Sinha *et al.,* 1990; Chauhan *et al.,* 1995). In addition to the *gora* accessions, 13 check varieties were used for phenotyping, while, 19 checks were included for genotyping. In this paper, '*gora'* (italics) is used when referring to gora cultivars as a whole, and 'gora' (normal font) for referring to different cultivar types such as black gora, brown gora, and white gora, etc.

Agro-morphological Characterization

Forty-nine *gora* and 13 check varieties were grown at CRURRS research farm during wet season (July-October) as rainfed crop in 2017 and 2018. The experiment was laid out in randomized complete block design with two replications and standard management practices were followed to raise a healthy crop. The entries were line sown in 3 rows having 2 m row length in the third week of July. After germination, the extra seedlings were hand removed to maintain a plant-to-plant distance of ~15 cm. Hand-weeding was done at 25 and 45 days after sowing. A recommended fertilizer dose of 60:30:30 ($N:P_2O_5:K_2O$) was applied. Data were recorded for 26 agro-morphological traits following Standard evaluation systems (SES) for rice (International Rice Research Institute, 2013). Grain yield plant^{-1} was calculated as the average yield of ten randomly selected hills from middle row of the plot.

Genotyping using SSR Markers

Thirty nine SSR markers, distributed across rice chromosomes, were selected from the GCP panel of 50 recommended markers for diversity analysis (Gramene marker database https://archive.gramene.org/markers/microsat/50_ssr.html) were used to assess genetic diversity among the accessions.

DNA was extracted from fresh leaves using the Qiagen DNeasy plant mini kit (Qiagen, CA, USA) following the manufacturer's instructions. Polymerase chain reaction (PCR) was carried out in a total volume of 10 µl reaction mixture having 25 ng template DNA, forward and reverse primers (5 pM each) and Master Mix (Thermo Fisher Scientific, USA). PCR was done in a thermocycler using following conditions: 5 min at 94°C; 35 cycles of 30 s at 94°C 30 s at annealing temperature and 30 s at 72°C; followed by 7 min at 72°C. Amplicons were visualized in Agarose gels stained with SYBR Safe DNA gel stains (Invitrogen). During scoring, the band with the lowest molecular weight was assigned allele number 1 and the progressively heavier bands were scored incrementally.

Data Analysis

The phenotyping data were subjected to analysis of variance and descriptive statistics using R v.3.4.4. (R Core Team, 2017). A factor analysis of mixed data

(FAMD) was performed in R using 'FactoMineR' and 'factoextra' packages in R to examine the variability including both quantitative and qualitative traits. FAMD algorithm can be seen as mixed between PCA and multiple correspondence analysis (MCA) and it ensures balance between the influences of both continuous and categorical variables to determine the dimensions of variability. Cluster analysis was done using 'cluster' package in R. The mixed data set (untransformed) of qualitative and quantitative traits was also used for cluster analysis by calculating the 'Gower' coefficient. A hierarchical cluster dendogram was generated using the 'Euclidean' distance and 'average' linkage between the objects.

The MCMC (Markov Chain Monte Carlo) population analysis program STRUCTURE (Falush *et al.,* 2003) was used to infer underlying population structure using an initial burn-in of 5,000 iterations, followed by a run length of 50,000 iterations. The population structure in the data was investigated using putative population *K* values ranging from 1-8 (10 replicates per *K* value) with a STRUCTURE model allowing for admixture and correlated allele frequencies. 'Structure Harvester' (Earl and VonHoldt, 2012) was used to determine an optimum *K* value. Subsequently, the SSR data was then reanalysed using STRUCTURE with the optimum *K* = 2, burn-in of 10,000 iterations and run length of 100,000 iterations to generate a STRUCTURE *Q* matrix. Major modes in the STRUCTURE output were identified using CLUMPAK (Kopelman *et al.,* 2015).

The following summary statistics of the SSR markers matrices were estimated: number of alleles (Na), major allele frequency (MAF), observed heterozygosity (Ho), expected heterozygosity (He) and polymorphism information content (PIC). The phylogenetic tree was constructed using Roger's 1972 genetic distance and neighbour joining method using PowerMarker V3.25 (Liu and Muse, 2005). To summarize the patterns of variation in multi-locus dataset, principal coordinate analysis (PCoA) was performed in GenAlex v6.5 software (Peakall and Smouse, 2012) using the genetic distance matrix among the accessions. Separate analyses were conducted by classifying the rice accessions into: cultivar groups (black gora, brown gora, white gora, gora and check) and STRUCTURE subpopulations (K1, K2 and admix). Accessions were only assigned to a STRUCTURE groups if the probablity of their group membership was >75%. Accessions with <75% probablity of a single group membership were classified as 'admix'.

Results and Discussion

Variability in Morpho-agronomic Traits

The *gora* accessions were classified into four groups: black grora, brown gora, white gora, and gora (other gora genotypes) based on traditional name. Overall, considerable variations were observed for seedling vigour (Vg), leaf blade pubescence (LBP), basal leaf sheath colour (BLSC), leaf angle (LA), apiculus colour (ApC), lemma and palea colour (LmPC) and seed coat colour (SCC). Frequency distribution indicated that seedlings of 85% *gora* accessions were extra-vigorous to vigorous. Awing was present in black gora accessions. Significant variations were also observed for LmPC within brown gora, white gora and gora subgroups. The LmPC of brown gora accessions varied from gold furrows on straw to brown furrows on straw. Majority (61%) of *gora* accessions had brown and red pericarp, with a few exceptions in white gora and gora where SCC varied from white to red (Fig. 1). The *gora* accessions predominantly had medium brown rice length and medium brown rice shape. Three black gora accessions (HRC82, HRC86, HRC88) had short-bold kernels.

Descriptive statistics of eleven quantitative traits revealed that all the traits showed significant variation within current germplasm collection (Table 1). Days to 50% flowering (DF) varied from 54 days (N22) to 95 days (Apo). Among the *gora* accessions, highest average DF was observed in white gora (66.56 days) followed by black gora (66.4 days). The highest average plant height (Ht) was observed in white gora (115.9 cm) followed by brown gora (113.5 cm) accessions. Most of the rice accessions had intermediate (90-125 cm) plant height. White gora cultivars recorded Panicle length (PnL) varied from 16.45 cm (HRC92) to 25.50 cm (HRC220) with an average value of 21.27 cm. The highest average brown rice length (BrRL) was observed in brown gora (6.23 mm) followed by white gora (5.99 mm). On an average, brown rice width (BrRW) was lowest in white gora (2.47 mm), and highest in brown gora and gora. The 100-grain weight (GW) varied from 1.54 g (Karhani) to 2.84 g (HRC94). Among the *gora* accessions, the gora group recorded the highest (2.12 g) GW, while black gora accessions had the lowest value (1.99 g). Grain yield plant^{-1} (Yld) under rainfed DSR varied from 0.72 g (HRC95) to 12.60 (Karhani).

Table 1. Range of variation in agro-morphological traits of *gora* rice landraces.

Groups	Stat	DF	Ht	PnN	PnL	GrL	GrW	SLmL	BrRL	BrRW	GW	Yld
All	Mean	64.42	110.82	10.17	21.27	8.35	3.22	2.56	5.98	2.59	2.09	5.97
n = 62	SD	6.91	12.28	2.61	2.49	0.52	0.20	0.29	0.39	0.20	0.23	2.77
	Min	54.00	69.00	4.67	16.45	6.62	2.36	1.83	4.67	1.99	1.54	0.72
	Max	95.00	134.33	16.33	27.50	9.47	3.70	3.25	6.87	3.00	2.84	12.60
	P	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.037
	%CV	10.73	11.08	25.66	11.71	6.23	6.21	11.33	6.52	7.72	11.00	38.02
Black gora	Mean	66.40	111.82	10.43	20.57	8.46	3.23	2.73	5.76	2.61	1.99	5.67
n = 10	SD	4.26	10.41	2.75	2.69	0.46	0.15	0.37	0.35	0.19	0.25	2.94
	Min	61.00	95.67	6.00	16.50	7.52	2.99	2.08	5.28	2.38	1.56	1.53
	Max	78.00	128.33	16.33	24.30	9.47	3.64	3.25	6.55	3.00	2.54	11.90
	P	0.000	0.104	0.079	0.000	0.231	0.010	0.003	0.000	0.000	0.279	0.795
	%CV	6.42	9.31	26.37	13.08	5.44	4.64	13.55	6.08	7.28	12.56	35.98
Brown gora	Mean	64.75	113.46	10.34	21.01	8.56	3.24	2.63	6.23	2.62	2.07	4.58
n = 12	SD	6.06	10.25	2.23	2.58	0.38	0.20	0.17	0.28	0.19	0.29	2.26
	Min	58.00	80.33	4.67	16.45	7.89	2.86	2.29	5.70	2.15	1.64	0.72
	Max	85.00	132.33	16.33	27.00	9.21	3.56	2.92	6.65	2.87	2.84	9.43
	P	0.000	0.076	0.999	0.000	0.002	0.000	0.000	0.000	0.000	0.257	0.712
	%CV	9.36	9.03	21.57	12.28	4.44	6.17	6.46	4.49	7.25	14.01	39.74
White gora	Mean	66.56	115.85	10.69	20.22	8.36	3.06	2.49	5.99	2.47	2.10	5.24
n = 8	SD	6.16	10.63	2.44	1.89	0.46	0.17	0.35	0.24	0.19	0.24	2.04
	Min	60.00	89.50	6.67	17.20	7.63	2.89	1.93	5.49	2.19	1.61	1.49
	Max	81.00	133.00	14.33	23.20	9.10	3.45	2.95	6.32	2.79	2.49	9.65
	P	0.007	0.173	0.214	0.000	0.001	0.004	0.000	0.000	0.000	0.070	0.265
	%CV	9.25	9.18	22.83	9.35	5.50	5.56	14.06	4.01	7.69	11.43	37.02
Gora	Mean	61.71	112.25	10.16	21.70	8.33	3.24	2.51	5.97	2.62	2.12	6.25
n = 19	SD	4.38	9.80	3.01	2.50	0.52	0.23	0.27	0.35	0.20	0.18	2.64
	Min	55.00	85.17	4.67	16.75	6.81	2.36	1.83	5.16	1.99	1.77	0.86
	Max	79.00	128.33	16.33	27.50	9.41	3.70	3.08	6.87	2.90	2.58	12.08
	P	0.000	0.000	0.267	0.000	0.139	0.000	0.000	0.000	0.000	0.253	0.098
	%CV	7.10	8.73	29.63	11.52	6.24	7.10	10.76	5.86	7.63	8.49	32.64
Checks	Mean	65.23	102.44	9.50	22.08	8.08	3.27	2.49	5.92	2.60	2.13	7.52
n = 13	SD	10.87	15.92	2.35	2.31	0.62	0.18	0.23	0.52	0.20	0.21	2.95
	Min	54.00	69.00	5.00	18.40	6.62	2.90	2.09	4.67	2.16	1.54	1.67
	Max	95.00	134.33	13.00	26.30	8.97	3.60	3.08	6.58	2.96	2.37	12.60
	P	0.000	0.000	0.004	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.068
	%CV	16.66	15.54	24.74	10.46	7.67	5.50	9.24	8.78	7.69	9.86	31.25

DF, Days to 50% flowering; Ht, Plant height; PnN, Panicle number plant^{-1}; PnL, Panicle length; GrL, Grain length; GrW, Grain width; SLmL, Sterile lemma length; BrRL, Brown rice length; BrRW, Brown rice width; GW, 100-grain weight; Yld, yield plant^{-1}; SD, Standard deviation; CV, Coefficient of variation

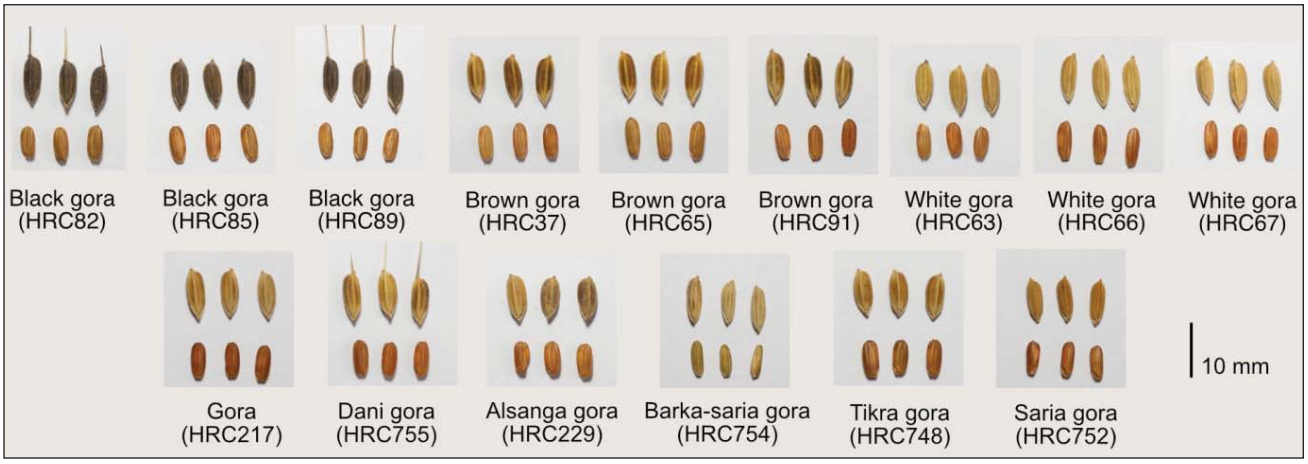

Fig. 1. Grain and kernel morphology of representative *gora* cultivars

The highest average Yld was recorded in checks (7.52 g) followed by gora (6.25 g), and the lowest Yld was observed in brown gora accessions (4.58 g). Considering the mean Yld of individual entries, only three accessions IR64Drt1, N22 and Karhani achieved Yld >10 g. The variation (% CV) for Yld was very high within four *gora* groups as well as within overall panel.

Ago-morphological Diversity within Gora Rices

The factorial analysis of mixed data (FAMD) using 26 traits extracted five factors (eigen value = 3.67 - 5.64) which collectively explained 33% of the total phenotypic variance. Among the traits, BrRL, An, AnC, ApC, LmPC and Len recorded higher contributions to factor 1 (Dim.1), while SLmL, Vg, An, ApC, LmPC and SCC showed greater contributions to factor 2 (Dim. 2). Overall, LmPC, ApC, SCC, An, AnC, Len, BrRL and Vg had contributed 69.19% to first two factors (Fig. 2a). Biplot of Dim.1 and Dim.2 explained about 16% of the total variance and separated the accessions mainly based on grain and kernel traits (Fig. 2b). The black gora accessions having morphologically distinct grains, formed separate group from the rest of the accessions. Similarly, the brown gora accessions formed a distinct group in the biplot. The white gora accessions along with improved check varieties grouped differentially

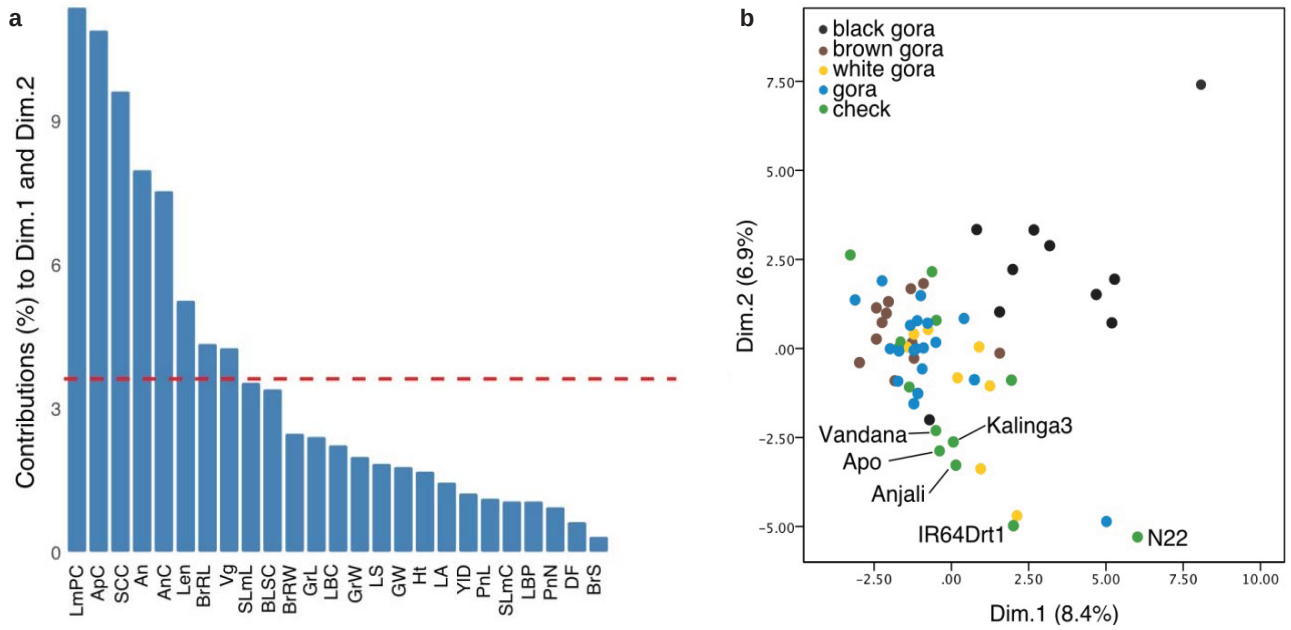

Fig. 2. Factorial analysis of mixed data. a. Percent contribution of the traits on factor 1 and 2; b. Biplot showing distribution of rice accessions based on trait loadings on first two factors

from the brown gora and gora and traditional checks. However, some overlapping between the cultivars of white gora and gora groups was found mostly due to their similarities in LmPC, ApC, SCC, and An.

Cluster analysis also supported the findings of FAMD. Dissimilarity (Gower's coefficient) among the accessions varied between 0.102 to 0.584 with an average value of 0.324. The dendogram depicting the morphological similarities of rice accessions have been drawn using 'average' linkage, due to having the highest cophenetic correlation (0.77) as obtained in the Mantel test (Fig. 3). Analysis of the optimal clusters following 'average silhouette' 'elbow' and 'Kelly-Gardener-Sutcliffe' methods suggested optimum cluster number of 2, 4 and 9. At $K = 2$, only N22 diverged from the rest of the genotypes. At $K = 4$, seven black gora accessions formed separate group from the rest of *gora* accessions. While, at $K = 9$, cluster 3 - 7 were represented by black gora accessions along with a traditional check Widd jong. The cluster 8 comprised two check varieties Kalinga III and IR64 Drt1. Finally, 48 accessions of brown gora, white gora, gora and check varieties formed cluster 9 with some sub-grouping. The white gora accessions distributed in three sub-clusters indicating considerable morphological variability within the white gora cultivars. However, it is apparent from both FAMD and clustering that most of the brown gora, gora and traditional checks are morphologically similar.

A comparison of phenotyping results revealed that the extent of variability in different agro-morphological traits is in line with the previous reports (Srivastava *et al.,* 1977; Sinha *et al.,* 1990, 1999). Most of the *gora* rice had intermediate to tall plant height. In general, drought-tolerant cultivars are tall mostly due

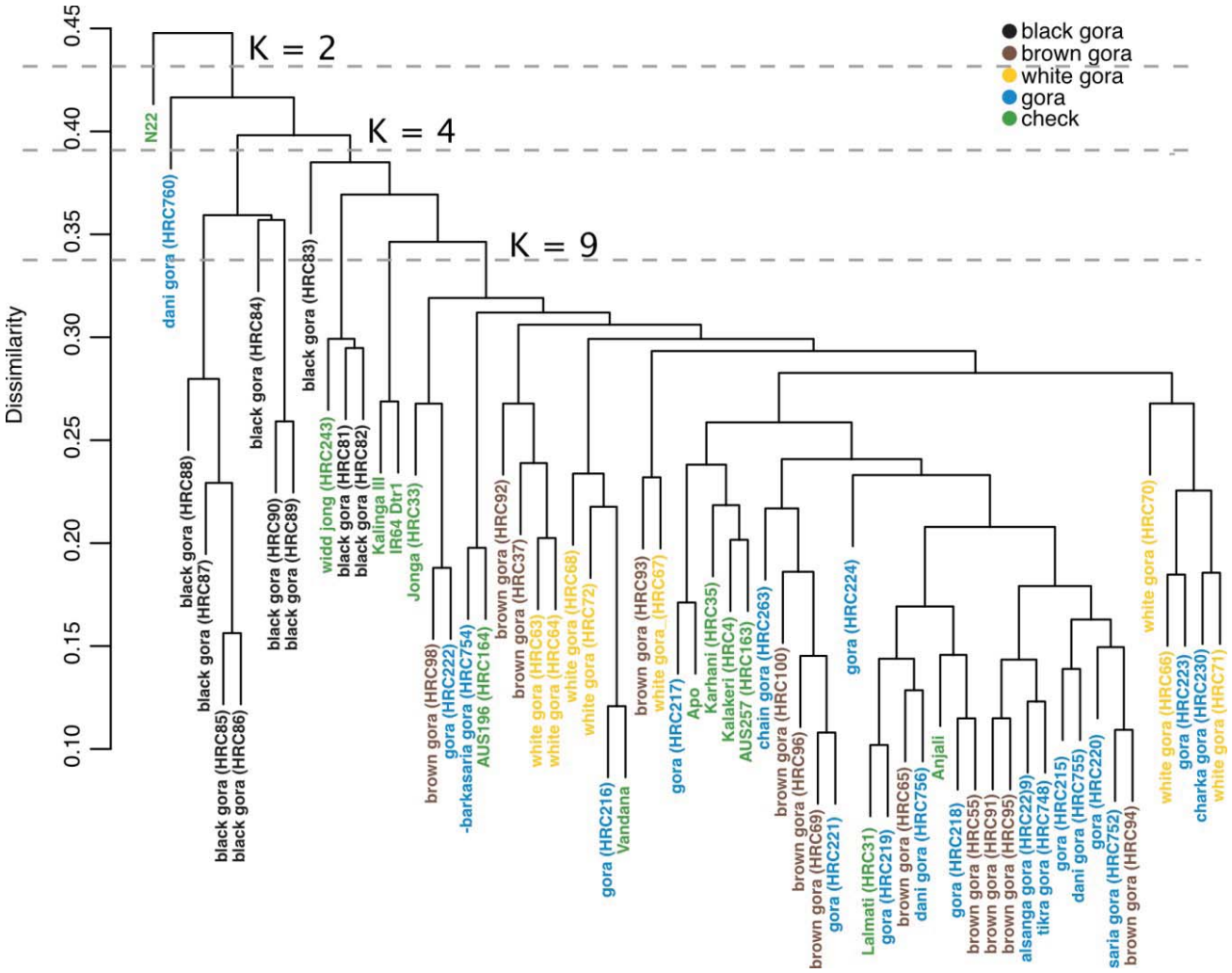

Fig. 3. Agro-morphological similarity among the *gora* rice landraces assessed using Gower's coefficient and clustering

to the tight linkage between the *sd1* gene and drought tolerance (Vikram *et al.,* 2015), and the 'tall' allele of *sd1* is present in most the drought tolerant landraces (Vikram *et al.,* 2016). Grain shape and size seem to vary appreciably in brown gora and white gora accessions as compared to black and gora rices, similar to earlier reports (Chauhan *et al.,* 1997). Among the different *gora* types brown gora was the most widely cultivated by upland farmers of Chotanagpur plateau and maximum number of collections were also made for this type. The lowest average grain yield per plant was registered in brown gora, while yield of all *gora* cultivars was lower than that of the checks. Sinha *et al.* (1998) also obtained very less yield for *gora* varieties and have the opinion that only a few good high yielding varieties could be sufficient to replace the *gora* cultivars. Multivariate analyses indicated that lemma-palea colour, apiculus colour, seed coat colour, awning, awn colour, grain length and grain width are the most influential traits in differentiating the accessions (Srivastava *et al.,* 1977; Sinha *et al.,* 1998). It is well documented that seed morphological features are generally been used as keys in cultivar identification and maintaining genetic purity of rice landraces by traditional farming communities (Roy *et al.,* 2016; Zapico *et al.,* 2020). The cluster analysis revealed that black gora cultivars are morphologically most distinct, while rest of the *gora* accessions are similar to each other and with improved drought tolerant varieties such as Anjali, Apo and Vandana. Hence, under typical upland ecologies, breeders also selected for similar sets of morphological traits that were favoured by traditional farmers over time.

SSR Polymorphisms

Altogether 154 alleles were identified from 68 tested germplasm using 39 SSR markers. On average 3.95 alleles were detected per marker. The highest number of alleles were identified for RM9 (AN = 9) followed by RM125 (AN = 7). The polymorphism information content (PIC) varied from 0.11 (RM25) to 0.73 (RM55) with an average of 0.47. Higher PIC (>0.60) was recorded for RM209, RM471, RM152, RM9, RM452, and RM19.

Population Structure and Genetic Diversity within Gora Rice Accessions

The results of the model-based STRUCTURE analysis (Fig. 4a), phylogenetic analysis (Fig. 4b) and principal coordinate analysis were consistent and 68 (49 *gora* plus 19 checks) accessions clearly separated into two clusters corresponding to *indica* and *aus*. Fifteen accessions including 13 *gora,* N22 and Kali aus were classified as admix, while, 18 (7 white gora and 11 check) and 35 (6 black gora, 8 brown gora, 15 gora, and 6 check) accessions were classified as *indica* and *aus,* respectively. When the NJ tree and PCoA were annotated based on cultivar groups, the distinctiveness of white gora accessions from the rest of the *gora* cultivars was obvious.

Assessment of genetic diversity indicators within the tested accessions revealed a higher level of genetic diversity within *aus* (He = 0.55) group compared to *indica* (He = 0.51) and admix (0.41) (Table 2). A similar pattern was observed for PIC. Gene diversity (He) at the cultivar level ranged from 0.41 (gora) to (0.57) checks. Among *gora* cultivars, brown gora recorded the highest genetic diversity (He = 0.45) (Table 2).

Although *gora* cultivars are generally classified under the *aus* subpopulation of rice, till date no molecular analysis has been done with a larger set of *gora* germplasm. Population structure analysis divided the current set of germplasm into two groups, K1 and K2, corresponding to *aus* (60%) and *indica* (40%) with average F_{st} of 0.349 and 0.035, respectively. The *gora* accessions were distributed in both the subpopulations, and interestingly seven out of eight white gora accessions were classified as *indica*. Rest of the 41 accessions were identified as *aus* (71%) and admix (29%). These findings are supported by the previous reports that *gora* rice is genetically *aus* (Courtois *et al.,* 1997; Ali *et al.,* 2011; Travis *et al.,* 2015). In the present study, four sub-clusters have been detected within the *gora* accessions falling under *aus* subpopulation, indicating considerable genetic diversity within them. A study with 183 rice landraces of East Kalimantan on the island of Borneo, Indonesia reported high population genetic structure even though there is little or no geographic differentiation within the landraces (Thomson *et al.,* 2009). Five groups were detected within the *japonica* accessions. A few other studies have also indicated that regional genetic diversity analysis with cultivars from a small geographic area (local-scale) often depict rich genetic diversity at micro-level (Barry *et al.,* 2007; Zhang *et al.,* 2007). Travis *et al.* (2015) reported two major groups within a large collection of *aus* germplasm originating from Eastern India and Bangladesh, and classified five *gora* accessions into *aus-1* (brown gora), *indica* (black gora) and *aus*-admix (black gora, dudhi gora and gora dhan). Courtois *et al.* (1997) observed

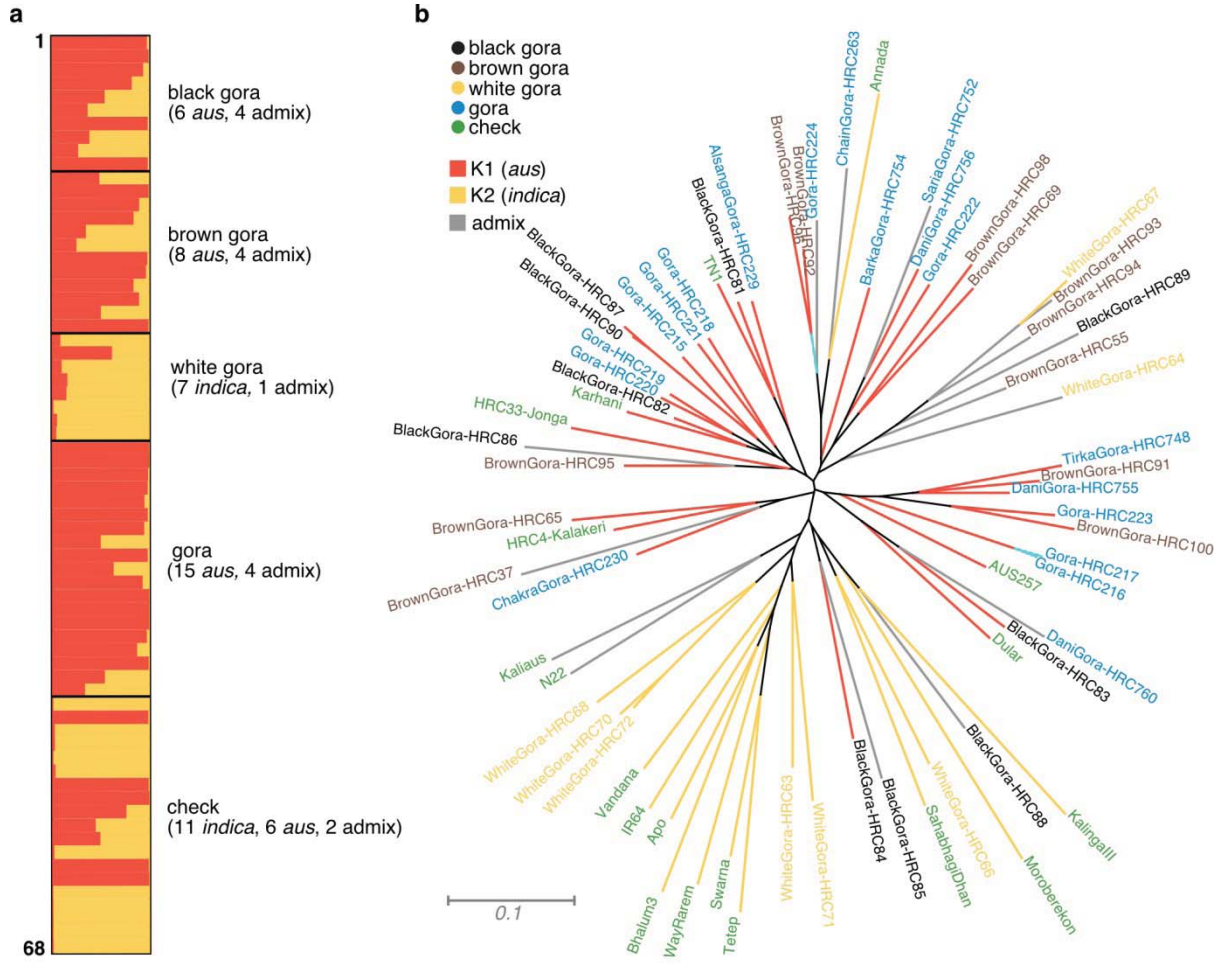

Fig. 4. Genetic diversity within *gora* rice. a. individual ancestry inferred with STRUCTURE. Each individual is represented by a bar partitioned by colour. The proportion of the colour making up each bar/ genotype represents the proportion contributed by the ancestral population. The clustering based on optimal K value divided the accessions into two main groups, corresponding to *indica* and *aus* rice types. b. Unrooted neighbour-joining tree of 68 rice accessions. Accession names and tree branches are colour coded based on cultivar types and STRUCTURE groups, respectively

Table 2. Genetic diversity indicators of *gora* rice landraces at different substructures

Sub-population	n	Na	MAF	He	Ho	PIC
STRUCTURE groups						
K1 (*aus*)	35	3.538	0.553	0.551	0.003	0.496
K2 (*indica*)	18	3.179	0.602	0.509	0.000	0.449
admix	15	3.051	0.704	0.406	0.004	0.353
Cultivar groups						
Black gora	10	2.667	0.682	0.425	0.000	0.369
Brown gora	12	2.769	0.663	0.448	0.006	0.388
White gora	8	2.462	0.667	0.432	0.000	0.370
Gora	19	2.974	0.699	0.408	0.005	0.358
Check	19	3.769	0.539	0.571	0.004	0.521
Mean	68	3.949	0.611	0.521	0.004	0.471

n, Number of genotypes; Na, Average number of alleles; MAF, Major allele frequency; He, Gene diversity; Ho, Observed heterozygosity; PIC, Polymorphism information content

that traditional upland cultivars mostly belong to *aus* group and appeared to be less diverse. In the present study, the morphological and genetic similarity of white gora accessions with improved drought tolerant varieties indicates that these cultivars may be some early *indica* cultivars being grown in the adjacent rainfed region and adopted by the traditional farmers for better yield in the specific ecology (relatively favourable uplands) of the region. This study also highlights considerable genetic diversity within the *aus* specific cluster (He = 0.551), as well as within *gora* cultivar types (He > 0.40). Genetic diversity is considered to be a function of ecological and evolutionary history (Thrupp, 2000). The high genetic diversity within *gora* cultivars could be associated with the diverse agro-ecological and ethno-cultural features of the region, as proposed in other studies (Wang *et al.,* 2016; Mbanjo *et al.,* 2019).

Conclusion

Agro-morphological analysis of *gora* rice accessions of Chotanagpur Plateau region in Eastern India indicated that although seed morphological features are traditionally used for differentiating landraces, based on overall agro-morphological features the cultivars could also be differentiated as found in case of black gora. Genetic diversity analysis revealed considerably high genetic diversity within the *gora* cultivars and classified white gora accessions as *indica,* and rest of the black gora, brown gora and other gora accessions as predominantly *aus*. The knowledge on the phenotypic variability and genetic structure of these trraditional upland rice landraces will provide essential foundation of decision making for conservation and utilization in breeding programmes, which is considered as an underexploited set of landraces. This germplasm set also provides scope for further genetic studies on multiple abiotic stress tolerance traits such as drought, submergenece and phosphorus starvation and traits for aerobic adaptation such as early vigour, weed competitiveness and well developed root system.

Acknowledgements

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RESEARCH ARTICLE

Genetic Resources of Genus *Allium* in India: Collection Status, Distribution and Diversity Mapping using GIS Tools

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The genetic resources of cultivated and wild *Allium* species collected from different states of the country have been discussed and analysed for distribution, diversity status and gaps. A total of 5,004 germplasm accessions have been collected during 1976-2020 by ICAR-NBPGR in collaboration with National Agricultural Research System (NARS) consisting 4,924 accessions of cultivated and 80 accessions of wild *Allium* species. Out of 5,004 accessions, 2,708 accessions have been conserved in National Genebank at ICAR-NBPGR, New Delhi. The cultivated alliums consist of 11 species, out of which nine species have been conserved (2,641 accessions). The wild *Allium* species comprise of 13 species out of which 11 species have been conserved (67 accessions). This study identified Western Himalaya as rich areas of diversity (H=1.491-2.0) for wild *Allium* species. Analysis indicated a significant gap for 21 wild taxa which are neither collected nor conserved in the genebank. Future thrust on explorations to be executed for collection of germplasm of these *Allium* species is discussed in this paper.

Key Words: *Allium* genetic resources, Diversity distribution mapping, Indian Himalayas, Wild *Allium* species

Introduction

The genus *Allium* L., one of the largest genera in the family Amaryllidaceae, has about 1,100 species distributed world-wide (The Plant List, 2020; Govaerts *et al.,* 2021). Mediterranean basin to Central Asia, and beyond is considered the centre of origin of *Allium* spp. which is the primary centre (Vavilov, 1926). Two main crops- onion (*Allium cepa* L.) and garlic (*A. sativum* L.) are commercially very important. About 40-45 species of *Allium* occur as cultivated and wild taxa from temperate to alpine regions of the Indian Himalaya. *Allium* species occurring in tropical areas are broadly distributed in different agro-ecological regions of India (Karthikeyan *et al.,* 1989; Pradheep *et al.,* 2014).

Allium species form an economically important group used as a vegetable, culinary salad, seasoning, spices and condiments, medicinal purposes and thus occupying an important place among the people of India (Verma *et al.,* 2008; Shah, 2014). In minor cultivated species *A. chinense* (lasan) and *A. tuberosum* are extensively grown as backyard cultigen in tribal dominated tracts of the Himalaya and other north-eastern states (Negi and Pant, 1992; Pandey *et al.,* 2008; Pandey *et al.,* 2019). *A. stracheyi* locally known as "*Faran"* grows wild in high altitude areas of Chamoli and Pithoragarh districts of Uttarakhand is declared as 'Vulnerable' and is used for seasoning purpose (Negi and Pant, 1992). Genetic resources of less-known *Allium*, their use and potential value have been discussed by some Indian workers (Negi and Pant, 1992; Pandey *et al.,* 2008; Shah, 2014; Pandey *et al.,* 2019).

ICAR-NBPGR has been carrying out explorations since 1976 in collaboration with crop-based institutes of the ICAR, State Agriculture University (SAUs) and Krishi Vigyan Kendras (KVKs). For alliums, the major collaborators were ICAR-Directorate of Onion and Garlic Research (ICAR-DOGR), Pune, Maharashtra; ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan (ICAR-VPKAS), Almora, Uttarakhand; ICAR-Central Institute of Temperate Horticulture (ICAR-CITH), Srinagar, Jammu and Kashmir; Mahatama Phule Krishi Vidyapeeth (MPKV), Rahuri, Maharashtra and National Horticulture Research and Development Foundation (NHRDF), New Delhi. These exploration missions have resulted in collection of diverse germplasm of several *Allium* species.

Crop wild relatives (CWR) of *Allium* have desirable traits/genes, which are generally not present in crops and recognized as a valuable resources; for crop improvement (Pandey *et al.,* 2019). Wild species, *Allium*

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roylei has provided genes resistant to powdery mildew and leaf blight to the *A. cepa* (Kofoet *et al.,* 1990; de Vries *et al.,* 1992; Khosa *et al.,* 2013). Molecular characterization performed by Khosa *et al.* (2013) for 10 indigenous *Allium* species, showed high transferability of different traits indicating their potential use in genetic transformation for crop improvement programmes. Germplasm characterization of Indian *Allium* especially those belonging to sub-genus *Cepa* deserve top priority for crop improvement (Pandey *et al.,* 2019).

The taxonomy of the genus *Allium* is poorly understood due to high polymorphism and wider adaptability to the habitats (de Vries *et al.,* 1992). Due to limited studies on taxonomy, morphology and eco-geography of wild taxa of *Allium* from the Indian region, species diversity remained uncollected and areas have remained unexplored. In present study geo-spatial tools and geographic information system (GIS) is used to analyze data of the collected and conserved germplasm of *Allium*. The aim is to assess the genus *Allium* particularly: (i) status of germplasm holding in national gene banks; and (ii) diversity mapping and identifying gaps in germplasm collection.

Materials and Methods

Scrutiny of Passport Data and Geo-referencing

ICAR-National Bureau of Plant Genetic Resources has augmented *Allium* germplasm since its inception in 1976, from various parts of the country through crop-specific/ multi-crop explorations conducted in collaboration with crop-based institutes of ICAR, SAUs and KVKs. This resulted in collection of a total of 5,004 accessions from different parts of the country, which were used in this study (NBPGR Annual Reports 1976-2019; Plant Germplasm Reporters, 2002-2018). The germplasm locality site details (village/tehsil/district) were checked thoroughly and wherever geo-coordinates (latitude and longitude) were not available, same were assigned with the help of passport data, gazetteers and Google map.

Gap Analysis and Mapping of Diversity

After a thorough screening of passport/germplasm data, geo-referenced map was prepared using geo-coordinates, WGS84 datum and geographic projection systems. To know spatial distribution and assessment of wild *Allium* species richness, DIVA-GIS software is used for point-to-grid analysis using simple-circular neighbourhood method (Hijmans *et al.,* 2001). Wild *Allium* species diversity is calculated using the Shannon-Weaver diversity index (Magurran, 2004) -

$$H = -\sum [(ni/N) \ln (ni/N)]$$

H = Shannon diversity index, ni = individuals of a species, N = total individuals of all

Species, ln = natural log

The diversity assessment vis-à-vis germplasm collected/conserved, literature survey/reports (Pandey *et al.,* 2008; Verma *et al.,* 2008; ICAR-DOGR Annual Report, 2016-17) and notes mentioned in germplasm reporter and exploration reports, collection gaps were identified to meet the objectives particularly areas representing deficit collection and wild *Allium* species which were neither collected nor conserved in the gene banks.

Results and Discussions

A. Status of Germplasm Collection

(i) *Allium cepa*: A total of 2,847 accessions of *A. cepa* have been collected from 240 districts of 29 states of the country. Geo-referenced map and ICAR-NBPGR passport database showed that Maharashtra (1,016) followed by Uttar Pradesh (295), Telangana (142), Haryana (133), Gujarat (98), Madhya Pradesh (89), Rajasthan (68), Chhattisgarh (63), Karnataka (61), Himachal Pradesh (40), Jammu & Kashmir (39) and Uttarakhand (38) were fairly well collected states (Fig. 1a). Least accessions were collected from Bihar, Jharkhand, Sikkim (5 each) and West Bengal (4). The data revealed that in Maharashtra, the Nashik (152 accns.), Akola (130), Dhule (91), Jalgaon (78) and Pune (75) districts represent significant collections. Though onion is cultivated in almost 29 states in smaller scale (kitchen garden), but several local varieties (70) and two hybrids (Arka Kirtiman, Arka Lalima) which are very widely adapted to specific regions (parts of Maharashtra and Karnataka) are currently cultivated on larger scale in the country (Mahajan *et al.,* 2018).

The production of onion is maximum in Maharashtra state which has share of 38.06 percent followed by Madhya Pradesh (15.91), Karnataka (12.84), Bihar (5.33), Rajasthan (4.28), Andhra Pradesh (3.94) and Haryana (3.02) out of total onion production in the country (HSR, 2018) which is in line with germplasm collected and conserved from these states.

(ii) *Allium sativum*: Germplasm of *A. sativum* (1,912 accns.) has been assembled from 304 districts of 28 states of the country and diversity distribution mapped (Fig. 1, b). Mapping of assembled diversity has shown that Gujarat (237) followed by Maharashtra (218), Uttarakhand (195), Telangana (170), Rajasthan (140), Himachal Pradesh (120) and Uttar Pradesh (107) have good representation in total collections (Fig. 1,b) while Sikkim (11), Punjab (9), Mizoram (7), Andhra Pradesh (5), Bihar (5) and Kerala (4) have poor representation and least collections. Multiplier onion (*A. cepa* var. *aggregatum*) is mainly grown in Andhra Pradesh, Karnataka and Tamil Nadu and only 85 germplasm accessions were collected from these states. Overlaying of geo-referenced layer on the black soil region (mapped by Mandal *et al.,* 2015) of the country revealed that maximum collections were from this soil, which is the suitable for cultivation of both cultivated species (onion and garlic). Similar studies have also been conducted on *Brassica* species (Semwal *et al.,* 2013), *Cajanus cajan* (Semwal *et al.,* 2018), *Vigna mungo* (Abraham *et al.,* 2010) and wild *Solanum* (Hijmans *et al.,* 2000), etc. in different parts of the world and provided quite valuable information.

(iii) *Other Less-known/ Minor Cultivated Species:* Among the less-known minor cultivated taxa namely- *A. ampeloprasum, A. cepa* var. *aggregatum, A. cepa* var. *viviparum, A. chinense, A. fistulosum, A. hookeri, A. porrum, Allium* × *proliferum* and *A. tuberosum* were collected from 19 states of the country (Table 1). Highest collections (>35%) were made in *A. cepa* var. *aggregatum* from Andhra Pradesh, Karnataka and Tamil Nadu. In *A. cepa* var. *viviparum* only four accessions were collected from Jammu & Kashmir. *A. tuberosum* is a widely distributed species in Himalayan region (1800-3000 m), and 13 accessions were collected from five states- Arunachal Pradesh, Jammu and Kashmir, Himachal Pradesh, Sikkim and Uttarakhand (Table 1).

(iv) Wild Allium Species: Data analysis revealed that out of 45 *Allium* species reported in the country (Kew Checklist, 2020; Pradheep *et al.,* 2014) the germplasm of only 13 wild *Allium* species were collected from different parts of the country (Table 2). Majority of the wild *Allium* species occur in high altitude regions of the Himalaya including cold desert of Himachal Pradesh, Ladakh and Uttarakhand (Fig. 3). Four economically important species namely *A. consanguineum, A. humile, A. przewalskianum* and *A. semenovii* were collected only from Pangi areas (3400 4600m) of Himachal Pradesh while *A. roylei* was collected from Jammu province especially Mendhar in Poonch; Gourwan in Reasi; Bani in Kathua; high altitude areas (1800-3500 m) of Malari in Chamoli, Milam valley in Pithoragarh district of Uttarakhand. Only three accessions of another economically important species – *A. stracheyi*, which is used as flavouring agent in high altitude areas of Uttarakhand (Chamoli- two accns. and Pithoragarh-one accn.), were collected. Collected diversity and literature revealed that temperate and high altitude areas of western and eastern Himalaya are the main habitats of wild *Allium* species diversity.

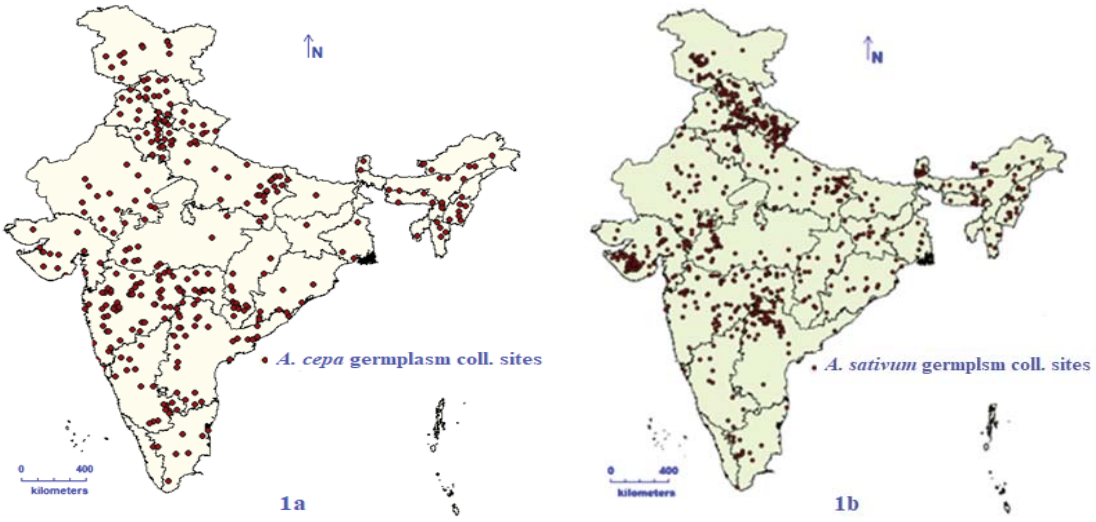

Fig. 1. Geo-referenced map of *A. cepa* (1a) and *A. sativum* (1b) germplasm collected from different states of India

Table 1. Status of *Allium* species indigenous collections (IC) from different states (1976-2020)

Cultivated species	Accessions[#] Collected	Wild species	Accessions[#]	Threatened status
A. cepa L. var. *cepa* L.	2,847	*A. carolinianum* DC.	25	
A. sativum L.	1,913	*A. auriculatum* Kunth	12	Endangered[$]
A. cepa var. *aggregatum* G.Don.	85	*A. griffithianum* Boiss.	11	
A. fistulosum L.	17	*A. wallichii* Kunth[#]	7	
A. tuberosum Rottler ex Spreng.*	13	*A. consanguineum* Kunth	6	
A. chinense G.Don	11	*A. przewalskianum* Regel[@]	5	
A. ampeloprasum L.	11	*A. humile* Kunth	5	
A. × *proliferum* (Moench) Schrad. ex Willd.	10	*A. stracheyi* Baker[@]	3	Vulnerable[$]
A. hookeri Thwaites*	10	*A. semenovii* Regel[@]	2	
A. cepa var. *viviparum* (Metz.) Alef.	4	*A. fasciculatum* Rendle	1	
A. porrum L.	3	*A. roylei* Stearn[#]	1	Endangered[$]
		A. prattii C.H.Wright	1	Rare[+]
		A. victorialis L.	1	
Total	4,924		80	

[#]ICAR-NBPGR Database *Also; wild occurring in India; @ also cultivated in kitchen garden, + Murti, 2001; $ Rao *et al.,* 2003

Table 2. *Ex-situ* conservation of cultivated and wild *Allium* species (IC) by ICAR-NBPGR.

Cult. Allium species	*Ex-situ* conservation methods				
	NGB	CB	IVR	FGB$	Total
A. cepa	991	9		606	1,606
A. sativum		134		779	913
A. fistulosum	16	3	1	6	26
A. chinense		11	9	3	23
*A. tuberosum**		7	4	18	29
*A. hookeri**		2	2	12	16
A. ampeloprasum		2		7	9
A. cepa var. *aggregatum*		1		3	4
*A. fasciculatum**			1	14	15
Sub-total	1,007	169	17	1,448	2,641
Wild *Allium* species					
A. przewalskianum#	1			19	20
A. griffithianum	2	1		8	11
A. carolinianum	3			5	8
A. stracheyi#	2			5	7
A. wallichii#		1		6	7
A. auriculatum	2	1		3	6
A. roylei#	1	1		1	3
A. humile	1			1	2
A. fasciculatum				1	1
A. prattii				1	1
A. victorialis	1				1
Sub-total	13	4		50	67
Total	1,020	173	17	1,498	2,708

NGB- national genebank; IVR- *in-vitro* repository; CB- cryo genebank; FGB- field genebank;
*also occurring in wild; [#]Also cultivated in kitchen garden [$]FGB at Bhowali, Uttarakhand and ICAR-Directorate of Onion and Garlic Research (ICAR-DOGR), Pune, Maharashtra.

B. Germplasm conserved Ex-situ

(i) ***Cultivated Allium species***: Among the two major *Allium* species, *A. sativum* (garlic) do not produce seeds hence it is conserved in field genebank and tissue culture repository. Out of the 24 species have been collected, only 11 produce seeds, while remaining non-seed producing or vegetatively propagated species are conserved in tissue culture repository, cryobank (CB)

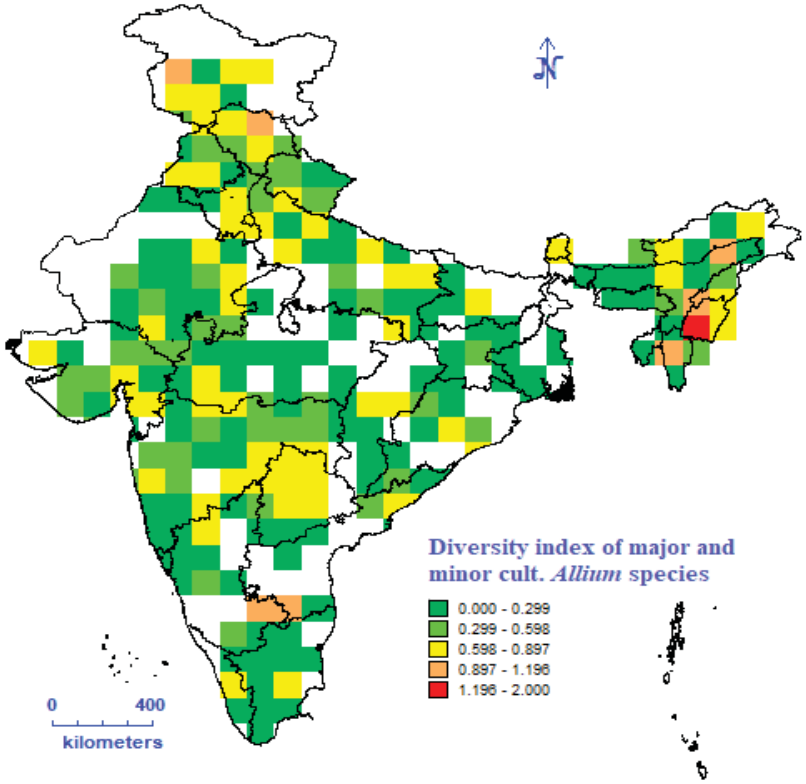

Fig. 2. Diversity index of major and minor cultivated *Allium* species

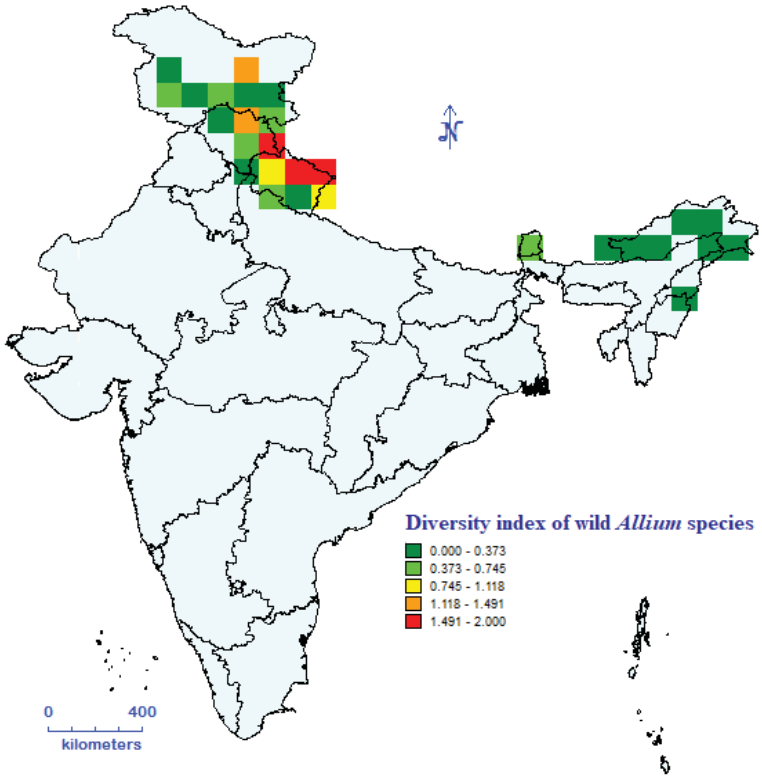

Fig. 3. Diversity index of wild *Allium* species

Table 3. Gaps and areas identified for collection of *Allium* species based on data from germplasm collected and conserved

Allium species (cult.)	Areas identified based on gaps in collections
A. cepa	Bihar (Chatra, Purnea, Sasaram, Samastipur, Vaishali districts), Jharkhand (Gumla, Garhwa, Hazaribagh, Ranchi), Tamil Nadu (Coimbatore, Cuddalore, Tiruchirappalli and Tirunelveli) and West Bengal (Darjeeling, Murshidabad, 24 South Parganas, West Medinipur)
A. sativum	Bihar (Nalanda, Nawada, Samastipur and Vaishali districts), Jharkhand (Garhwa, Gumla, Hazaribagh and Palamu), Tamil Nadu (Dindigul, Salem, and Tiruchirappalli) and West Bengal (Darjeeling, Murshidabad, West Medinipur)
A. cepa var. *aggregatum*	Andhra Pradesh (Chitoor, East and West Godavari, Kurnool, Ranga Reddy), Karnataka (Belgaum, Chikkabalapura, Dharwad, Medak, Mysore) and Tamil Nadu (Coimbatore, Cuddalore, Dindigul, Namakkal, Perambalur, Tiruppur, Tirunelveli, Thoothukudi, and Trichy)
Germplasm collected but not conserved	
A. porrum	Low altitude (1800-2800 m) areas (Kangra and Chamba) of Himachal Pradesh and Uttarakhand (low altitude areas of Chamoli and Pithoragarh districts)
Allium × *proliferum*	Jammu & Kashmir (Bandipura and Kupwara)
A. cepa var. *viviparum*	Anantnag, Bandipura, Kupwara and Parimpora village of Jammu and Kashmir and adjoining areas of Himachal Pradesh
A. consanguineum	High altitude (2800-4700 m) areas of Lahaul and Spiti, Kinnaur of Himachal Pradesh
A. semenovii	Pangi high altitude (3400-4600 m) areas of Himachal Pradesh
Species-wise least collection (in wild spp.)	
A. carolinianum	Hanupata, Khaltse, Lahaul areas of Ladakh (3700- 3950 m); Gilgit, Naltar lake, Kishenganga Valley (Jammu and Kashmir); High altitude areas (2400-4600 m) of Himachal Pradesh and Uttarakhand (Dasgupta, 2006)
A. humile	High altitude (2800-4700 m) areas of Himachal Pradesh (Chanchal pass, Chamba, Larot, Lahaul and Spiti, Kinnaur), Bashaur, high altitude areas of Gulmarg, Liddar Valley, Zojpal (Jammu and Kashmir), Hari Ki Dun (Uttarkashi district), high altitude areas of Pithoragarh Uttarakhand (Dasgupta, 2006; GBIF, 2021)
A. fasciculatum	Naku La, high altitude (1800-3500 m) areas of North Sikkim (Sikkim) (GBIF, 2021)
A. prattii	Tangu, Lachen and Tallum Sandong areas of Sikkim (GBIF, 2021)
A. roylei	Jammu province especially Mendhar in Poonch; Gourwan in Reasi; Bani in Kathua, Sanjhi, Chat Bhairoin temple (Jammu and Kashmir); high altitude (1800-3500 m) areas of Chamoli, Pithoragarh Rudraprayag districts of Uttarakhand (Dasgupta, 2006)
A. stracheyi	High altitude (2400-4600 m) Chamba, Kakcham hill slopes, Pangi, Lahaul and Spiti, Kinnaur areas of Himachal Pradesh and Lata, Gamshali, Niti, Valley of flowers (Chamoli district) (Dasgupta, 2006)
A. victorialis	Bal tal, Sonamarg areas of Jammu and Kashmir (GBIF, 2021)
A. wallichii	Banihal ridge of Jammu and Kashmir (Dasgupta, 2006), Chirbasa, Gangotri (Uttarkashi district), high altitude areas of Pithoragarh and Rudraprayag districts of Uttarakhand (Dasgupta, 2006) and Yakchi, Lachung and Islumbo sites (3000- 3300 m) of Sikkim (GBIF, 2021)
Areas representing deficit collection	
Arunachal Pradesh,	High altitude (1800-4600 m) areas of Dibang valley, Upper Siang and Tawang districts
Ladakh	Valley and remote areas of Leh, Kargil and Turtuk
Himachal Pradesh	Lahaul and Spiti, high altitude (1800-4200 m asl) areas of Kinnaur and adjoining areas
Jammu and Kashmir	High altitude (1800-3200 m) areas of Anantnag, Bandipura and Kupwara districts
Sikkim	High altitude (1800-4600 m) areas of West and North districts of Sikkim
Uttarakhand	Mana, Malari and Niti valley areas of Chamoli, Kedarnath valley of Rudraprayag, Dayara Bugyal and Nelong valley of Uttarakashi district, Milam valley of Pithoragarh district

and field genebank (FGB). Out of total 4,924 collected germplasm, only 2,641 accessions of cultivated *Allium* species including minor cultivated species are conserved in national gene bank, *in-vitro* repository (IVR), cryobank and field genebank (Table 2). Major part of that (1,335 accessions) comprising of *A. cepa* (584 accns.) and *A. sativum* (751 accns.) is conserved in the field gene bank at ICAR-DOGR, Pune, Maharashtra (ICAR-DOGR Annual Report, 2016-19).

(ii) *Wild Allium species:* Data analysis revealed that out of 34 wild *Allium* species reported in the country, germplasm of only 13 wild *Allium* species are conserved in gene bank, cryo genebank and field genebank (FGB) for utilization in future breeding programme of the country (Table 2). Maximum accessions are conserved in *A. przewalskianum* (20) and *A. griffithianum* (12). Meager conservation of wild germplasm in gene banks may be attributed to various reasons like niche-specificity,

Table 4. Wild *Allium* species not represented in genebanks and priority for collection

Wild *Allium* spp. and RET status	Distribution (altitudinal range)	References
A. atropurpureum L.	High altitude (2700-3400 m) areas of Himachal Pradesh (Lahaul and Spiti, Kinnaur), remote areas of Ladakh and Uttarakhand.	(Pandey *et al.,* 2008; Kew Checklist, 2020*)
A. atrosanguineum Schrenk var. *atrosanguineum*	Alampila, Gilgit and Nittar Valley (Jammu and Kashmir), remote and high altitude (2400-3100 m) areas of Himachal Pradesh	(Dasgupta, 2006; Pradheep *et al.,* 2014)
A. atrosanguineum Schrenk var. *fedschenkoanum* (Regel) G.H.Zhu & Turland	High altitude (3200-4400 m) areas of Himachal Pradesh and Jammu and Kashmir (Gilgit, Dras, Suru, Zanskar and Zojila)	(Murti, 2001; Pradheep *et al.,* 2014)
A. barsczewskii Lipsky	Kashmir Valley (Jammu and Kashmir),remote and high altitude (1900-3200 m) areas of Himachal Pradesh	(Dasgupta, 2006; Kew Checklist, 2020)
A. blandum Wall.	High altitude (2200-3600 m) areas of Himachal Pradesh, Jammu and Kashmir and Uttarakhand	(Kew Checklist, 2020)*
A. caesioides Wendelbo. Threatened	Rocky slopes from 2700-4000 m. areas of Lahual (Himachal Pradesh), Chenab Valley, Kashmir Valley and Gilgit (Jammu and Kashmir), Afghanistan and Pakistan	(Dasgupta, 2006; Pradheep *et al.,* 2014)
A. chitralicum F.T. Wang & Tang Rare	High altitude (2200-3400 m) areas of Kinnaur (Himachal Pradesh) and Gilgit (Jammu and Kashmir) and Ladakh	(Dasgupta, 2006; Murti, 2001)
A. chrysanthum Regel	Remote and high altitude areas (3700-4900 m) of Pangi (Himachal Pradesh) and Kashmir, Pajroti (Jammu and Kashmir)	(Dasgupta, 2006)
A. farctum Wendelbo.	High altitude (1900-3200 m) areas of Kalpa (Himachal Pradesh) and Jammu and Kashmir	(Dasgupta, 2006)
A. gilgiticum F.T. Wang & Tang Endangered	Remote and high altitude areas (2100-3100 m) of Gilgit, Kashmir (Jammu and Kashmir), Himachal Pradesh,. Endemic to Kashmir	(Dasgupta, 2006; Singh, 2017)
A. jacquemontii Kunth Threatened	High altitude areas (1100-3400 m) of Trilokinath (Himachal Pradesh), Rajaouri, Jammu, Kashmir (Jammu and Kashmir) and Zanskar Lahaul (Ladakh, threatened in Ladakh) and Tehri (Uttarakhand)	(Murti, 2001; Dasgupta, 2006; Pradheep *et al.,* 2014)
A. kokanicum Regel	Remote and high altitude (2200-3800 m) areas of Himachal Pradesh, Jammu and Kashmir and Uttarakhand	(Kew Checklist, 2020)*
A. loratum Baker Endangered	Remote and high altitude areas (2900-4100 m) of Himachal Pradesh, Chenab Valley, Kishtwar (Jammu and Kashmir), Nubra, Zanskar (Ladakh) and Bhaironghati (Tehri Garhwal). Uttarakhand	(Murti, 2001; Rao *et al.,* 2003; Dasgupta, 2006; Singh, 2017)
A. macleanii H.Lev.	Chenab Valley, Chamba, Kilar, Pangi (Himachal Pradesh), Kishtwar (Jammu and Kashmir).	(Dasgupta, 2006; Kew Checklist, 2020)
A. macranthum Baker Threatened	High altitude (3700-4300 m) areas of North and West districts, Lachen and Senthang (Sikkim), Tawang (Arunachal Pradesh)	(Dasgupta, 2006; Pradheep *et al.,* 2014)
A. mairei Baker	High altitude areas (2300-3200 m) of Tawang and Dichu gorge (Arunachal Pradesh) and other places in NEH	(Dasgupta, 2006)
A. oreoprasum Schrenk	Hanupata, Khaltse of Ladakh and high altitude (3700- 3900 m) areas of Jammu and Kashmir ; Zalung, Karpo pass (Himalayas)	(Dasgupta, 2006)
A. phariense Rendle Threatened	Remote and high altitude (3200-4600 m) areas of Arunachal Pradesh and other places in NEH	(Pradheep *et al.,* 2014; Kew Checklist, 2020)
A. schrenkii Regel	Remote areas (2900-4800 m) of Ladakh; Losar, Spiti and Kangra (Himachal Pradesh)	(Orrell, 2021)
A. sikkimense Baker	High altitude (3500-5200 m) areas particularly on open grassy hill sides, Cholamo, Lhonak, Naku Chu, Lachen and Tangu areas of Sikkim	(Dasgupta, 2006; GBIF, 2021)
A. spicatum (Prain) N. Friesen syn. *Milula spicata* Prain Threatened	High altitude (2900-4500 m) areas of Chamoli, Bageshwar and Pithoragarh districts of Uttarakhand	(Govaerts, 2011; Pradheep *et al.,* 2014; Kew Checklist, 2020)

*Kew Checklist, 2020 (accessed on 30.12.2020); http://wcsp.science.kew.org/prepareChecklist.do;jsessionid;

http://www.plantsoftheworldonline.org/taxon/urn:lsid:ipni.org:names:77068854-1

lack of *ex-situ* conservation protocols, rapid loss of viability, poor performance/non-suitability to climatic conditions of field gene bank at Pune and Bhowali. Asynchronous maturity and seed shattering pose great problems in collecting their sufficient number of seed for conservation and regeneration.

Out of 80 accessions, only 67 accessions of wild *Allium* species are conserved (Table 2) in national

genebank, *in-vitro* repository, cryobank and field genebank. Among these, maximum accessions (50) are conserved in the FGB at ICAR-NBPGR, Regional Station, Bhowali, Uttarakhand. Besides these, the ICAR- Directorate of Onion and Garlic Research (ICAR-DOGR), Pune, Maharashtra reported that 139 accessions of 17 wild *Allium* species were conserved in their FGB (ICAR-DOGR Annual Report, 2016-17).

C. *Diversity Mapping of Cultivated Species*

GIS-based grid mapping technique has proved to analyze species richness, assessment of variability and occurrence of trait-specific germplasm (Ramirez-Villegas *et al.*, 2010; Semwal *et al*., 2018). The GIS mapping using diversity indices have identified species rich areas in collected accessions of different cultivated species with different colour grids and Shannon diversity (H) values. In cultivated *Allium* species, dark red coloured grids (H= 1.196-2.00) represent regions with high diversity/more number of species (*A. cepa. A. sativum, A. ampeloprasum*, *A. chinense, A. hookeri* and *A. tuberosum)* collected from these sites; yellow to orange colour (H=0.00-0.598) areas represent regions with occurrence of moderate number of species (*A. proliferum, A. porrum, A. cepa* var. *aggregatum, A. cepa var. viviparum*), while dark green to light green (H=0.00-0.598) areas represent regions with occurrence of minimum species (*A. fistulosum*, *A. cepa, A. sativum*) from these collection sites (Fig. 2). In a map of country level like India, which has 3.28 million km^2 areas, it is very difficult to identify diversity hot-spots, this technique has identified high/low diversity areas in a very short time for ease of understanding of researchers and explorers to plan further collection. The geo-referenced map of collected diversity also indicated that parts of western plains (mainly Gujarat and Maharashtra); western Himalaya (Himachal Pradesh and Uttarakhand) and Telangana had extensive collections for major cultivated species.

D. *Diversity Mapping of Wild Allium Species*

Similar to cultivated species, geospatial software (DIVA-GIS) was used to generate diversity map of wild species to demarcate areas vis-à-vis species richness. Dark red colour (H= 1.491-2.0) grid on the map is showing maximum number of wild *Allium* species (*A. humile, A. roylei, A, stracheyi* and *A. wallichii*) collections from the high altitude areas of Uttarakhand and Himachal Pradesh. The second species-rich (*A. humile, A. roylei*) area has comparatively low value (H=1.118 -1.491) of Shannon diversity depicted with orange colour grid, displayed in Leh region of Ladakh and northern region of Himachal Pradesh (Fig. 3). This revealed that high altitude areas/districts of Himachal Pradesh and Uttarakhand adjoining to the border areas would form the target for future exploration and collection through fine grid survey. Diversity map has also showed that most of the wild *Allium* species are distributed in high altitude areas of Arunachal Pradesh, Himachal Pradesh, Jammu and Kashmir, Ladakh, Sikkim and Uttarakhand. Most of these species have meager representation in the NBPGR collections.

Based on high Shannon diversity value (H=1.491-2.0) for the Western Himalaya region, literature survey (sites surveyed and visited) and availability of maximum number of species in Malari-Niti valley (a part of Nanda Devi Biosphere Reserve) may be a probable *in-situ* conservation site for wild *Allium* species. Similar site for *Citrus* spp. was located and established as citrus gene sanctuary in Garo hills, Meghalaya by ICAR during 1981 based on availability of maximum citrus species represented in that area for *in-situ* conservation (Singh, 1981). Alpine meadows (locally known as *Bugyals*) in Himalayas are home to the several tuberous plant species including *Alliums*. Hence, there is a need for extensive survey of temperate, sub-alpine and alpine regions of Himalayas for this purpose.

E. *Gaps in Germplasm Collection and Conservation*

Based on germplasm collections data of cultivated and wild *Allium* species, their distribution, diversity mapping through GIS grid method, inputs from floristic and relevant literature, the gaps were identified with detail description of distribution and altitudinal range (Table 3).

F. *Gaps in Collection-germplasm of Wild Allium Species not Represented in Genebank*

Analysis has revealed that twenty one wild *Allium* species are not represented in any of the gene banks (table 4) and need to be explored and collecting on priority. Majority of these species have origin in Central Asia, extended to Iran, Afghanistan, Pakistan and Himalayas in India. Reports on availability of these species in Western Himalayas (WH), eastern Himalaya (EH)/ north-eastern hill (NEH) region are scanty, mostly mentioned by explorers, botanists and others on floristic surveys, which generally have not collected for the purpose of

germplasm conservation and use. These reports have insufficient information on their locations, altitudinal range, frequency and population density. In most of the cases, their distribution is reported like WH, EH or Himalayas, which covers 5 lakh km^2 (about 16.2% of country's total geographical area) in three states in WH and seven states in NEH including Sikkim. Hence, it is very difficult to pin-point their specific locations. There is drastic loss in habitat and species composition in past decades due to increase in frequency of erratic rainfall and cloud burst in Himachal Pradesh and Uttarakhand would be affecting their niche habitat and population. Climate change is adversely affecting all the temperate species of the Himalayas. Now it is an urgent need to conduct *Allium* specific explorations in Himalayan region and report their current status on availability as well as rare, endangered and threatened (RET) status of these twenty one species.

Conclusions

Significant amount of germplasm samples of cultivated *Allium* species have been assembled from all over the country, still there are gaps in lesser cultivated areas and different agro-ecological zones. *Allium cepa* being cross pollinated crop, a large variability developed naturally through introgression and honey bee pollination, while collection gaps exist in wild and less-known *Alliums* in the Himalayan region. *Allium* species as revealed through diversity mapping using GIS tools, the following conclusions are:

- Prioritized and unattended taxa need to be explored to collect and conserve on priority
- Prioritization of sites/ areas for collecting wild *Allium* species through specific exploration mission.
- Identification of areas/sites suitable for *Allium* gene sanctuary to facilitate *in-situ* conservation, multiplication, evaluation studies of collected germplasm.
- Need to study the reproductive biology of rare/ endangered taxa- *A. stracheyi, A. wallichii, A. auriculatum, A. humile* and *A. roylei*.
- Multiplication and development of protocols for conservation in cryo/in-vitro repository of *A. przewalskianum, A. stracheyi, A. wallichii* and *A. auriculatum.*

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RESEARCH ARTICLE

Germplasm Access from ICAR-NBPGR and Use within India

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Plant genetic resources for food and agriculture support the livelihoods of every person and encompass the diversity of genetic material. Rapid progress in the field of agriculture was witnessed in the last three decades of this century with respect to collection, conservation, exchange and sustainable utilization of PGR (http://www.fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/conservation/en/). At the national level, the ICAR-NBPGR is the nodal institution for the management of PGR under the umbrella of the Indian Council of Agricultural Research (ICAR), New Delhi. The ICAR-NBPGR has developed a very strong Indian Plant Germplasm Management System which operates in a collaborative and partnership mode with other organizations. The system has contributed immensely towards safeguarding and exchanging the PGR from other countries for enhancing the agricultural production and productivity in the country. ICAR-NBPGR is also serving the needs of researchers for various crop improvement program through supply of the desired germplasm from National Genebank and from active collections maintained at regional stations in different agro-climatic zones of the country. National Active Germplasm Sites (NAGS) are effective partners in collaborating with ICAR- NBPGR for meeting the requirements of researchers in the country. The present study was undertaken to learn more about the use and distribution of germplasm accessions, which may help to assess the areas of constraint and hence, to encourage policies to enhance germplasm use/utilization.

Key Words: Distribution, Exchange, India, NBPGR, PGR, Use

Introduction

Plant genetic resources (PGR) are the biological basis of world food security and, directly or indirectly, support the livelihoods of every person on Earth. PGRFA encompass the diversity of genetic material in traditional varieties and modern cultivars, as well as crop wild relatives and other wild plant species used as food. Plant domestication produced numerous landrace populations that served as the founder material for further genetic improvement through more recent selective breeding. (Bradshaw, 2017). In fact, most of the contemporary crop varieties descend from a relatively small number of founder landraces. Exchange of PGR and their utilization is a continuous process. This exchange of germplasm has benefited agriculture across the globe. The exotic and indigenous germplasm offer enormous opportunity for addressing the needs of the breeders/ researchers for developing varieties resistant to various pests and diseases and to improve quality, quantity and other value addition traits. There is continuous search for newer resources to meet the future demands that arise with the emergence of climate change, new diseases, and enhanced demands food and nutritional security (De Jonge, 2009). ICAR-NBPGR is the nodal institution under Indian Council of Agricultural Research (ICAR), New Delhi for the management of PGR. NBPGR works with the mandate for promotion of sustainable use, of PGR and policy issues. NBPGR operates in collaboration mode and in strong partnership mode with other organizations. Since its establishment, NBPGR has continually contributed significantly towards import and exchange of germplasm from over 150 countries for further utilization in crop improvement programmes. To understand the extent of use/ utilization of exotic as well as indeigenously collected germplasm, the study was undertaken. The study also reflects on the constraints in accessing the germplasm from National Gene Bank or National Active Germplasm Sites so that the mechanisms may be developed to encourage the access regulations and their further us and distribution.

Any researcher/user in India if needs to access seed or planting material from other countries, the germplasm must be introduced/ imported following the Plant Quarantine (Regulation of Import) Into India, Order 2003. The Director of the National Bureau of Plant Genetic Resources (NBPGR) is authorized to issue an

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import permit for the purpose. However, to access the germplasm from NBPGR very simple procedure is laid out.

Materials & Methods

Access at national level is based on the provisions of Biological Diversity Act, (BDA), 2002 and Rules (2004). The request for supply of germplasm in small quantities and only for research purposes are being considered by Director, ICAR-NBPGR. The indentor is desired to submit its request in requisition proforma for supply of seed/ planting material in small quantities (GEX 01). The applicant is also required to fill in and submit the duly signed Material Transfer Agreement for research use within India for public and private entities (MTA). The two documents are available at NBPGR website. NBPGR arranges for the supply of germplasm germplasm maintained in network mode from its regional stations and other National Active Germplasm Sites (NAGS), where the active collections are held. If the desired material are available at ICAR-NBPGR, they are collected and forwarded to the indentor, or else the requests are forwarded to various sources in India including NAGS and the material thus procured is forwarded to the indentor. The material is always transferred under a Material Transfer Agreement, though the practice of sending materials using the Standard Material Transfer Agreement (SMTA) under the International Treaty is still rare. Since 1976 a total of 5,04,679 samples are supplied from NBPGR within country for use by researchers. For this study the documented information was analyzed from year 2014 to 2019. The data was assembled for this study through the records/ online database of Germplasm Exchange Unit and compiled by the author. All information kept as records in NBPGR. NBPGR receives large number of requests and they are serially registered in ledger books).

Results & Discussion

In the period of five years from 2014 -19, a total of seventy five thousand six hundred and twenty two (75, 622) accessions were distributed to researchers in 190 crops within the country. For the supply of seed/planting material nearly 90% of the requests were met by NBPGR, New Delhi and its regional stations at Akola, Cuttack, Bhowali, Ranchi, Jodhpur, Hyderabad, Shimla, Srinagar, Shillong and Thrissur and for the rest 10% NAGs played active role in meeting the demands of the researchers. These samples were supplied against 2055 requests registered during the period. Large number of requests are receied by NBPGR. There is a prescribed proforma (GEX01) for requisition of seed/ planting material. The indentor is required to fill in all details relating to the name of crop, number of accessions/ samples requested and type of study to be carried out. These proformas were studied and Based on the frequency of requests received for a particular crop and the based on the number of samples supplied a rank list was prepared which indicated information on the number of times the crop was requested by different institutes thus giving information on the top scorer crop the research is being carried on. According top 25 requests for different crops were ranked for the frequency of request and another 25 based on number of samples supplied (Table 1 & 2).

Earlier the seed material was supplied by ICAR-NBPGR to private sector based on their specific requests, however after the enactment of Biological Diversity Act, 2002, the requested were regulated as per the provisions of BDA, 2002. In 2017, a revision in the MTA (reference) was brought into effect and procedures laid out and 544

Table 1. Top 25 crops based on the number of requests received (2014-2019)

Crop	No of requests registered	Rank
Tomato (*Solanum* sp.)	137	1
Rice (*Oryza* sp.)	126	2
Okra (*Abelmoschus* sp.)	125	2
Brinjal (*Solanum melongena*)	77	4
Chilli (*Capsicum annuum*)	99	5
Wheat (*Triticum* sp.)	95	6
Bitter gourd (*Momordica charantia*)	68	7
Maize (*Zea mays*)	66	8
Mungbean (*Vigna radiata*)	59	9
Cowpea (*Vigna unguiculata*)	58	10
Cucumis (*Cucumis melo*)	56	11
French bean (*Phaseolus vulgaris)*	52	12
Chickpea (*Cicer arietinum*)	51	13
Mustard (*Brassica juncea*)	49	14
Urd bean (*Vigna mungo*)	48	15
Amaranth (*Amaranthus tricolor*)	42	16
Pigeonpea (*Cajanus cajan*)	36	17
Pea (*Pisum sativum*)	33	18
Chenopodium (*Chenopodium quinoa*)	32	19
Barley (*Hordeum vulgare*)	29	20
Lentil (*Lens culinaris*)	27	21
Cluster bean (*Cyamopsis tetragonoloba*)	23	22
Bottle gourd (*Lagenaria ciceraria)*	23	23
Buckwheat (*Fagopyrum esculentum*) & rice bean (*Vigna umbellata)*	22	24
Onion (*Allium cepa*)	21	25

Table 2. Top 25 crops based on number of samples supplied (2014-2019)

Crop	Number of samples supplied	Rank
Wheat	12216	1
Chickpea	8683	2
Okra	3445	3
Rice	3213	4
Rice bean	2424	5
Pigeonpea	2305	6
Chilli	2287	7
Tomato	2237	8
Maize	2183	9
Brinjal	2133	10
Sesame	2078	11
Finger millet	1900	12
Mustard	1636	13
Horsegram	1394	14
Urdbean	1351	15
Cowpea	1333	16
Frenchbean	1314	17
Amaranth	1302	18
Mungbean	1285	19
Soybean	1170	20
Pea	1145	21
Barley	1144	22
Lentil	1111	23
Foxtail millet	1102	24
Barnyard millet	1024	25

samples were supplied to Indian private seed companies in 2017-18 (Table 3). The types of users (users submit their requests in a prescribed proforma which have all the details of the user of the seed/ planting material) who submit requests for germplasm are mainly plant breeders, researchers, students engaged in research activities.

Although, NBPGR conserves a vast repository of novel genes that may be utilized in breeding new crop varieties, mostly the requests are not very specific in nature. On the basis of the requests submitted, the access is mainly for carrying out biochemical analysis, molecular characterization, phyto-chemical evaluation, screening, evaluation, breeding and for grafting studies. Total number of samples supplied for research purposes from NBPGR and other National Active Germplasm Sites and the number of samples supplied in different crop are shown in Figure 1 and Figure 2. Analysis of recipient groups exhibit that 45% of the total samples were received by students of State Agriculture Universities (SAU's) followed by scientists of ICAR institutes (41%), traditional/ central universities (11%), private and other government institutions (1%). The distribution

Table 3. List of Private Seed Companies which received seed material in different crops (2017-2019)

Indentor	Crop
Ambrocia Seed Producer Company Ltd.	Wheat
Ananya Seeds Private Limited,	Brinjal, Tomato, Chilli
Arizona Seeds Private Limited,	Tomato
Arjuna Natural Extracts Ltd	Amaranth
Basant Agro Tech (I) Ltd.,	Soybean
Daftari Agro Bio-tech Pvt.,	Ethiopian mustard
Eagle Seeds & Biotech Ltd	Wheat
M/s ACSEN Hy. Veg. Private Ltd.,	Onion, Carrot, Cauliflower
Noble Seeds Private Limited	Okra
Nuziveedu Seeds Limited,	Mustard, Wheat
Pahuja Seeds Private Limited	Cucumber
Rasi Seeds (P) Ltd.s	Cotton, Wheat, Rice
Seed works Seed Works International Private Limited	Mustard
Shreeoswal Seed and Chemical Ltd.,	Wheat, Mustard, Triticale
Somani Kanak Seedz Pvt. Ltd.	Bottle gourd, Sponge gourd, Brinjal
Tierra Seeds Science Pvt. Ltd.,	Mustard
VNR Seeds Pvt Ltd	Bitter gourd, Tomato, Okra

is depicted in Figure 3. More or less similar type of study was also carried out by Bonham *et al.* (2010) on Plant Genetic Resources and Germplasm use in India depicting breeder's approaches to germplasm acquisition, accessing information about germplasm and benefits associated with germplasm use.

Feedback on the Use of Germplasm

It is always pertinent to know about the performance and utilization of the material sent to indenters. While sending the material, a feedback form is also being attached which includes reference number, crop name, accession number, purpose of request, information about establishment of material, seed supplied back to Genebank, details of utilization in experiment/ crop improvement and publication, if any. Most of the indenters send duly filled feedback form but did not mention performance/ utilization of the germplasm received. However, some of the indenters send full details of the material and readily use them in their breeding programme while some also send enough quantity of multiplied seeds for deposition in Genebank.

Some examples of feedback received for the germplasm supplied during 2016 and 2017 are described here. Wheat lines imported from UK were established well and are being utilized for tilling. Four genetic

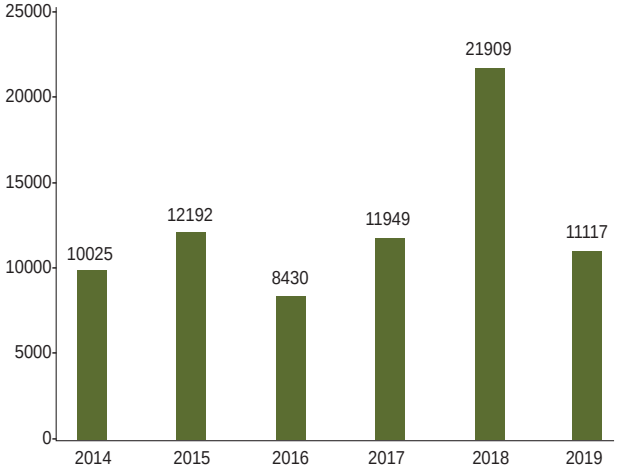

Fig. 1. Total number of samples supplied to researchers within country from ICAR-NBPGR from its Headquarter at Delhi and Regional Stations (2014-2019)

stocks of wheat. On the basis of APR and SRT data, promising stem rust resistant genotypes were selected for use in crossing programme to target novel rust resistance genomic regions. Crosses were attempted using prominent Indian wheat genotypes like DPW621-50, HD2967, DBW14, HUW510, HI977 and PBW343 to introgress Sr39 gene from exotic source HR22 (Hartog) (feedback from ICAR-IIWBR, Karnal and ITC, Bangalore).

Five wild species of okra high degree of resistance to *Yellow vein mosaic virus* (YVMV) and *Okra enation leaf curl virus* (OELCV). The lines will be further utilized for interspecific gene transfer for resistance to YVMV and OELCV. All the wild derived materials having *A. mizoramensis* sp Nova as male parent showed high degree of resistance to both these diseases (feedback from ICAR-IIVR, Varanasi). Bottlegourd and sponge gourd indigenous collections showed good variability in fruit shape and are being utilized in breeding programme (feedback from. Accession IC49581 of *Catharanthus roseus* was found promising under salt stress condition (feedback from Delhi University).

Imported *Vasconcellea qercifolia* is resistant to papaya ringspot virus (PRSV); *V. pubenscens* is reported to immune to PRSV, but it is cross incompatible with Papaya. *V. parviflora* is susceptible to PRSV but it is compatible with *V. pubenscens.* Therefore, it can be a good bridge species to transfer PRSV resistance gene from *V. pubescens* to papaya (feedback from ICAR-IARI, New Delhi). Though some of the indenters are sincerely doing their job in keeping the track of material

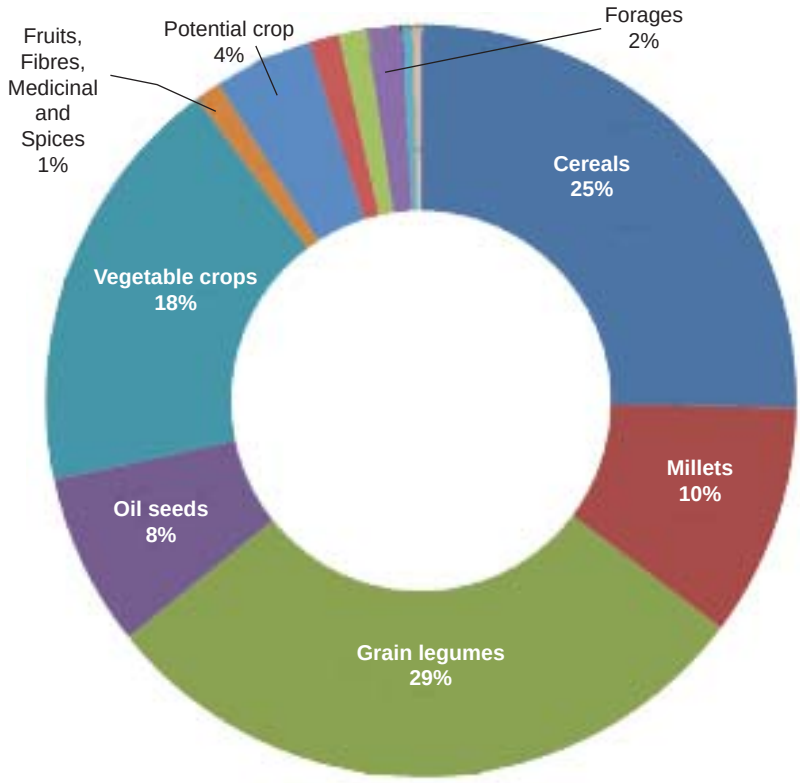

Fig. 2. Number of samples supplied in different crop groups (2014-2019)

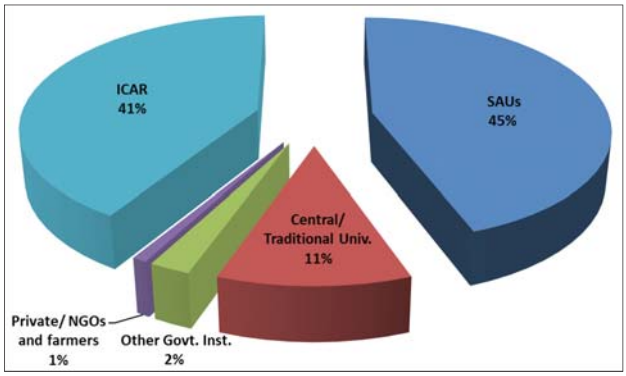

Fig. 3. Germplasm distribution from NBPGR to different Recipient Groups (2014-19)

supplied, all the indenters should follow the same making it a success story. Feedback information received on establishment of hing accessions is a success story (Fig. 4).

Superior quality & best tasting berries of seabuckthorn and Monk Fruit (EC938819) a new introduction from China is established at Institute of Himalayan Bioresource Technology (IHBT), Palampur (Fig. 5)

ICAR-NBPGR has been playing the pivotal role in germplasm exchange among countries as well as catering to the needs of researchers/users within country, meeting their demands of desired genetic resources. A large number of wild species/crop wild relatives are also

Fig. 5. Monk fruit established at IHBT, Palampur

Fig. 4. Heeng accessions introduced first time from Iran established at Institute of Himalayan Bioresource Technology, (IHBT), Palampur

being conserved which at National Genebank which are finding their routes to the crop improvement programmes in different crops.

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RESEARCH ARTICLE

Morphological Characterization of 58 Chilli Genotypes

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Chilli is an important vegetable and condiment crop having immense commercial and therapeutic value with great export potential. Current research was aimed to characterize resolving power of morphological traits for reliable identification of 58 chilli accessions using 25 morphological descriptors. All the characters genotypes showed a wide range of variation. UPGMA based clustering using morphological markers distributes all genotypes into three separate major clusters and six sub clusters with unique traits specific genotypes in each. Fruit calyx cover, fruit neck (basal end) and stem pubescence were the most prominent descriptors as that were showing highest PIC value. High discriminating power of number of petals and anthers was found in our study.

Key Words: Chilli, Diversity, DUS, Morphotypes, Variability

Introduction

Chilli (*Capsicum annuum* L.) is an important vegetable and condiment crop having immense commercial and therapeutic value with great export potential (Kaur *et al*. 2018); also known as bird pepper, cayenne, paprika, hot and sweet pepper belongs to the genus *Capsicum* of Solanaceae family, subfamily Solanoideae and tribe Capsiceae (Hunziker, 2001; Knapp *et al*., 2004). It is a diploid (2n = 2X = 24), annual or short-lived perennial herb with several cultivated forms. The Genus *Capsicum* consists of approximately 22 wild and 5 cultivated species, which includes *C. annuum*, C. *baccatum*, *C. chinense*, *C. frutescens*, and *C. pubenscens*. Molecular analysis confirmed that the center of domestication of *C. annuum var. longum*, the cultivated variety, is the upland region of central-eastern Mexico (Loaiza Figueroa *et al.,* 1989), while Guatemala is considered as a secondary centre of origin (Salvador, 2002). In the world, the production of Chilli in green form is about 7 to 8 million tons and 2 to 3 million tons in dry form. India is the largest producer of Chilli in the world accounting for 1.1 million tons of production annually (Rahevar *et al.* 2019).

With the introduction of Indian Legislation Protection of Plant Varieties and Farmers Rights Act (PPV and FRA, 2001), the release of new crop varieties is possible only if it is distinct (D) from other varieties, uniform (U) in their characteristics and generally stable (S) over the time (DUS). To identify cultivars, standardized descriptor list based on morphological traits developed by the International Union for the Protection of New Varieties of Plants (UPOV) was used as published in the Guidelines for the Conduct of Tests for Distinctness, Uniformity and Stability (UPOV 2006; available online at: www.upov.int/edocs/tgdocs/en/tg0 76_08.pdf). The UPOV system of plant variety protection based on individual test guidelines represent an agreed and harmonized approach for the examination of new cultivars of a species of interest. Morphological characters of both qualitative and quantitative have long been used to identify species and to discriminate between varieties. DUS study based on morphological characters is carried out with the strident visual observations in the field during seedling, vegetative and reproductive stages, but it is an expensive and time-consuming process and the purity of seed will be known only after the seed harvest. There is no general rule for cultivar identified or rejection purely by examining only seed or morphological characters in the field. Therefore, for keeping the purity of cultivars, stable visual diagnostic characters of seed, seedling, and plant morphology are utmost essential to know (Lalitha, 2007). Keeping this in view, the present investigation was carried out to differentiate fifty-eight chilli genotypes based on morphological characters.

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Table 1. Details of genotypes and their sources

Genotypes	Source	Genotypes	Source	Genotypes	Source
ACGP – 2	A.A.U., Anand, Gujarat	ACGP-74	A.A.U., Anand, Gujarat	GAVC – 112	A. A. U., Anand,
ACGP –7		ACGP –76		Anugraha	N. A. U., Navsari, Gujarat
ACGP –10		ACGP –78		Byadagi Dabbi	
ACGP –15		ACGP –84		Ajeet-6	
ACGP –19		ACGP –88		Arka Abhir	
ACGP –25		ACGP –96		DCL-2	
ACGP –26		ACGP –99		PC-56	
ACGP –27		ACGP –111		Kashi Anmol	I.I.V.R., UP.
ACGP –29		ACGP –112		Mathania Type – 1	C.I.A.H, RJ.
ACGP –37		ACGP –113		Arka Lohit	I.I.H.R., KA.
ACGP –38		ACGP –119		Arka Suphal	
ACGP –46		ACGP –125		Jaweri Vani	Nipani, KA.
ACGP –48		ACGP –129		Gondal Dhholar	Gondal, GJ.
ACGP –49		ACGP –130		US Agri 702	
ACGP –50		ACGP –134		Seedco – 202	Anand (Pvt.), GJ.
ACGP –57		ACGP –135		Gujarat Chilli – 1	S. D. A. U., GJ.
ACGP –58		AVNPC – 131		Gujarat Chilli – 3	
ACGP –66		GVC – 101		Local Selection	Modasa, GJ.
ACGP –67		GVC – 111			
ACGP –69		GVC – 121			

Materials and Methods

Plant materials: Fifty-eight diverse chilli accession (Table 1) collected from different research stations were evaluated at the Main Vegetable Research Station, Anand Agricultural University, Anand during the late rainy season in 2017.

Field experiments: The thirty-five days old seedlings were transplanted using 60.0 cm × 60.0 cm plant to plant and row to row distance using a randomized complete block design. Data on twenty-five morphological characters such as plant habit, plant spread (cm), stem pubescence, stem shape, length of leaf blade, width of leaf blade, plant anthocyanin colouration of nodes, leaf colour, leaf shape, petal colour, anther colour, flower orientation, fruit orientation, fruit bearing habit, fruit colour (mature stage), fruit curvature, fruit neck (basal end), fruit shape of apex, fruit sinuation of pericarp, fruit shape at the base, fruit calyx cover, fruit calyx margin, fruit calyx constriction, stigma length, and number of petals and anthers etc., were recorded on five randomly selected plants.

Cluster analysis: The qualitative trait data were subjected to cluster analysis. Genetic association between genotypes was evaluated by calculating the similarity matrix coefficient for pairwise comparisons based on the morphological characters using software power marker 3.25; Euclidean distance was calculated and a dendrogram was constructed using the unweighted pair group method on arithmetic average (UPGMA).

Results and Discussion

Morphological Characters

Twenty-five morphological characters of fifty-eight chilli genotypes were characterized. All the traits were recorded and genotypes were classified based on phenotypic observations following DUS guidelines specified by Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA) of India.

Plant Habit: In accordance with plant habit, fifty-eight genotypes were categorized into three different classes as spreading, semi-upright and upright plant growth habit with 19, 13 and 26 genotypes in each class, respectively. GVC – 101, GVC – 121, byadagi dabbi, arka abhir and kashi anmol were found to have a spreading type of growth habit, whereas DCL-2, PC-56, jaweri vani, gondal dhholar and gujarat chilli–1 were observed with semi upright growth habit. AVNPC – 131, GVC – 111, GAVC – 112, anugraha, ajeet-6, arka lohit, arka suphal and gujarat chilli–3 were observed with upright plant growth habit. Similar classes concerning plant growth

habits were reported by Farwah *et al.* (2019), Padma *et al.* (2017), Sood *at al.* (2011), Sudre *et al.* (2010) and Manju and Sreelathakumary (2002).

Plant Spread: Fifty-eight genotypes were classified into three different classes as broad, medium and narrow plant spread (cm) with 17, 22 and 19 genotypes in each class, respectively. Gujarat chilli–1, arka abhir, kashi anmol, mathania type–1, seedco – 202, GVC – 111, ajeet-6 and arka lohit were found having broad plant spread, whereas PC-56, jaweri vani, gondal dhholar, GVC – 121, byadagi dabbi, US Agri 702, local selection, AVNPC – 131, GAVC – 112, arka suphal and gujarat chilli–3 were observed with medium plant canopy spread. DCL-2, GVC – 101 and anugraha were observed with narrow plant spreading habits. Farwah *et al.* (2019) observed the same result concerning plant spread.

Stem Pubescence: Based on stem pubescence, fifty-eight genotypes were categorized into two altered sets as presence and absence of stem pubescence with 35 and 23 genotypes in each set, respectively. Stem pubescence was present in gujarat chilli–1, arka abhir, mathania type–1, seedco – 202, GVC – 111, ajeet-6, arka lohit, PC-56, gondal dhholar, GVC – 121, AVNPC – 131 and GAVC – 112, whereas absent in kashi anmol, jaweri vani, byadagi dabbi, US Agri 702, local selection, arka suphal, gujarat chilli–3, DCL-2, GVC – 101 and anugraha. Similar variation along with two different classes for stem pubescence was observed by Farwah *et al.* (2019), Padma *et al.* (2017), Sood *at al.* (2011) and Manju and Sreelathakumary (2002).

Stem Shape: Stem shape classified fifty-eight genotypes into two classes as round and angled with 36 and 22 genotypes in each class, respectively. Stem shape was round in jaweri vani, US Agri 702, local selection, arka suphal, gujarat chilli–3, DCL-2, gujarat chilli–1, Mathania type–1, seedco – 202, GVC – 111, arka lohit, PC-56, gondal dhholar, GVC – 121, AVNPC – 131 and GAVC – 112, whereas angled in kashi anmol, byadagi dabbi, GVC – 101, anugraha, arka abhir and ajeet-6. A similar result for stem shape was observed by Farwah *et al.* (2019) and Sood *at al.* (2011).

Length of the Leaf Blade: Following the length of the leaf blade, fifty-eight genotypes categorized into three different classes as long, medium and short with 6, 47 and 5 genotypes in each class, respectively. GVC – 101, anugraha, ACGP –10, arka suphal, gujarat chilli–1 and GAVC – 112 were found having long leaf blade, whereas kashi anmol, byadagi dabbi, arka abhir, ajeet-6, jaweri vani, US Agri 702, gujarat chilli–3, DCL-2, GVC – 111, arka lohit, PC-56, gondal dhholar, GVC – 121 and AVNPC – 131 were observed with medium length of leaf blade. ACGP –111, local selection, mathania type–1, seedco – 202, ACGP –15 were observed with a short length of leaf blade. Farwah *et al.* (2019) observed the same result with respect to plant spread.

Width of Leaf Blade: Fifty-eight genotypes were categorized into three different classes as broad, medium and narrow width of leaf blade with 1, 19 and 38 genotypes in each class, respectively. Broad width of leaf blade was observed for genotype ACGP – 10, whereas arka suphal, gujarat chilli–1, GAVC – 112, ajeet-6, US Agri 702, gujarat chilli–3, arka lohit and GVC – 121 were observed with medium width of leaf blade. GVC – 101, anugraha, kashi anmol, byadagi dabbi, arka abhir, jaweri vani, DCL-2, GVC – 111, PC-56, local selection, mathania type–1 and seedco – 202 were observed with narrow width of leaf blade. Farwah *et al.* (2019) observed the same result with respect to width of leaf blade.

Plant Anthocyanin Coloration of Nodes: Plant Anthocyanin coloration of nodes was the visual assessment by a single observation on a group of plants. Fifty-eight genotypes categorized into two different classes as present and absent with 37 and 21 genotypes in each class, respectively. Plant Anthocyanin coloration of nodes was present in AVNPC – 131, GVC – 121, anugraha, byadagi dabbi, ajeet-6, PC-56, kashi anmol, mathania type–1, arka suphal, jaweri vani and gujarat chilli–1, whereas absent in GVC – 101, GVC – 111, GAVC – 112, arka abhir, DCL-2, arka lohit, gondal dhholar, gujarat chilli–3 and local selection. Similar variation along with two different classes for stem pubescence was observed by Farwah *et al.* (2019), Padma *et al.* (2017), Sudre *et al.* (2010) and Manju and Sreelathakumary (2002).

Leaf Colour: Leaf colour was green for all the fifty-eight genotypes, so all the genotypes were fallen in the same class. Farwah *et al.* (2019), Padma *et al.* (2017), Sood *at al.* (2011) and Manju and Sreelathakumary (2002) also have a similar result.

Leaf Shape: In accordance with leaf shape fifty-eight genotypes categorized into three different classes as broad elliptic, lanceolate and ovate type of leaf shape with 6, 34 and 18 genotypes in each class, respectively.

GVC – 101, ACGP –67, AVNPC – 131 and US Agri 702 were found having the broad elliptic type of leaf shape, whereas GVC – 111, GAVC – 112, arka abhir, DCL-2, arka lohit, gujarat chilli–3, local selection, GVC – 121, byadagi dabbi, ajeet-6, kashi anmol, mathania type–1 and seedco – 202 were observed with lanceolate type of leaf shape. Gondal dhholar, anugraha, PC-56, gujarat chilli–1 were observed with the ovate type of leaf shape. Similar classes with respect to leaf shape were reported by Farwah *et al.* (2019), Padma *et al.* (2017) and Sood *at al.* (2011).

Petal Colour: Following petal colour fifty-eight genotypes categorized into three different classes as purple, white and yellow green petal colour with 2, 55 and 1 genotypes in each class, respectively. ACGP –15 and ACGP –29 were found having purple petal colour, whereas GVC – 101, AVNPC – 131, US Agri 702, GVC – 111, GAVC – 112, arka abhir, DCL-2, arka lohit, gujarat chilli–3, local selection, gondal dhholar, anugraha and PC-56 were observed with white petal colour. ACGP –129 was observed with yellow green petal colour. Farwah *et al.* (2019) observed the same result with respect to petal colour.

Anther Colour: In keeping with anther colour fifty-eight genotypes categorized into four different classes as green, pale blue, purple and yellow anther colour with 8, 44, 5 and 1 genotypes in each class, respectively. DCL-2, GVC – 121, ACGP –10, ACGP –50, ACGP –130 and ACGP –129 were found having green anther colour, whereas GVC – 101, AVNPC – 131, US Agri 702, GVC – 111, GAVC – 112, gondal dhholar, anugraha, PC-56 and gujarat chilli–1 were observed with pale blue anther colour. Genotypes with purple anther colour were ACGP –29, ACGP –69, arka lohit, ACGP –66, ACGP –26, whereas genotype mathania type–1 was fall in fourth class with yellow anther colour. Farwah *et al.* (2019), Padma *et al.* (2017) and Manju and Sreelathakumary (2002) observed the same result with respect to anther colour.

Flower Orientation and Fruit Orientation: Generally, flower orientation and fruit orientation remains always alike; so we can assume one character by observing another one. Compliant with flower and fruit orientation fifty-eight genotypes were categorized into three different classes as drooping, semi drooping and erect type of flower and fruit orientation with 50, 5 and 3 genotypes in each class, respectively. Genotypes DCL-2, arka abhir, gujarat chilli–3, local selection, ajeet-6, arka lohit and mathania type–1 were observed with drooping type of flower and fruit orientation, whereas ACGP –76, ACGP –48, byadagi dabbi, ACGP –27 and ACGP –66 were fall in semi drooping type and ACGP –49, ACGP –129 and anugraha were fall in erect type of flower and fruit orientation. Similar classis with respect to flower and fruit orientation were reported by Farwah *et al.* (2019), Padma *et al.* (2017) and Sudre *et al.* (2010).

Fruit Bearing Habit: Fifty-eight accessions of chilli were classified in two distinct classes as cluster and solitary fruit bearing habit with 4 and 54 genotypes in each class, respectively. Genotypes ACGP –48, ACGP –66, ACGP –76 and ACGP –99 were found having fruit bearing habit in cluster, whereas all the other genotypes were found having fruit bearing habit of solitary. Similar variation along with two different classes for fruit bearing habit was observed by Farwah *et al.* (2019).

Fruit Colour (Mature stage): In accordance with fruit colour (Mature stage), fifty-eight genotypes were categorized into four different classes as green with 55 genotypes, while greenish white (ACGP –57), orange (ACGP –25) and purple (ACGP –29) fruit colour (Mature stage) had 1 genotype in each class. Similar classis with respect to fruit colour (Mature stage) was reported by Farwah *et al.* (2019), Sood *at al.* (2011), Sudre *et al.* (2010), Pradheep and Veeraragavathatham (2006) and Manju and Sreelathakumary (2002).

Fruit Curvature and Fruit Neck (Basal end): Observations of fruit curvature and fruit neck (basal end) were recorded by visual assessment of a group of plants which dispense fifty-eight genotypes in two different classes as presence and absence of fruit curvature and fruit neck (basal end) with 14 and 44 genotypes in each class of fruit curvature and with 35 and 23 genotypes in each class of fruit neck (basal end), respectively. Fruit curvature was absent in genotypes AVNPC – 131, GVC – 101, GVC – 121, anugraha, ajeet-6, arka abhir, PC-56 and local selection, whereas all the other genotypes have fruit curvature, whereas fruit neck (basal end) was absent in genotypes AVNPC – 131, GVC – 121, byadagi dabbi, ajeet-6, arka abhir, and gondal dhholar. Result was in accordance with findings of the Farwah *et al.* (2019), Sudre *et al.* (2010) and Manju and Sreelathakumary (2002).

Fruit Shape of Apex: In accordance with fruit shape of apex fifty-eight genotypes categorized into three different classes as acute, blunt and depressed with 43, 13 and 2

genotypes in each class, respectively. GVC – 121, byadagi dabbi, ajeet-6, PC-56, anugraha, DCL-2, kashi anmol, mathania type–1, arka lohit, gujarat chilli–1, gujarat chilli–3 and local selection were found having acute type of fruit shape at apex, whereas AVNPC – 131, arka abhir, arka suphal and jaweri vani were observed with blunt type of fruit shape at apex. ACGP –84 and ACGP –135 were observed with depressed fruit shape at apex. Farwah *et al.* (2019) and Manju and Sreelathakumary (2002) have the similar result for fruit shape at apex.

Fruit Sinuation of Pericarp: In keeping with fruit sinuation of pericarp; fifty-eight genotypes were categorized into three different classes as week, medium and strong sinuation with 36, 13 and 9 genotypes in each class, respectively. AVNPC – 131, GVC – 101, GVC – 121, GAVC – 112, ajeet-6, kashi anmol, arka suphal and local selection were found having week sinuation, whereas mathania type–1, Arka lohit, Gondal dhholar, Gujarat chilli–1 and Gujarat chilli–3 were observed with medium sinuation. Genotypes with strong sinuation were GVC – 111, anugraha, byadagi dabbi, arka abhir, DCL-2, PC-56 and jaweri vani. Farwah *et al.* (2019) observed the same result with respect to fruit sinuation of pericarp.

Fruit Shape (At the base): Fifty-eight genotypes of chilli were categorized in to three classes based on fruit shape (at the base) as acute, round and sunken with 42, 14 and 2 genotype in each class. Genotypes mathania type–1, arka lohit, byadagi dabbi, anugraha, DCL-2, ajeet-6, GVC – 101, GAVC – 112, kashi anmol, US Agri 702, seedco – 202, local selection and AVNPC – 131 were found having acute fruit shape at the base, whereas gondal dhholar, arka abhir, jaweri vani and arka suphal were found having round fruit shape at the base while genotypes PC-56 and ACGP –84 had sunken fruit shape at the base. Farwah *et al.* (2019) and Manju and Sreelathakumary (2002) have the similar result for fruit shape at the base.

Fruit Calyx Cover: Fruit Calyx Cover at the base of the fruit was a good visual character for differentiating two genotypes as enveloping and non-enveloping type. Fifty-eight genotypes of chilli were categorized in to two different classes as enveloping and non-enveloping with 35 and 23 genotypes in each class based on fruit calyx cover. Genotypes mathania type–1, arka lohit, anugraha, DCL-2, GVC – 121, ACGP –15, GAVC – 112, kashi anmol, US Agri 702, seedco – 202, local selection and AVNPC – 131 were fall in to class enveloping, whereas genotypes gondal dhholar, byadagi dabbi, PC-56, arka abhir, jaweri vani, ajeet-6, GVC – 101 and arka suphal were fall in to class non enveloping. Farwah *et al.* (2019) have the similar result for fruit calyx cover at the base.

Fruit Calyx Margin: Fifty-eight accessions of chilli were classified into two distinct classes as dented and smooth fruit calyx margin with 41 and 17 genotypes in each class, respectively. Genotypes mathania type–1, GVC – 111, anugraha, DCL-2, GVC – 121, GAVC – 112, AVNPC – 131, gondal dhholar, byadagi dabbi, PC-56, arka abhir, jaweri vani, GVC – 101 and arka suphal were found having dented fruit calyx margin, whereas all the other genotypes were found having smooth fruit calyx margin. Similar result with respect to fruit calyx margin was observed by Farwah *et al.* (2019).

Fruit Calyx Constriction: Fifty-eight genotypes categorized into two different classes as presence and absence of fruit calyx constriction with 48 and 10 genotypes in each class, respectively. Fruit calyx constriction was present in ACGP –37, ACGP –112, ACGP –25, ACGP –50, ACGP –66, GAVC – 112, AVNPC – 131, ACGP –67, ACGP –57 and ACGP –26, whereas absent in mathania type–1, gujarat chilli–1, gujarat chilli–3, GVC – 111, anugraha, DCL-2, GVC – 121, gondal dhholar, byadagi dabbi, PC-56, arka abhir, jaweri vani, GVC – 101, arka suphal, arka lohit, kashi anmol local selection and ajeet-6. Similar variation along with two different classes for fruit calyx constriction was observed by Farwah *et al.* (2019).

Stigma Length: Based on flower stigma length; chilli was classified into three different classes as short (Stigma was shorter then anther length so remains inside anther cone), medium (Stigma was same in length to anther) and long (Stigma was longer then anther so appears out of the anther cone). Compliant with stigma length fifty-eight genotypes were categorized into three different classes as short, medium and long with 24, 22 and 12 genotypes in each class, respectively. DCL-2, GVC – 121, byadagi dabbi, arka abhir, arka suphal and ajeet-6 were found having short stigma length, whereas mathania type–1, anugraha, gondal dhholar, PC-56, GVC – 101, arka lohit, US Agri 702, seedco – 202, GAVC – 112, and AVNPC – 131 were observed with medium stigma length. Sood *at al.* (2011) observed similar result for stigma length.

Number of Petals and Anthers: Based on petal and anther number, fifty-eight genotypes were categorized into four different classes as 5, 6, 7 and 8 petals and anthers with 24, 27, 6 and 1 genotypes in each class, respectively. Gujarat chilli–1, jaweri vani, kashi anmol, PC-56, DCL-2, GVC – 121 and byadagi dabbi were found having 5 petals and anthers, whereas local selection, mathania type–1, anugraha, GVC – 101, arka lohit, GAVC – 112, AVNPC – 131 and arka suphal were observed with 6 petals and anthers. Genotypes with 7 petals and anthers were ACGP –66, gondal dhholar, ACGP –96, ACGP –134, arka abhir and ACGP –25, whereas genotype Ajeet-6 was fall in fourth class with 8 petals and anthers. The number of petals and anther were serving large variability, but due to the absence of DUS guidelines to evaluate them; these characters were

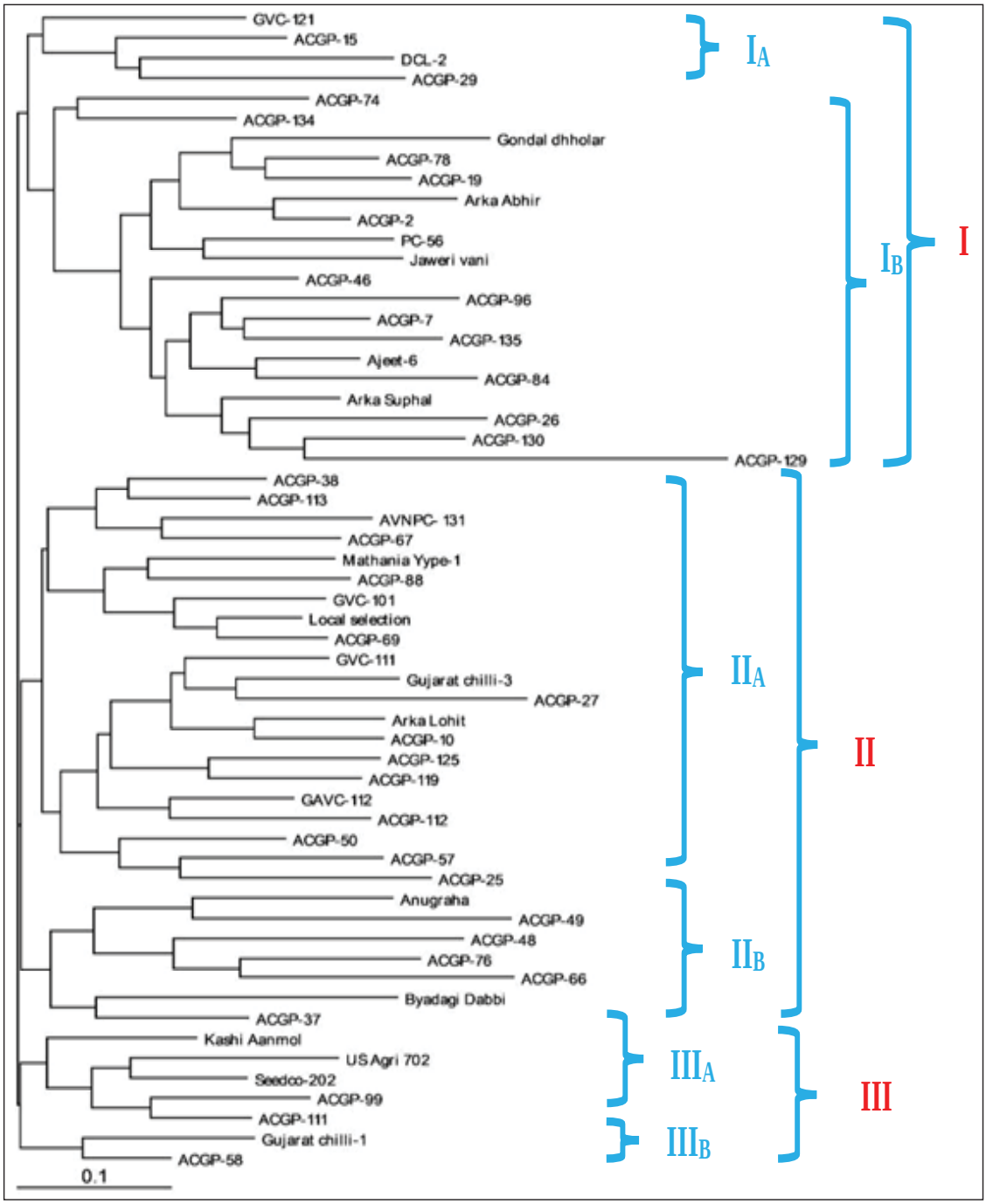

Fig. 1. Grouping of 58 chilli genotypes

not studied till today. The authority should add them and publish a proper guideline to investigate them well.

Cluster analysis: Cluster analysis based on dissimilarity matrix was performed using the UPGMA. Three clearly defined clusters have been detected (Fig. 1); representing distinct morphotypes. The dendrogram depicted 23, 21 and 14 genotypes have diverged under cluster I, II and III, respectively. Cluster I represent genotypes with lanceolate leaf shape, drooping flower orientation, drooping fruit orientation, solitary fruit bearing habit, acute fruit shape of apex, acute fruit shape at the base, dented fruit calyx margin, absence of fruit calyx constriction, short stigma length, green fruit colour (mature stage), absence of fruit curvature and 5 number of petals. Sub cluster I_A composed of 4 genotypes and represent genotypes with lanceolate leaf shape and short stigma length, whereas sub-cluster I_B consists of 19 genotypes and represents genotypes with the absence of fruit curvature. Genotypes of Cluster I_A and I_B have dissimilar fruit Calyx Cover as enveloping and non-enveloping, respectively. Cluster II contain 28 genotypes with 21 genotypes in sub-cluster II_A and 7 in II_B. Cluster II represent genotypes with white petal colour and 6 number of petals in flower. 7 out of 58 genotypes were falling under cluster III with 2 sub-clusters and 5 genotypes in sub-cluster III_A whereas 2 in sub-cluster III_B. Cluster III represent genotypes with Pale blue anther colour and presence of fruit neck (basal end). Padma *et al.* (2017) studied 11 genotypes and detected comparable output with 3 clusters.

Clusters based on distinct morphotypes unfold the evolutionary development of studied chilli. Highest euclidean (0.8443) was observed between genotypes ACGP – 129 and ACGP – 99 suggesting best diverse genotypes for hybridization program and creating transgressive segregants. Second highest distance was observed between genotype (0.8021) ACGP-129 and ACGP-66, whereas lowest distance (0.1266) was observed between ACGP – 69 and local selection, suggesting most similar genotypes among all the studied genotypes.

A total of twenty-five phenotypic markers were taken under consideration; as each phenotypic variable was a one selection marker for varietal identification. Fruit calyx cover, fruit neck (basal end) and stem pubescence were the most prominent descriptors as that were responsible for showing the highest PIC value (0.3641) followed by stem shape (0.36) and plant anthocyanin coloration of nodes (0.3553), whereas lowest PIC (0.00) was observed for green leaf colour. All the descriptors were well explanatory for available diversity in the germplasm understudy with high (0.7774) mean major allele frequency and mean allele number (2.68), whereas low mean PIC (0.2437) value in the study suggests either to use of more descriptors or elimination of extra descriptors with poor discriminating power from the study.

Conclusion

It was concluded that the fifty-eight chilli genotypes could be effectively distinguished by its' morphological characters based as twenty-five characters.

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RESEARCH ARTICLE

Characterization, Diversity Analysis and Stability Testing of Extant Tomato Cultivars for Pheno-morphological Traits

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Tomato (*Solanum lycopersicum* L.), is cultivated globally. Its cultivation faces several problems such as shrinking genetic diversity, morphological variability and stability. Therefore, a study was conducted to characterize, classify, assess the diversity and test stability in 100 extant cultivars of tomato for 35 pheno-morphological traits. Data were recorded on the basis of distinctiveness, uniformity and stability test guidelines of tomato. All the cultivars exhibited distinct and uniform characters. The 100 cultivars of tomato were grouped into five major clusters based on their characteristics in the coefficient range of 0.48-1.00. In the stability test analysis, interaction of cultivars and environment was significant for various morphological characteristics. These traits were stability in most of the cultivars across different environments. The characterized pheno-morphological traits in study would be helpful for creating a database on tomato.

Key Words : DUS testing, Genetic diversity, Morphological traits, Stability analysis, Tomato

Introduction

Tomato (*Solanum lycopersicum* L.), is cultivated globally as annual and a well-studied crop for variety development (Peralta and Spooner, 2000). It belongs from large and diverse family of *Solanaceae*, which have more than three thousand species (Bauchet and Causse, 2012). Today, a drastic reduction found in genetic diversity of tomato by which these crop has faced several jams over the years, it may be due to its origin, domestication, and morpho-physio-chemical variability etc. (Peralta and Spooner, 2000; Scintu *et al.*, 2014; Athinodorou *et al.*, 2021).

Tomato fruits have rich source of antioxidant biomolecules *viz.*, lycopene, betacarotene, provitamin-A, carotenoid, ascorbic acid, phenolics, flavonoids and vitamin E. Lycopene is the major carotenoid in tomato fruit with the nutraceutical properties related to a powerful anti-oxidant which can reduce the risk of cancers, heart diseases, age-related diseases and increase the glow on human face (Giovannucci, 1999; Shi and LeMaguer, 2000; Nasir *et al.*, 2015). Besides lycopene a class of pigment anthocyanins is also available in tomato which protects to human body by serious diseases and showed a significant extension of life span (Rick *et al.*, 1994; Andersen, 2001; Lazze *et al.*, 2004; Butelli *et al.*, 2008). The skin colour pigments of cultivated tomato are mainly found in three types, red, yellow and tangerine due to the complex mixtures of carotenoid pigments (Fraser *et al.*, 1994). The red-fruited tomatoes hold several carotenoid pigments and sufficient amount of lycopene (Shi and LeMaguer, 2000; Nasir *et al.*, 2015). The yellow tomatoes have low total content of carotenoid pigments and small quantities of lycopene but this is most important natural source, directly or indirectly of vitamin A. While, the tangerine colour of tomato closely related to orange carotenoid pigment as pro-lycopene (Fraser *et al.*, 1994; Shi and LeMaguer, 2000). Earlier it has been reported that the red colour in tomato fruits is due to the degradation of chlorophyll and synthesis of lycopene because that time chloroplasts are converted into chromoplasts (Fraser *et al.*, 1994; Shi and LeMaguer, 2000; Camelo and Gomez, 2004). Fruit shape and size along with quality traits like pericarp thickness, number of locules, firmness of fruit and total soluble solid are major issues for public interest (Osei *et al.*, 2014).

Besides the multiuse of tomato fruits, the leaves, stems and flowers also have high economic value in ecosystem (Osei *et al.*, 2014). There was a strong positive relationship between plant growth and fruit yield. Stem growth rate of plants are also a reason of

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total stomatal number. Similar scope for high yield and high stomatal density were found in broad leaf area because stomata facilitate photosynthesis procedure in plants (Li *et al.,* 2014). A myth about leaves and stems of many nightshade plants are poisonous containing toxic alkaloid and solanine but tomato is not one of them (http://www.thekitchn.com/fresh-tip-use-tomato-leaves-to-123288). In this self-pollinated crop flowers are appearing on apical meristem with size of 1-2 cm in yellow colour (https://en.wikipedia.org/wiki/Tomato).

The morphological traits of cultivated tomatoes are easily altered by environmental conditions (Osei *et al.,* 2014; Mahbubar *et al*., 2020) because morphological description and classification is a traditional approach to elucidate the economic importance of tomato. Due to their widespread use in many centuries, the conserved tomato cultivars save diversity of the species thereby comprising a precious genetic material for selection and breeding. Breeders are devoted in utilizing the tomato cultivars from different locations in order to develop improved varieties with high nutritional value and stable yield potential. The stability test has indicated the inert nature of phenotypic and genetic characters of tomato under different climates (Spaldon *et al.,* 2017). The quantitative traits of stable genotypes depended upon level of genotype × environmental interaction (Kumar *et al.,* 2013). The environmental interactions between genotypes and stability in morphological traits are important in selection of better varieties along with yield capacity for improvement of varieties in different environments (Singh *et al.,* 2015a; Spaldon *et al*., 2017; Athinodorou *et al*., 2021). Since, on the basis of best of my knowledge limited literatures published with huge morphological traits in tomato on a single platform. This study will provide sufficient fictions on tomato and may be helpful for students and researchers. Therefore, the objective of this study was to classify the extant cultivars of tomato on the basis of distinct pheno-morphological traits for analysing the distinctiveness, uniformity and stability and to identify the divers and stable cultivars for developing new varieties of tomato.

Materials and Methods

Plant materials and transplanting

A total of hundred extant cultivars of tomato developed through different pedigree (Table 1**)** and obtained from many research institutes, SAUs (State Agricultural Universities) and CUs (Central Universities) across the India, and maintained at the vegetable research experimental field of DUS testing, ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, U.P., India. For observation of pheno-morphological characteristics a total 150 tomato plants of each cultivar were transplanted in three replications (50 plants in each) in randomized block design during main cropping season September to March of 2013, 2014, 2015 and 2016. The spacing was maintained at 60 cm × 60 cm (line to line and plant to plant). All cultural practices and crop protection management were applied for surviving healthy crops.

Data observation

Data was recorded from each replication (avoiding the border rows) at quantified growth stages of crop when the specified characters had on full expression (PPV&FRA, 2009). For the measurement of colour characteristics, the latest Royal Horticultural Society (RHS) colour chart was used. Observations of seedling, plants, leaves, flowers and fruits were recorded from the stages of cotyledon completely unfolded to harvest maturity of fruits. The data was recorded of 35 botany based characters as discussed in descriptor of distinctiveness, uniformity and stability (DUS) guidelines of tomato (PPV&FRA, 2009). Growth stages recorded on specific characteristic codes, e.g., 'code 10' on cotyledons completely unfolded (seedling: anthocyanin colouration of hypocotyl), 'code 20' on active vegetative growth before flowering (leaf: intensity of green colour), 'code 30' on appearance of first flower flush (stem characteristics), 'code 40' on 50% flowering (leaf and flower characteristics), 'code 50' on first harvest stage (number of inflorescence on main stem), 'code 60' on fruit fully developed before colour break (fruit colour and intensity before maturity), 'code 70' on harvest maturity (fruit characteristics) from different types of assessment group (Table 1-3) as prescribed in DUS guidelines of tomato (PPV&FRA, 2009).

Leaf area index (leaf size): Leaf area index was calculated by dividing leaf length from leaf width (Singh *et al*., 2015b). Leaf area index was measured by scales <1cm=small, 1-2cm=medium and >2cm=large. These scales were indicated to leaf length (<25cm=short, 25-30cm=medium,>30cm=long) and leaf width (<15cm=narrow, 15-20cm=medium, >20cm=broad).

Leaflet area index (leaflet size): Leaflet area index was calculated by dividing leaflet length from leaflet width (Singh *et al*., 2015b). Leaflet area index was measured by scales <1cm=small, 1-2cm=medium and

Table 1. Details of 100 extant cultivars of tomato

Name of extant cultivars	Pedigree of extant cultivars	Origin centre where from seed received
Ageta-32	Selction	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
ALT-4-19	Pure line selection	Anand Agricultural University (AAU), Anand, Gujarat, India
Anand Tomato-3 (AT-3)	Mahabaleshwar-2 × Sel.-7	Anand Agricultural University (AAU), Anand, Gujarat, India
Anand Tomato-4 (AT-4)	Pure line selection	Anand Agricultural University (AAU), Anand, Gujarat, India
Angha (LE-415)	Pure line selection	Kerala Agricultural University (KAU), Vellanikkara, Thrissur, Kerala, India
Angoorlata (Kalyanpur)	Selection from local germplasm	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Arka Abha	Selection from IIHR 663-12-3-SB-SB (VC-8-1-2-1) from AVRDC, Taiwan	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Arka Ahuti (Sel 11)	Selection from IIHR 143-3-7-SB-1 (Ottawa 60 from Canada)	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Arka Alok	Selection from IIHR 719-1-6 (CL-114-5-1-0) from AVRDC, Taiwan	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Arka Ashish (IHR674SBSB)	Improvement over UC83 B from California	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Arka Meghali	Arka Vikash x IIHR-554	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Arka Saurabh (Sel-4)	Selection from V-685 (Canadian line)	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Arka Vikash (Sel-22)	Selection from American introduction (Tip Top)	ICAR-Indian Institute of Horticultural Research (IIHR), Hessaraghatta lake post, Bangalore, Karnataka, India
Azad T-2 (KS-2)	HB-5 × Kuber	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Azad T-3	Pure line selection	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Azad T-4	Pure line selection	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Azad T-5 (KS-17)	Pure line selection	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Azad T-6 (KS-118)	Pure line selection	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Azad T-8	Pure line selection	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Best of All	Introduction from American line	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
Bhagyashree	Selection from local germplasm	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, Maharashtra, India
BT-11	Pure line selection	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
BT-136	Pure line selection	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
CO-3 (Marutham)	Induced mutant from CO-1	Tamil Nadu Agricultural University (TNAU), Coimbatore, India
Colambia	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
CTS-06	Selction	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAS&T), Jammu, India
DARL-68	EC-386032 × BL-342	Defence Agricultural Research Laboratory (DARL), Pithoragarh, Uttarakhand, India
DCT-1	Selction	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
DCT-2	Selction	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
Dhanshree	407 DPDBK × LA-124	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, Maharashtra, India
Dhrubya	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
DMT-1	Selction	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India

Name of extant cultivars	Pedigree of extant cultivars	Origin centre where from seed received
Feb-2	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
Flora Dade	Open pollinated and heirloom variety	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
Gujarat Tomato-1 (GT-1)	Angoorlata x Punjab Chhuhara	Junagadh Agricultural University (JAU), Junagadh, Gujarat, India
Gujarat Tomato (GT-2)	Angoorlata × Punjab Chhuhara	Anand Agricultural University (AAU), Anand, Gujarat, India
Hisar Anmol (H-24)	Hisar Arun × *L.hirsutumf.glabratum*	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, Haryana, India
Hisar Arun (Sel-7)	Pusa Early Dwarf × K-1	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, Haryana, India
Hisar Lalit (NT-8)	HS-101 × Resistant Banglore	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, Haryana, India
JT-3	Pure line selection	Junagadh Agricultural University (JAU), Junagadh, Gujarat, India
Kalyanpur T-1	Selection from local collection	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Kalyanpur T-3	Type 1 × KS-2 (through pedigree method)	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Kashi Adarsh	Pedigree & marker assisted selection from Indam 2013 × Vaibhav	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Aman	Backcross pedigree of Sel-7 x *L. Hirsutam f. Glabratum* B6013	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Amrit	Backcross pedigree of Sel-7 × *L. Hirsutam f. Glabratum* B6013	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Anupam	Sel-7 × *L. Hirsutum f. Glabratum* B6013	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Chayan	Selection from RILs of H-86 × H-88-78-2	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Hemant (IIVR Sel-1)	Sel-18 × Flora Dade	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Sharad (IIVR Sel-2)	MTH-6 x Kalyani Eunish	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashi Vishesh	Selection using *S. habrochaites f. glaboratum* (B-6013) as donar parent (back cross)	ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh, India
Kashmiria	Introduction from exotic collection	ICAR-ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
KS-16	5414 × Type 1 (through pedigree method)	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
KS-7	Punjab Chuhara × 7019 (Selection through pedigree method)	Chandra Shekhar Azad University of Agriculture and Technology (CSAU&T), Kanpur, Uttar Pradesh, India
Manileima (Sel-2)	Pure line selection	ICAR-Research Complex for North Eastern Hill Region (ICAR RC NEH), Umiam, Meghalaya, India
Marglobe	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
Mukthi (LE-79-5)	Selection from LE79 (CL32D-0-1-19GS)	Kerala Agricultural University (KAU), Vellanikkara, Thrissur, Kerala, India
NDT-1	Selection	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDT-2	Developed from EC 119201	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDT-3	Resistant Bangalore × Kalyanpur Kuber	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDT-4	Pusa Ruby × Kalyanpur Kuber	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDT-5	Selection from EC 130041	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDT-7	Selection	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India

Name of extant cultivars	Pedigree of extant cultivars	Origin centre where from seed received
NDT-8	Selection	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDT-9	Pusa Ruby × Kalyanpur Kuber	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
NDTVR-73	Selection	Narendra Dev University of Agriculture and Technology (NDUA&T), Faizabad, Uttar Pradesh, India
Pant T-3	Pure line selection	Govind Ballabh Pant University of Agriculture and Technology (GBPUA&T), Pantnagar, Uttarakhand, India
Pant T-5	Pure line selection	Govind Ballabh Pant University of Agriculture and Technology (GBPUA&T), Pantnagar, Uttarakhand, India
Patharkuchi	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
PNR-7	Sel-12 × NMR-1	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Prestige	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
PT-11	Selection	Govind Ballabh Pant University of Agriculture and Technology (GBPUA&T), Pantnagar, Uttarakhand, India
Punjab Varkha Bahar-1	Pedigree selection	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Punjab Varkha Bahar-2	Pedigree selection	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Punjab Chhuhara	Introduction from Israel and Shimla Gold	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Punjab Keshari	Punjab Tropic × EC 55055	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Punjab Ratta	Pedigree selection	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Punjab Upma	Pedigree selection	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Pusa Gaurav	Glamour × Watch	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
Pusa Ruby	Selection from Sioux × Improved Meruthi	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
Pusa Upma	Pedigree selection	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
Pusa-120	Selection from introduction	ICAR-Indian Agricultural Research Institute (IARI), Hill Side Road, Pusa, New Delhi, India
Roma	Introduction from exotic collection	ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
Sel-12	Selection	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Sel-18	Selection	Punjab Agricultural University (PAU), Ludhiana, Punjab, India
Sioux	Introduction from exotic collection	ICAR-ICAR-National Bureau of Plant Genetic Resources (NBPGR), Pusa campus, New Delhi, India
Solan Lalima	Pure line selection	Dr.Yashwant Singh Parmar University of Horticulture and Forestry (DYSPUH&F), Solan, Himachal Pradesh, India
Solan Vajra	Pure line selection	Dr.Yashwant Singh Parmar University of Horticulture and Forestry (DYSPUH&F), Solan, Himachal Pradesh, India
Swarna Deepti	Pedigree selection	ICAR-Horticulture and Agro-forestry Research Programme (HARP), Ranchi, Jharkhand, India
Swarna Gola	Pure line selection	ICAR-Horticulture and Agro-forestry Research Programme (HARP), Ranchi, Jharkhand, India
Swarna Lalima	Pure line selection	ICAR-Horticulture and Agro-forestry Research Programme (HARP), Ranchi, Jharkhand, India
Swarna Naveen	Pure line selection	ICAR-Horticulture and Agro-forestry Research Programme (HARP), Ranchi, Jharkhand, India
Utkal Upahar (BT-120)	Selection	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
Utkal Deepti (BT-2)	Selection	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
Utkal Kumari (BT-10)	Sel-22 × BT-2	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
Utkal Pragyan (BT116-3-2)	Sel- 4 × BT- 1	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
Utkal Raja (BT-20-2-1)	Azad Kirti × BWR- 5	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India

Name of extant cultivars	Pedigree of extant cultivars	Origin centre where from seed received
Utkal Urvashi (BT-12)	Punjab Chhuhara × LE-79	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
Utkal Pallavi (BT-1)	Punjab Chhuhara X AC- 142	Orissa University of Agriculture and Technology (OUA&T), Bhubaneswar, Odisha, India
Vaibhaw	Pure line selection	University of Agricultural Sciences (UAS), Bangalore, Karnataka, India
VL Tamatar-4	Introduction and selection from AVRDC line CL 5915-206 (EC 461691)	ICAR-Vivekanand Parvatiya Krishi Anusandhan Sansthan (VPKAS), Almora-263601 (Uttarakhand), India

Table 2. Analysis of variance for stability analysis in 36 extant cultivars of tomato under different environments for 10 morphological traits (SLI, LL, LW, TF, AFW, FL, FD, FTP, FLN, TFM)

Source of Variation	DF	SLI	LL	LW	TF	AFW	FL	FD	FTP	FLN	TFM
Variety	35	273.60**	112.40**	63.05**	81.28**	1828.74**	4.15**	3.36**	0.88**	3.36**	212.98**
Environment	3	249.31**	10.90**	10.13**	316.48**	94.16**	1.00**	1.13**	242.32**	1.60**	622.27**
Var. × Envion.	105	0.39**	0.01*	0.01*	0.04*	0.21**	0.02*	0.05*	0.20**	0.00**	0.06*
Env + Var × Env	108	7.30**	0.32**	0.29**	8.83**	2.82**	0.03*	0.03**	6.93**	0.05**	17.35**
Env (Linear)	1	747.93**	32.70**	30.40**	949.43**	282.48**	3.01**	3.39**	726.97**	4.79**	1866.82**
Env × Var (Lin)	35	1.16**	0.04*	0.03*	0.11*	0.62**	0.01*	0.02*	0.61**	0.01**	0.19**
Pooled Deviation	72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Pooled Error	280	5.87	2.02	10.91	5.94	2.17	0.07	0.08	0.04	0.03	11.96

*,**Significance Levels at P=<0.05, P=<0.01; **DF**= Degree of freedom; **SLI**=Stem: Length of internode between 1st and 4th inflorescence (cm); **LL**=Leaf length (cm); **LW**=Leaf width (cm); **TF**=Time of flowering (50% of the plants with at least one open flower from seed sowing) (days); **AFW**=Average Fruit Weight (g); **FL**=Fruit length (cm); **FD**=Fruit diameter (cm); **FTP**=Fruit thickness of the pericarp (cm); **FLN**- Fruit locule number; **TFM**= Time of fruit maturity (from seed sowing) (days).

>2cm=large. These scales were indicated to leaflet length (<5cm=short, 5-10cm=medium, >10cm=long) and leaflet width (<4cm=narrow, 4-6cm=medium, >6cm=broad).

Fruit size: Fruit size was determined on the basis of average weight of 10 fruits as given in DUS descriptor e.g., <100g=very small, 100-200g=small, 201-700g=medium, large=701-1000g, very large=>1000g.

Genetic diversity

For analyzing the genetic diversity a dendrogram was constructed by using 100 extant cultivars of tomato (Table 1) based on 32 morphological characters (Figure 1). Cluster analysis constructed on the basis of Euclidian distance coefficient and unweighted pair-group method of arithmetic means (UPGMA) by using the SAHN program in numerical taxonomy and multivariate analysis system (NTSYS-PC software) version 2.11s (Rohlf, 2005).

Stability test analysis

To analyse the data over four environments the stability model was used for isolation of the stable genotypes from ten yield related morphological traits *viz.*, Stem length of internode between 1st and 4th inflorescence (SLI), Leaf length (LL), Leaf width (LW), Time of flowering at 50% of the plants with at least one open flower from seed sowing (TF), Average Fruit Weight (AFW), Fruit length (FL), Fruit diameter (FD), Fruit thickness of the pericarp (FTP), Fruit locule number (FLN), Time of fruit maturity from seed sowing (TFM). Among the 100 extant cultivars of tomato only 36 were selected for the stability test on the basis of better yield related morphological traits. The data was analysed on genotypes × environmental interaction model proposed by Eberhart and Russell (1966).

Results

Pheno-morphological characterization

Seedling, stem and leaves

Observation of pheno-morphological characteristics of seedling, stems and leaves of 100 extant cultivars of tomato were presented in Supplementary Table 1. A total 96 extant cultivars of tomato were initiated anthocyanin colouration of hypocotyls on their seedlings. However, after transplanting and vigorous growth of plants the anthocyanin colouration was displayed on upper third portion of stem in 79 cultivars with different intensity like, weak (29), medium (40) and strong (10) (Supplementary Table 1). Although, in present study the determinate and indeterminate nature of plant growth habit of tomato were observed in 49 and 51 cultivars, respectively. Whereas, in another finding all the extant cultivars were present the pubescence (hairs or trichomes) on their stem (Supplementary Figure 1) excluding 'Hisar

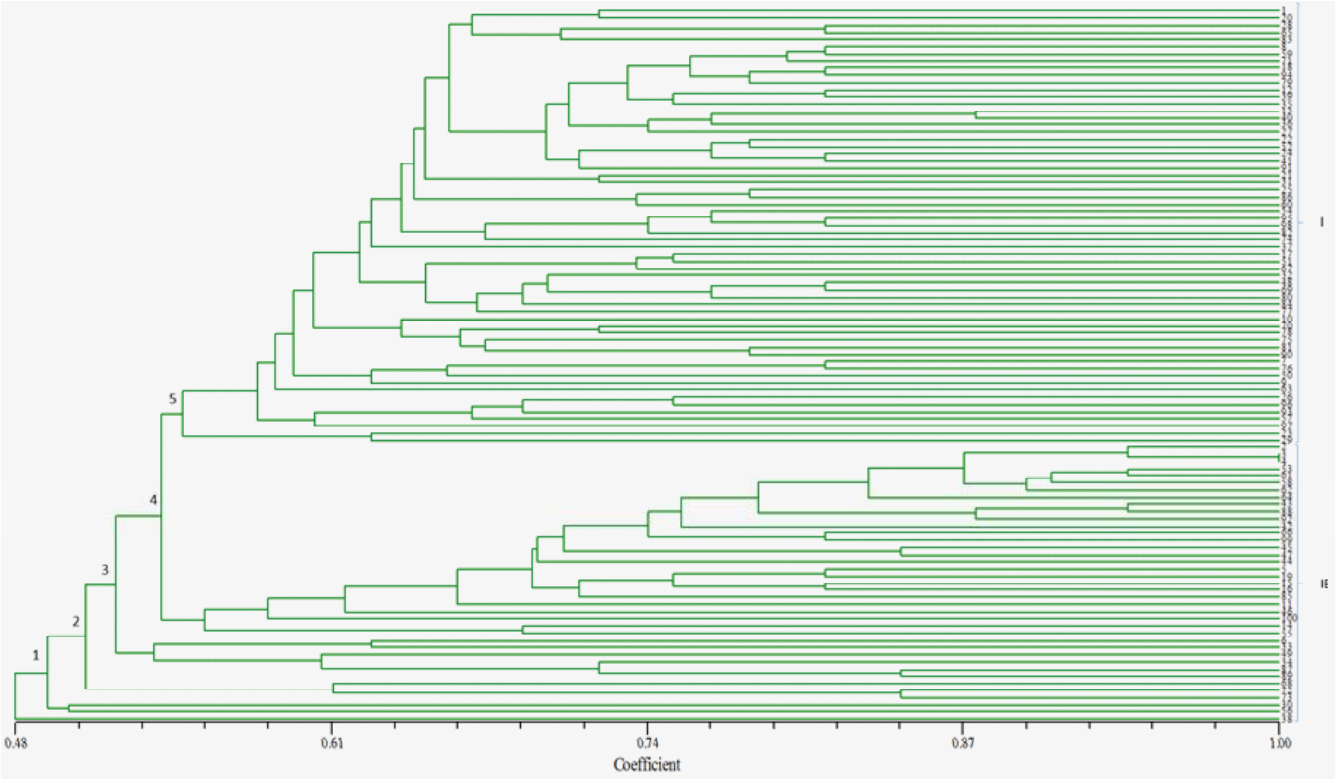

Fig. 1. Unweighted Pair Group Method with Arithmetic mean (UPGMA) dendrogram (with Euclidean distance coefficient) of generated by 100 extant cultivars of tomato based on 32 pheno-morphological characters [1-100 extant cultivar's order as mentioned in Table 1]

Anmol' (Supplementary Table 1). Intensity of green colour in tomato leaves was recorded in three categories light, medium and dark of 16, 62 and 22 extant cultivars, respectively (Supplementary Table 1). In present study it was observed that 22, 74 and 4 tomato cultivars were displayed short, medium and large in leaf and leaflet size (Supplementary Figure 2). Similarly, leaf structure of 100 cultivars categorized into open (22), intermediate (71) and closed (7). While, leaflet serration was classified in 5 (absent or potato type), 79 (less serrated) and 16 (highly serrated) cultivars. However, the attitude of leaf and leaflet in relation to main stem or axis were observed semi-erect, horizontal and drooping in 68, 9 and 23 cultivars of tomato, respectively (Supplementary Table 1).

Flowers

In present study, type of inflorescence was classified into three categories of uniparous (19 cultivars), intermediate (47 cultivars) and multiparous (34 cultivars). Flower fascinations were absent in 66 extant cultivars while it was present in 34 extant cultivars (Supplementary Table 2). Out of 100 extant cultivars, 91 were adopted non-exerted nature of stigma and remaining 9 cultivars were found stigma exerted in their flowers. Correspondingly, stigma nature was classified into three categories unilobe, bilobe and multilobe for 13, 34 and 53 extant cultivars, respectively (Supplementary Table 2; Supplementary Figure 3). In this study, presence of pubescence on style of flowers was present in all cultivars excluding two cultivars 'Dhanshree' and 'Mukti'. Whereas, abscission layer in peduncle was presented in all cultivars (Supplementary Table 2). It was also observed that the colour of flowers exhibited yellow (97 cultivars) and orange (3 cultivars), while colour of anthers of flowers were green (14 cultivars) and yellow (86 cultivars), respectively. During observation it was also recorded that the time of flowering (50% of the plant) was recorded as early, medium and late in 17, 76 and 7 cultivars, respectively (Supplementary Table 2).

Fruits

In current study, the intensity of green colour of fruits skin before maturity was monitored in 100 extant

Table 3. Stability test analysis in 36 extant cultivars of tomato under different environments for 10 morphological traits (SLI, LL, LW, TF, AFW, FL, FD, FTP, FLN, TFM)

Genotypes	SLI			LL			LW			TF			AFW		
	m	b	S²di	m	b	S²di	m	b	S²di	m	b	S²di	m	b	S²di
Ageta-32	44.92	1.29	-1.96	17.38	0.67	-0.67	14.17	0.70	-3.64	71.71	1.01	-1.98	55.36	0.72	-0.72
Arka Ahuti	29.95	0.85	-1.96	30.33	1.17	-0.67	20.32	1.03	-3.64	70.70	1.00	-1.98	73.46	0.97	-0.72
Arka Alok	48.03	1.38	-1.96	25.66	0.98	-0.67	22.49	1.13	-3.64	72.38	1.02	-1.98	97.78	1.29	-0.72
Arka Vikash	33.56	0.96	-1.96	23.58	0.91	-0.67	16.83	0.84	-3.64	70.70	1.00	-1.98	66.76	0.87	-0.72
Azad T-2 (KS-2)	29.30	0.85	-1.96	19.43	0.78	-0.67	14.84	0.76	-3.64	72.05	1.02	-1.98	65.68	0.86	-0.72
Azad T-3	36.18	1.04	-1.96	19.39	0.78	-0.67	16.73	0.84	-3.64	72.36	1.02	-1.98	63.58	0.83	-0.72
Azad T-6 (KS-118)	26.99	0.77	-1.96	22.01	0.82	-0.67	17.93	0.91	-3.64	72.03	1.02	-1.98	54.50	0.72	-0.72
Bhagyashree	17.68	0.51	-1.96	23.55	0.91	-0.67	19.43	0.96	-3.64	74.38	1.05	-1.98	58.34	0.76	-0.72
Colambia	31.32	0.90	-1.96	21.59	0.82	-0.67	17.79	0.91	-3.64	71.04	1.00	-1.98	104.65	1.38	-0.72
DARL-66	56.21	1.61	-1.96	23.38	0.89	-0.67	17.23	0.87	-3.64	70.69	1.00	-1.98	56.53	0.74	-0.72
Dhanshree	33.64	0.96	-1.96	30.86	1.22	-0.67	25.98	1.33	-3.64	74.38	1.05	-1.98	77.41	1.02	-0.72
Floradade	27.54	0.79	-1.96	24.63	0.97	-0.67	19.88	0.99	-3.64	71.71	1.01	-1.98	116.06	1.52	-0.72
Hisar Arun (Sel-7)	34.33	0.99	-1.96	23.24	0.90	-0.67	18.79	0.96	-3.64	72.03	1.02	-1.98	76.65	1.00	-0.72
Kalyanpur T-1	50.92	1.46	-1.96	27.61	1.06	-0.67	17.07	0.84	-3.64	70.69	1.00	-1.98	81.83	1.07	-0.72
Kashi Adarsh	31.58	0.90	-1.96	28.18	1.11	-0.67	21.59	1.09	-3.64	72.36	1.02	-1.98	67.58	0.88	-0.72
Kashi Amrit	51.38	1.47	-1.96	27.11	1.06	-0.67	18.39	0.91	-3.64	72.03	1.02	-1.98	62.73	0.82	-0.72
Kashi Hemant	25.28	0.73	-1.96	23.26	0.92	-0.67	17.73	0.88	-3.64	71.71	1.01	-1.98	54.67	0.72	-0.72
Kashi Sharad	34.43	0.98	-1.96	28.34	1.11	-0.67	17.63	0.88	-3.64	82.75	1.17	-1.98	107.50	1.41	-0.72
Kashi Vishesh	35.31	1.01	-1.96	24.62	0.96	-0.67	20.73	1.00	-3.64	73.04	1.03	-1.98	76.48	1.00	-0.72
Manileima (Sel-2)	35.48	1.02	-1.96	27.64	1.06	-0.67	18.19	0.91	-3.64	71.71	1.01	-1.98	98.28	1.29	-0.72
Marglobe	35.19	1.01	-1.96	27.94	1.09	-0.67	18.78	0.94	-3.64	71.37	1.01	-1.98	114.71	1.51	-0.72
NDTVR-73	32.93	0.95	-1.96	23.64	0.90	-0.67	26.68	1.34	-3.64	60.64	0.86	-1.98	56.36	0.74	-0.72
Pant T-5	33.38	0.96	-1.96	22.24	0.82	-0.67	18.90	0.93	-3.64	72.36	1.02	-1.98	121.76	1.59	-0.72
Prestige	33.48	0.96	-1.96	22.84	0.85	-0.67	16.19	0.82	-3.64	72.03	1.02	-1.98	54.33	0.72	-0.72
Punjab Chhuhara	24.73	0.71	-1.96	37.14	1.40	-0.67	30.58	1.53	-3.64	74.72	1.05	-1.98	64.90	0.85	-0.72
Punjab Keshari	31.91	0.92	-1.96	29.13	1.14	-0.67	21.16	1.05	-3.64	73.05	1.03	-1.98	64.58	0.85	-0.72
Punjab Upma	35.72	1.03	-1.96	22.39	0.87	-0.67	18.62	0.94	-3.64	60.98	0.86	-1.98	65.42	0.86	-0.72
Punjab Varkha Bahar-1	31.62	0.91	-1.96	28.13	1.08	-0.67	21.98	1.13	-3.64	72.36	1.02	-1.98	85.38	1.13	-0.72
Punjab Varkha Bahar-2	33.58	0.96	-1.96	28.61	1.11	-0.67	24.61	1.24	-3.64	71.71	1.01	-1.98	116.73	1.53	-0.72
Pusa Gaurav	34.66	1.00	-1.96	27.51	1.06	-0.67	20.40	1.02	-3.64	72.03	1.02	-1.98	78.15	1.03	-0.72
Pusa-120	23.67	0.68	-1.96	21.00	0.83	-0.67	14.58	0.76	-3.64	60.30	0.85	-1.98	53.33	0.70	-0.72
Sel-12	49.36	1.42	-1.96	20.19	0.78	-0.67	17.73	0.88	-3.64	57.96	0.82	-1.98	46.79	0.62	-0.72
Solan Vajra	32.83	0.94	-1.96	39.98	1.53	-0.67	26.74	1.33	-3.64	72.38	1.02	-1.98	93.92	1.23	-0.72
Swarna Naveen	42.61	1.22	-1.96	37.58	1.45	-0.67	22.10	1.15	-3.64	70.70	1.00	-1.98	85.54	1.13	-0.72
Utkal Pragyan (BT-116-3-2)	33.85	0.98	-1.96	18.96	0.73	-0.67	14.91	0.76	-3.64	73.05	1.03	-1.98	52.50	0.69	-0.72
Vaibhav	31.25	0.90	-1.96	33.68	1.29	-0.67	28.31	1.42	-3.64	67.69	0.95	-1.98	69.19	0.92	-0.72
PM±SE	34.85 ±0.01	1.0 ±0.003		25.91 ±0.01	1.0 ±0.015		19.89 ±0.01	1.0 ±0.015		70.94 ±0.01	1.0 ±0.002		76.09 ±0.01	1.0 ±0.004	

m= mean; **b**= regression coefficient; **S²di**= deviation from regression; **SLI**=Stem: Length of internode between 1st and 4th inflorescence (cm); **LL**=Leaf length (cm); **LW**=Leaf width (cm); **TF**=Time of flowering (50% of the plants with at least one open flower from seed sowing) (days); **AFW**=Average Fruit Weight (g); **PM±SE**= Pooled mean± standard error

cultivars. These cultivars were exposed in light (52), medium (38) and dark (10) green colour. However, green shoulder on tomato fruits before maturity was present in 11 extant cultivars (Supplementary Table 3, Supplementary Figure 4). In case of fruit size of tomato was measured by average weight of 10 fruits which was categorized in very small <100g (0), small 100-200g (1), medium 201-700g (53), large 701-1000g (32) and very large >1000g (14) fruit size. Whereas, fruit shape in longitudinal section (Supplementary Table 3, Supplementary Figure 4) was examined in flattened (5), slightly flattened (30), circular (38), rectangular (3),

Table 3 (Contd.). Cont. Stability analysis in 36 extant cultivars of tomato under different environments for 10 morphological traits (SLI, LL, LW, TF, AFW, FL, FD, FTP, FLN, TFM)

Genotypes	FL			FD			FTP			FLN			TFM		
	m	b	S^2di	m	b	S^2di	m	b	S^2di	m	b	S^2di	m	b	S^2di
Ageta-32	4.58	0.77	-0.02	4.59	0.96	-0.03	1.63	0.90	-0.01	3.08	1.05	-0.01	119.83	1.00	-3.99
Arka Ahuti	7.33	1.54	-0.02	4.36	0.96	-0.03	1.63	0.84	-0.01	2.05	0.61	-0.01	118.82	0.99	-3.99
Arka Alok	4.52	0.77	-0.02	5.90	0.99	-0.03	1.95	1.20	-0.01	5.13	1.66	-0.01	124.54	1.04	-3.99
Arka Vikash	3.65	0.77	-0.02	5.23	0.96	-0.03	1.75	1.07	-0.01	4.10	1.22	-0.01	119.49	1.00	-3.99
Azad T-2 (KS-2)	3.75	0.77	-0.02	3.53	0.67	-0.03	1.26	0.69	-0.01	3.08	1.05	-0.01	105.65	0.88	-3.99
Azad T-3	5.54	1.33	-0.02	4.49	0.96	-0.03	1.68	0.86	-0.01	2.05	0.61	-0.01	122.53	1.02	-3.99
Azad T-6 (KS-118)	4.38	0.77	-0.02	4.56	0.96	-0.03	1.60	0.90	-0.01	3.08	1.05	-0.01	116.45	0.97	-3.99
Bhagyashree	4.18	0.77	-0.02	4.63	0.96	-0.03	1.57	0.93	-0.01	3.08	1.05	-0.01	121.50	1.01	-3.99
Colambia	6.14	1.33	-0.02	6.31	1.17	-0.03	3.19	1.00	-0.01	4.10	1.22	-0.01	119.82	1.00	-3.99
DARL-66	4.65	0.77	-0.02	4.73	0.96	-0.03	1.65	0.94	-0.01	2.05	0.61	-0.01	120.84	1.01	-3.99
Dhanshree	4.68	0.77	-0.02	5.59	0.96	-0.03	1.84	1.14	-0.01	3.08	1.05	-0.01	119.83	1.00	-3.99
Floradade	6.64	1.33	-0.02	7.42	1.49	-0.03	2.48	1.50	-0.01	5.13	1.66	-0.01	117.13	0.98	-3.99
Hisar Arun (Sel-7)	4.66	0.96	-0.02	5.73	0.99	-0.03	1.92	1.17	-0.01	5.13	1.66	-0.01	116.78	0.97	-3.99
Kalyanpur T-1	4.45	0.77	-0.02	5.49	0.96	-0.03	2.68	0.90	-0.01	3.08	1.05	-0.01	119.15	0.99	-3.99
Kashi Adarsh	4.22	0.77	-0.02	4.79	0.96	-0.03	1.59	0.97	-0.01	3.08	1.05	-0.01	122.85	1.02	-3.99
Kashi Amrit	4.45	0.77	-0.02	4.89	0.96	-0.03	1.68	0.98	-0.01	4.10	1.22	-0.01	108.35	0.90	-3.99
Kashi Hemant	4.38	0.77	-0.02	4.49	0.96	-0.03	1.51	0.91	-0.01	3.08	1.05	-0.01	117.80	0.98	-3.99
Kashi Sharad	5.71	1.33	-0.02	5.93	0.99	-0.03	1.96	1.20	-0.01	4.10	1.22	-0.01	121.53	1.01	-3.99
Kashi Vishesh	4.45	0.77	-0.02	5.43	0.96	-0.03	1.83	1.10	-0.01	3.08	1.05	-0.01	139.74	1.16	-3.99
Manileima (Sel-2)	6.28	1.33	-0.02	5.49	0.96	-0.03	1.99	1.07	-0.01	2.39	0.76	-0.01	122.87	1.03	-3.99
Marglobe	6.48	1.33	-0.02	8.12	1.49	-0.03	3.65	1.40	-0.01	4.10	1.22	-0.01	118.13	0.98	-3.99
NDTVR-73	3.85	0.77	-0.02	4.43	0.96	-0.03	1.59	0.87	-0.01	2.73	0.90	-0.01	116.12	0.96	-3.99
Pant T-5	6.01	1.33	-0.02	5.49	0.96	-0.03	1.87	1.11	-0.01	2.05	0.61	-0.01	117.80	0.98	-3.99
Prestige	4.15	0.77	-0.02	4.33	0.96	-0.03	1.56	0.84	-0.01	3.08	1.05	-0.01	121.53	1.01	-3.99
Punjab Chhuhara	7.02	1.40	-0.02	4.46	0.96	-0.03	1.63	0.87	-0.01	3.08	1.05	-0.01	119.15	0.99	-3.99
Punjab Keshari	6.41	1.33	-0.02	4.23	0.96	-0.03	1.53	0.82	-0.01	2.05	0.61	-0.01	139.40	1.16	-3.99
Punjab Upma	5.94	1.33	-0.02	5.23	0.96	-0.03	1.85	1.04	-0.01	3.08	1.05	-0.01	116.79	0.98	-3.99
Punjab Varkha Bahar-1	4.52	0.77	-0.02	5.39	0.96	-0.03	1.94	1.06	-0.01	3.08	1.05	-0.01	139.40	1.16	-3.99
Punjab Varkha Bahar-2	4.82	0.77	-0.02	5.23	0.96	-0.03	1.88	1.03	-0.01	4.10	1.22	-0.01	116.45	0.97	-3.99
Pusa Gaurav	6.41	1.33	-0.02	4.56	0.96	-0.03	1.78	0.85	-0.01	2.05	0.61	-0.01	120.15	1.00	-3.99
Pusa-120	4.35	0.77	-0.02	4.86	0.96	-0.03	1.84	0.93	-0.01	3.08	1.05	-0.01	123.19	1.03	-3.99
Sel-12	4.55	0.77	-0.02	4.46	0.96	-0.03	1.60	0.87	-0.01	2.05	0.61	-0.01	105.65	0.88	-3.99
Solan Vajra	4.89	0.96	-0.02	5.97	0.99	-0.03	2.20	1.16	-0.01	2.05	0.61	-0.01	116.45	0.97	-3.99
Swarna Naveen	5.13	1.14	-0.02	6.25	1.20	-0.03	2.10	1.26	-0.01	3.08	1.05	-0.01	117.80	0.98	-3.99
Utkal Pragyan (BT-116-3-2)	5.81	1.33	-0.02	4.36	0.96	-0.03	1.57	0.85	-0.01	2.05	0.61	-0.01	122.53	1.02	-3.99
Vaibhav	3.65	0.77	-0.02	4.43	0.96	-0.03	1.83	0.81	-0.01	2.39	0.76	-0.01	122.18	1.02	-3.99
PM±SE	5.07 ±0.01	1.0 ±0.050		5.15 ±0.01	1.0 ±0.038		1.88 ±0.01	1.0 ±0.006		3.11 ±0.01	1.0 ±0.045		120.23 ±0.01	1.0 ±0.001	

m= mean; **b**= regression coefficient; **S^2di**= deviation from regression; **FL**=Fruit length (cm); **FD**=Fruit diameter (cm); **FTP**=Fruit thickness of the pericarp (cm); **FLN**= Fruit locule number; **TFM**= Time of fruit maturity (from seed sowing) (days); **PM**±**SE**= Pooledmean± standard error.

cylindrical (0), heart shaped (3), obovoid (13), ovoid (5) and pear shaped (3). Similarly, fruit shape in cross section was noticed as round and not round in 56 and 44 cultivars, respectively. Ribbing at peduncle end was absent in 21 cultivars. While, ribbing at peduncle end was present in 79 cultivars which were categorized into different intensity of weak (37 cultivars), medium (33 cultivars) and strong (9 cultivars). However, fruit depression at peduncle end was present in 30, 50, and 18 cultivars with the intensity of shallow, medium and deep but 2 cultivars were absent the depression at peduncle end. Among the 100 cultivars size of scar around peduncle and size of blossom scar of all cultivar's fruits were categorized in small (52 and 64),

medium (45 and 34) and large (3 and 2). While, shape of blossom end at fruit was observed in different shape like indented, indented to flat, flat, flat to indented and pointed for 18, 39, 30, 10 and 3 cultivars, respectively. In this study colour of skin and flesh were recorded in yellow (3 and 3), orange (11 and 9), pink (9 and 44) and red (77 and 44) colour (Supplementary Table 3; Supplementary Figure 4). Whereas, the fruit firmness was measured as soft, medium and firms in 17, 72, and 11 cultivar's fruit. While, the time of fruit maturity from date of seed sowing was recorded as early (110 days), medium (110-130 days) and late (>130 days) in 8, 81 and 11 extant cultivars, respectively.

Genetic diversity

In the present finding, a dendrogram was developed with five major clusters (clusters '1', '2', '3', '4' and '5') by using 100 cultivars of tomato and 32 morphological traits (Figure 1). These five clusters were classified into two groups 'I' and 'II' including 62 (cluster '5') and 38 (clusters '1', '2', '3' and '4') extant cultivars in the coefficient range of 0.48%–1.00%. Two cultivars 'Agata-32' and 'Best of All' were close in group 'I'. Similarly, the cultivars 'Anand Tomato-3' and 'Anand Tomato-4' were found very close in group 'II'. A cultivar 'Hisar Arun' was isolated individually in cluster '1' of group 'II'.

Stability test analysis

The estimates of genotypes, environment and G × E variances were highly significant for all the characters (Table 2). The estimates of mean (m), deviation from regression (s^2di) and regression coefficient (b) for morphological traits (SLI, LL, LW, TF, AFW, FL, FD, FTP, FLN, TFM) were calculated for stability test in 36 cultivars of tomato (Table 3). Out of 36 a total 29, 26, 27, 35, 25, 22, 32, 26, 27 and 33 cultivars were showed less than or equal to '1' (b<1 or b=1) for the characters SLI, LL, LW, TF, AFW, FL, FD, FTP, FLN and TFM, respectively (Table 3). Whereas, 22 and 32 cultivars were showed less than '1' regression coefficient (b<1). It was also observed that all the cultivars were occupied less than '1' or close to '0' deviation from regression ($s^2di<1$ or $s^2di=0$) for the characters LL, AFW, FL, FD, FTP and FLN.

Discussion

According to literatures many vegetable crops have been reported for black or purple fruit colour pigments due to the anthocyanins but tomato is in queue for producing purple or black colours in farmer's field. In present study, the anthocyanin coloration was present at the stages of seedlings and vigorous growth in most of cultivars (Supplementary Figure 1). In some other studies the cultivated tomato expressed the anthocyanins in vegetative tissues, it may be possible due to transfer of anthocyanin-pigments by wild tomato relatives (Rick *et al.*, 1994; Andersen, 2001). Earlier, it has been reported that the anthocyanins are natural pigments which protects the plants from damage by UV radiations and found in the cell vacuole of flowers, fruits, leaves, stems and some time in roots with different colours red, purple and blue (Rick *et al.*, 1994; Qiu *et al.*, 2016). Anthocyanin has been detected mainly in outer cell layers such as the epidermis and peripheral mesophyll cells of plant parts (Qiu *et al.*, 2016). The changes in anthocyanin colour pigments depend on the range of pH because these anthocyanins have degraded at higher pH effect (Rick *et al.*, 1994; Andersen, 2001; Qiu *et al.*, 2016). The anthocyanins known for its antioxidant properties against reactive oxygen and extreme temperatures and is reported to protect tomato plants by cold stress with countering reactive oxygen and leading a lower rate of cell death in leaves (Rick *et al.*, 1994; Andersen, 2001; Qiu *et al.*, 2016). Plant growth type in tomato are classified into two categories, determinate or bush type and indeterminate or vining type (Supplementary Figure 1). Vigorousness in plants caused by more plant height and spreading of branches and may be deserved for producing high yield in crop (Singh *et al.*, 2014, 2015a, 2015b). It was also found that all the cultivars had pubescence (hairs or trichomes) on their stem (Supplementary Figure 1). Theoretically these dense covering of pubescence protects the living cell surface from insects, direct flow of air, frost and heat in open habitats and also reducing the transpiration rate in plant (Peralta and Spooner, 2000). In agreement of this finding only 'H-24' cultivar was reported as pubescenceless and also discussed in DUS descriptor of tomato (2009). In present study, the intensity of green colour leaves in tomato were categorized as light, medim and dark green colour and indicated the presence of chlorophyll content (Rick *et al.*, 1994; Peralta and Spooner, 2000; Singh *et al.*, 2015b). Correspondingly, other characters of leaves or leaflets *e.g.*, attitude, serration, structure, morphology and size (Supplementary Figure 2) are also responsible for the photosynthetic processes and also

helpful in food accumulations (Peralta and Spooner, 2000; Jones, 2000; Singh *et al.*, 2015b). It may be light or deform green colour of leaves due to nitrogen or iron or sulphur deficiency but in the present observation it was determined by the genetic characters of tomato cultivars. Healthy green colour and vigorousness in leaves or leaflets may also support for producing high yield in tomato (Rick *et al.*, 1994; Jones, 2000; Singh *et al.*, 2015b).

Flowers play very important role to obtain an expected high yield in any crops. Only presence of flower will not be responsible for producing high yield, while, the nature and structure of stigma and the morphology, size, number and earliness of flowers and fruits (Supplementary Figure 3) are also important. In present finding, many characters of flowers *viz.*, type of inflorescence (uniparous, intermediate or biparous and multiparous), fasciations (absent and present), stigma exertion (exerted and non-exerted) and nature of stigma (unilobe, bilobe and multilobe) had direct relation by significant and potential yield capacity (Rashid *et al.*, 2016). In present study, the pubescence on style of flowers and abscission layer was present in most of cultivars. Presence of pubescence is known to help in reducing the transpiration rate and protects by insects (Peralta and Spooner, 2000). While, presence of abscission layer indicated to strong joint between fruits and peduncles. Some time, formation of abscisic acid (ABA) take place in abscission layer and may be caused bud dormancy or dropness of fruits and leaves (deMelo *et al.*, 2015; Rashid *et al.*, 2016). It was also found that the colour of flowers and anthers was yellow in many cultivars but few cultivars were displayed orange flowers and green anthers. Earlier it has been studied that the yellow colour of flowers in tomato is due to xanthophyll pigments (Peralta and Spooner, 2000; Ariizumi *et al.*, 2014; deMelo *et al.*, 2015). In this study the time of flowering (50% of the plant) was recorded medium in many cultivars. Early flowering is responsible for early fruiting and may be beneficial for breeders and farmers (Moya *et al.*, 1995; Rashid *et al.*, 2016).

Fruit attributes (fruit colour, size, shapes, yield, qualities and time of maturity) are demanding issue for any crop and has been need of breeders, researchers, and farmers. In results of this study it was observed that the few tomato cultivars had dark green colour intensity on their fruit's skin and shoulder (Supplementary Figure 4). Earlier it has been studied that the green colour of fruits indicated presence of chlorophyll content (Rick *et al.*, 1994; Mahbubar *et al.*, 2020; Goodenough *et al.*, 1982; D'souza *et al.*, 1992) but the presence of green shoulder is due to high availability of chlorophyll content along with high phenol and ethylene (D'souza *et al.*, 1992; Rick *et al.*, 1994). The green colour of tomato fruits convert into deep red colour after ripening due to presence of phenol and ethylene, either it may also be due to chlorophyll convert into lycopene (D'souza *et al.*, 1992; Rick *et al.*, 1994). In case of fruit size most of the cultivars were found medium fruit size but none was in very small size. Very small fruit size is found only in cherry tomato and wild species because most of tomato cultivars having small to very large size (Singh *et al.*, 2015a). Whereas, fruit shape in longitudinal section was categorized as flattened, slightly flattened, circular, rectangular, cylindrical, heart shaped, obovoid, ovoid and pear shaped as prescribed in DUS guideline of tomato, 2009 (Supplementary Figure 4). Size and shape of tomato fruits are deciding to the demand of consumers (Sheldrake, 1989; Singh *et al.*, 2015a). Similarly, some morphological characters *e.g.*, ribbing at peduncle, depression at peduncle end, size of scar around peduncle end, size of blossom scar and shape of blossom end at fruit (indented, indented to flat, flat, flat to indented and pointed) were noticed among the cultivars. Presence or absence of these characters in tomato fruits has decided to better and poor fruit shape and demands of growers and consumers (Sheldrake, 1989). In results of this study, the colour of fruit's skin and flesh were recorded in yellow, orange, pink and red in many cultivars at the maturity stage (Figure 4). Earlier, tomato fruits has been found in a range of colours like red, yellow, white, pink, green, purple, brown and black but these colours are influenced only for two traits skin and flesh. It may be due to origin of various pigments of carotenoids at the ripening stages of fruits. (D'souza *et al.*, 1992; Fraser *et al.*, 1994). Red and yellow colours of fruit indicates to presence of high level of lycopene and beta-carotene while, the pink and orange colour may be indicated to low lycopene and beta-carotene in tomato fruits (Goodenough *et al.*, 1982; D'souza *et al.*, 1992; Fraser *et al.*, 1994; Nasir *et al.*, 2015). Earlier, it has been studied that during maturity of fruits the chlorophyll (green colour) was reduced and increased the carotenoids (red, yellow and orange colour) or induces yellowing of green tissues due to decolouration and

degradation in chlorophyll pigments by the secretion of small amount of ethylene in fruits (Goodenough *et al.,* 1982; D'souza *et al.,* 1992; Fraser *et al.,* 1994). In another study, when the colour of skin is genetically controlled by a single recessive gene 'y' then the 'y'+ (wild type) is dominant and gave results in yellow skin ('y'+'y' = yellow skin), and when the 'y' is expressed in a recessive pairing then the result was red skin ('yy' = red skin) (Gorini and Testoni, 1990). Sometimes, the flesh or pericarp of tomato is the interior tissue of the fruit. Various genes for control of flesh colour can be expressed at the same time. Likewise, the red flesh or green flesh and other colours expressed with the bicolour (red + green flesh) trait at the same time because it has different alleles which produced slight variations to the expression of the gene (Gormley and Egan, 1978; Gorini and Testoni, 1990; Goodenough *et al.,* 1982). These pigments not only affect fruit appearance but they also influenced nutrition and flavour (Gormley and Egan, 1978; Gorini and Testoni, 1990). Another finding was the fruit firmness measured as soft, medium and firms in many cultivars which is determine to quality and post-harvest capacity of fruits (Gormley and Egan, 1978; Goodenough *et al.,* 1982). It was also observed that many cultivars noticed for their fruit maturity as early, medium and late. Early or medium days of maturity and ripening of fruits may be good for quality as well as commercialization of seeds by farmers, entrepreneurs and companies. Time of maturity of tomato decides to the attitude of market and also helpful in breeding program for a breeder (Sheldrake, 1989; Gorini and Testoni, 1990; Henareh *et al.,* 2015).

The genetic diversity represents the number of genetic characteristics and genetic makeup of populations to adapt the changing climate. Tomatoes have conserved rich diversity towards quantity and quality resources but among the cultivars (*S. lycopersicum*) a limited diversity has been reported (Bauchet and Causse, 2012). The cluster dendrogram is a way of presenting the distance and closeness between genotypes. In present finding, five clusters in two major groups were developed which was located in a dendrogram made by hundred extant cultivars (Figure 1). These two groups were indicated genetically difference because of using different pedigree and showed different morphological characters (Table 1). It was also noticed that most of the cultivars were very close with each other and came in same group but some cultivars were diverse to each other and went with different group. It may be due to these same group cultivars developed from similar research centres and showed similar morphology (Table 1 and supplementary Table 1-3). Earlier, it has been studied that tomato has many simple and complex traits and low genetic variation (Scintu *et al.,* 2014; Athinodorou *et al.,* 2021). Another finding was that the cultivar 'Hisar Arun' clustered individually in a group, it may be possible due to involving wild parentage and covering genetically different morphology (Singh *et al.,* 2015a, 2015b). The differences and closeness indicated to genetic relationship between the extant cultivars which may be utilized during hybridization (Bauchet and Causse, 2012; Singh *et al.,* 2014).

Stability test is a way to confirm the stability rate of varieties for growing in difficult circumstances. In present study, those characters of the cultivars were showed less than '1' (b<1) or equal to '1' (b=1) regression coefficient either they sowed less than '1' (s2di<1) or close to '0' (s2di=0) deviation from regression, that cultivars can stable for cultivation in each environment. In support of this finding several workers has been reported that the results of less or equal to '1' regression coefficient (b=<1 and b=1) and close to '0' deviation from regression (s^2di=0) indicated most stable and adaptive genotypes of tomato which can be utilized for cultivation in any climatic zone (Eberhart and Russell, 1966; Singh *et al.,* 2012; Kumar *et al.,* 2013; Singh *et al.,* 2015a; Spaldon *et al.,* 2017; Athinodorou *et al*., 2021).

Conclusions

From present study, it was concluded that hundred extant cultivars of tomato were represented quite a good diversity for morphological and mopho-physio-chemical properties. For example, the presence of pubescence in tomato protects to plant by insect and speedy winds; presence of anthocyanin protects to plant by UV rays and protect to human by cancerous diseases; intensity of green colour and vigorousness of plant morphology helps in photosynthetic processes; fruit size, shape and firmness determines to the quality and demands of consumers; early flowering and fruiting will be beneficial for producers to achieve the market demand; red, orange, yellow and pink colour of ripen tomato fruit was due to conversion of chlorophyll into carotenoids pigments in presence of ethylene etc. Moreover, the characterization of these cultivars on the basis of their various morphological traits would be helpful for

generating a data base on tomato and also will be time saver and helpful for students, industrialists and breeders to know about behaviour of tomato varieties from a single platform. The evaluation of the genetic diversity and closeness between the tomato cultivars could be utilized in conservation, evolution and improvement of crop. Consequently, the stable cultivars of tomato can be grown in any climatic zone and could be utilized in varietal improvement programme for desired characteristics. Furthermore, these categorized cultivars can be protected and registered under PPV&FRA, New Delhi on the basis of DUS testing and may be protected by IPR issues.

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*Supplementary Table or Figure mentioned in the article are available in the online version.

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RESEARCH ARTICLE

Agro-morphometric Diversity Analysis in Carrot Germplasm from Indian Genebank

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Carrot is a nutrient rich and commercially important root vegetable in India. A study was undertaken in *rabi* seasons of 2015-16 and 2016-17 to assess the agro-morphological diversity in 100 accessions collected from different regions of India and from other countries. Wide variation was observed in accessions for qualitative (root and core colour) and quantitative (plant length, root length and length, shoulder, root, core size, number of leaves per plant, total plant weight root yield etc.) traits. Maximum accessions had red and mixture of light red (45) to light purple roots (38). Only orange accessions had uniformity in root shape and colour. Wide variation was observed in root length (13.6-25.6 cm) and shoot length (25.0 - 88.3 cm). The study revealed wide variation in carrot germplasm maintained by Indian genebank, however, intra-population variation needs to be fixed before use in breeding.

Key Words: Diversity analysis, Germplasm, Morphometric traits, National Genebank, Tropical carrot

Introduction

Carrot (*Daucus carota* L.) is one of the most important and nutritious vegetables grown in the world. Its production has increased to 42.8 million tons from 1.15 million ha area (FAOSTAT, 2017) with average annual growth rate is 4.26%. The primitive purple and yellow carrots were source for evolution of modern-day edible carrots (Bradeen and Simon, 2007; Simon *et al*., 2008) which have diverse colours *i.e.* red (lycopene), orange (β-carotene), black (anthocyanin), white (lutein) and yellow (xanthophylls). Carrot is typically of two types, namely (i) Asiatic/tropical type which form edible roots and produce seeds profusely in tropical and sub-tropical climate without vernalization requirement and (ii) the temperate or European type which forms good quality roots in cool months in sub-tropical environment, but needs vernalization to initiate bolting (initiation of flower stalk). In India, tropical carrots are preferred for juice, pudding (*gajar halwa*), vegetable and fresh salad, pickle purposes (Kushlaf and Kalia, 2012) but remain available in winter season only while European/ temperate type are available throughout the year due to their storability. India has good extent of diversity in carrot germplasm as reported by Saha *et al*. (2016). However, they used only 38 tropical carrot inbred lines, whereas more than 100 collections have been reported by ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Hence, evaluation of germplasm for economically important traits was prerequisite for breeding use.

Agro-morphometric traits are functional representation of gene(s) and environment interaction and they are simple, inexpensive and easily observable. Such traits have been effectively used in understanding diversity in *Capsicum* from Peninsula of Baja California (Murillo-Amador *et al*., 2016), mulberry from Giardinello, Sicily, Italy (Lo Bianco *et al*., 2018), maize from different regions (Yousaf *et al*., 2007) and diverse plant species in northern China (Meng *et al*., 2009). Morphological description of inter- and intra-accession in a germplasm helps in deciding the use of molecular markers, particularly in carrot which is a highly cross-pollinated crop and has high level of inbreeding depression. Diversity in carrot germplasm was also reported from Turkey (Balakaya *et al*., 2005), United States of America (Luby *et al*., 2016) and China (Ma *et al*., 2016). In India, 27 genotypes of temperate carrot were evaluated for economic traits in North Western Himalayas (Kumar *et al*., 2009), 32 genotypes of temperate carrot (Saha *et al*., 2015) and 38 genotypes

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of tropical carrot (Saha *et al*., 2016) for morphological traits and heat tolerance, respectively in Delhi. Amin *et al*. (2010) reported morphological variation in 48 genotypes (both temperate and tropical types) in Punjab, India. However, these studies were only aimed to investigate the advance genotypes available with respective centres and none of them targeted germplasm available with national genebanks such as NBPGR, New Delhi. The present investigation was aimed to characterize the carrot germplasm available at National Genebank for agro-morphometric traits.

Materials and Methods

A set of 108 germplasm from Indian Council of Agricultural Research (ICAR)-National Bureau of Plant Genetic Resources (NBPGR), New Delhi was received for characterization based on morphological traits. It comprised of traditional cultivars/folk varieties (17), released varieties (16), Elite lines (11), landraces (6), registered germplasm/genetic stock (6), breeding lines (5), parental lines (2) and others (45). These were predominantly collected from different parts of India while three were exotic lines. The checks used were four open-pollinated varieties, namely Pusa Rudhira (tropical, red colour, self core and main season), Pusa Vrishti (tropical, light red colour, self core and heat tolerant variety), Pusa Asita (tropical, black colour, self core and main season) and Pusa Meghali (tropical, light orange colour, self core and main season).

The germplasm was evaluated at Division of Vegetable Science, ICAR- IARI, New Delhi in *rabi* seasons of 2015-16 and 2016-17. The trials were conducted in randomized block design with two replications. The crop was raised on ridges (15 cm height, 20 cm width) made 30 cm apart in paired row system in plots of 3 × 1 m size (3 sq m). Sowing was done at 5 cm distance and maintained a spacing of 10 cm by thinning after 30 days of sowing and recommended package of practices were followed during crop growth.

The observations for agro-morphometric traits namely plant height (cm), shoot length (cm), total plant weight (g), number of leaves per plant, root length (cm), shoulder diameter (cm), root diameter (mm), core diameter (mm), cortex diameter (cm), individual root weight (g) and shoot weight (g) were recorded from five random plants using standard rulers and electronic balance. Marketable root yield was derived from plot yield. The root to gross plant weight ratio and root to shoot weight ratio were derived from the component traits. Number of marketable roots were counted per plot and percentage of the same was calculated by using formula as, marketable roots (%) = (Number of marketable roots per plot/Total number of roots per plot) × 100.

The statistical analysis of the data was performed using R Software for principal component analysis, correlation coefficient, basic statistics creating heatmap and K-means analysis while DARWIN 6.0 version was used for diversity analysis.

Results and Discussion

In total, 101 accessions germinated and one accession IC-330367 did not form carrot type roots and bolted directly, which was not included in present study. Hence, the current experiment and analysis has been carried out using 100 accessions along with four commercial checks. The root and core colours of investigated accessions are given in Table 1. These 100 accessions were grouped on the basis of root skin colour as black (04), orange (14), mixture of light purple, white, pale or red (38) and light to dark red (44).

Plant Traits

The observations on plant traits in germplasm evaluated are presented in Table 2. Whole plant height (root + shoot length) ranged from 41.4 to 103.7 cm, the highest in IC0347795 followed by IC0537770, IC0361562-X, IC0371696, IC0570071 and EC0171367 while it was minimum in IC526888. Accessions showed wide variation for root length which was ranged from 13.5 (IC0606225) to 25.5 cm (IC0598342) and none of the accessions had root length more than commercial variety Pusa Rudhira (25.6 cm) and Pusa Asita (31.4 cm) while IC0598342 had better than Pusa Meghali (25.3 cm). Pusa Vrishti is a heat tolerant open pollinated variety of tropical red carrot and 50 accessions had root length greater than this indicating scope for screening germplasm in early group for longer roots and other desirable traits. Shoot length was prominent over the check varieties in almost all the accessions and highest was observed in IC0347795 (88.3 cm) followed by IC0537770 (82.1 cm), IC0144374 (79.2 cm) and EC0171374 (77.84 cm). However, shoot length was minimum in IC0143948 (23.5 cm) and IC0121429 (22.7 cm). The shoot length should be less so that plant can divert more photosynthates towards root development.

An optimum number of leaves are desirable because excessively low or high affect root yield. Broader

Table 1. Observations on root and core colours of carrot germplasm

Accessions	Root colour	Core colour
EC0171367	Purple, red, white	Light purple
EC0171374	Light purple, white, red	Light purple, white
EC0368401	Purple, white, red	Red
IC0121429	Orange	Pale
IC0143948	White, light purple	Pale
IC0143949	Purple, red, white	Purple
IC0143950	Purple, orange, white	Purple, pale, light red
IC0143951	Purple	Purple, pale, red
IC0143952	Purple, light purple, white	Red, pale
IC0143953	Purple, white, red	Pale
IC0143954	Red, purple	Purple, pale
IC0143955	Red, purple, white	Pale, light red pale
IC0143956	Purple, white, light red, purple	Light purple, pale
IC0143957	Red, purple, white	Light purple
IC0143958	Red, purple	Medium purple, pale
IC0144373	Red, white, purple	Light red
IC0144374	Purple, light, red	Pale
IC0144375	White, red	Medium purple
IC0144376	White, purple, red	Purple
IC0144377	Light purple	Purple pale
IC0144378	White, red	Red
IC0144379	White, red	Light purple, pale, light red
IC0144380	White, red	Purple white
IC0144381	White, red	Red
IC0144382	Red, purple	Pale
IC0144383	Purple	Medium red purple
IC0144384	Red, light purple	Red, pale
IC0146714	Purple, white, red	Red
IC0146715	White, purple, red	Red
IC0265265	Red	Red
IC0284904	Red, white	Red
IC0284927	Orange	Orange
IC0312821	Red	Red
IC0312835	Red	Red
IC0312919	Red, white	Light purple
IC0312928	Red, yellow	Light red
IC0312942	Red	Light red
IC0312956	Red	Light red
IC0312995	Purple, white	Pale
IC0313041	Red	Pale
IC0318887	Red	Red, light red
IC0325192	Red, light	Red
IC0325192-X	Purple, white	Pale
IC0325193	Red	Red
IC0325194	Red, light purple	Light purple
IC0325197	Medium red	Pale
IC0331877	Medium red	Light purple, white
IC0331885	Red	Light red
IC0331978	Black	Pale, light purple
IC0339571	Black	Light purple, pale
IC0339572	Orange	Orange
IC0361562	Orange	Orange
IC0361562-X	Purple, white, pale	Pale
IC0369523	Purple, white	Red
IC0371696	Black	Purple, white
IC0374708	Red	Red
IC0399065	Red	Red
IC0399657	Purple	Red
IC03399658	Red	Red
IC0399659	Red	Red
IC0405214	Orange	Orange
IC0411726	Purple, white	Pale
IC0141736	Purple	Light purple
IC0411817	Black	Light purple
IC0470032	Orange	Orange
IC0970062	Orange	Orange
IC0512325	Red	Purple
IC0524226	Red	Light red
IC0537770	Purple, white	Pale
IC0565022	Red	Light purple
IC0565023	Purple	Red
IC 0566229	Orange	Orange
IC0566230	Orange	Orange
IC0570071	Purple, white	Red
IC0570261	Light red	Light red
IC0591033	Red, pale	Pale, red, pale green
IC0593950	Orange	Orange
IC0596514	Red, purple	Purple
IC0598342	Red	Red
IC0598343	Red	Pale
IC0598344	Red	Purple
IC0606225	Purple, white	Pale
IC0607364	Purple, white	Light red, pale green
IC0614611	Red	Light red
IC0614612	Purple	Light purple
IC0312995	Red	Light red
IC0312948	Red, white red	Light red
IC0313048	Red	Light red
IC0342261	Orange	Orange
IC0342291	Red	Light red
IC0342466	Medium red	Light red
IC0347722	Red	Light red
IC0347795	Orange	Orange
IC0347829	Red	Red
IC0347850	Red	Red
IC0429963	Red	Light red
IC432018	Purple	Red
IC433539	Red	Pale
IC526888	Orange	Orange
IC537826	Orange	Orange
Pusa Rudhira (check)	Red	Red
Pusa Vrishti (check)	Red	Red
Pusa Asita (check	Black	Black
Pusa Meghali (check)	Orange	Orange

shoulder, of course is an undesirable trait. It is essential to identify the accessions which have high net assimilation rate and maintain proper growing potential. Ideally, the accessions should have an optimal level of harvest index (a ratio of economic part to total biomass of plant or crop), to ensure efficient partitioning to root part while preserving a sufficient photosynthetic leaf area (Suojala, 2000).

Root Traits

Root shoulder width is important trait for marketing perspective and narrow shoulder is a preferred trait. It ranged from 22.7 to 64.7 mm (Table 2). Similarly, root diameter is a yield trait and it ranged from 17.2 to 41.3 mm. Germplasm also showed variation for core diameter (7.06 - 27.94 mm), smaller core diameter is desirable trait. Total plant weight, which includes both root and shoot portions weight, was highest in IC0325197 (602.5 g/plant) which also had highest values for root weight as well. But, the roots were excessively bulky and undesirable. Other accessions with highest plant weight were IC0325194, IC0312928, IC0399657 and IC0399657. IC0312942 and IC0399659 had individual root weight greater than Pusa Rudhira (165.0 g) while IC0325197 (201.7 g) had higher root weight than Pusa Asita (195.0 g). The root: gross plant weight ratio is important indicator for yield potential and it should be higher. It was highest in IC433539 (0.80) followed by IC0570261 (0.78) and IC0284927 (0.77) while minimum in IC0361562-X (0.21), IC0399065 (0.25) and IC0596514 (0.25). The root: shoot ratio was maximum in IC0361562-X (3.9) followed by IC0399065 (2.94) and IC0596514 (2.85) while it was minimum in IC433539, IC0570261 and C0284927 (<0.3).

Intra-population variation within the accessions was minimal in all the orange root coloured accessions while it was maximum in red and light purple colour groups. The orange color accessions represent germplasm introduced from European countries by public and or private sectors for commercial or immediate breeding use which later on multiplied/refined and resubmitted to Genebank. However, the red and purple colour accessions are predominately collected locally as landraces or farmers varieties which rarely undergone for purification, hence showed wide variation in root and plant traits. Occurrence of light to purple colour roots within the germplasm indicates for existence of sub-groups as also indicated by Ipek *et al*. (2016) within the purple carrot populations in Eregli District of Turkey. Intra-population variation in carrot accessions might be due to highly cross-pollinated nature of the crop which allows out-crossing along with high degree of inbreeding depression which restricts survival of selfed progenies beyond 3-4 generations (Kalia, 2005).

In germplasm, the share of marketable roots is one of the important criteria which determines the yield potential. It was highest in orange coloured accessions

Table 2. Basic statistics of agro-morphometric evaluation of carrot germplasm

Characters	Germplasm accessions				Check varieties				C.D. (p=0.05)	SE(m)	C.V. (%)
	Mean	Minimum	Maximum	Standard deviation	Pusa Rudhira	Pusa Vrishti	Pusa Asita	Pusa Meghali			
Plant height (cm)	77.3	41.4	103.7	13.8	85.0	69.1	87.5	73.1	13.4	4.8	8.8
Root length (cm)	19.6	13.6	25.6	2.8	25.6	19.5	31.4	25.3	5.1	1.8	6.8
Shoot length	57.5	25.0	88.3	14.0	59.4	49.6	56.1	47.8	13.5	4.8	
Shoulder diameter (cm)	41.3	22.7	64.7	9.1	44.5	39.8	58.2	51.7	3	1.1	
Root diameter (mm)	30.9	17.2	41.3	5.7	37.4	34.2	38.7	41.3	11.1	3.9	
Core diameter (mm)	14.9	7.1	27.9	4.9	10.8	12.4	36.8	35.6	10.1	3.6	
Cortex diameter (cm)	16.0	5.4	29.5	5.2	26.6	21.8	9.5	16.2	2.2	0.71	
No. of leaf per plant	11.1	7.0	28.6	3.5	8.5	8.5	27.3	19.4	1.5	0.5	6.5
Total plant weight (g)		79.3	602.5	86.7	310.0			172.7	113.6	40.4	
Individual root weight (g)		41.5	201.7	32.3	165.0			135.0	55.7	19.8	
Avg shoot weight (g)		20.4	400.8	66.3	145.0	64.0		37.7	97.3	34.6	
Root:gross plant weight ratio	0.5	0.2	0.8	0.1	0.5	0.7	0.5	0.8	0.34	0.11	
Root:shoot ratio	1.2	0.2	3.8	0.6	0.9	0.4	0.8	0.3	3.36	1.2	
Marketable roots (%)	40.6	21.0	73.0	13.4	71.0	58.0	67.0	67.0	-	-	-
Root yield (t/ha)	10.2	4.2	24.2	4.1	29.3	20.8	32.7	23.9	13.4	4.8	6.7

and maximum was observed in IC0361562 and IC537826 (73.0%) followed by IC0284927 (72%). In 96 accessions, it was less than the commercial variety Pusa Rudhira (71.0%) and 84 accessions had less than Pusa Meghali (62.0%) and Pusa Vrishti (58.0%).

Root Yield

The yield potential in the germplasm ranged from 4.2 to 24.2 t/ha, the highest was in IC0325192-X and minimum in IC0374708 (Table 2). Two accessions, namely IC0325192 and IC0361562 outperformed Pusa Vrishti (20.0 t/ha) and Pusa Meghali (23.9 t/ha) for root yield. Most of the higher yielding accessions were of orange colour European carrot because they had high level of uniform marketable roots and low share of unmarketable roots.

Variation in accessions for foliage and root traits appears to be in the line of earlier reports of Hole (1996) who stated that the genotype is the primarily responsible factor for difference in distribution of dry matter between shoot and storage root. The tropical type accessions have less root:shoot ratio compared to European type, which could be due to their genetic makeup to adapt to higher temperature conditions and also that the high temperature is more favourable for shoot growth than for storage root growth (Hole, 1996).

Cluster Analysis

The unweighted pair group method with arithmetic mean (UPGMA) method-based clustering of germplasm accessions using 15 morphometric observations revealed six main clusters and one accession IC0325197 was not part of any of these clusters (Fig. 1). Most of the orange coloured accessions (12) were grouped into a single cluster while purple coloured accessions were distributed across the clusters. The purple and red coloured accessions are part of tropical carrot while orange carrot mainly represents European type. The root and plant traits are distinct in both groups, hence they showed clear grouping pattern. Cluster-1 had nine accessions, cluster-2 had 16 and 12 of them were orange type, cluster-3 had 30 accessions all of which were red to light purple except one purple root accession IC0371696. Cluster-4 had only six accessions, three of which were orange type and one purple root type. Cluster-5 was represented by eight accessions and all of them were grouped in red or light purple category. In cluster-6, there were two sub-clusters each having 11 and 10 accessions. In cluster-7, 13 accessions were of

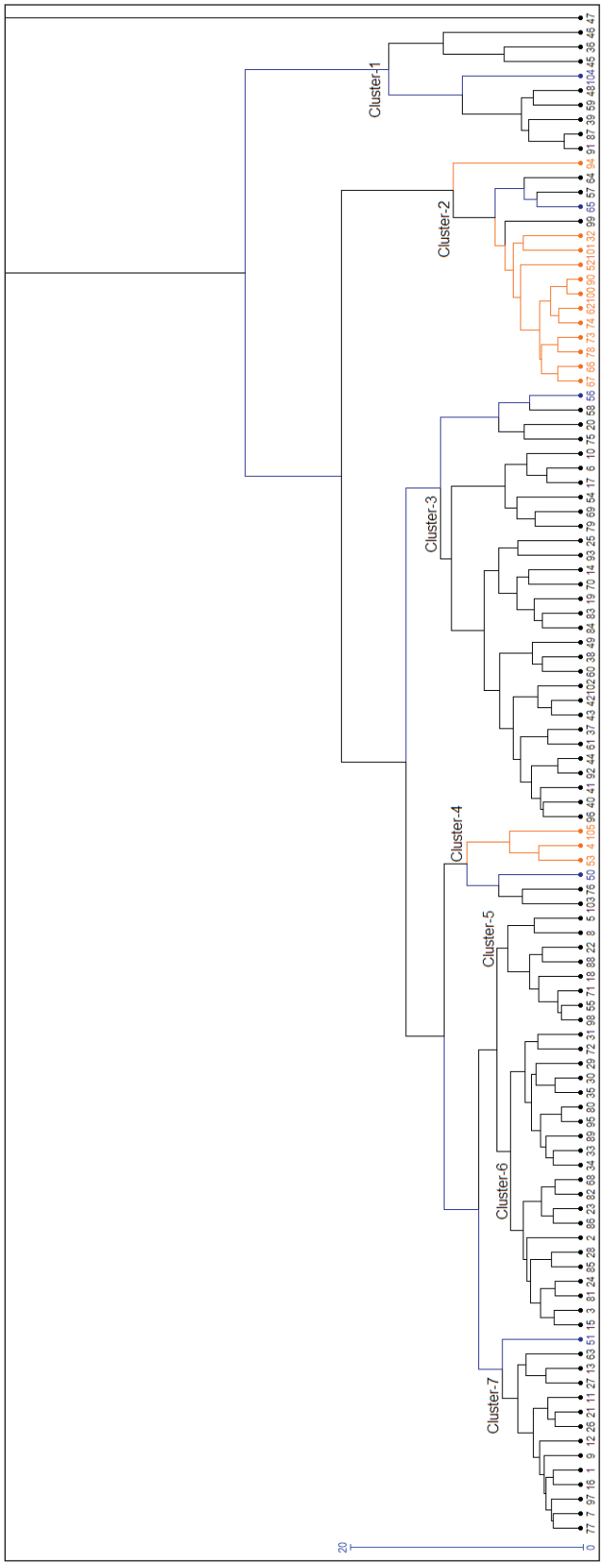

Fig. 1. Hierarchical clustering of carrot germplasm by UPGMA method using 15 morphometric traits (Details of 1-104 are given in Table 1)

red and light purple colour while accession IC0339571 was of purple root colour.

Correlation Analysis

The correlation analysis of 15 morphological (observed and calculated) traits showed significant level of association between plant and root traits (Table 3). It was significantly high between shoot length and plant length (r=0.951), total plant weight (r=0.386) and shoot weight (r=0.394). Root length had negative correlation with shoot length (r= - 0.179) but positively correlated with shoulder diameter (r=0.325), core diameter (r=0.196) and number of leaves per plant (r=0.316). Root diameter was positively correlated with root length (0.274), root weight (r=0.610) and root yield (r=0.237). Per cent marketable roots and root yield was significantly correlated with root yield (r=0.644). Number of leaves per plant was negatively correlated with plant height shoot length, but positively correlated with root length, root shoulder diameter, and root diameter. Hence, breeding for a smaller number of leaves may affect root yield which was also positively correlated.

The morphological variation in the carrot accessions appears to be due to their ancestry because all the accessions were of domesticated carrots which have two groups, the Eastern/Asiatic (var. *altorubens*) and Western (var. *sativus*) groups, and these are genetically distinct (Clotault *et al.*, 2010; Baranski *et al.*, 2012; Iorizzo *et al.*, 2013). The Asiatic types have anthocyanin-pigmented roots and are generally purple, red/pink or orange/yellow in colour and plants are often prone to early flowering and bolt easily. The center of diversity for this group is the Himalayan-Hindu Kush region (Stolarczyk and Janick, 2011). They suggested that the Western sub-group evolved slightly later and are characterized by carotenoid-pigmented roots that are orange, yellow or occasionally red or white in color. Orange carrots were selected from yellow cultivars as indicated by genetic analyses performed by Shim and Jorgensen (2000) and Iorizzo *et al*. (2013). Orange carrot roots require extended exposure to cold temperatures in order to produce flowers and are, thus, adapted to cooler climates (Atherton *et al*., 1990).

Saha *et al*. (2016) also attempted cluster analysis by UPGMA method using 38 inbred lines of tropical carrot with four quantitative traits. They grouped the genotypes into two clusters with 35 and 3 inbreds with maximum distance of 76.67. Amin *et al*. (2010) performed diversity analysis in carrot and reported a wide range of D^2 values (7.71 to 727.17) observed in 48 carrot germplasm, the lowest in IPC-122 and CA-05-01, whereas the upper end is the D^2 between CCA-05-01 and Nantes. The 48 genotypes were grouped into 14 clusters and the pattern of clustering of genotypes is independent of their place of collection or development. They concluded that selection based on weight of marketable roots per plot, root weight, shoot weight per plant and per cent marketable roots would be more efficient for the improvement of better-quality roots in carrot crop. Ibanez *et al*. (2014) performed multivariate analysis of morphological diversity and clearly differentiated two accessions, however, the results

Table 3. Pearson correlation matrix of carrot germplasm

	Plant height (cm)	Root length (cm)	Shoot length	Shoulder diameter (cm)	Root diameter (mm)	Core diameter (mm)	Cortex diameter (cm)	No. of leaf per plant	Total plant weight (g)	Individual root weight (g)	Avg shoot weight (g)	Root: Gross plant weight ratio	Root: shoot ratio	Market-able roots (%)
Root length (cm)	0.043^{NS}													
Shoot length (cm)	0.951^{**}	-0.179^{NS}												
Shoulder diameter (mm)	0.233^{*}	0.325^{**}	0.142^{NS}											
Root diameter (mm)	0.274^{**}	0.296^{**}	0.191^{NS}	0.761^{**}										
Core diameter (mm)	0.211^{*}	0.196^{*}	0.109^{NS}	0.572^{**}	0.533^{**}									
Cortex diameter (mm)	0.078^{NS}	0.133^{NS}	0.073^{NS}	0.267^{**}	0.576^{**}	-0.363^{**}								
No. of leaf per plant	-0.050^{NS}	0.316^{**}	-0.159^{NS}	0.441^{**}	0.417^{**}	0.526^{**}	-0.010^{NS}							
Total plant weight (g)	0.386^{**}	0.230^{*}	0.279^{**}	0.585^{**}	0.610^{**}	0.535^{**}	0.106^{NS}	0.522^{**}						
Root weight (g)	0.221^{*}	0.229^{*}	0.110^{NS}	0.449^{**}	0.610^{**}	0.464^{**}	0.226^{*}	0.450^{**}	0.733^{**}					
Shoot weight (g)	0.394^{**}	0.184^{NS}	0.310^{**}	0.537^{**}	0.487^{**}	0.464^{**}	0.022^{NS}	0.455^{**}	0.937^{**}	0.449^{**}				
Root: plant weight ratio	-0.405^{**}	-0.149^{NS}	-0.371^{**}	-0.377^{**}	-0.208^{*}	-0.256^{**}	0.095^{NS}	-0.215^{*}	-0.541^{**}	0.108^{NS}	-0.766^{**}			
Root:shoot ratio	0.373^{**}	0.139^{NS}	0.334^{**}	0.340^{**}	0.188^{NS}	0.220^{*}	-0.064^{NS}	0.191^{NS}	0.481^{**}	-0.190^{NS}	0.730^{**}	-0.929^{**}		
Marketable roots (%)	-0.334^{**}	0.011^{NS}	-0.358^{**}	-0.179^{NS}	-0.125^{NS}	-0.186^{NS}	0.122^{NS}	-0.010^{NS}	-0.320^{**}	-0.036^{NS}	-0.402^{**}	0.550^{**}	-0.430^{**}	
Root yield (t/ha)	-0.010^{NS}	0.236^{*}	-0.135^{NS}	0.237^{*}	0.389^{**}	0.265^{**}	0.247^{*}	0.345^{**}	0.311^{**}	0.700^{**}	0.049^{NS}	0.412^{**}	-0.391^{**}	0.644^{**}

*, ** Significance at 1 and 5%, respectively. NS- Non-significant.

were not in line with molecular diversity. Baranski *et al*. (2012) reported higher morphological and genetic diversity in Asian genepool than Western type accessions by using 17 and 61 accessions, respectively. Variation within accessions could be due to allelic variation among plants populations as earlier reported by Maksylewicz and Baranski (2013) while studying Intra-population genetic diversity of cultivated carrot from continental Asia, Europe, Japan and USA. They found that allelic richness and variability in landraces was higher than F_1 hybrids and open-pollinated cultivars. Luby *et al*. (2016) investigated 140 accessions in United States of America carrot germplasm and reported that the cultivated carrot germplasm in the USA forms an unstructured population and their findings suggested that the genetic diversity present in carrot cultivars have freedom to operate and is potentially large enough to support carrot breeding efforts in most market classes given present levels of intellectual property protection.

Conclusion

Observations on agro-morphological diversity in carrot accessions conserved in National Genebank highlighted that (i) it has diverse root colour groups i.e. red, light to dark purple, pale to light yellow and orange, (ii) except orange colour accessions, most of others had intra-population variation for root colour and root morphometric traits which was predominant in purple colour accessions, (iii) orange colour accessions showed uniformity in root traits, however, they are of temperate type and did not flower in Delhi condition (because of vernalization requirement) and (iv) none of the accession outperformed commercial varieties except for one or two traits indicating rare possibility of immediate commercial use. The present study revealed significant variation in carrot germplasm at agro-morphological level, however, we suggest for use of molecular tools in assessing the diversity and characterize the accessions after reinforcing homozygosity by attempting selfing for 3-4 generations.

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RESEARCH ARTICLE

Characterisation of Exotic Rice Germplasm for Qualitative Traits

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Characterization of exotic germplasm of rice for qualitative traits was done in the Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University during 2019. Eighty-nine exotic rice accessions received from IRRI, Philippines were characterized along with five check varieties. The experiment was set in augmented block design with five blocks. Accessions were characterized for qualitative traits as per DUS descriptor. Out of the 25 qualitative traits observed, eight each had one and two character states. The traits flag leaf attitude, lemma and palea colour, colour of apiculus, distribution of awns, panicle attitude of main axis, panicle exsertion, and pericarp colour were having three character states. Colour of awns and caryopsis shape had four classes. Qualitative traits, less affected by environment can be used as morphological marker for identifying genotypes. Twenty-two accessions with superior characteristics like erect leaf, erect flag leaf, erect and strong culm and well exserted panicle were identified.

Key Words: Characterization, Exotic rice germplasm, Qualitative traits

Introduction

Genetic diversity in rice, the most ancient and major food crop of the world far exceeds that in any other crops as it is highly adaptable to its environment of growth. Today rice is cultivated in all parts of the world except Antarctica (Priya *et al*., 2019). This diversity can be used in breeding programmes. In order to provide superior lines for plant breeding programmes, agro-morphological characterization of germplasm accessions is one of the most essential aspects. Evaluation of germplasm collections is essential for assessing the variability, maintenance of the diversity and identification of valuable genes. Numerous morphological features acts as crucial aspect of rice grain yield. Plant height, tillering and panicle morphology are significantly associated with grain production in rice. Hence, the present study has been taken up to evaluate exotic germplasm of rice based on qualitative traits and to identify accessions with superior plant ideotype.

Materials and Methods

Characterization of exotic germplasm of rice (*Oryza sativa* L.) for qualitative traits was done in the Department of Plant Breeding and Genetics, College of Agriculture, during June 2019 to October 2019. Eighty nine exotic accessions of rice received from IRRI, Philippines at NBPGR Regional Station Thrissur were evaluated along with check varieties, Jyothi, Jaya, Thulasi, Vaishak and Manurathna. The experiment was set in augmented block design with 5 blocks; each block consisted of 20 exotic accessions and check varieties in plots of $5m^2$ at a spacing of 20 cm x 15cm. Plants were raised as rainfed crop in upland condition. Observations were recorded from five plants of each line for the qualitative traits as per DUS descriptor by Rani *et al*., 2006 at appropriate stage.

Results and Discussion

Among the 25 qualitative traits observed, coleoptile, auricle, ligule, collar and sterile lemma were colourless in all the accessions. Anthocyanin colouration of leaf sheath, distribution of anthocyanin colouration on the leaf blade and shape of ligule were same in all the accessions. Threshability was intermediate in all accessions. Rao *et al*., 2013 and Islam *et al*., 2018 also observed green basal leaf in majority of accessions. Among the 64 farmer varieties Rao *et al*., 2013 studied, two varieties were having green coleoptile, while, one variety had purple coleoptile,while others were colourless. They observed that 56 out of 65 farmer varieties were having no anthocyanin colouration on leaf sheath. As per their study three classes of auricle colouration was observed with majority being colourless (83.07%). Five varieties

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had light purple auricle, while 6 varieties had purple auricle.

Basal leaf sheath colour of the accessions were categorized as green and purple. Out of 89 accessions, eleven accessions exhibited purple colour and the rest seventy-eight accessions and check varieties had green coloured basal leaf sheath. (Table 1). Rao *et al.,* 2013 and Islam *et al*., 2018, also observed majority of germplasm having green basal sheath colour, while a few had coloured basal leaf sheath. Based on these studies it can be assumed that purple colour of basal leaf is a trait which is present only in a few genotypes and hence, can be used as a marker for identification of genotypes.

On the basis of leaf blade attitude, eighteen accessions and check variety Jaya were having semi-erect leaf blade attitude and the rest seventy-one accessions and other four check varieties were having erect leaf blade attitude as presented in Table 1. Twenty accessions and one check variety exhibited erect flag leaf attitude, five accessions showed horizontal type flag leaf attitude and the rest sixty-four accessions along with four check varieties were having semi-erect flag leaf attitude. Burgess *et al.,* 2015 suggested that reduced susceptibility to photo inhibition and reduced risk of overheating was observed with erect leaf stature. According to Tafere and Irie 2019, erect leaf angles lead to improvement in whole day carbon gain by enhancing light absorption at low solar angles under dense canopies. There was a positive correlation between flag leaf angle and photosynthesis material translocation which increases spikelets fertility and grain yield in rice. Jennings *et al*., 2003, reported that modifications of leaf angle and flag leaf angle have been emphasized by many investigators as a means to obtain better light utilization. Hence, the accessions with erect leaf and flag leaf might have more light use effiency.

Observation on culm habit showed that thirty-nine accessions were having semi-erect and the rest fifty accessions and five check varieties were having erect culm habit. There was no open and spreading culm habit among the accessions. Islam *et al*., 2018 observed culm angle as erect in 29 per cent of the genotypes, while intermediate types of culm was seen in 60 per cent and open types in 11 per cent of the genotypes they studied. Tafere and Irie. (2019), reported that short culm erect cultivar produced significantly higher photosynthesis rate, poor stomatal conductance, maximum PAR, higher canopy photosynthesis and grain yield than short culm open cultivar. Hence, accessions with erect stem may have these advantages over other accessions

Culm lodging resistance observed in accessions showed that four accessions had weak culm and the rest 85 accessions and five check varieties were recorded with strong culm. According to Rani *et al*., 2017, lodging of the rice crop is the major limiting factor to rice productivity. Lodging not only reduces the yield but also it deteriorates grain quality, impedes mechanical harvesting, increases harvesting and drying costs. Lodging resistance is a complex trait influenced by environment and structural properties of the stem. Hence, the accessions showing lodging resistance can be used in breeding programme.

Stigma colour visually observed showed that fourteen accessions and two check varieties possessed purple stigma colour and the rest seventy-five accessions and three check varieties had white stigma colour. Manjunatha *et al*., 2018, observed purple stigma in 62 per cent of land races, while in three per cent of landraces it was light green and in 35 per cent of cultivars it was white when they evaluated 60 landraces of rice. Islam *et al*., 2018, based on their studies in 113 aromatic rice varieties observed that 88.49 per cent of genotypes had white colour of stigma and 5.31, 6.19 per cent of accessions had light purple and purple coloured stigma, respectively. All these studies points to the fact that stigma colour can be used to morphologically distinguish between genotypes.

Eleven accessions exhibited brown spots on lemma and palea, twenty-two accessions had golden straw colour and the rest fifty-six accessions and five check varieties had straw colour for lemma and palea. Manjunatha *et al*., 2018 observed six states of expression for lemma and palea colour among 60 landraces they evaluated. They were straw, gold and gold furrows on straw background, brown spots on straw, brown furrows on straw, brown and purple black. Islam *et al*., 2018, observed nine different types for lemma and palea colour. They were gold, brown furrows on straw, brown, reddish to light purple, purple spots on straw, purple furrows on straw, purple and black. Being a qualitative trait showing wide variability and not influenced by environment, this can be used for identification of specific genotypes.

According to the observations recorded, two accessions possessed strong colour for apiculus, thirty-nine accessions along with two check varieties exhibited

Table 1. Qualitative traits of exotic accessions as per DUS criteria

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
EC 207747	1	1	1	0	3	1	1	3	1	3	3	1	1	1	5	1	1	0	0	7	5	7	2	5	3
EC 204847	1	1	1	0	3	1	1	3	1	3	3	1	5	4	5	1	9	1	4	5	5	7	2	1	3
EC 204863	1	1	1	0	3	1	1	3	1	3	3	1	1	4	7	1	9	5	4	5	5	5	2	5	3
EC 204865	1	1	1	0	3	1	1	3	1	3	1	1	5	4	1	1	9	1	4	5	5	5	2	5	1
EC 204868	1	1	1	0	1	1	1	3	1	3	1	1	5	1	5	1	9	5	4	5	5	5	2	5	1
EC 204928	1	1	1	0	3	1	1	3	1	1	1	1	5	1	5	1	9	1	1	5	5	7	2	6	1
EC 204970	1	1	1	0	3	1	1	3	1	1	3	1	5	3	1	1	9	1	1	5	5	7	2	5	1
EC 204991	1	1	1	0	3	1	1	3	1	3	3	3	1	3	1	1	1	0	0	2	5	5	2	5	3
EC 204999	1	1	1	0	3	1	1	3	1	1	3	1	1	1	5	1	1	0	0	2	5	7	2	5	1
EC 205001	1	1	1	0	3	1	1	3	1	5	3	1	1	3	5	1	9	5	4	5	5	7	2	1	3
EC 205042	1	1	1	0	3	1	1	3	1	3	3	1	1	3	1	1	9	3	4	5	5	7	2	5	3
EC 205047	1	1	1	0	1	1	1	3	1	1	2	1	1	3	1	1	9	5	4	5	5	5	2	1	1
EC 205070	1	1	1	0	3	1	1	3	1	5	3	1	1	3	5	1	9	5	1	7	5	7	2	5	3
EC 205072	1	1	1	0	3	1	1	3	1	3	1	1	1	3	1	1	9	5	1	5	5	7	2	5	3
EC 205128	1	3	1	0	1	1	1	3	1	3	1	1	1	3	1	1	1	0	0	2	5	5	2	6	3
EC 205192	1	1	1	0	3	1	1	3	1	1	1	1	1	3	1	1	9	5	1	5	9	7	2	5	2
EC 205205	1	1	1	0	1	1	1	3	1	1	1	1	1	1	5	1	1	0	0	5	5	5	2	5	2
EC 205223	1	1	1	0	1	1	1	3	1	1	3	1	1	3	1	1	1	0	0	5	5	7	2	6	1
EC 205252	1	1	1	0	1	1	1	3	1	1	3	1	1	3	1	1	9	1	1	2	9	7	2	6	1
EC 205264	1	1	1	0	3	1	1	3	1	5	3	1	5	1	1	1	9	1	1	2	5	7	2	5	3
EC 205269	1	1	1	0	1	1	1	3	1	1	3	1	1	3	1	1	1	0	0	5	5	5	2	6	1
EC 205275	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	1	0	0	5	5	5	2	5	1
EC 205305	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	1	0	0	5	5	5	2	6	2
EC 205314	1	1	1	0	1	1	1	3	1	3	1	1	1	4	1	1	1	0	0	5	5	5	2	1	3
EC 205321	1	3	1	0	1	1	1	3	1	5	1	1	5	1	1	1	9	1	4	5	9	7	2	1	3
EC 205333	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	9	1	1	5	5	7	2	6	3
EC 415392	1	1	1	0	1	1	1	3	1	1	1	1	1	1	5	1	1	0	0	5	5	5	2	1	4
EC 415393	1	1	1	0	1	1	1	3	1	3	1	1	1	3	1	1	9	5	1	5	5	5	2	1	3
EC 415394	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	9	1	1	5	5	5	2	1	4
EC 415396	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	9	1	1	5	5	5	2	1	4
EC 415397	1	3	1	0	1	1	1	3	1	3	3	1	5	1	1	1	9	1	4	5	5	7	2	1	3
EC 415399	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	5	2	1	3
EC 415401	1	1	1	0	1	1	1	3	1	3	1	1	1	3	1	1	9	1	1	5	5	5	2	6	3
EC 415402	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	9	5	1	5	5	5	2	1	3
EC 415403	1	1	1	0	1	1	1	3	1	1	1	1	1	1	5	1	9	5	1	5	5	7	2	1	3
EC 415404	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	7	2	1	3
EC 415405	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	1	0	0	5	5	7	2	1	4
EC 415406	1	1	1	0	1	1	1	3	1	1	1	1	1	1	1	1	1	0	0	5	5	5	2	1	3
EC 415407	1	1	1	0	1	1	1	3	1	1	1	1	1	1	5	1	1	0	0	5	5	7	2	1	3
EC 415408	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	9	1	1	5	5	5	2	1	3
EC 415409	1	1	1	0	1	1	1	3	1	5	3	1	1	4	5	1	1	0	0	5	5	5	2	1	3
EC 415410	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	5	2	1	3
EC 415411	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	9	5	1	5	5	7	2	1	3
EC 415412	1	1	1	0	1	1	1	3	1	3	3	1	1	1	1	1	1	0	0	5	5	7	2	1	4
EC 415413	1	1	1	0	1	1	1	3	1	1	1	1	1	1	5	1	9	3	1	5	5	7	2	1	3
EC 415414	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	9	1	1	5	5	5	2	5	3
EC 415415	1	1	1	0	1	1	1	3	1	3	3	1	1	1	1	1	1	0	0	5	5	7	2	5	3
EC 415416	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	1	0	0	5	5	5	2	1	3
EC 415417	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	9	1	1	2	5	5	2	1	3
EC 415420	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	1	0	0	5	5	7	2	1	3
EC 415421	1	1	1	0	1	1	1	3	1	1	1	1	1	4	5	1	9	1	1	5	5	7	2	1	3
EC 415422	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	7	2	1	3
EC 415423	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	1	0	0	7	5	5	2	1	3

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
EC 415425	1	1	1	0	1	1	1	3	1	3	3	1	1	1	1	1	1	0	0	5	5	5	2	1	3
EC 415426	1	3	1	0	1	1	1	3	1	1	1	1	1	1	1	1	1	0	0	7	5	7	2	1	3
EC 415427	1	1	1	0	1	1	1	3	1	3	1	1	5	1	1	1	9	1	4	5	5	5	2	1	3
EC415428	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	7	2	1	1
EC 415429	1	3	1	0	1	1	1	3	1	3	3	1	5	1	1	1	1	0	0	5	5	7	2	1	3
EC 415431	1	1	1	0	1	1	1	3	1	3	3	1	1	1	1	1	1	0	0	5	5	5	2	1	4
EC 415433	1	3	1	0	1	1	1	3	1	3	3	1	5	1	1	1	9	3	4	5	5	5	2	1	3
EC 415434	1	3	1	0	1	1	1	3	1	3	3	3	5	1	1	1	9	5	1	5	5	5	2	1	3
EC 415435	1	3	1	0	1	1	1	3	1	3	3	3	1	1	1	1	1	0	0	5	5	5	2	1	3
EC 415436	1	1	1	0	1	1	1	3	1	3	3	3	1	1	5	1	1	0	0	5	5	3	2	1	4
EC 415437	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	1	0	0	5	5	5	2	1	3
EC 415438	1	3	1	0	1	1	1	3	1	3	1	1	5	1	5	1	1	0	0	5	5	5	2	1	3
EC 415439	1	3	1	0	1	1	1	3	1	3	1	1	5	1	1	1	9	5	4	7	9	5	2	1	4
EC 415441	1	1	1	0	1	1	1	3	1	3	3	1	1	4	5	1	9	3	1	5	5	5	2	1	3
EC 415442	1	1	1	0	3	1	1	3	1	3	1	1	1	1	5	1	9	5	1	7	5	5	2	1	1
EC 415444	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	9	5	1	5	5	5	2	1	3
EC 415445	1	1	1	0	1	1	1	3	1	3	1	1	1	1	5	1	9	5	1	5	5	5	2	1	4
EC 415446	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	9	1	1	5	5	5	2	1	3
EC 415448	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	5	2	1	3
EC 415449	1	1	1	0	1	1	1	3	1	3	1	1	1	4	5	1	9	1	1	2	5	5	2	1	4
EC 415450	1	1	1	0	1	1	1	3	1	3	3	1	1	1	5	1	1	0	0	5	5	5	2	1	4
EC 415451	1	1	1	0	3	1	1	3	1	3	1	1	1	4	1	1	1	0	0	5	5	5	2	1	3
EC 415452	1	3	1	0	1	1	1	3	1	1	1	1	1	3	1	1	1	0	0	5	5	5	2	1	4
EC 415454	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	1	0	0	5	5	7	2	1	3
EC 415455	1	1	1	0	1	1	1	3	1	3	1	1	1	3	1	1	9	3	1	5	5	7	2	1	3
EC 415456	1	1	1	0	3	1	1	3	1	3	3	1	1	3	1	1	1	0	0	5	5	7	2	1	3
EC 415458	1	1	1	0	1	1	1	3	1	1	1	1	1	1	1	1	1	0	0	5	5	7	2	1	3
EC 415459	1	1	1	0	1	1	1	3	1	1	1	1	1	4	5	1	9	3	2	7	5	5	2	1	2
EC 415460	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	1	0	0	5	5	7	2	1	1
EC 415461	1	1	1	0	1	1	1	3	1	3	1	1	1	1	1	1	9	1	1	7	5	7	2	1	4
EC 415462	1	1	1	0	1	1	1	3	1	1	3	1	1	3	1	1	1	0	0	5	5	5	2	1	3
EC 415463	1	1	1	0	1	1	1	3	1	3	1	1	1	3	1	1	1	0	0	5	5	5	2	1	3
EC 415464	1	1	1	0	3	1	1	3	1	3	1	1	1	3	1	1	1	0	0	5	5	7	2	1	3
EC 415465	1	1	1	0	1	1	1	3	1	3	3	1	1	3	1	1	1	0	0	5	5	7	2	1	3
EC 415468	1	1	1	0	1	1	1	3	1	3	1	1	1	3	1	1	9	1	1	5	5	5	2	1	3
EC 415470	1	1	1	0	1	1	1	3	1	3	3	1	1	3	1	1	1	0	0	5	5	7	2	1	3
Check Varieties																									
Jyoti	1	1	1	1	1	1	1	3	1	3	1	1	1	1	1	1	9	5	1	5	5	5	2	5	3
Jaya	1	1	1	1	2	1	1	3	1	3	1	1	5	1	5	1	9	3	1	4	3	5	2	5	3
Thulasi	1	1	1	1	1	1	1	3	1	1	1	1	5	1	1	1	9	5	1	5	5	5	2	5	3
Vaisakh	1	1	1	1	1	1	1	3	1	3	1	1	1	1	1	1	1	0	0	5	5	7	2	5	3
Manurathna	1	1	1	1	1	1	1	3	1	3	1	1	1	1	5	1	1	0	0	5	5	5	2	5	3

A-coleoptile colour; **B-** basal leaf sheath colour; **C-** leaf sheath anothocyanin colouration; **D-**leaf blade distribution of anthocyanin; **E-** leaf blade attitude; **F-** auricle colour; **G-** colour of collar; **H-** ligule shape; **I-** ligule colour; **J-** flag leaf attitude; **K-** culm habit; **L-** culm lodging resistance; **M-** stigma colour; **N-** lemma and palea colour; **O-** lemma colour of apiculus; **P- s**terile lemma colour; **Q-** presence of awns; **R-** distribution of awns; **S-** colour of awns; **T-** panicle attitude of main axis; **U-** panicle attitude of branches; **V-** panicle exsertion; **W-** panicle threshability; **X-** caryopsis pericarp colour; **Y-** caryopsis shape.
Numbers indicate the character state in the descriptor

medium colour and the rest forty-eight accessions and three check varieties did not have any colour. Islam *et al*., 2018 observed five classes in colour of apiculus in 113 aromatic rice lines they evaluated. This polymorphic trait also can be used in identification of rice genotypes.

Forty-six accessions along with two check varieties were without awns and forty-three accessions and three check varieties exhibited the presence of awns. Islam *et al*., 2018 observed awns in about one third of the accessions they studied. According to Guo *et al*., 2018, awns, which are derived from floral structures in grasses,

Table 2. Exotic accessions of rice with superior qualitative traits

Accession	Erect Leaf	Erect flag leaf	Erect culm	Strong culm	Well exsetred panicle	Total score
EC 204928		√	√	√	√	4
EC 205192		√	√	√	√	4
EC 205205	√	√	√	√	√	5
EC 205223	√	√		√	√	4
EC 205252	√	√		√	√	4
EC 205333	√		√	√	√	4
EC 415392	√	√	√	√		4
EC 415403	√	√	√	√	√	4
EC 415405	√		√	√	√	4
EC 415406	√	√	√	√		4
EC 415407	√	√	√	√	√	5
EC 415411	√		√	√	√	4
EC 415413	√	√	√	√	√	5
EC 415420	√		√	√	√	4
EC 415421	√	√	√	√	√	5
EC 415426	√	√	√	√	√	5
EC 415452	√	√	√	√		4
EC 415454	√		√	√	√	4
EC 415455	√		√	√	√	4
EC 415458	√	√	√	√	√	5
EC 415460	√		√	√	√	4
EC 415461	√		√	√	√	4

are known to be critically important for photosynthesis and transpiration. However, domestication and human selection resulted in awnless types to facilitate grain harvesting, handling and storage (March, 2015).

In the present study 21 accessions along with two check varieties had awns on the grains which are present on tip of the panicle. Six accessions and one check variety possessed awns on the grains towards the upper half of the panicle. Sixteen genotypes exhibited awns on whole length of panicle and the rest forty-six accessions and two check varieties were awn-less. Islam *et al*., 2018, characterized 36 aromatic rice germplasm of Bangladesh and found that among 13 genotypes having awn, in nine genotypes awns were present only in the tip and in remaining four it was present in the upper half of panicle. With domestication awns become eliminated from the genotypes or became restricted to a limited portion of the panicle facilitating easy harvest and threshing.

The colour of awn recorded at ripening stage showed that thirty accessions and three check varieties had yellowish white awns, only one genotype showed yellowish awn, twelve accessions had reddish brown and the rest forty-six accessions with two check varieties were awnless as indicated in Table 1. Mondal *et al*., 2014 observed colour of awn as a polymorphic trait.

The panicle attitude of main axis was determined by curvature of panicle base. Seven accessions had semi-straight panicle, while, eight accessions had deflexed drooping and seventy-four accessions along with check varieties had drooping deflexed panicle attitude of main axis. According to Xu *et al*., 2005, one of the parameters of rice ideal panicle type for Liaoning province of China was neck-panicle curvature <40°. In the present study majority of the accessions had this more than 40° an ideal character.

According to Liang *et al*., 2017, erect panicle type is an important characteristic for japonica super rice and plays a significant role in enhancing yield. The erect panicle type can be considered as a genetic ideotype resource to japonica super rice group by virtue of its agronomic advantages such as grain number per panicle and biomass. Also erect panicle optimizes canopy structure. Rice plants with drooping panicle can be lodged easily. However, when the panicle is heavy there will always be a tendency for drooping. Hence, the axis of panicle suitable for different situation may vary and breeder has to choose the best type.

Attitude of panicle branches was characterized by the compactness of the panicle and was classified with respect to its mode of branching, angle of primary branches and spikelet density. Only four accessions

were observed to have spreading panicle and the rest eighty-five accessions along with check varieties showed semi-erect type of panicle attitude of branches. Rice breeders selectively breed for compact panicle type and open panicle type is selected against, for maximizing crop grain production and harvest (Fageria, 2007). Semi erect panicle observed in the present study is an indication that some amount of breeding intervention might have happened in the accessions with respect to branching attitude of panicle.

Panicle exertion was recorded at near ripening stage. On the basis of observations recorded there was only one accession having partly exserted panicle, thirty-nine accessions along with one check variety exhibited well exserted panicle, the rest forty-nine accessions and four check varieties were having mostly exserted panicle. Manjunatha *et al*., 2018 and Islam *et al.,* 2018 observed exerted or well exerted panicles in majority of accessions. If upper internode of panicle is short lower panicle branches remain enclosed, spikelets in that branches become sterile or partially filled and are often blackened by secondary pathogens, resulting in yield losses (Jennings *et al*.,1979). For better yield and for enhancing crossing in hybrid rice programme well exerted panicle is essential.

Eight accessions exhibited red pericarp colour, sixteen accessions along with five check varieties showed light red colour and the rest of sixty-five accessions were having white pericarp colour. Manjunatha *et al*., 2018, observed red pericarp colour in 50 per cent of landraces from Kerala,while, Islam *et al*., 2018 observed white pericarp colour in 61 per cent of Bangladesh accessions. Colour of pericarp is considered as a grain quality of commercial importance. In Kerala, people prefer red kernelled rice and that might have resulted in rice germplasm rich in red pericarp colour as observed by Manjunatha *et al*., 2018. However, as the present study was carried out in exotic germplasm we could observe more white kernelled accessions.

The observations recorded based on the length to width ratio of grain showed that out of 89 accessions ten were short slender, four had short bold grains, six were long bold and rest sixty-nine along with five check varieties were medium slender. Mondal *et al*., 2014 observed highest polymorphism for decorticated grain shape. Manjunatha *et al*., 2018 observed five states of expression for decorticated grain shape. Being highly polymorphic, this trait also can be used in identification of genotypes and seed certification programmes.

Grouping of Aaccessions based on Ideal Plant Characteristics

Accessions were grouped based on superior characteristics such as erect angle of leaf and flag leaf, strong and erect culm with well exserted panicle and is given in Table 2. Qualitative traits less affected by the environment can be used as a robust marker for identifying genotypes. Erect attitude of leaf and stem has a positive effect on yield through high photosynthesis. Hence, accessions EC204928, EC205192, EC205205, EC205223, EC205252, EC205333, EC415392, EC415403, EC415405, EC415406, EC415407, EC415411, EC415413, EC415420, EC415421, EC415426, EC415452, EC415454, EC415455, EC415458, EC415460 and EC415461 were identified as superior with erect leaf, flag leaf, erect and strong culm and fully exserted panicle. These can be utilized in breeding programmes to transfer superior traits

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RESEARCH ARTICLE

Morpho-physiological Characterization of Bread Wheat Accessions for Heat Stress Tolerance under Late Sown Conditions of North-Western Plain Zone of India

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Bread wheat is grown in the sub-tropical and tropical regions world-wide. Terminal-heat stress is a major abiotic stress in wheat and global warming due to climate change has negatively impacted its production and productivity. We evaluated 96 accessions of bread wheat germplasm, which included 79 indigenous and 17 exotic collections, by investigating 16 morpho-physiological and yield-related traits during two successive *Rabi* seasons of 2018-19 and 2019-20 under non-stressed and heat-stressed (as a delayed sown crop) environments. Heat susceptibility index (HSI) was used to classify tolerant (HSI <1.0) and susceptible (HSI >1.0) accessions. The heat-stress showed negative impact on the phenotypic expression of 14 morpho-physiological and yield related traits by reducing the traits more prominently in susceptible accessions than the tolerant. However, early ground cover showed the increased expression in the tolerant accessions and higher variability in the germplasm under the heat-stress. Grain length/width ratio (LWR) also improved in the germplasm under heat-stress, while, there was a marked increase in LWR of the susceptible accessions mainly due to relatively higher decrease of grain width in these accessions under heat-stress. The plot yield associated positively with its contributing traits namely yield per plant, number of grains per plant, number of grains per spike, grain weight per spike and plant biomass under both the non-stressed and the heat-stressed environments, but its association with chlorophyll fluorescence was only under heat-stress. The germplasm accessions IC574476 (HD2967), IC393878 (WH157), IC296383 (WR544), EC534487 (PAU351), IC519900 (HD2932) and IC539221 {EIGN-I-(04-05)/149} produced high yield and were stable across the environments. The identified bread wheat germplasm lines could be used as potential parents for bi-parental and multi-parental populations.

Key Words: Bread wheat, Characterization, Germplasm accessions, Heat-stress, Morpho-physiological traits

Introduction

Bread wheat (*Triticum aestivum* L.), an important cereal crop, is a staple food for 40% of the global population (Acevedo *et al*., 2018). It provides 20% of the total dietary calories consumed world-wide (Shiferaw *et al*., 2013). Wheat crop was cultivated on 215.9 million ha land with global production of 765.8 million tonnes during 2019 and contributed 8% to world's food basket (FAO, 2021). Global warming has negatively impacted the production and productivity of food crops in different regions of world during the last decade (Wang *et al*., 2018). Effective utilization of genetic resources conserved in the genebanks is vital for crop breeding to increase genetic gains and thus addressing the challenges posed by global warming (Reynolds *et al*., 2015; Mondal *et al*., 2016). Studies using global and country based models suggest that every 1°C rise in average global surface temperature will lead to decline in wheat yields from 4.1 to 6.4% world-wide and 8.0% in India (Liu *et al*., 2016). High temperature during grain development

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stage is a major limiting factor in wheat production in many production environments (Farooq *et al*., 2011). Late sown wheat is exposed to high temperature-stress at grain filling stage, commonly known as terminal-heat stress, and it adversely affects plant growth and consequently the grain yield.

Late sowing of the bread wheat is prevalent in the western part of the Indo-Gangetic Plain (IGP) region of India, where popular rice-wheat cropping system is followed. As a result, it delays sowing of wheat and leads to exposing the crop to terminal-heat stress. A large area in eastern and central parts of India is under late-sown condition due to delayed harvesting of *Kharif* crops, which exposes wheat crop to terminal-heat stress resulting in significant yield losses (Rane *et al*., 2007; Kumar *et al*., 2014). The substantial area of eastern IGP, peninsular and central parts of India are under severely heat-stressed, whereas it is moderate in north-western part of IGP (Joshi *et al*. 2007b,c). Hence, the assessment of impact of heat-stress on the productivity of wheat has emerged as top priority in the climate change scenario (Joshi *et al*. 2007a,b). Selection of stress tolerant germplasm lines by screening large genebank collections is a pragmatic approach to develop climate-resilience (McCouch *et al*., 2020).

The morpho-physiological adaptive traits like early or rapid ground cover, stay-green, chlorophyll fluorescence, biomass and flag-leaf area contribute towards heat-stress tolerance ability of wheat plant (Reynolds *et al*., 1994, 2001; Cossani and Reynolds, 2012; Latif *et al*., 2020). High temperature during crop growth and grain filling stage in wheat significantly decreases morphological, yield and its component traits *viz*., plant height, number of tillers per plant, spike length, number of spikelets per spike, number of grains per spike, grain weight and yield (Mondal *et al*., 2015; Akter and Islam, 2017; Telfer *et al*., 2018). However, Telfer *et al.* (2021) advocated that adaption to heat stress should be considered as the combination of total performance and responsiveness to heat stress. Each genotype responds to the changed environment differently due to its genetic makeup and its interaction with environment (Rane *et al*., 2007; Elbasyoni, 2018; Yashavanthakumar *et al*., 2021). The genotypes, which maintain high grain weight and yield under heat-stressed environment, seem to possess higher tolerance to hot environment (Sharma *et al*., 2008; Fleitas *et al*., 2020).

Genotype-environment interaction is an important factor in the expression of quantitative traits such as yield and its contributing traits. The G × E interactions are major bottlenecks in selection of superior breeding lines. Therefore, stratification of the environment has been used to reduce the G × E interaction (Eberhart and Russell, 1966). Germplasm being heterogeneous and heterozygous population offers the best opportunity to develop varieties, which might show small G × E interaction. GGEbiplot is useful for ranking the cultivars based on their performance in a specific environment, comparing the performance of pair of cultivars in different environments and identifying the best cultivars in each environment (Yan and Kang, 2002). It is also used in evaluating the cultivars based on both average yield and stability and provides visual analysis of G×E interactions (Frutos *et al*., 2014). The aim of this study was to characterize bread wheat germplasm accessions based on morpho-physiological traits and to assess their yield stability in heat-stressed environment for identification of parents for the development of biparental and multi-parental mapping populations, and their further utilization as donor lines in wheat breeding programmes.

Materials and Methods

Plant Materials and Experimental Design

A select set of 96 bread wheat accessions, which included released varieties, germplasm lines and genetic stocks, was used in the present experiment. The bread wheat accessions were acquired from the working collection of National Gene Bank (NGB), ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The details of these accessions are provided in Table 1. The geo-referencing of bread wheat accessions carried out using software 'DIVA-GIS' (Hijmans *et al*., 2001) and are depicted in Figure 1. The germplasm lines selected were diverse in nature covering all the wheat growing zones of India. The experimental trials were conducted at New Area Research Farm of ICAR-NBPGR, New Delhi, located at latitude 28.649°N, longitude 77.152°E and altitude 220 m, during *Rabi* crop seasons of 2018-19 and 2019-20. The accessions were evaluated for two consecutive crop seasons using two sowing dates: Normal (sown in 1st week of December) and very late sown wheat (sown in 1st week of January) using Augmented block design (ABD) with five blocks, where four national checks namely Raj3765, HD2932, WR544 and HD2967 were randomized and replicated in each

Table 1. Details of bread wheat accessions used in the study along with their IC/EC (Indigenous/Exotic Collection) number, alternate identity and original source of acquisition

Accession Number	Alternate id	Original Source	Accession Number	Alternate id	Original Source
IC443766	RAJ3765	RARI, Jaipur	IC542652	PAU4061	PAU, Ludhiana
IC519900	HD2932	IARI, New Delhi	IC536468	K8415	CSUAT, Kanpur
IC296383	WR544	IARI, New Delhi	IC536483	CPAN2039	IIWBR, Karnal
IC574476	HD2967	IARI, New Delhi	EC574735	8842	CIMMYT, Mexico
EC574731	8832	CIMMYT, Mexico	IC531191	PBW103	PAU, Ludhiana
EC576707	E4828	CIMMYT, Mexico	IC333095	NKD/YSR2910	Barwani, MP
IC252725	HUW467	BHU, Varanasi	IC572925	HPW185	Malan, Kangra, HP
IC252816	KRL13	IIWBR, Karnal	IC252867	NW1014	NDUAT, Ayodhya
IC277741	Dharwad680	Dharwad, Karnataka	IC524299	HW2012	IARI RS, Wellington
IC536081	WL3226	PAU, Ludhiana	IC573461	GW11 (GW396)	Mehsana, Gujarat
IC279617	KHH416	Tehri, Uttarakhand	IC252444	BW/SH49	Kolkata, WB
IC535176	WON-D14	IARI, New Delhi	IC529207	VWFW2150	VPKAS, Almora
IC401976	PHR1011	IIWBR, Karnal	IC290191	HW971	Wellington, TN
IC539221	EIGN-I-(04-05)/149	IIWBR, Karnal	IC112258	VL401	VPKAS, Almora
IC539287	MC2003-71	IIWBR, Karnal	IC627711	CAZ/JSM/AP/01	Jaisalmer, Rajasthan
IC539531	EIGN1(03-04)/112	IIWBR, Karnal	IC443653	HD2851	IARI, New Delhi
IC443661	PHR1017	IIWBR, Karnal	IC252431	BW/SH30	Kolkata, WB
EC534487	VEE/KOEL(PAU351)	USDA, USA	IC252619	HD2590	IARI, New Delhi
IC416018	PAU438 (W 7484)	PAU, Ludhiana	IC529242	VWFW1290	VPKAS, Almora
IC416075	PAU495 (W 8067)	PAU, Ludhiana	IC536162	WL4996	PAU, Ludhiana
IC416078	PAU498 (W 8093)	PAU, Ludhiana	IC536050	WL1803	PAU, Ludhiana
IC416019	PAU439 (W 7485)	PAU, Ludhiana	IC252999	WH594	CCSHAU, Hisar
IC446713	PSR11489	Nizamabad, Telangana	IC443640	DWR240	IIWBR, Karnal
IC075240	C306	CCSHAU, Hisar	IC445365	7th EGPSN78	IIWBR, Karnal
EC178071	NA	CIMMYT, Mexico	IC303071	RAJ3777	RARI, Jaipur
IC542509	PAU1453	PAU, Ludhiana	IC252414	BW1050	Kolkata, WB
IC252348	AKW2294	PDKV, Akola	IC372643	KRR/AK7	Mandi, HP
IC543293	PAU1218	PAU, Ludhiana	IC252620	HD2615	IARI, New Delhi
IC128454	HB602	Bhowali, Uttarakhand	IC240818	GW273	Mehsana, Gujarat
IC416055	PAU475 (W 7883)	PAU, Ludhiana	IC401940	K8962 (Indra)	CSUAT, Kanpur
IC111800	J1-7	Junagadh, Gujarat	IC443694	PBW527	PAU, Ludhiana
IC111931	K101	CSUAT, Kanpur	IC542547	PAU4091	PAU, Ludhiana
EC576317	E1804	CIMMYT, Mexico	EC190962	Cultivar No.30	CIMMYT, Mexico
EC577013	E8826	CIMMYT, Mexico	EC576066	410	CIMMYT, Mexico
EC414149	CHNQIRR 95S OCHN	CIMMYT, Mexico	EC573527	3850	CIMMYT, Mexico
IC252653	HI1433	IARI, RS, Indore	EC576585	E3228	CIMMYT, Mexico
IC252739	HW1058	Wellington, TN	EC190899	Cultivar No.37	CIMMYT, Mexico
IC335792	KAUZ+1B.1R	IIWBR, Karnal	EC574849	9008	CIMMYT, Mexico
IC543425	10TH HTWYT38	IARI, New Delhi	EC576175	E10906	CIMMYT, Mexico
IC402055	K20008 (KRL35)	IIWBR, Karnal	IC582706	HPW240	Malan, Kangra (HP)
IC265318	NKD2671	Sawai Madhopur, Raj	IC393878	WH157	CCSHAU, Hisar
IC445449	ET99745	IIWBR, Karnal	IC542544	PAU4088	PAU, Ludhiana
IC528965	VWFW182	VPKAS, Almora	IC566223	HS492	IARI RS, Shimla
IC549437	PHR1032	IIWBR, Karnal	IC342668	VKG21/72	Chatra, Jharkhand
IC144911	VW120 (GW120)	Mehsana, Gujarat	IC535717	PBW139	PAU, Ludhiana
IC542578	PAU558	PAU, Ludhiana	IC553599	HI1544	IARI RS, Indore
IC535704	PBW124	PAU, Ludhiana	EC277134	713	CIMMYT, Mexico
EC542533	NA*	USDA, USA	NA	CUO/79/Pru 11A	CIMMYT, Mexico

*NA-Not available; **RARI-**Rajasthan Agricultural Research Institute, Jaipur, Rajasthan; **IARI-**Indian Agriculture Research Institute, New Delhi; **CIMMYT-**International Maize and Wheat Improvement Center, Mexico; **BHU-**Banaras Hindu University, Varanasi, Uttar Pradesh; **IIWBR-**Indian Institute of Wheat and Barley Research, Karnal, Haryana; **PAU-**Punjab Agricultural University, Ludhiana, Punjab; **USDA-**United States Department of Agriculture, USA; **CCSHAU- CCS** Haryana Agricultural University, Hisar, Haryana; **PDKV-**Panjabaro Deshmukh Krishi Vidyapeeth, Akola, Maharashtra; **CSUAT-**Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, Uttar Pradesh; **VPKAS-**Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarakhand; **NDUAT-**Acharya Narendra Deva University of Agriculture and Technology, Ayodhya, Uttar Pradesh.

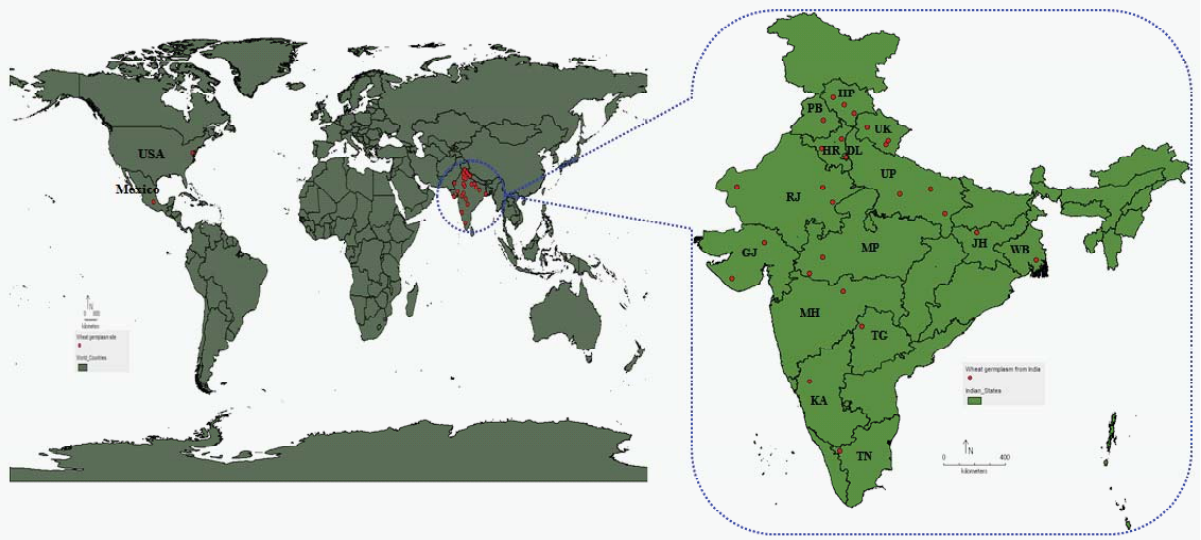

Fig. 1. Geo-referencing map of bread wheat accessions comprised of exotic (17) and indigenous (79) collections used in the screening for terminal heat-stress tolerance

block. The very late sown trial was exposed to high temperatures during grain filling stage. The experimental plot consisted of three rows of 2 m length with 25 cm spacing covering an area of 1.5 m^2. Standard agronomic and cultural practices were followed for raising the healthy wheat crops.

Field Phenotyping and Data Recording

The morpho-physiological and yield related traits for terminal heat-stress tolerance were recorded as per Manual on Physiological Breeding II: A field guide to wheat phenotyping (Pask *et al*., 2012). The phenological parameters were recorded using Zadoks scale observing whole plot (Zadoks *et al*., 1974). Sixteen traits were recorded during different growth phases of the bread wheat crop (Table 2).

Statistical Analysis

The adjusted mean values were used for the statistical analysis of ABD trial data for 16 morpho-physiological and yield contributing traits tested under non-stressed (NS) and heat-stressed (HS) environments over two years. Combined analysis of variance (ANOVA) was performed following a test of homogeneity of variances and applying Aitkin's transformation using SAS software version 9.4 (SAS Institute, 2013). The descriptive statistics and Pearson's correlation coefficients (r) among traits were derived using IBM SPSS statistics software version 20.0 (IBM SPSS, 2011) for both NS and HS environments. We also performed boxplot analysis of 16 morpho-physiological and yield-related traits for both NS and HS environments. The bread wheat accessions were categorized as heat-stress tolerant or susceptible based on heat susceptibility index (HSI) values calculated on grain yield per plot (YPP) data using following formula (Fischer and Maurer, 1978).

$$HSI = (1 - X_a/X_b)/(1 - Y_a/Y_b)$$

Where, X_a and X_b are mean value of YPP of individual accession under HS and NS environment, respectively, and Y_a and Y_b are mean value of YPP of all accessions under HS and NS environment, respectively. HSI values were used to categorize bread wheat accessions as tolerant (HSI <1.0) or susceptible (HSI >1.0).

GGE biplot analysis: The GGE biplot is based on the concept of the biplot (Gabriel, 1971), and provides graphical analysis of genotype (G) and genotype (G) × Environment (E) interaction of multi-environment trials (Yan *et al*., 2000). The GGE biplot analysis was carried out using four environments (two non-stressed: E1, E3 and two heat-stressed: E2, E4) datasets of grain yield per plot using R software version 3.6.1, package GGE Biplot GUI (R Core Team, 2019). The interpretation of GGE biplots was carried out according to Yan and Tinker (2006). The model for constructing a GGE biplot (Yan, 2001) is as follows: $Y_{ij} - \bar{Y}_j = \lambda_1\xi_{i1}\eta_{j1} + \lambda_2\xi_{i2}\eta_{j2} + \varepsilon_{ij}$

Where, Y_{ij}- average yield of i^{th} accession in j^{th} environment, $\bar{Y}_j$- average yield over all accession in j^{th} environment; λ_1 and λ_2 - singular values for PC1 and

Table 2. Morpho-physiological and yield related traits studied in 96 bread wheat accessions grown in non-stressed and heat-stressed conditions during *Rabi* seasons of 2018-19 and 2019-20

Trait studied	Code	How was the trait measured?
Early ground cover (0-10 scale)	EGC	EGC measured by visual observation of whole plot at 45 days after sowing and scored using the scale from 0 (0%) to 10 (100%) by estimating the percentage cover in increments of 10%.
Chlorophyll Fluorescence	CF	CF measured on three randomly selected flag leaves in each plot using hand-held chlorophyll fluorometer (Model OS-30p Chlorophyll Fluorometer, Opti-Science, USA) and dark adaptation leaf clips (Pask *et al*., 2012).
Days to 50% heading	DH	DH recorded as the duration between date of sowing and date at which base of 50% of the spikes have emerged from the flag leaf sheath (Zadoks *et al*., 1974).
Spike Bearing Tillers per Plant	SBT	Number of tillers with fully developed spikes counted each plant and expressed as spike bearing tillers per plant.
Plant Height (cm)	PH	Plant height measured from base of the plant to the top of spike excluding awns of the main tiller at maturity.
Flag Leaf Length (cm)	FLL	FLL measured from base to the tip of flag-leaves of five randomly selected plants on main tillers during grain filling period.
Flag Leaf Width (cm)	FLW	FLW measured from the widest part of the flag leaf of randomly selected five flag leaves of main tillers during grain filling period.
Spike Length (cm)	SL	SL measured from the spike collar to the tip of the spike excluding awns of the main tiller in three plants per accession.
Physiological maturity (days)	PM	PM recorded as the period between date of sowing and date when 50% peduncle in a plot were matured or turned yellow and at this point the glumes will also be losing their colour (Zadoks *et al*., 1974).
Biological yield per plant (g)	BYP	Three plants per accession randomly selected, uprooted at maturity, adhering soil removed and the weight of total biomass recorded for individual plant.
Number of Grains per Plant	NGP	All spikes of each plant were threshed together, debris cleaned and all grains were counted.
Number of Grains per Spikes	NGS	NGS was calculated by dividing total number of grains per plant by number of spikes produced in that particular plant.
Grain weight per spikes	GWS	Total grains of each spike weighed using electronic balance.
Grain L/W Ratio	LWR	LWR was calculated by dividing the length of wheat grain with its width.
Grain Yield per Plant (g)	GYP	Five plants per accession were randomly selected, harvested at maturity and threshed separately. Weight of total grains per plant was taken using electronic balance.
Yield per Plot (g)	YPP	The whole plot (1.5 m^2) was harvested at maturity and thrashed manually. After threshing whole plot grains were weighted using electronic balance machine.

PC2, respectively; ξ_{i1} and ξ_{i2} - PC1 and PC2 scores, respectively for i^{th} accession; η_{j1} and η_{j2} - PC1 and PC2 scores, respectively, for j^{th} environment; and ε_{ij} - residual of the model associated with the i^{th} accession in j^{th} environment.

Results

Genetic Variability for Morpho-physiological Traits

Mean sum of squares estimated for year, genotype (= accession), G × Y interaction and model from ANOVA for 16 morpho-physiological and yield traits in 96 accessions of bread wheat under NS and HS environments are presented in Supplementary Table 1. Accessions showed significant differences for most of the traits under NS environment except SBT, BYP, NGP and GYP. However, these traits showed significant differences due to year and model effects. All the traits except chlorophyll fluorescence showed significant differences due to genotype effect under HS environment. This revealed that the accessions exhibited diverse responses under heat-stress and hence showed significant variability for these traits. The accessions revealed non-significant differences for chlorophyll fluorescence under both the environments, where the effect due to year was significant. Descriptive statistics derived for 16 morpho-physiological and yield-related traits recorded in 96 accessions of bread wheat under both NS and HS environments are presented in Table 3. Accessions showed remarkable variability for early ground cover and days to 50% heading traits. The terminal heat-stress exerted an adverse effect on most of the traits and the reduced values were observed for these traits except early ground cover and grain L/W ratio, which showed higher values under HS environment (Table 3). Phenological traits like days to 50% heading and physiological maturity were significantly reduced by 16.4 days and 23.4 days, respectively, under HS environment. Similarly, plant height and spike length also decreased due to heat-stress by 9.7 cm and 1.1 cm,

Table 3. Descriptive statistics for 16 morpho-physiological and yield contributing traits recorded in 96 accessions of bread wheat grown in non-stressed and heat-stressed environments during two *Rabi* seasons of 2018-19 and 2019-20

Characters	Environment	Range		Mean ± S.E.	Standard deviation	CV (%)
		Min.	Maxi.			
Early Ground Cover (0-10 scale)	Non-stressed	3.0	8.0	5.0±0.11	1.12	22.20
	Heat-stressed	3.0	9.0	5.1±0.13	1.23	24.21
Chlorophyll Fluorescence	Non-stressed	0.72	0.80	0.76±0.01	0.02	2.05
	Heat-stressed	0.62	0.77	0.72±0.01	0.03	3.80
Days to 50% Heading	Non-stressed	77.0	112.0	87.3±0.50	4.94	5.66
	Heat-stressed	62.7	89.5	70.9±0.41	3.98	5.62
Spike Bearing Tillers per Plant	Non-stressed	7.8	17.5	10.9±0.17	1.65	15.16
	Heat-stressed	7.0	14.7	9.7±0.15	1.49	15.39
Plant Height (cm)	Non-stressed	84.9	150.9	106.6±1.31	12.83	12.03
	Heat-stressed	73.2	127.0	96.9±1.25	12.23	12.63
Flag Leaf Length (cm)	Non-stressed	18.4	35.4	24.7±0.34	3.33	13.48
	Heat-stressed	12.6	29.4	18.6±0.31	3.03	16.29
Flag Leaf Width (cm)	Non-stressed	1.6	2.9	2.0±0.02	0.23	11.55
	Heat-stressed	1.3	2.4	1.7±0.02	0.18	10.55
Spike Length (cm)	Non-stressed	8.7	15.6	11.7±0.12	1.18	10.14
	Heat-stressed	8.1	13.5	10.6±0.11	1.10	10.38
Physiological Maturity (days)	Non-stressed	121.0	143.0	126.1±0.31	3.04	2.41
	Heat-stressed	94.5	118.0	102.7±0.32	3.18	3.10
Biological yield per Plant (g)	Non-stressed	32.8	93.6	55.8±1.16	11.40	20.44
	Heat-stressed	27.6	74.1	43.8±0.94	9.22	21.07
Number of Grains per Plant	Non-stressed	243.0	831.8	530.9±10.56	103.45	19.49
	Heat-stressed	246.0	636.7	418.9±8.46	82.86	19.78
Number of Grains per Spike	Non-stressed	27.9	71.2	48.9±0.89	8.69	17.78
	Heat-stressed	25.6	70.6	43.8±0.84	8.28	18.90
Grain Weight per Spike (g)	Non-stressed	0.9	3.6	2.0±0.04	0.40	19.83
	Heat-stressed	0.9	3.2	1.6±0.04	0.37	23.54
Grain L/W Ratio	Non-stressed	1.70	3.09	1.99±0.02	0.18	8.82
	Heat-stressed	1.78	3.28	2.05±0.02	0.19	9.06
Grain yield per plant (g)	Non-stressed	9.5	40.6	22.0±0.52	5.08	23.02
	Heat-stressed	8.7	26.5	15.1±0.37	3.62	24.06
Yield Per Plot (g)	Non-stressed	450.1	1203.8	844.0±13.39	131.23	15.59
	Heat-stressed	265.1	897.1	635.2±11.09	108.69	17.09

respectively. Flag-leaf length and width decreased under HS environment by 6.1 cm and 0.3 cm, respectively. Likewise, heat-stress significantly reduced spike bearing tillers from 10.9 to 9.7 and biological yield from 55.8 to 43.8 g. The numbers of grains per spike and grain weight per spike were also reduced in HS condition. Furthermore, the heat-stress condition showed adverse effects on number of grains per plant, grain yield per plant and yield per plot, and the decrease was from 530.9 to 418.9, from 22.0 to 15.1 g and from 844.0 to 635.2 g, respectively. The value of chlorophyll fluorescence was also reduced from 0.76 to 0.72 under HS environment. However, the values of early ground cover and grain L/W ratio were slightly increased from 5.0 to 5.1 and 1.99 to 2.05, respectively, under HS environment. The highest CV was observed for early ground cover (24.21%) followed by grain yield per plant (24.02%) under HS environment. The lowest CV was recorded for chlorophyll fluorescence (2.05%) closely followed by physiological maturity (2.41%) under heat-stress.

Check variety 3 (WR544) showed the earliest heading on 77.0 and 62.7 days under NS and HS environment, respectively. Accession 34 (EC577013) was the tallest (150.9 cm) under NS environment, while the accession 84 (EC576585) was the tallest (127.0 cm) under HS environment. Similarly, the shortest plant height was recorded in accession 38 (IC335792; 84.9 cm) under NS and in accession 64 (IC443653; 73.2 cm) under HS condition. Accession 96 (CUO/79/PRU11A) exhibited the highest yield per plant (40.6 g) under NS, whereas, accession 86 (EC574849) showed the highest yield per plant (26.5 g) under HS condition.

Accession 15 (IC539287) produced the lowest yield per plant (9.5 g) under NS environment, while accession 34 (EC577013) produced the lowest yield per plant (8.7 g) under HS environment. Accession 86 (EC574849), which produced the highest yield/plant, also exhibited the highest biological yield (74.1 g) under heat-stress. Under NS environment, the highest yield per plot was recorded in accession 9 (IC277741; 1203.8 g), whereas accession 91 (IC566223) produced the highest yield (897.1 g) under HS environment. The lowest yield per plot (450.1 g) was produced by accession 26 (IC542509) under NS, whereas, accession 15 (IC539287), produced the lowest yield (265.1 g) under HS environment. The highest EGC recorded in accessions 24 (IC075240), 57 (IC524299) and 91 (IC566223). Accessions 85 (EC190899), 84 (EC576585), 17 (IC443661) and 60 (IC529207) showed early ear-heading.

Boxplot analysis showed diverse pattern of genetic variability for 16 morpho-physiological and yield related traits under NS and HS environments. Boxplot analysis clearly depicted minimum, maximum, mean, median and outliers' values under both the NS and HS environments (Fig. 2). All the traits, except EGC and grain L/W ratio, showed lower values of mean and median in boxplots under HS environment as compared to the NS environment. EGC showed more variable expression by different accessions under heat-stress than under non-stress condition. However, boxplot revealed almost similar mean and median for EGC under both environments. Some of the traits (CF, FLL, NGS, SL and PL) showed comparatively more variability, as depicted by spreads of boxplots, under the HS environment. The boxplot showed that the accessions took significantly less time for 50% heading and physiological maturity under heat-stress as compared to non-stress condition. It was interesting to note that the grain L/W ratio was increased mainly due to more reduction of grain width under heat-stress. Traits like DH, SBT, PM, BYP, NGP, GYP, GWS and YPP expressed more variability under non-stress condition.

Correlation of Grain Yield with Other Traits

Correlation coefficients were estimated among 16 morpho-physiological and yield-related traits in 96 bread wheat accessions under NS and HS environments (Table 4). Among the various traits studied, grain yield per plot (YPP) positively associated with GYP, NGP, NGS, GWS and BYP under both NS and HS environments. However, YPP positively correlated with EBT under NS environment and chlorophyll fluorescence under HS environment only. YPP showed negative association with LWR under both the environments, and with DH and PM under NS environment only. The grain yield per plant (GYP) showed moderate positive association with its component traits such spike length, SBT, NGS and strong association with NGP, GWS and BYP under both NS and HS environments, while it showed moderate positive association with plant height, FLL and FLW only under HS environment. Early ground cover (EGC) was found to be positively associated with DH, PM, PH and FLL under both the environments, and with BYP under NS environment. Similarly, chlorophyll fluorescence (CF) exhibited positive correlation with FLL, SL and BYP under NS environment and with YPP under HS environment. Days to 50% heading (DH) showed strong positive association with physiological maturity (PM) under both the environments. Yield contributing traits like SL, NGP, NGS, GWS, GYP and BYP also showed moderate to strong positive association with each other. Spike length (SL) also showed moderate positive association with DH, PM, FLL and FLW under both the environments, but with CF only in NS environment.

Impact of Heat Stress on Morpho-Physiological Traits in Tolerant and Susceptible Accessions

The effect of heat-stress on 16 morpho-physiological traits was investigated after classifying the accessions into tolerant or susceptible one based on HSI values (Table 5). Most of the traits (CF, DH, SBT, PH, FLL, FLW, SL, PM, GYP, NGP, NGS, GWS, GYP and YPP) were negatively impacted by the heat-stress and showed reduced expression under HS environment (Fig. 3). There was marked reduction in the trait values in the susceptible accessions than the tolerant ones in CF, PH, FLL, SL, BYP, NGP, NGS, GWS, GYP and YPP under heat-stress condition. However, physiological trait like EGC showed increased expression under heat-stress specifically in the tolerant accessions. The grain trait namely LWR also exhibited increased value under heat-stress in both the tolerant and susceptible accessions but the susceptible accessions showed comparatively more increase in LWR.

GGE Biplot Analysis and Selection of Heat-stress Adapted Wheat Germplasm

Graphical representation of relationship between accessions and test environments based on grain yield

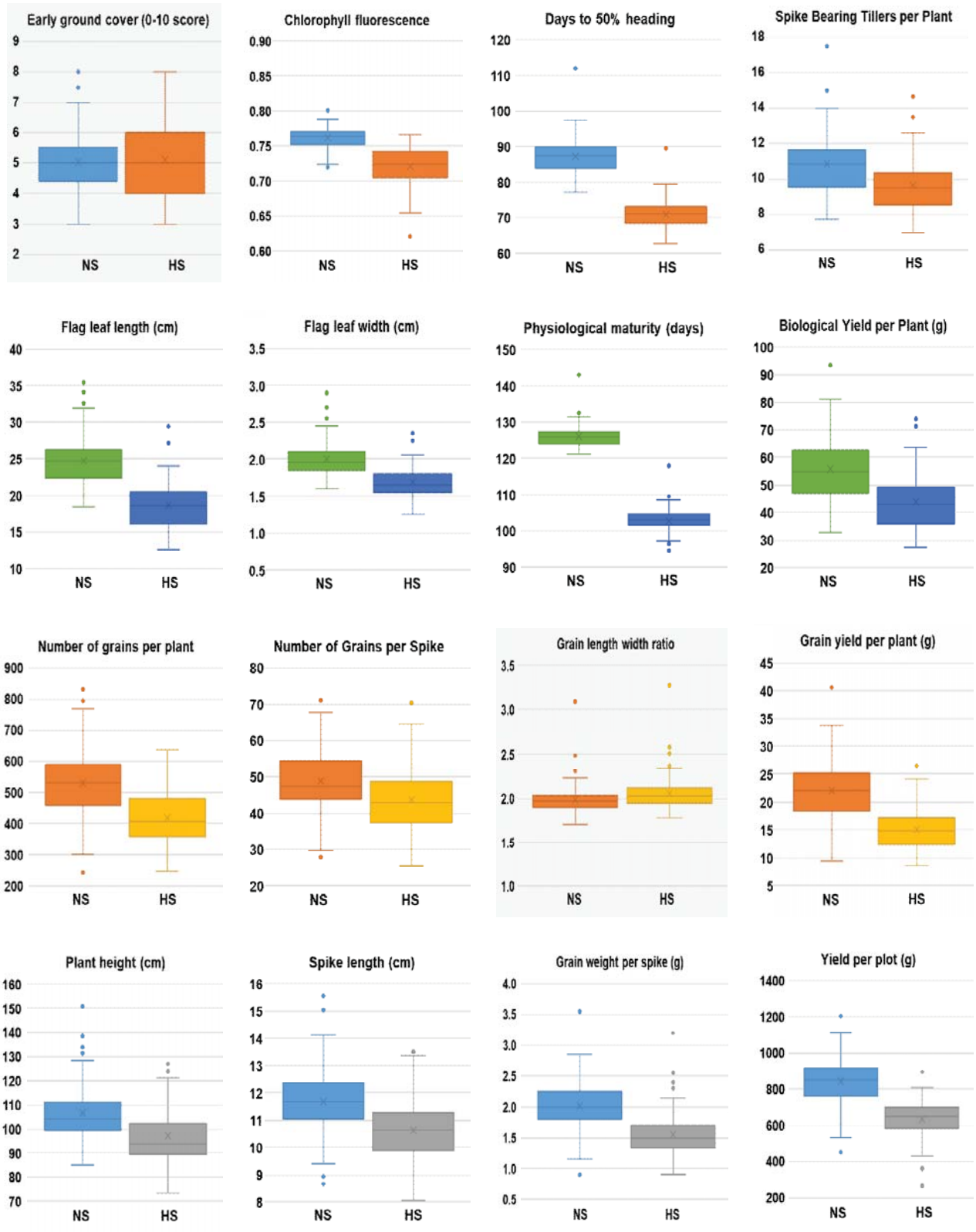

Fig. 2. Box plot analysis of variability in 16 morpho-physiological and yield contributing traits observed in 96 bread wheat accessions tested under non-stressed (NS) and heat-stressed (HS) environments

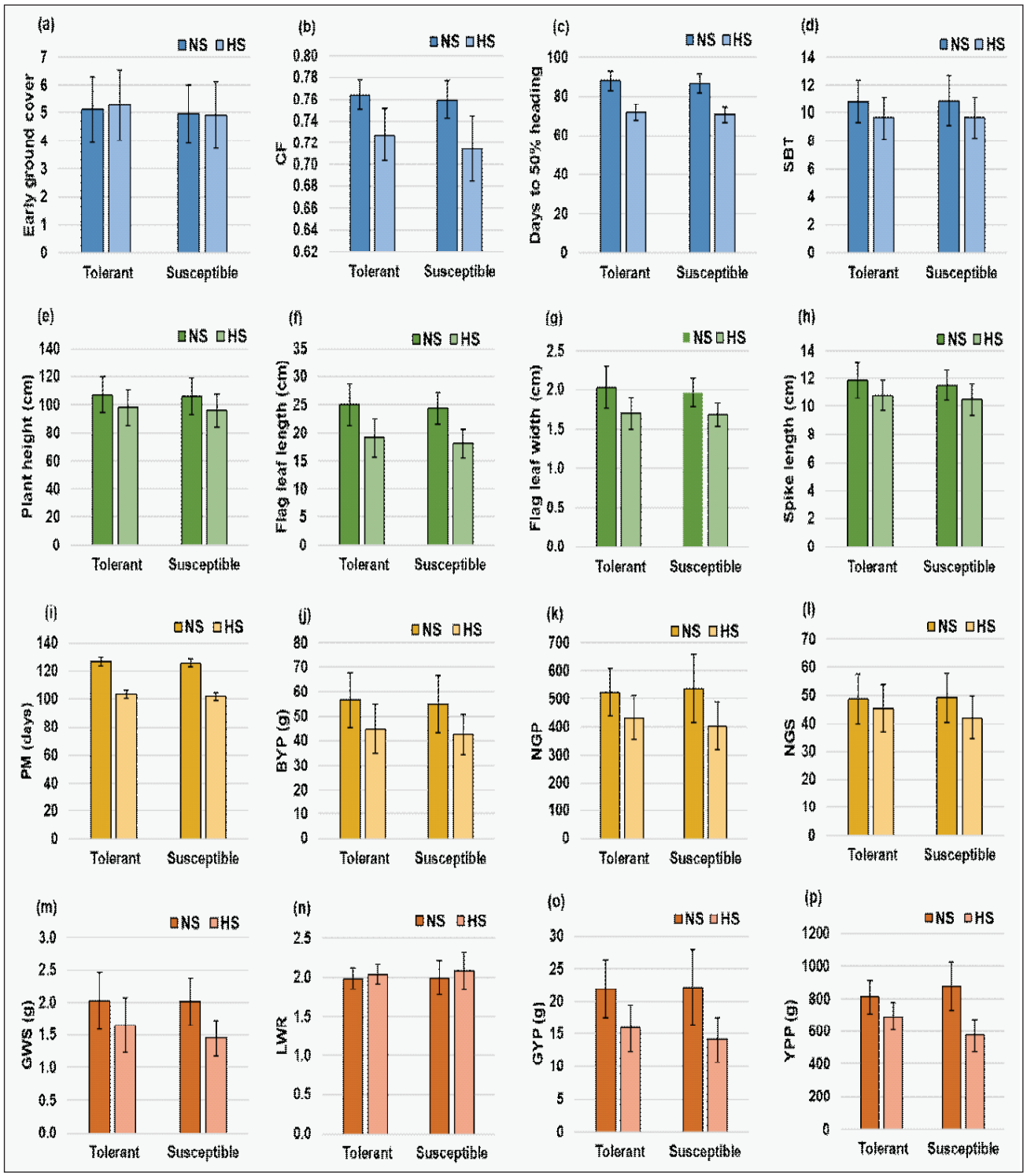

Fig. 3. Effects of heat-stress on different morpho-physiological and yield-related traits in tolerant and susceptible accessions (a-p). Early ground cover was higher in tolerant accessions under HS environment (a). Grain length width ratio (LWR) were relatively higher in susceptible accessions than the tolerant accessions under HS environment (n). CF-Chlorophyll fluorescence, SBT-Spike bearing tillers per plant, PM-Physiological maturity (days), BYP-Biological yield per plant (g), NGP-Number of grains per plant, NGS-Number of grains per spikes, GWS-Grain weight per spikes (g), LWR-Grain length width ratio, GYP-Grain yield per plant (g), YPP-Yield per plot (g)

per plot is presented in Figure 4. The principal component (PC) 1 and PC2 together explained 99.3 % of the total variation.

Characterization of test environments: The characterization of four test environments is explained by Figure 4a. The single-arrowed line represents the average environment axis (AEA). Highly positive correlations (acute angle) observed between E1 and E3, and between E2 and E4 environments. Environment E3 showed more representativeness because of the small angle with AEA followed by E4 and E1, while environment E2 was the least representative test environment. Among group 1, environment E1 was more discriminative (longest environment vector) than E3, whereas in group 2, E2 and E4 environments were of equal discriminative nature. Thus, E3 environment was more representative and discriminative test environment in comparison to others for selecting adapted genotypes.

Mean performance and stability: GGE biplot showing mean performance and stability of the bread wheat accessions for yield per plot are depicted by Figure 4b. An ideal genotype produces high yield with high stability across the environments. The direction of AEA points to higher mean yield across environments. Thus, accessions 65 (IC252431), 9 (IC277741) and 4 (HD2967) were the top yielding accessions followed by 91 (IC566223), 85 (IC566223), 96 (CUO/79/Pru 11A) and 89 (IC393878), whereas the accessions 15 (IC539287), 26 (IC542509), 34 (EC577013), 35 (EC414149) and 33 (EC576317) were the low yielding accessions across the environments. The vector or line which joined the accessions with the AEA showed stability in either direction. Thus, accessions having very small vector or positioned very near to the AEA showed high stability. Accordingly, the mean *vs.* stability biplot showed that accessions 4 (HD2967), 89 (IC393878), 3 (WR544), 18 (EC534487), 2 (HD2932) and 14 (IC539221) produced high yield and were stable across the environments. However, accessions 9 (IC277741) and 91 (IC566223) were the high yielder with low stability across the environments. Further, the accessions 15 (IC539287), 26 (IC542509) and 34 (EC577013) were low yielder with poor stability across the environments.

Performance of genotypes to specific environments: The which-won-where view of the GGE biplot (Fig. 4c) expressed which genotypes performed best in which

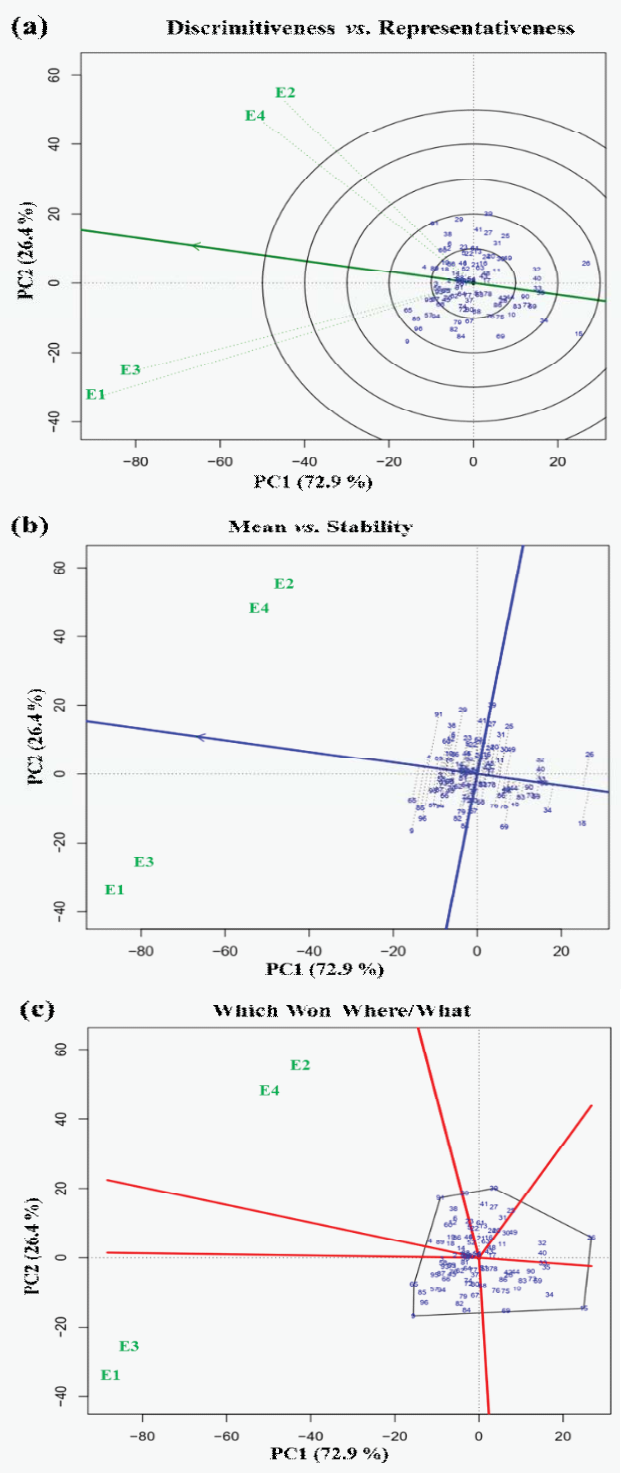

Fig. 4. GGE biplot showing genotype, G × E interactions with discrimitiveness vs. representativeness view of test environments (a), the mean performance and stability of wheat accessions (b) and which-won-where pattern of genotypes (c). Two principal components, PC1 and PC2 showed genetic variability of 99.3%. E1: NS environment 2018-19, E2: HS environment 2018-19, E3: NS environment 2019-20, E4: HS environment 2019-20

Table 4. Pearson's correlation coefficients for 16 morpho-physiological and yield related traits in 96 bread wheat accessions in non-stressed (above diagonal) and heat-stressed (below diagonal) environments during two *Rabi* crop seasons of 2018-19 and 2019-20

Trait	EGC	CF	DH	PM	PH	FLL	FLW	SL	LWR	SBT	NGP	NGS	GYP	GWS	BYP	YPP
EGC	--	0.10	0.25*	0.25*	0.40**	0.24*	0.13	0.18	0.09	0.14	-0.01	-0.14	0.14	0.04	0.33**	-0.06
CF	0.02	--	0.11	0.14	-0.02	0.21*	0.18	0.23*	-0.09	0.07	0.15	0.11	0.20	0.18	0.26*	-0.05
DH	0.32**	0.14	--	0.87**	0.13	0.19	0.17	0.35**	0.17	-0.14	-0.03	0.11	-0.23*	-0.14	0.01	-0.28**
PM	0.30**	0.19	0.86**	--	0.08	0.27**	0.23*	0.45**	0.10	-0.09	-0.04	0.07	-0.18	-0.09	0.07	-0.23*
PH	0.35**	-0.14	0.08	0.05	--	0.34**	-0.03	0.11	0.21*	0.13	-0.06	-0.18	-0.01	-0.10	0.32**	0.03
FLL	0.22*	-0.05	0.19	0.19	0.37**	--	0.54**	0.53**	0.19	-0.23*	-0.06	0.18	0.03	0.28**	0.31**	-0.02
FLW	0.10	0.05	0.19	0.26*	-0.06	0.54**	--	0.53**	0.16	-0.22*	0.04	0.29**	0.17	0.46**	0.34**	-0.14
SL	0.13	0.07	0.27**	0.37**	0.12	0.28**	0.28**	--	0.06	0.04	0.34**	0.40**	0.35**	0.46**	0.49**	0.02
LWR	0.08	-0.08	0.14	-0.02	0.12	-0.01	-0.02	-0.03	--	-0.04	-0.31**	-0.33**	-0.26**	-0.30**	-0.12	-0.28**
SBT	0.08	0.01	-0.09	-0.04	0.17	0.10	0.03	0.01	0.02	--	0.53**	-0.30**	0.56**	-0.19	0.51**	0.21*
NGP	-0.08	0.11	0.05	0.13	0.03	0.23*	0.22*	0.44**	-0.21*	0.49**	--	0.63**	0.85**	0.53**	0.71**	0.46**
NGS	-0.15	0.11	0.14	0.21*	-0.12	0.18	0.22*	0.50**	-0.27**	-0.33**	0.65**	--	0.43**	0.78**	0.34**	0.32**
GYP	0.05	0.11	-0.16	0.01	0.21*	0.37**	0.36**	0.44**	-0.18	0.44**	0.83**	0.52**	--	0.68**	0.85**	0.50**
GWS	-0.02	0.10	-0.09	0.07	0.09	0.35**	0.38**	0.50**	-0.22*	-0.24*	0.53**	0.82**	0.74**	--	0.59**	0.39**
BYP	0.20	0.08	0.16	0.23*	0.35**	0.46**	0.46**	0.43**	0.01	0.49**	0.71**	0.36**	0.85**	0.55**	--	0.28**
YPP	0.05	0.23*	-0.10	0.07	0.05	0.05	0.04	0.20	-0.28**	0.12	0.39**	0.33**	0.42**	0.38**	0.22*	--

**, * significant at 0.01 and 0.05 probability level, respectively.

Abbreviations: EGC-Early ground cover (0-10 score), **CF**-Chlorophyll fluorescence, **DH**-Days to 50% heading, **PM**-Physiological maturity (days), **PH**-Plant height (cm), **FLL**-Flag leaf length (cm), **FLW**-Flag leaf width (cm), **SL**-Spike length (cm), **LWR**-Grain length width ratio, **SBT**-Spike bearing tillers per plant, **NGP**-Number of grains per plant, **NGS**-Number of grains per spike, **GYP**-Grain yield per plant (g), **GWS**-Grain weight per spike (g), **BYP**-Biological yield per plant (g), **YPP**-Yield per plot (g),

environments. A polygon was drawn on genotypes at the extreme from the biplot origin so that all other genotypes are enclosed within the polygon. The genotype at the vertex of the polygon performs best in the environment falling within the sectors. The hexagon was drawn which has eight accessions at the vertices *viz*. 91 (IC566223), 65 (IC252431), 9 (IC277741), 69 (IC536050), 15 (IC539287), 26 (IC542509), 39 (IC543425) and 29 (IC128454). Based on the which-won-where view of the GGE biplot the accessions 9 (IC277741), 65 (IC252431), 96 (CUO/79/ Pru 11A), 85 (EC190899), 57 (IC524299), 94 (IC553599), 84 (EC576585), 82 (EC576066) and 95 (EC277134) fall in E1 and E3 (Non-stressed) environment sectors, which were the superior performer in the favourable environment but highly susceptible for unfavourable (heat-stressed) environment. Similarly, accessions 91 (IC566223), 29 (IC128454), 38 (IC335792), 6 (EC576707), 12 (IC535176), 60 (IC529207), 23 (IC446713) and 22 (IC416019) were included in E2 and E4 (heat-stressed) environment and hence these accessions were the excellent performer in HS environment and were the highly tolerant to heat-stress. The winning accession for NS environment was 9 (IC277741), whereas accession 91 (IC566223) was the winning accession for HS environment because these accessions were found to be located on the vertex of NS and HS environment, respectively.

Discussion

Evaluation of diverse germplasm under heat-stress would help us in understanding the complexity of crop response to global warming and identification of superior lines for the development of mapping populations, which may be utilized for the development of heat tolerant cultivars. In present investigation, we have evaluated a diverse set of 96 accessions of bread wheat along with four national checks to analyse plant responses in terms of effect of heat-stress on morpho-physiological and yield related traits. The late sown wheat crop is exposed to higher temperatures at reproductive and grain filling stages and has been the widely used strategy to screen germplasm for yield and other traits under heat-stress (Ullah *et al*., 2020). Grain yield is complex quantitative trait and is an end-product of many interactions between genes for physiological and yield component traits. High temperature stress has a wide range of effects on plants in terms of physiological, biochemical and gene regulation pathways (Bita and Gerats, 2013). Wheat

Table 5. The mean yield and heat susceptibility index (HSI) of 96 accessions of bread wheat grown under non-stressed (NS) and heat-stressed environments during *Rabi* seasons of 2018-19 and 2019-20

Accession	Yield per plot (g)		HSI	Accession	Yield per plot (g)		HSI
	NS	LS			NS	LS	
IC265318	762.1	756.1	0.03	IC536468	879.3	653.1	1.05
IC566223	906.4	897.1	0.04	IC401940	793.3	587.6	1.06
IC128454	819.0	807.1	0.06	IC252867	896.3	658.1	1.09
IC543425	762.0	747.0	0.08	IC443640	938.3	684.6	1.11
EC178071	694.1	681.1	0.08	IC240818	863.3	628.6	1.11
IC252348	732.1	715.1	0.09	WR544	982.6	708.2	1.14
IC111800	699.1	678.1	0.12	EC576317	634.1	455.1	1.15
IC542509	450.1	431.1	0.17	IC535717	973.6	696.1	1.17
IC416075	724.8	687.1	0.21	IC303071	662.3	470.6	1.18
IC401976	765.8	717.1	0.26	EC573527	694.3	492.6	1.19
IC542652	673.3	627.1	0.28	IC252999	941.3	665.6	1.20
IC446713	817.8	758.1	0.30	IC573461	982.3	694.1	1.20
EC576707	868.8	802.1	0.31	EC414149	633.1	447.1	1.20
IC290191	783.3	724.1	0.31	IC572925	951.3	669.1	1.21
IC075240	752.8	690.1	0.34	IC531191	836.3	586.1	1.22
EC574731	823.8	751.1	0.36	IC536483	846.3	592.1	1.23
IC335792	890.1	809.1	0.37	IC443653	899.3	626.1	1.24
IC416019	813.8	735.1	0.40	EC574849	760.6	530.1	1.24
IC535176	890.8	798.1	0.43	EC576175	992.6	685.1	1.27
IC529207	907.3	791.1	0.52	IC112258	931.3	637.1	1.29
IC539531	775.8	678.1	0.52	IC252444	645.3	441.1	1.29
IC279617	723.8	630.1	0.53	EC277134	1020.6	697.1	1.30
IC416078	795.8	693.1	0.53	IC252619	989.3	662.6	1.35
IC111931	603.1	521.1	0.56	IC549437	752.1	500.1	1.37
Raj3765	828.8	708.0	0.60	IC445365	902.3	600.6	1.37
IC416055	736.1	628.1	0.60	IC252414	908.3	604.6	1.37
IC416018	908.8	762.1	0.66	IC445449	776.1	515.1	1.38
IC627711	787.3	661.1	0.66	IC542547	887.3	586.6	1.39
IC542578	850.3	711.1	0.67	IC536162	856.3	564.6	1.39
IC393878	950.6	775.1	0.75	IC144911	973.3	638.1	1.41
EC534487	914.8	744.1	0.76	IC543293	784.1	512.1	1.42
EC574735	848.3	688.1	0.77	IC252431	1109.3	717.6	1.44
EC542533	786.3	629.1	0.82	IC372643	778.3	499.6	1.46
IC402055	619.1	493.1	0.83	IC252620	813.3	521.6	1.47
IC539221	889.8	703.1	0.86	IC252739	913.1	580.1	1.49
IC582706	872.6	689.1	0.86	IC536081	748.8	474.1	1.50
IC443661	784.8	620.1	0.86	IC553599	1028.6	637.1	1.56
IC252653	920.1	722.1	0.88	IC443694	946.3	581.6	1.58
HD2967	997.8	778.0	0.90	IC529242	901.3	553.6	1.58
IC252816	831.8	647.1	0.91	EC190899	1098.6	673.1	1.58
IC342668	873.6	676.1	0.92	IC524299	1064.3	634.1	1.65
IC252725	897.8	689.1	0.95	EC576066	969.3	564.6	1.71
IC542544	653.6	497.1	0.98	CUO/79/ PRU 11A	1111.6	635.1	1.75
IC333095	850.3	645.1	0.99	EC576585	956.3	530.6	1.82
IC528965	812.1	613.1	1.00	EC577013	662.1	363.1	1.85
IC535704	865.3	652.1	1.01	IC536050	808.3	438.6	1.87
EC190962	892.3	666.6	1.03	IC277741	1203.8	624.1	1.97
HD2932	922.0	688.2	1.04	IC539287	529.8	265.1	2.04

HSI value <0.50 considered as highly tolerant, HSI value = 0.51 to 1.04 as tolerant, HSI value = 1.05 to 1.50 as susceptible and HSI value of >1.51 as highly susceptible accessions of bread wheat.

achieves adaptation through variation in phenology and related traits determining plant architecture (Hyles *et al.*, 2020). Hence, it is crucial to understand the genes that underpin the variations in plant phenology and their interactions with other genes, morpho-physiological traits and the environment.

Trait Variability in Germplasm and Impact of Heat-stress

The ANOVA revealed that the bread wheat accessions possess significant differences for most of the traits under both NS and HS environments, which shows that the accessions have varied response to heat-stress and it provides ample scope for further selection of positively associated traits for terminal heat-tolerance. The heat-stress showed an adverse effect on crop growth, development, morpho-physiological and yield traits. Most of the traits showed reduced values under HS environment except early ground cover and grain length/ width ratio, which were increased under heat-stress. The similar results were also reported by Gowda *et al*. (2011) and Elbasyoni (2018). According to Pinto *et al*. (2017), the heat-adapted genotypes with best yielding ability also showed high early biomass and high grain filling rates. In most of the traits, the reduction was more prominent in susceptible accessions as compared to the tolerant. Heat-stress reduced plant height, days to heading, spike length, maturity, grain weight and yield between 4-7% with every 1°C rise in average maximum temperature above the optimal 25°C (Ullah *et al*., 2020). Mondal *et al*. (2015) also observed that the values of days to heading, plant height, grain weight and yield were reduced in HS environment. Sharma *et al*. (2008) reported significantly lower values for days to heading, grain weight, and yield in late sown wheat. Similarly, Fleitas *et al.* (2020) found that the grain yield and yield component traits were more severely affected as the heat-stress increases. High temperature applied at post-anthesis shortened maturity and grain filling duration, and reduced grain weight and yield (Kaur and Behl, 2010). Agarwal *et al.* (2021) reported that days to anthesis and yield traits were reduced in late sown wheat as compared to normal. These previous studies support our finding of reduction in 14 out of the 16 morpho-physiological and yield traits analysed under the heat-stress.

Association of Grain Yield with Other Traits

Yield is complex character and determined by many morphological, physiological and yield related parameters. Under heat-stress, yield showed significantly positive association with yield per plant and yield contributing traits like number of grains (NGP, NGS), grain weight (GWS) and plant biomass (BYP). Sharma *et al.* (2008) reported significantly positive association of grain yield with grain weight under both normal and terminal-heat stress conditions, and corroborates our results. Yashavanthakumar *et al.* (2021) reported the positive association of yield with TGW and GFP, and negative association with days to heading and maturity. However, there was no association of yield with days to 50% heading and plant height in the present study under HS environment, which also confirmed by Ullah *et al*. (2020). Hence, to increase the yield in wheat under heat-stress, the focus should be given on traits which have high and significant association with grain yield for the selection of heat tolerant lines. Lordkaew *et al.* (2019) reported positive correlation between days to heading and grain yield and opined that longer time before heading enables the development of larger spikes and more numbers of spikelets producing enhanced grain numbers per plant. Positive association of grain yield with number of grains per spike and grain weight per spike was also reported by Sharma *et al*. (2016). They found that the phenological characters such as days to heading and days to maturity showed strong positive correlation (0.96) and validates our finding. The present and earlier association studies revealed that yield is positively correlated with its contributing traits under HS environment. Therefore, selection for these traits could be valuable in wheat breeding programme designed for heat-stress tolerance.

Yield Stability and Identification of Accessions Adapted to Heat-stress

Yield stability analysis is used to identify the accessions exhibiting superior performance and stability in one or more groups of environments. The graphical presentation of GGE biplots have been used to identify and select the accessions which were adapted to unfavorable HS environment, favorable NS environment and both environments (Yan and Tinker, 2006). Yield stability across the environments is a reliable criterion for the selection of heat-stress adapted germplasm (Kang

et al., 2004). The GGE biplot showed that accessions HD2967, IC393878, WR544, EC534487, HD2932 and IC539221 produced high yield and were stable across environments and may be used as donor parents in heat-stress adaptation breeding programme. Similar studies were also carried by Elbasyoni (2018) and Fleitas *et al*. (2020) using GGE biplot to select superior yielding lines under heat-stress. The G×E interaction biplots for grain yield showed that genotypes Raj3765 and Raj4027 were more stable across all environments (Rane *et al*., 2007). The significant influence of environment, genotype and G × E interactions on the grain yield was reported by Yashavanthakumar *et al.* (2021). They selected three superior genotypes namely MACS 6729, HD 2932, and MACS 6733 based on yield and stability performance across the environments. The stable and higher yielding accessions identified under HS environment in our study could be utilized for the development of terminal heat-stressed tolerant cultivars in bread wheat.

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*Supplementary Table or Figure mentioned in the article are available in the online version.

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RESEARCH ARTICLE

Genetic Divergence Study in Maize (*Zea mays* L.) Inbred Lines under North Western Himalayan Conditions

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Genetic divergence in 50 maize inbreds including five checks was assessed based on some morpho-physiological and yield contributing traits using Mahalanobis D^2 statistics. The experiment was carried out in an augmented block design at Maize Research Station, SKUAST-J, Udhampur, J&K during *Kharif* 2019-20. All the inbreds were grouped into ten clusters based on D^2 analysis. Maximum numbers of genotypes (12) were grouped in cluster III whereas cluster X (1) was the smallest. Maximum inter-cluster distance was observed between cluster VIII and cluster IX indicating presence of maximum diversity among the genotypes falling within these clusters. The genotypes in the cluster VIII showed better performances having high shelling percentage (%), grain yield per plot (g), cob length, kernels per row and 1000 kernel weight (g). It is expected that crossing of inbred lines belonging to high-medium D^2 values may tend to produce high heterosis for yield. Perusal of the data indicated that moisture percentage contributed maximum of 8.90 per cent whereas, days to 50 % silking contributed the lowest of 0.73 per cent to the total genetic divergence.

Key Words: Clusters, Divergence, Inbred, Maize, PCA

Introduction

Maize (*Zea mays* L.) is one of the three most important food crops in the world agricultural economy both as food for human beings and feed for animals. It is grown primarily for grain and secondarily for fodder, raw material for industrial process and diversified products. Maize is a member of Poaceae family (2n=2x=20). Worldwide, approximately 21% of total produced maize is consumed directly as food while the rest part of produce is used in other purposes (Jaiswal *et al.,* 2019). In India, maize is third important cereal crop after rice and wheat. It is cultivated on an area of 9.3 million hectares with a production of 27.2 million metric tonnes and a productivity of 2.92 tonnes per hectare (FAOSTAT, 2018). In Jammu and Kashmir, it is cultivated on an area of 0.29 million hectares with a production and productivity of 5411 thousands quintals and 18.33 quintals per hectare, respectively (Shazia *et al*., 2017). It is mainly concentrated in mid hill zones and rainfed areas of the state. For developing high yielding hybrids in maize, inbred lines need to be evaluated for their diverse gene pool. Precise information about genetic divergence is critical for a productive breeding programme, as genetically diverse parents are known to produce high heterotic effects increasing consequently recovery of yield suitable segregants (Sharma *et al.,* 2020). Information on genetic diversity and relationship among different maize genotypes is very important in hybrid maize breeding programme (Punya *et al.,* 2020*)* Maize shows heterosis in recombinants, particularly when inbreds differing for many genes affecting yield or some other character of importance are used as parents (Udaykumar *et al*., 2013). Several studies on maize have shown that inbred lines from diverse genetic base to be more productive than crosses of inbred lines derived from closely related stocks (Moll *et al*., 1965; Vasal, 1998; Udaykumar *et al*., 2013). It has become possible to quantify magnitude of genetic diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics. Maize inbred lines developed at Maize Research Station, Udhampur and inbred lines received from IIMR, New Delhi as part of coordinated programme needed assessment of diversity

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among them for evaluation of their potential use in hybrid breeding programs. With this view, diversity among 50 maize inbred lines was studied using multivariate approaches of analysis.

Materials and Methods

Fifty inbred lines of maize (*Zea mays* L.) were grown in an Augmented Block Design (ABD) with five blocks including five checks at Maize Research Station, SKUAST-J, Udhampur, J&K during *Kharif* 2019-20. The detail pedigree and source of all fifty maize inbred lines are listed in Table 1. Unit plot size was 3 m x 1.2 m maintaining 60 cm x 20 cm spacing. Intercultural operations were done at appropriate time according to the necessity. Data was recorded on different morpho-physiological and yield contributing traits such as, days to 50% tasseling, days to 50% silking, days to 75% dry husk, plant height (cm), ear height (cm), number of leaves, number of plants per plot, stem girth (cm), number of cobs per plant, shelling percentage (%), moisture percentage (%), grain yield per plot (g), cob length (cm), cob girth (cm), kernel rows per cob, kernels per row and 1000 kernel weight (g). Data was subjected to analysis of Mahalanobis D^2 statistics using windostat 9.1 software. Intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985).

Results and Discussion

The analysis of variance for significances different genotypes for all the character under study. The highest number of days to 50% flowering was observed in G 29 and G 40 genotypes. The maximum plant height was observed in G 22 and G 40 genotypes. The highest 1000 kernel weight was observed in G 21 and G 45 genotypes. The highest grain yield per plot was observed in G 22 and G 40 genotypes. The variation among the genotypes of 50 inbred lines was studied on a multivariate scale using Mahalanobis, D^2 statistics. Assuming the D^2 values as χ^2, it appears that there were significant variations among all the genotypes. Fifty genotypes were grouped into ten clusters, which are presented in the Table 2. Cluster III was the largest, containing twelve genotypes whereas cluster X was the smallest cluster containing only one genotype. Average intra and inter cluster distance of four clusters are presented in Table 3. The magnitude of intra cluster distances indicated the extent of genetic diversity among genotypes within the same

Table 1. Maize inbred lines studied for morpho-physiological traits

Code	Udhampur code	Inbreds	Source
G1	UDMI 401	CM 153	IIMR
G2	UDMI 402	WN 1069	WNC Hyderabad
G3	UDMI 403	CM 141	IIMR
G4	UDMI 404	CM 212	IIMR
G5	UDMI 405	WN 1207	WNC Hyderabad
G6	UDMI 406	CML 116	CIMMYT
G7	UDMI 407	WN 24249-1	WNC Hyderabad
G8	UDMI 408	WN 689-1	WNC Hyderabad
G9	UDMI 409	CM 140	IIMR
G10	UDMI 410	CML 295	CIMMYT
G11	UDMI 411	WN 1079	CIMMYT
G12	UDMI 412	WN 4615	WNC Hyderabad
G13	UDMI 413	WN 2456	IIMR
G14	UDMI 414	WN 547	CIMMYT
G15	UDMI 415	EV1465	WNC Hyderabad
G16	UDMI 416	WN 2449	IIMR
G17	UDMI 417	WN 2469	IIMR
G18	UDMI 418	PFSR 10109	IIMR
G19	UDMI 419	WN 2436	IIMR
G20	UDMI 420	CML 130	CIMMYT
G21	UDMI 421	CML 31	CIMMYT
G22	UDMI 422	VP14114	CIMMYT
G23	UDMI 423	CM123	IIMR
G24	UDMI 424	VP14109	CIMMYT
G25	UDMI 425	CML 433	CIMMYT
G26	UDMI 426	EV1463	WNC Hyderabad
G27	UDMI 427	WN 4614	WNC Hyderabad
G28	UDMI 428	HKI 323	Karnal
G29	UDMI 429	CML 427	CIMMYT
G30	UDMI 430	WN 52362	IIMR
G31	UDMI 431	CML 300	CIMMYT
G32	UDMI 432	CM 143	IIMR
G33	UDMI 433	WN 52343	CIMMYT
G34	UDMI 434	WN 52218	CIMMYT
G35	UDMI 435	WN 516	IIMR
G36	UDMI 436	WN 52011	MANDYA
G37	UDMI 437	HKI 287	Karnal
G38	UDMI 438	WN 241-1	IIMR
G39	UDMI 439	CM 128	IIMR
G40	UDMI 440	VL144077	CIMMYT
G41	UDMI 441	SNL 142836	CIMMYT
G42	UDMI 442	HKI 139-1	Karnal
G43	UDMI 443	WN 52361	IIMR
G44	UDMI 444	Z490-26	CIMMYT
G45	UDMI 445	WN 52188	CIMMYT
G46	UDMI 446	HKI 1105-2-2	Karnal
G47	UDMI 447	V351	Almora
G48	UDMI 448	CM I52	IIMR
G49	UDMI 449	HKI 536	Karnal
G50	UDMI 450	WN2453-2	IIMR

Table 2. Distribution of 50 genotypes of maize inbreds into ten clusters

Cluster	No. of entries	Name of entries
I	9	G6, G39, G5, G1, G8, G4, G28, G13, G3
II	2	G10, G17
III	12	G7, G42, C47, G15, G9, G48, G24, G26, G35, G41, G25, G50
IV	3	G37, G46, G14
V	6	G34, G36, G38, G31, G44, G2
VI	2	G20, G33
VII	7	G27, G45, G23, G12, G16, G21, G49
VIII	5	G22, G40, G11, G29, G30
IX	3	G32, G43, G19
X	1	G18

cluster. The distance between the clusters were more than the intra clusters distances indicating that diversity in between clusters was more than within clusters. The highest distance was obtained between cluster VIII and cluster IX (10580240.00) indicating the wider genetic divergence between genotypes of these two clusters. Wider diversity shows high heterosis (Singh *et al*., 1980). It was followed by cluster II and cluster IX, cluster V and cluster VIII, cluster IV and cluster IX, and cluster I and cluster VIII. The cluster VIII had the highest distance from the rest indicating that the genotypes in the cluster VIII were distinctly different from others. Low inter cluster distances were observed between cluster I and cluster VI (46018.47) followed by cluster I and cluster V (71727.68) indicating that the genotypes belonging to these clusters were comparatively less diverse. Hence, crossing of genotypes from these clusters may not produce high level of heterotic expression in the F_1's and broad-spectrum of variability in segregating (F_2) populations. The clusters with comparatively less magnitude of divergence showed instability, while widely divergent clusters remained distinct in different environments (Raut *et al*., 1985; Singh *et al*., 1980; Somayajulu *et al*., 1970). Parents for hybridization programmes could be selected on the basis of large inter-cluster distance for isolating useful recombinants in the segregating generations. Increasing parental distance implies a better chance at greater number of constraining alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generations, following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of interest (Ghaderi *et al*., 1984).

Principal Component Analysis (PCA) also helps in assessment of diversity on multivariate scales. The principal components formed were equal to number number of characters. The criteria followed for selecting the principal components to be included in further analysis was based on Eigen values of principal components (Kovacic, 1994). Only 5 principal components were taken having Eigen values greater than one (>1) and they accounted for the 79.99% of total variation. The fact that Eigen values are above unity indicates that the evaluated principal component weight is reliable (Mohammadi and Prassanna, 2003). This clustering pattern confirmed the results obtained by D^2 analysis. For principal component-1, grain yield per plot contributed highest percentage of 36.60. For component-2 highest percentage was contributed by days to 50% tasseling (44.20%), For principal component-3 the highest percentage was contributed by days to 50% silking (29.80%), while as for component-4 and component-5 kernels per row and number of leaves contributed highest with percenatage of 51.10 and 47.90, respectively (Table 4).

Cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in the two dimensional scattered diagram and the genotypes falling in same cluster were present closer to each other in the scattered diagram.

Table 3. Average inter and intra cluster distances in maize inbreds

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster	10 Cluster
1 Cluster	12532.28	3526052.00	223767.50	2449302.00	71727.68	46018.47	803570.60	5664764.00	778316.50	1680888.00
2 Cluster		296.85	2030856.00	99205.24	4516543.00	2811707.00	1036380.00	287172.10	7578075.00	341690.50
3 Cluster			24011.69	1238961.00	509359.10	76684.87	219682.10	3719944.00	1787615.00	715419.30
4 Cluster				1281.77	3282782.00	1859391.00	506582.30	694161.40	5952360.00	73711.17
5 Cluster					7338.01	204152.80	1295608.00	6897718.00	403977.60	2379302.00
6 Cluster						1013.79	488339.10	4752457.00	1162232.00	1197817.00
7 Cluster							75431.66	2310397.00	3101456.00	208235.20
8 Cluster								106742.80	10580240.00	1201257.00
9 Cluster									18623.37	4711829.00
10 Cluster										0.00

Table 4. Eigen values, proportion of the total variance represented by first five Principal components, cumulative per cent variance and component loading of different characters in maize (*Zea mays* L.)

	PC1	PC2	PC3	PC4	PC5
Eigen Value	2.48	1.82	1.24	1.21	1.04
% variance Expressed	36.18	19.56	9.11	8.71	6.42
Cumulative variance Expressed	36.18	55.74	64.84	73.56	79.99
GYP	0.366	-0.155	0.009	-0.068	-0.020
CL	0.334	-0.133	0.247	0.048	-0.230
CG	0.301	-0.134	0.265	0.115	-0.309
KRPC	0.217	-0.284	0.065	0.066	0.150
1000KW	0.218	-0.047	0.259	-0.519	0.130
KPR	0.173	-0.210	0.012	0.511	-0.309
MP	0.122	0.115	-0.248	-0.213	-0.518
SP	0.070	-0.233	0.295	-0.180	0.388
NCP	0.256	0.067	-0.392	-0.321	-0.044
SG	0.132	0.341	-0.221	0.126	-0.033
NPPP	0.273	0.164	-0.292	-0.197	0.074
NOL	0.147	0.017	-0.325	0.413	0.479
EH	0.350	-0.091	-0.220	0.038	0.099
PH	0.352	-0.142	-0.066	0.070	0.171
DDH	0.184	0.428	0.164	0.018	0.124
DS	0.172	0.432	0.298	0.122	0.0377
DT	0.162	0.442	0.288	0.118	0.037

GYP= grain yield plot-^{1} (g), CL= cob length (cm), CG= cob girth (cm), KRPC= kernels rows cob-^{1}, 1000KW= 1000 kernel weight (g), KPR= kernels row-^{1}, MP= moisture percentage (%), SP= shelling percentage (%), NCP= No. of cobs plant-^{1}, SG= stem girth (cm), NPPP= No. of plants plot-^{1}, NOL= No. of leaves, EH= Ear height (cm), PH= plant height (cm), DDH= days to 75% dry husk, , DS= days to 50% silking, DT= days to 50% tasseling.

Genetically distant parents are usually able to produce higher heterosis (Falconar, 1960; Moll *et al.*, 1962; Mian and Bhal 1989). Endang *et al.,* (1971) stated that the clustering pattern could be utilized in choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic traits. Keeping this in view, the findings from the present study indicated that variability existed among the studied maize inbreds. The choice of parents for further breeding programme can be made by selecting individuals from the maximum divergent cluster such as cluster VIII and cluster IX and clusters have single or few genotypes II, VI and X in the present study, which would exert high heterosis and wide variability in genetic architecture in subsequent generations. The lines UDMI 433 (G33), UDMI 410 (G10), UDMI 422 (G22), UDMI 440 (G40), UDMI 411 (G11), UDMI 429 (G29), UDMI 430 (G30), UDMI 432 (G32), UDMI 443 (G43) and UDMI 418 (G18) belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregants.

Conclusion

Most of the maize inbred lines significantly differed for all the characters under study indicating sufficient amount of variability present in the inbreds. Selection based on characters which are significant positive and direct association with grain yield may increase the grain yield in maize inbreds. High number of clustes and there values for genetic divergence showed presence of significant amount of genetic diversity. The inbred lines showing higher genetic divergence can further be utilised for crossing programme to achieve high yielding hybrids in maize.

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RESEARCH ARTICLE

Deciphering Morpho-taxonomic Variability in *Lathyrus* Species

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Twenty accessions of *Lathyrus* belonging to four different species such as *L. sativus*, *L. cicera*, *L. aphaca* and *L. odoratus* were obtained from ICAR-National Bureau of Plant Genetic Resources (NBPGR) genebank, New Delhi and the International Center for Agricultural Research in the Dry Areas (ICARDA). All the accessions were grown at the experimental farm of ICAR-NBPGR, New Delhi, India, during the *rabi* seasons of 2018–2019 and 2019–2020. Agro-morphological delineation was carried out using 24 qualitative and 18 quantitative traits by following standard *Lathyrus* descriptors. The results indicated a wide range of variation for both qualitative and quantitative characteristics among the accessions. Remarkable distinguishing feature was observed at the different crop growth stages like seedling, pod and maturity stage. Among the species, *L. odoratus* had early maturity, whereas *L. aphaca* exhibited late maturity. The average value of hundred seed weight was highest in *L. sativus* followed by *L. cicera* and *L. odoratus* while the lowest value was recorded in *L. aphaca*. Based on hierarchical clustering, all accessions were grouped into four clusters. Our findings could be used as reference in species identification and understanding the diversity within and among *Lathyrus* species.

Key Words: *Lathyrus aphaca, L. cicera, L. odoratus, L. sativus*, Morphology, Taxonomy

Introduction

The genus *Lathyrus* is an important, underutilized species, which has the immense potential to be used as human food, animal feed and sustainable agriculture (Campbell, 1997; Tripathi *et al*., 2020) (Fig. 1). It includes about 182 species (POWO, 2019) cultivated around 1.5 m ha throughout the world (Kumar *et al*., 2013; Vaz Patto and Rubiales, 2014). Due to its high biological potential, it can thrive well in various environmental conditions and capacity to improve soil fertility (Polignano *et al*., 2009; Sidorova *et al*., 2013). It is believed that it was originated in two separate regions, *namely*, the Central Asiatic region and the Abyssinian centre of origin (Vavilov, 1951). It is grown in India from 2000 BC (Saraswat, 1980). Sanjappa (1992) mentioned nine species of the genus *Lathyrus* are distributed in India, namely *L. aphaca* L., *L. inconspicuous* L., *L. hirsutus* L., *L. humilis* (Seringe) Fischer ex Spreng., *L. laevigatus* (Waldst. & Kit.), *L. odoratus* L., *L. pratensis* L., *L. sativus* L., *L. sphaericus* Retz. However, Bhellum (2016) reported a new existence of *L. cicera* in the country. Among them, *L. sativus,* commonly known as grasspea is predominantly grown in India, has the great potential to use as grain and forage legume crop in arid areas. It is resilient to several abiotic stresses such as drought, flood and salinity. *L. cicera* is the progenitor of *L. sativus* (Campbell, 1997), which reported as potential donor for cold-tolerance (Robertson *et al*., 1996) and crossable with *L. sativus* (Yunus *et al*., 1991). Apart from this, *L. aphaca* is commonly found as weed and resistant to powdery mildew and thrips (Pandey *et al*., 1996; Pradeep *et al*., 2014). *L. odoratus* was discovered in Sicily in 1695 and has been extensively used as an ornamental plant (Inoue *et al*., 2000; Rice, 2002; Vaz-Patto and Rubiales, 2014).

In the present age of changing climate, there is a need to diversify the cropping system by introducing

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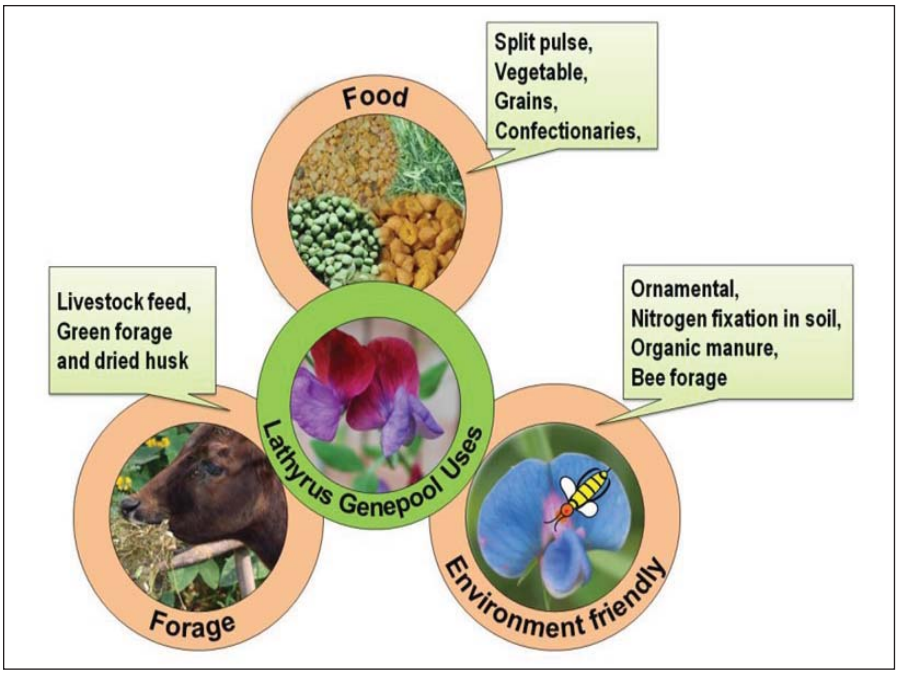

Fig. 1. Manifold use of the *Lathyrus* genepool

the diversity of species, varieties and forms of grain legumes in cropping systems for sustainable agricultural production (Mihailovic *et al*., 2013). The assessment of the genetic diversity and phenotypic characterization of the genetic resources remains the first step for the evaluation, description and categorization of germplasm collections to enhance their proper and rational utilization in crop breeding programs (Bisht *et al*., 2005; Tripathi *et al*., 2018). Principal component analysis (PCA) and clustering are the two main multivariate approaches for genetic diversity estimation. They have been utilized in analyzing the extent of diversity in many *Lathyrus* species (Grela *et al*., 2010). Therefore, the present research was carried out to compare the morphological traits of the selected *Lathyrus* accessions representing four economic species and reveal diversity among accessions by using clustering and PCA approach.

Materials and Methods

Plant Materials

A total of 20 accessions comprising of four species of *Lathyrus viz. L. aphaca*, *L. cicera*, *L. odoratus* and *L. sativus* were obtained from National genebank, ICAR-NBPGR, New Delhi and ICARDA-Food Legume Research Platform, Amlaha, Madhya Pradesh, India. The details of species and accessions, along with passport data, are presented in Table 1.

Table 1. Passport data of experimental materials

Accession	Species	Source of Country
IC572435	*Lathyrus aphaca* L.	India
IC572423	*Lathyrus aphaca* L.	India
IG 64838	*Lathyrus cicera* L.	Syria Arab Republic
IG 64839	*Lathyrus cicera* L.	Syria Arab Republic
EC540952	*Lathyrus cicera* L.	Syria Arab Republic
IC420786	*Lathyrus cicera* L.	India
IG 64857	*Lathyrus cicera* L.	Syria Arab Republic
EC540954	*Lathyrus cicera* L.	Syria Arab Republic
EC720816	*Lathyrus cicera* L.	Syria Arab Republic
EC720817	*Lathyrus cicera* L.	Syria Arab Republic
IC311167	*Lathyrus odoratus* L.	Jharkhand, India
IC319832	*Lathyrus odoratus* L.	India
IC396040	*Lathyrus sativus* L.	India
IC394579	*Lathyrus sativus* L.	India
IC396037	*Lathyrus sativus* L.	India
IC396038	*Lathyrus sativus* L.	India
IC396040	*Lathyrus sativus* L.	India
IC396041	*Lathyrus sativus* L.	India
IC396042	*Lathyrus sativus* L.	India
IC444256	*Lathyrus sativus* L.	India

Experimentation, Data Collection and Statistical Analysis

All accessions were grown at ICAR-NBPGR, New Delhi, India (28.08 °N, 77.12 °E and the height above mean sea level 228.61 meters) during the winter (*Rabi*) season

of 2018–2019 and 2019–2020 for agro-morphological characterization and evaluation.

Seeds of each accession were sown in pots in five replications. Due to the staggered germination factors, to avoid the hardiness of seed coat, scarification was done to facilitate proper water imbibitions for promoting good germination in all accessions (Gore *et al*., 2019, Singh *et al*., 2020). Standard agronomic practices were followed as and when necessary to obtain healthy crop growth. All these annual *Lathyrus* species were characterized for 24 qualitative and 18 quantitative traits using standard *Lathyrus* descriptors published by Bioversity International (Table 2). During observations, the plant parts were observed with the help of the naked eye, hand lens (10x), and some typical vegetative characters like stipules and all the floral characters noted using stereo-microscope (Lmi, SZM 12) with dissected floral parts. Ten random samples were taken from each accession of the particular species to record the data on quantitative characters. The data were subjected to statistical analysis using MS Office Excel and SPSS software.

Results

Distinctive morphological characters of the *L. sativus, L. cicera, L. aphaca* and *L. odoratus* were recorded at the vegetative, flowering, podding and post-harvest stages.

Vegetative Characteristics

Semi-erect type of plant growth habit was recorded in *L. sativus* and *L. cicera*, whereas spreading type was found in *L. aphaca* and *L. odoratus.* The three species *L. sativus, L. cicera* and *L. odoratus* had one pair of leaflets while *L. aphaca* had reduced into simple tendril leaflets. The shape of the leaflet was linear in *L. sativus* and *L. cicera,* whereas ovate in *L. odoratus.* Stipules were prominent and persistent in all four species. The shape of stipules was semi-sagittate in *L. sativus;* semi-hastate in *L. cicera* and *L. odoratus,* while fallacious ovate-hastate in *L. aphaca.* Stem sections were square in *L. sativus*, *L. cicera* and *L. aphaca* while cylindrical in *L. odoratus.* The waxiness on the stem was observed in all studied species (Fig. 2).

Flower Characteristics

Blue coloured flower was recorded in *L. sativus*. Red coloured flower was recorded in *L. cicera,* creamish white to light yellow in *L. aphaca*; while in *L. odoratus* standard petal were bright pink colour and purple colour wing petals. All species possess single flower per peduncle except *L. odoratus* where 2-3 flowers were observed. The smallest flower size was recorded in *L. aphaca*; medium in *L. sativus and L. aphaca,* while flower was largest in *L. odoratus* (Fig. 3).

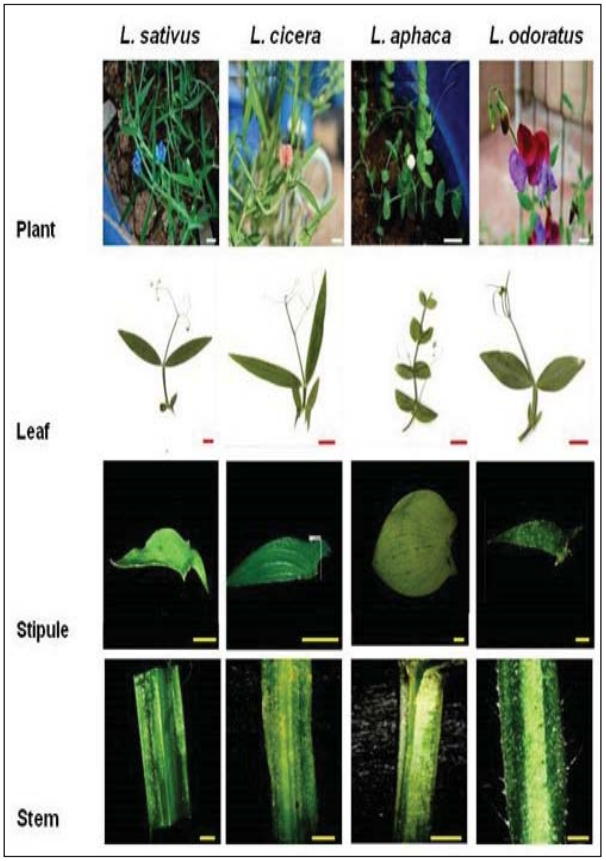

Fig. 2. Vegetative characteristics of *L. sativus, L. cicera, L. aphaca* and *L. odoratus* (bar scale: white colour bar = 10 cm, red colour bar = 1 cm, yellow colour bar = 0.1 cm)

Pod Characteristics

The morphology of pod was one of the essential characters in distinguishing all four species. Pod shape was medium oblong elliptical in *L. sativus* and *L. cicera*; beaded in *L. aphaca* while broad linear in *L. odoratus.* The colour of the mature pod was yellowish-brown in *L. sativus* and *L. cicera;* brown in *L. aphaca* and creamy yellow *L. odoratus.* Pod beak shape was pointed in *L. sativus, L. cicera* and *L. aphaca* whereas, blunt in *L. odoratus*. Wings on the pod were narrow observed in *L. sativus* while other species (*L. odoratus*, *L. aphaca* and *L. cicera*) were wingless. All species had glabrous pod except *L. odoratus* where it was pubescent (Fig. 3). Shattering of pods at maturity was observed only in *L. aphaca.*

Table 2. Descriptor traits used in study of *Lathyrus* species

Qualitative	Descriptor State
Early plant vigour	Poor (1), Good (2), Very good (3)
Plant Growth Habit	Prostate (1), Spreading (2), Semi-erect (3), Erect (4)
Plant type	Indeterminate (1) Determinate (2)
Nodes per plant	Few (3), Medium (5), Many (7)
Stem colour	Light green (1), Green (2), Purple-green (3), Purple (4), Other (99)
Stem wing width	Wingless (0), Small (3), Medium (5), Large (7)
Stem waxy coating	No coating (0), Small (3), Medium (5), Large (7)
Stem section shape	Round (1) Square (2) Deeply fasciated (3), Other (99)
Root nodulation	No nodules (0), Low (3), Intermediate (5), High (7)
Branch arrangement	Evenly distributed throughout the whole plant (1), Mainly on lower part of the plant (2) Mainly in middle part of the plant (3)
Anthocyanin pigment colour	Absent (0), Present (1)
Leaf type	Tendril (1), Phyllody (2), Simple (3), Bipinnate (4), Multipinnate (5), Other (99)
No of leaflets per leaf	One pair (1), Two pairs (2), More than two pairs (3)
Leaf colour	Light green (1), Green (2), Dark green (3), Other (99)
Prominence of leaf vein	No (0), Yes (1)
Pigmentation of leaf vein	No (0), Yes (1)
leaf size	Small (3), Medium (5), Large (7)
Leaflet shape	Linear (1), Lanceolate (2), Ovate (3)
Leaf petiole colour	Green (1), Purple-green (2) Other (99)
Leaf tendrils	Absent (0), Short (1), Medium (2), Long (3), Other (99)
Top leaves petiole end	Tendril subulate (1) Tendril simple (2), Tendril compound (3), Other (99)
Lower leaves petiole end	Tendril subulate (1), Tendril simple (2), Tendril compound (3), Other (99)
Leaf persistance	Low (3), Moderate (5), High (7)
Leaf senescence	No visual senescence (0), Slight visual senescence (3), Moderate senescence (5), Conspicuous concurrent senescence (7)
Leaf pubescence	Absent (0), Present (1)
Stipule shape	Sagittate (1), Semi-sagitatte (2)
Flower colour	White (1), White blue (2), Blue (3), Grey (4), Light Yellow (5), Yellow (6), Pink (7), Orange (8), Red (9), Violet-blue (10), Violet (11), Other (99)
Flower size	Small (3), Medium (5), Large (7)
Pod colour immature	Yellow-cream (1), Light green (2), Green (3), Dark green (4), Green-purple (5), Light purple (6), Purple (7), Other (99)
Pod colour mature	Yellow-green (1), Violet mottled (2), Grey (3), Other (99)
Pod pigmentation	Uniformly green (1), Uniformly pigmented (2), Mottled (3), Other (99)
Pod shape	Oblong-elliptical (1), Medium oblong-elliptical (2), Curved (3), Beaded (4), Broad-linear (5), Broad-elliptical (6), Other (99)
Pod curvature	Straight (1), Slightly curved (2), Curved (3)
Pod beak shape	Pointed (1), Blunt (2), Other (99)
Pod pubescence	Absent (0), Low (3), Medium (5), High (7)
Pod dehiscence	No shattering (0), Low shattering (3), Medium shattering (5), High shattering (7)
Pod wings	Absent (0), Narrow (3), Medium (5), Wide (7)
Seed shape	Oblate or flattened (1), Triangular (2), Rhomboid (3), Square (4), Obtriangular (5), Spherical (6), Other (99)
Seed coat colour	Greyed-white (1), Yellow-white (2), Grey (3), Brown (4), Yellow-green (5), Pink (6), Red-purple (7), Black (8), Grey mottled (9), Green mottled (10), Other (99)
Seed coat surface	Smooth (1), Tubercular (2)
Seed coat pattern	Absent (0), Marbled (1), Dotted (2), Streaked (3), Mixture (4)
Seed coat pattern colour	Cream (1), Green (2), Brown (3), Red-purple (4), Black (5), Other (99)
Seed size	Small (3), Medium (5), Large (7)
Cotyledon colour	Yellow (1), Orange (2), Other (99)
Seed ornamentation	Absent (0), Present (1)

Table 3. Distinctive characteristics of four species of *Lathyrus*

Traits	*L. sativus*	*L. cicera*	*L. aphaca*	*L. odoratus*
Vegetative characteristics				
Plant growth habit	Semi-Erect	Semi-Erect	Spreading	Spreading
Leaflet shape	Linear	Linear	Tendril	Ovate
Number of leaflets	One pair	One pair	Reduced to a simple tendril	One pair
Stipule shape	Semi-saggitate	Semi-hastate	Fallacious ovate-hastate	Semi-hastate
Stem wing	Present	Narrow	Absent	Present
Stem section	Square	Square	Cylindrical	Square
Floral characteristics				
Number of flowers per inflorescence	1	1	1	2-3
Flower colour	Blue	Brick Red	Light Yellow	Pink
Flower size	Medium	Medium	Small	Large
Pod and seed characteristics				
Pod shape	Medium oblong elliptical	Medium oblong elliptical	Beaded	Broad linear
Mature pod colour	Yellowish Brown	Yellowish Brown	Brown	Yellowish
Immature pod colour	Light Green	Light Green	Dark Green	Light Green
Pod beak shape	Pointed	Pointed	Pointed	Blunt
Pod wings	Narrow	Absent	Absent	Absent
Pod pubescence	Absent	Absent	Absent	High
Pod dehiscence	No shattering	No shattering	Medium shattering	No shattering
Seed shape	Rhomboid-Obtriangular	Rhomboid-Obtriangular	Spherical	Spherical
Seed coat colour	Grey Mottled	Brown Mottled	Grey Mottled	Blackish Grey
Seed size	Large	Medium	Small	Medium
Seed coat surface	Tubercular	Tubercular	Smooth	Smooth
Seed coat pattern	Marbled	Absent	Marbled	Dotted
Seed eye width	Narrow	Narrow	Narrow	Wide
Shattering	Absent	Absent	Present	Absent

Seed Characteristics

The morphology of seed characters was studied with the naked eye and under the stereo-microscope are presented in Table 3 and Figure 3. The four species can be identified easily at the seed stage prominently by observing the seed's size, colour, and shape. Seeds of *L. sativus* and *L. cicera* were rhomboidal obtriangular in shape with tuberculate surface. The seed shape was spherical, with smooth surface observed in *L. aphaca* and *L. odoratus*. Seed coat colour was observed grey mottled in *L. sativus* and *L. aphaca* whereas brown mottled in *L. cicera* and blackish-grey in *L. odoratus.* Among all studied species, the smallest seed was observed in the *L. aphaca*; medium in *L. cicera* and *L. odoratus* while the largest in *L. sativus*.

Quantitative Traits

Wide variation for quantitative traits was recorded in *L. sativus, L. cicera, L. odoratus* and *L. aphaca* (Table 4). The mean value of plant height was 91.70 and 91.21 cm in *L. sativus* and *L. cicera*, respectively. The tallest plant was recorded (113 cm average plant height) in *L. odoratus*, whereas two times shorter plant height was recorded (an average of 51.63 cm) in *L. aphaca*. Length of internode was also similar in case of *L. sativus* (5.35 cm) and *L. cicera* (5.52 cm), whereas, *L. odoratus* had comparatively shorter internode length (4.00 cm) followed by *L. aphaca* (2.50 cm). Petiole and pedicle length were short in *L. aphaca* whereas, the longest in *L. odoratus* followed by *L. sativus* and *L. cicera.* In the present study, an average number of primary branches 3.50, 3.62, 5.00 and 5.54 were recorded on *L. aphaca, L. sativus, L. odoratus and L. cicera*, respectively. The mean number of days to flowering of *L. sativus* and *L. cicera* was recorded 70 and 75 days, respectively. The *L. aphaca* accessions was flowered in 89 days, while the lowest was recorded in *L. odoratus* (60 days). The average number of pods in *L. sativus* accessions amounted to 37.62, while it was lesser in *L. aphaca* (27.33) and *L. odoratus* (25.17) than *L. sativus*. Highest number of pods per plant was recorded in *L. cicera* (45.62). The pod was longer in *L. odoratus* (5.52 × 1.10 cm) while the medium in *L. sativus* (2.96 × 0.82 cm) and *L. cicera* (2.75 × 0.76 cm) and smallest in *L. aphaca*

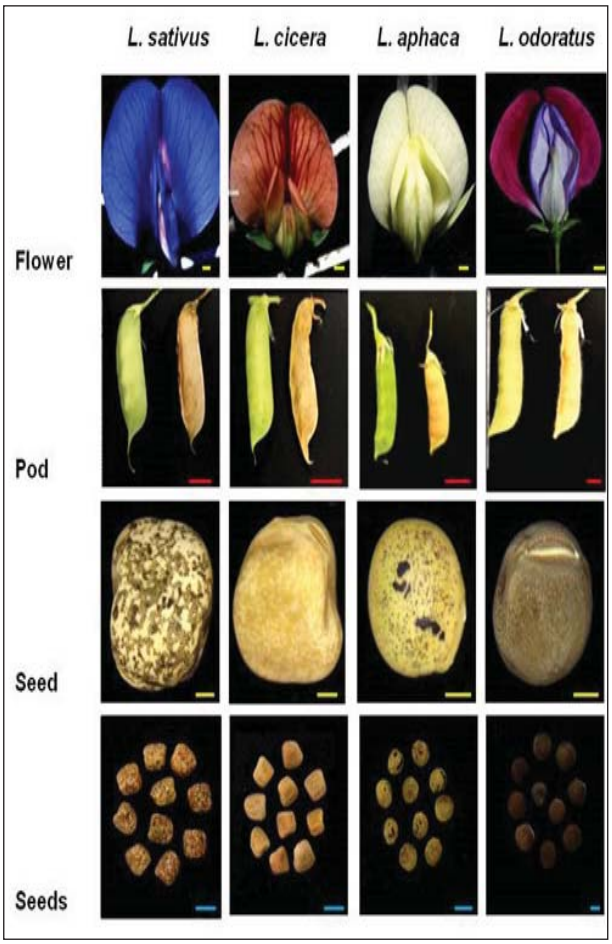

Fig. 3. Floral and pod characteristics of *L. sativus, L. cicera, L. aphaca* and *L. odoratus* (bar scale: white colour bar = 10 cm, red color bar = 1 cm, yellow colour bar = 0.1 cm, blue colour bar = 0.5 cm)

(2.05 × 0.587). The average number of seeds per pod was the highest in *L. odoratus* followed by *L. aphaca, L. sativus* and *L. cicera.* Wide variation was observed for 100-seed weight among the *Lathyrus* species. The mean highest value for 100-seed weight was recorded in *L. sativus* (8.83 g) followed by *L. cicera* (6.99 g) and *L. odoratus* (5.11 g), whereas *L. aphaca* (1.30 g) showed the lowest 100-seeds weight. Seed diameter was correlated with 100-seed weight as it was the highest in *L. sativus* (0.47 cm) followed by *L. cicera* (0.41cm) and *L. odoratus* (0.34 cm) whereas lowest in *L. aphaca* (0.26 cm).

Inter-relationship Studies among Quantitative Traits

Correlation analysis revealed that plant height strongly correlated with leaflet, standard petal, pod size, petiole and pedicle length, and 100-seeds weight. In contrast, a strong negative correlation was observed with the number of days to flowering and maturity. Hundred seed weight positively correlated with pod length, leaflet length and seed diameter (Table 5). The number of seeds per pod had a positive relation with petiole and pedicle length and pod length while negative with seed diameter. Pod length and plant height were negatively correlated with days to flowering and maturity.

Hierarchical Clustering and Principal Component Analysis

Based on hierarchical clustering dependent upon Euclidian distance using the Wards method, all accessions were grouped into four clusters. Cluster-I contained accessions of *L. aphaca,* and cluster-II had *L. odoratus,* while III and IV clusters contain *L. sativus* and *L. cicera* both (Figure 4). The interrelationships among the different parameters were studied through PCA based on correlations. The first three principal components summarized a realistic summary of all data explaining 87.16% variance in *Lathyrus* germplasm considered in

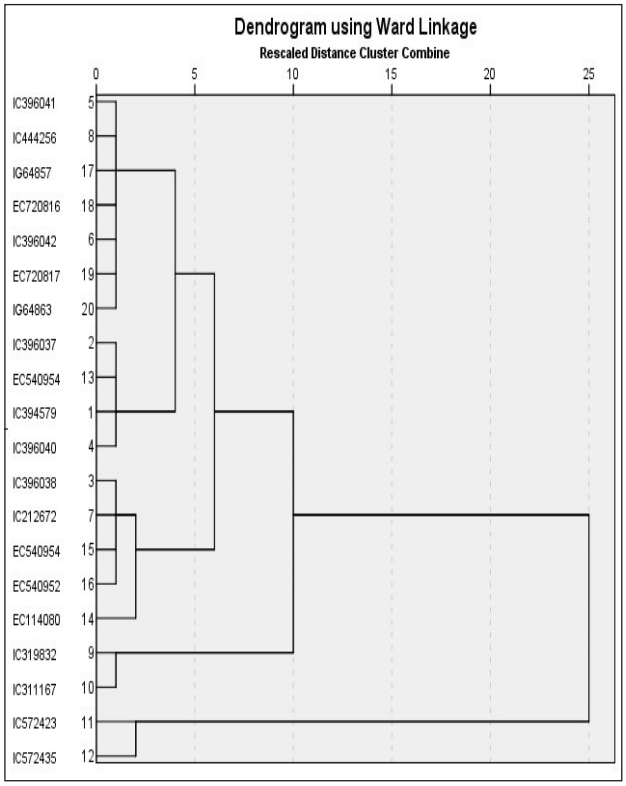

Fig. 4. Dendrogram by Ward's method based on Euclidian distance revealing genetic diversity and relationship among 20 accessions of *Lathyrus* as indicated by quantitative traits

Table 4. Mean value of quantitative characters

Trait	*L. sativus*	*L. cicera*	*L. aphaca*	*L. odoratus*
Plant height (cm)	91.70* ± 1.95**	91.21 ± 2.09	52.63 ± 4.20	113.00 ± 2.5
Internode length (cm)	5.35 ± 0.43	5.52 ± 0.19	2.50 ± 0.50	4.00 ± 0.215
Petiole length (cm)	1.56 ± 0.19	1.25 ± 0.06	0.50 ± 0.08	2.65 ± 0.11
Pedicel length (cm)	3.45 ± 0.32	3.12 ± 0.05	2.43 ± 0.10	5.27 ± 0.13
Leaflet length (cm)	5.9 ± 0.24	5.45 ± 0.13	2.28 ± 0.12	5.55 ± 0.28
Leaflet width (cm)	0.62 ± 0.05	0.58 ± 0.05	0.37 ± 0.03	2.68 ± 0.38
Number of primary branches	3.62 ± 0.35	5.54 ± 0.36	3.50 ± 0.50	5.00 ±1
Nodes to the first bearing pod	8.66 ± 0.17	8.20 ± 0.22	7.17 ± 0.17	5.00 ±0.5
Number of days to first flowering	70.91 ± 1.03	75.66 ± 2.29	89.33 ± 2.83	60.00 ± 2
Standard petal length (cm)	2.04 ± 0.02	2.75 ± 0.02	1.42 ± 0.05	3.20 ± 0.17
Standard petal width (cm)	2.20 ± 0.02	2.36 ± 0.03	1.47 ± 0.10	3.08 ± 0.01
Number of days to 80% maturity	101.45 ± 0.89	101.25 ± 2.78	121.17 ± 0.50	95.17 ± 0.16
Number of pods per plant	37.62 ± 2.76	45.62 ± 2.70	27.33 ± 3.17	25.17 ± 1.16
Pod length (cm)	2.96 ± 0.16	2.75 ± 0.07	2.05 ± 0.25	5.52 ± 0.28
Pod width (cm)	0.82 ± 0.09	0.76 ± 0.03	0.57 ± 0.04	1.10 ±0.095
Number of seed per pod	3.97 ± 0.16	3.91 ± 0.12	4.00 ± 0.33	5.00 ±1
100 seed weight (g)	8.83 ± 0.38	6.99 ± 0.27	1.30 ± 0.02	5.11 ± 0.04
Seed diameter (cm)	0.47 ± 0.01	0.41 ± 0.01	0.26 ± 0.03	0.34 ± 0.03

*: Average value; **: Standard Errors (SE)

Table 5. Correlation matrix of quantitative traits

Traits	PH	IL	NFPB	DF	DM	NPB	LL	LW	PL	PDL	SPL	SPW	NPP	PoL	PoW	NSP	HSW	SD
PH																		
IL	0.595**																	
NFPB	-0.007	0.301																
DF	-0.738**	-0.133	0.037															
DM	-0.850**	-0.427	-0.129	0.814**														
NPB	0.332	0.018	-0.324	0.016	-0.304													
LL	0.841**	0.828**	0.224	-0.526*	-0.713**	0.131												
LW	0.515*	-0.059	-0.714**	-0.525*	-0.342	0.321	0.211											
PL	0.759**	0.417	-0.363	-0.665**	-0.582**	0.053	0.609**	0.768**										
PDL	0.647**	0.227	-0.508*	-0.495*	-0.450*	0.25	0.445*	0.720**	0.831**									
SPL	0.723**	0.328	-0.376	-0.433	-0.590**	.666**	0.432	0.640**	0.532*	0.505*								
SPW	0.831**	0.326	-0.407	-0.628**	-0.661**	.490*	0.561*	0.789**	0.738**	0.679**	0.896**							
NPP	0.258	0.607**	0.460*	0.278	-0.124	0.323	0.369	-0.373	-0.086	-0.062	0.191	0.058						
PoL	0.653**	0.116	-0.658**	-0.667**	-0.540*	0.258	0.389	0.885**	0.881**	0.840**	0.617**	0.802**	-0.289					
PoW	0.540*	0.398	-0.510*	-0.294	-0.391	0.318	0.538*	0.664**	0.736**	0.782**	0.421	0.599**	0.043	0.714**				
NSP	0.33	-0.225	-.618**	-0.342	-0.219	0.409	0.042	0.812**	0.477*	0.661**	0.486*	0.581**	-0.377	0.665**	0.556*			
HSW	0.653**	0.530*	0.308	-0.595**	-0.541*	-0.247	0.784**	0.192	0.577**	0.351	0.031	0.347	0.089	0.358	0.383	0.04		
SD	0.466*	0.685**	0.603**	-0.274	-0.394	-0.236	0.766**	-0.291	0.134	0.012	-0.013	0.126	0.358	-0.135	0.054	-0.351	0.700**	

(PH: plant height; IL: internode length; NFPB: nodes to the first bearing pod: DF: days to flowering; DM: days to maturity; NPB: number of primary branches; LL: leaflet length; LW: leaflet width; PL: petiole length; PDL: pedicel length; SPL: standard petal length; SPW: standard petal width; NPP: number of pods per plant; PoL: pod length; PoW: pod width; NSP: number of seeds per pod; HSW: 100 seed weight; SD: seed diameter)

this study. The first Principal Component (PC1) was the most important, accounting for 47.12% of the total variation. PC1 was loaded on plant height, petiole and pedicel length, leaflet length and width, pod length and width and the number of seeds per pod. PC2 accounted for 23.92 % variance, and it was loaded on internode length, nodes to the first bearing pod, 100-seed weight and seed diameter. PC3 contributed 10.91% variance mainly through a number of primary branches, number of days to first flowering and number of pods per plant (Table 6).

Discussion

The phenetic or taximetrics concept attempts to classify organisms based on morphology or other observable traits of the species delineation for their evolutionary or phylogeny relation (Schneider *et al*., 2016; Gore *et al*., 2019; Ivana *et al*., 2020). The present study highlighted

Table 6. Principal component (PC) matrix explaining loading of variables.

Trait	Component		
	1	2	3
Plant height	0.90	0.35	0.09
Internode length	0.43	0.73	0.23
Petiole length	0.90	-0.01	-0.24
Pedicel length	0.83	-0.21	-0.07
Leaflet length	0.71	0.66	0.02
Leaflet width	0.79	-0.53	-0.10
No of primary branches	0.37	-0.25	0.79
Nodes to the first bearing pod	-0.37	0.82	-0.05
No of days to first flowering	-0.73	-0.13	0.43
stranded petal length	0.75	-0.13	0.50
stranded petal width	0.91	-0.09	0.20
No of days to 80% Maturity	-0.75	-0.35	-0.01
No of pods/plant	0.00	0.59	0.69
Pod length	0.89	-0.35	-0.17
Pod width	0.77	-0.12	0.05
No of seed per pod	0.60	-0.61	-0.02
100 seed weight	0.55	0.59	-0.45
Seed diameter	0.21	0.88	-0.14
Total	8.48	4.31	1.96
% of Variance	47.12	23.92	10.91
Cumulative %	47.12	71.04	81.96

the characterization of the morphological traits for delineating and revealing the diversity pattern.

During morphological characterization of different accessions of the selected species, it was observed that *L. sativus, L. cicera* and *L. odoratus* had one pair of leaflets and it is reduced into simple tendril leaflets in *L. aphaca*. Hofer *et al*. (2009) suggested selective advantage of the tendril enable plants to reach the canopy, increase the opportunity for pollination, photosynthesis and seed dispersal with minimal energy investment. Whereas, Gianoli (2004) emphasized that the climbing habit (tendril) is associated with species/cultivars richness compared with non-climbing habit sister taxa. The waxy coating on the stem was observed in all studied species. Mitra *et al.* (2020) suggested that the amount and composition of the waxy coating and their chemical compounds (alkanes, esters, aldehydes, fatty acids, and alcohols) may vary widely within species. *L. sativus* had blue coloured flowers. IPGRI (2000) also reported that in *L. sativus*, the blue-flowered type is common in South Asia, while the white-flowered type is commonly found in the Mediterranean region. Shattering of pods at maturity is one of the prominent traits of wild species. In the present study, shattering was observed only in *L. aphaca*. Ogutcen *et al*. (2018) reported that indehiscence is a preferred trait in cultivated crops, especially in legumes by breeders, because shattering makes harvesting difficult and lead to significant yield loss. In *L. sativus* and *L. cicera,* seed shape was rhomboidal obtriangular with tuberculate surface. Similarly, Singh and Roy (2013) and Barpete (2015) demonstrated a highly predominating rhomboid seed shape in *L. sativus*. Based on morphological traits, all four studied species can be differentiated. Similar studies were carried out in genus *Vigna* (Gore *et al*. 2019), suggested that morphological characteristics can be used to delineate closely related species.

Several researchers have carried out the morphological characterization of Lathyrus species (Tay *et al*., 2000; Benkova and Zakova, 2001; Dela Rosa and Martın, 2001; Kumari, 2001; Tavoletti *et al*., 2005; Grela *et al*., 2012). All the previous studies suggested a wide range of exploitable variations in *Lathyrus* species. In the present study, wide variation for quantitative traits was recorded. Similar plant height was recorded for *L. sativus* and *L. cicera*. Earlier studies on *L. sativus* and *L. cicera* suggested that plant height varies in different environmental conditions (Campbell, 1997; IPGRI, 2000; Grela *et al.,* 2010). The number of branches per plant is an essential character that has a substantial impact on plant productivity (Basaran *et al*., 2013). In the present study, *L. odoratus and L. cicera* were recorded with more number of primary branches as compared to the *L. aphaca* and *L. sativus,* and similar observations were made by Kosev and Vasileva (2019). The flowering is a complex phenomenon (from vegetative to reproductive stage), and it varies among species as well as genotypes in legumes (Putterill *et al*., 2013; Barpete *et al.,* 2020). In the present study, *L. aphaca* was late maturing, and *L. odoratus* had early maturity among all the species studied. The highest number of pods per plant was recorded in *L. cicera*. Wide variation was observed for 100-seed weight among the *Lathyrus* species. The highest value for 100-seed weight was recorded in *L. sativus* while the lowest in *L. aphaca*. Rybinski *et al.* (2008) reported wide variation for 100-seeds weight in *L. sativus.* The grain productivity in *L. sativus* was dependent mainly number of pods per plant and seeds per pod (Donskoy, 2013). Seed diameter was correlated with

100-seed weight as it was highest in *L. sativus*. Larger seeds are always preferred for selections by a breeder (Chowdhury and Slinkard, 2000). Because, large seed size may increase seed yield that desired for any crop improvement programmes, including *Lathyrus* gene pool (Campbell, 1997). Polignano *et al.* (2005) emphasized that *L. sativus* has tremendous potential for cultivation, mainly for grain purposes. Similar studies reported high variability in morphological and agronomical traits in field evaluation of *Lathyrus* species, indicated high breeding potential in *Lathyrus* gene pool (Tay *et al*., 2000; De la Rosa and Martın, 2001; Kumari, 2001; Benkova and Zakova, 2001; Tadesse and Bekele, 2003; Tavoletti *et al*., 2005; Grela *et al*., 2012).

Correlation analysis revealed that plant height strongly correlated with leaflet, standard petal, pod size, petiole and pedicle length, and 100-seeds weight. Hanbury *et al*. (1995) reported that increased seed size is positively correlated with higher seed yield. Therefore, plant breeders considered increasing seeds per pods in large-seeded cultivars as an effective means of increasing yield. In the present study, the number of seeds per pod positively related to petiole and pedicle length and pod length while negative with seed diameter. Pod length and plant height were negatively correlated with days to flowering and maturity. These results were in consonance with previous studies (Jackson *et al*., 1984; Hanbury *et al*., 1999; Nakamura *et al*., 2010; Kosev and Vasileva, 2019) on studies of different *Lathyrus* species.

Possibility to distinguish a large number of accessions into small homogenous clusters make it easier to select diverse parents for future breeding programme. It does not only facilitates a comparison among the feasible pairs of individuals but also helps in bringing together all possible combinations of gene constellations, thereby making it possible to construct desirable progenies with multiple traits through hybridization. Based on hierarchical clustering dependent upon Euclidian distance using the Wards method, all accessions were grouped into four clusters. Cluster-I contained accessions of *L. aphaca,* and cluster-II had *L. odoratus,* while III and IV clusters contain *L. sativus* and *L. cicera* both. The interrelationships among the different parameters were studied through PCA based on correlations. DelaRosa and Martin (2001) reported similar results of variability distribution from a study with 150 accessions of *L. sativus.*

The present study demonstrated substantial morphological variation in studied *Lathyrus* species. These species were characterized for morpho-taxonomical descriptor traits. Based on descriptor traits, results indicated the similarity in characteristics of *L. cicera* and *L. sativus*. The *Lathyrus* species showed a substantial variation for days to flowering and maturity. A positive correlation between pod size and 100-seed weight was found in the study. This study of *Lathyrus* provide insights on exploiting wild germplasm and information on floral traits for the readily crossable wild species with cultivated genepool. In India, characterization of available *Lathyrus* genepool and collection of new germplasm from untapped areas should be prioritized to enhance the utilization of this minor multi-purpose legume.

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RESEARCH ARTICLE

Characterization of Selected Sweet Cherry (*Prunus avium* L.) Varieties using DUS Test Guidelines

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The present study was conducted to characterize and decipher the genetic variability among twenty sweet cherry (*Prunus avium* L.) varieties. Different morphological traits namely, growth habit, foliage, flower, fruit and stone characteristics were studied for further improvement and utilization. Growth habit varied from upright (5 varieties) to semi-upright and spreading (15 varieties). Shape of leaves was observed as obovate and lanceolate. Most of the varieties were late in maturity early. Huge variation was recorded for quality determining traits namely, fruit size, shape, flesh and skin colour. Fruit shape was observed as reniform in fourteen varieties and elliptic in rest of the varieties except cordate in Rainier. Fruit firmness was found to be soft and intermediate for the most of the varieties, whereas, varieties *viz.*, Lambert, Rainier, Red Heart, Stella and Sunburst had hard fruit firmness.

Key Words: Characterization, DUS, Fruit quality, Sweet cherry

Introduction

Sweet cherry (*Prunus avium* L.) belonging to the family Rosaceae and sub-family Prunoideae is one of the most important and delicious fruits of temperate regions of the world (Wunsch and Hormaza, 2004). Sweet cherries contain high nutritional content and are available in market from mid-week of May until July with non-competence among different temperate fruit crops (Zheng *et al*., 2016).

Sweet cherry is native to the areas adjoining Black Sea and Caspian Sea (Watkins, 1976) from where it diversified to different regions of the World. They are usually grown in the coldest climates at an altitude of about 1600 to 2700 m above mean sea level and its cultivation is mainly confined between 35 °N and 55 °S latitude. Jammu and Kashmir is the major producer, (90 % of total production) of sweet cherry in India with 2713 ha area and 11789 MT production (Anonymous, 2019a). In Himachal Pradesh, it is grown under 453 ha area having 225 MT production (Anonymous, 2019b). Shimla, Kullu, Mandi, Chamba and Lahaul & Spiti are the main districts in Himachal Pradesh where cherries are grown extensively. Shimla district alone accounts for 80 per cent of total production of the state.

The fruits of sweet cherries are highly perishable in nature as it has a short shelf life which is a serious bottleneck for efficient handling, transportation and marketing of the produce. Moreover, with the sudden upsurge of global warming, standard varieties of sweet cherry, due to their inability to meet the chilling requirement in temperate areas of Himachal Pradesh face the risk of crop failure. Besides, the dominance of few cherry varieties such as Black Heart, Red Heart, Stella, Durone Nero and Van in cherry growing pockets of Himachal Pradesh at times, leads to glut in the market resulting in colossal economic loss to the farmers. This situation may be only countered by broadening the germplasm base through introduction and characterization of improved sweet cherry varieties.

Characterization helps in recording and compilation of data for important characteristics which distinguish genotype within a species or between the species and allows for easy and quick discrimination among them. It aids in easy accession grouping, gap identification and extraction of valuable germplasm for breeding programs, resulting in a greater understanding of the collection's composition and genetic diversity. It also enables a check on the true-to-type nature of homogeneous samples, allowing the detection of misidentifications or duplicates, as well as highlighting possible errors made during other operations.

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Although, the characterization and evaluation work on selected sweet cherry varieties has been carried out earlier, by several workers. The study was put forward to check the performance (qualitatively as well as quantitatively) of these sweet cherry varieties under wet temperate zone to extend their farming in Himachal Pradesh by selecting the most promising varieties, that perform good at this elevation. This will also help in the identification, description, assessment of uniformity of traits and stabilization of their expression at different locations over the time period. Keeping in view its significance, the characterization and evaluation of different sweet cherry varieties was performed at the Regional Horticultural Research and Training Station, Mashobra, Shimla (HP).

Materials and Methods

The present investigation was carried out in the experimental block of Regional Horticultural Research and Training Station, Mashobra, Shimla (H.P.) at an elevation of 2286 m amsl (latitude 31.1° N and longitude 77.1° E) during the years 2019 and 2020. The following varieties *viz*. Bing, Black Heart, Bradbourne Black, Durone Nero - II, Durone Nero - III, Early Rivers, Lambert, Lapins, Merton Glory, Noir De Guben, Rainier, Red Heart, Roundel Heart, Sam, Seneca, Stella, Sunburst, Triumph Domini, Van and Vega were characterized for the tree, foliage, floral and fruit characters. 20-24 years old plants of each variety, maintained at a spacing of 6.0 m × 6.0 m were selected and arranged in Randomized Complete Block Design with 3 replications for recording data on various quantitative characters.

The varieties were characterized for 29 morphological characters at specific growth stage when character had full expression, as per UPOV (2006) and PPV&FRA (2012) descriptors. Among 29 characters, 10 (tree habit, leaf: presence of nectaries, nectaries colour, flower diameter, flower: arrangement of petals, flower: shape of petals, fruit shape, fruit pistil end, colour of fruit juice and fruit juiciness) characters were characterized as per UPOV descriptor, whereas, PPV&FRA descriptor was used to characterize rest of the 19 (one year old shoot: length of internodes, leaf length, leaf width, leaf length/leaf width ratio, leaf shape, leaf: angle of apex, leaf: shape of base, leaf: length of petiole, days from full bloom to harvest, fruit weight, fruit length, fruit width, fruit skin colour, fruit flesh colour, fruit firmness, length of fruit stalk, eating quality, stone weight and stone shape) characters. The observations for the assessment of distinctiveness, uniformity and stability were made on plants from each replication selected randomly. All observations on the tree and the branches were made during dormancy. For foliage characters randomly picked thirty fully matured leaves (ten in each replication) from the middle portion of the current season's flush at the end of summer growth. Similarly, for fruit and stone characters, 15 representative fruit samples (five in each replication) were taken at optimum maturity. Observations on the mature fruit were recorded when fruit was ready for harvesting.

Results and Discussion

Tree growth characters such as growth habit and length of internode were observed as per UPOV (2006) descriptor

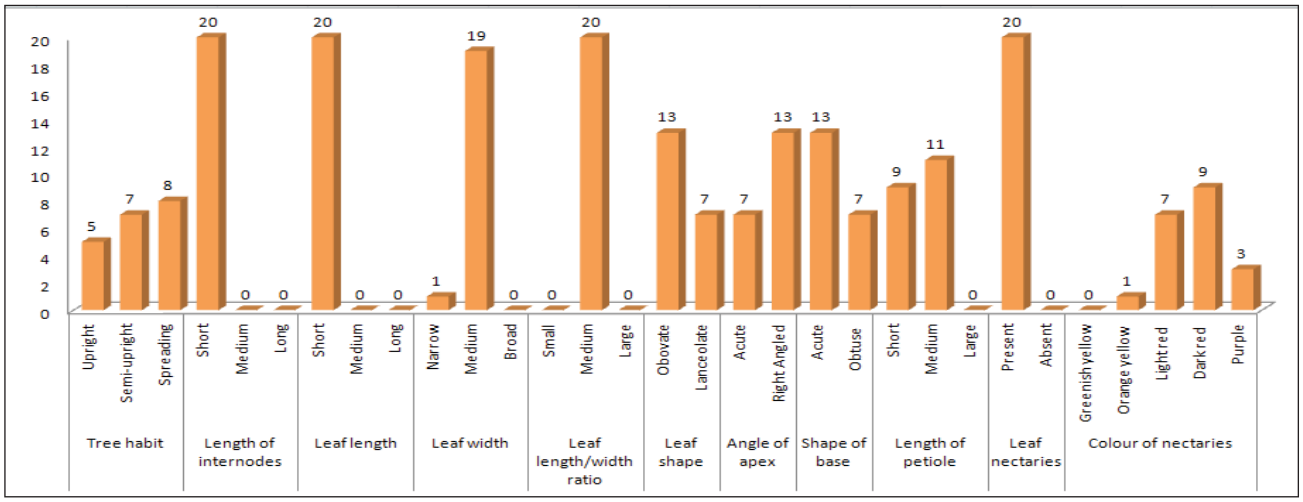

Fig 1. Frequency distribution of 20 sweet cherry varieties based on tree and foliage characters

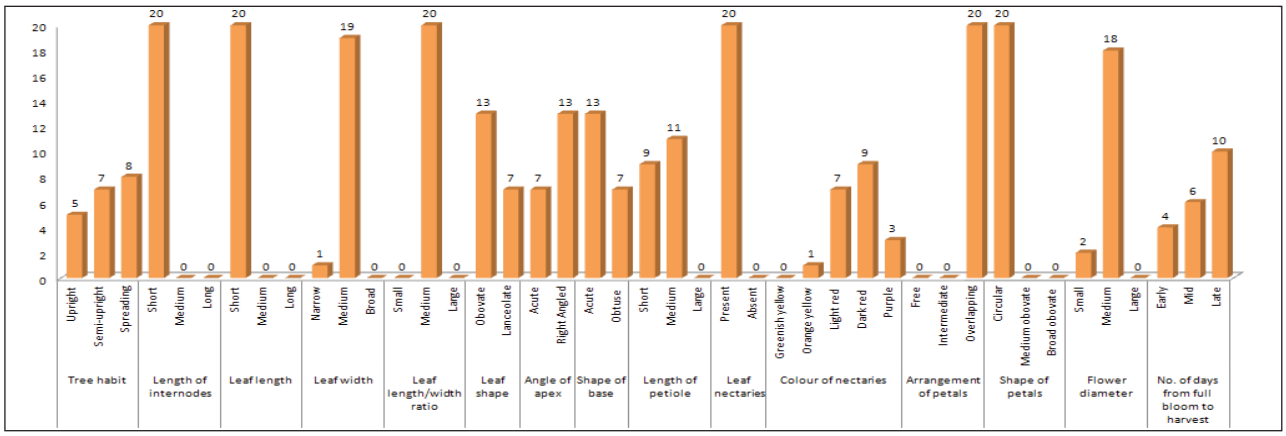

Fig. 2. Frequency distribution of 20 sweet cherry varieties based on tree, foliage and flower characters

and PPV&FRA (2012) descriptor. These guidelines varied considerably amongst the sweet cherry varieties under study which fell into distinct classes. Out of twenty sweet cherry varieties as many as eight varieties were found to have spreading type of growth habit (Black Heart, Bradbourne Black, Durone Nero-III, Lambert, Roundel Heart, Seneca, Stella and Sunburst), whereas, seven varieties had semi-upright growth habit (Durone Nero-II, Merton Glory, Red Heart, Sam, Triumph Domini, Van and Vega) and five had upright type of growth habit (Bing, Early River, Lapins, Noir De Guben and Rainier). No such variation in internodal length was reported in the present study. Upright growth habit observed in these varieties (Bing, Early River, Lapins, Noir De Guben and Rainier) suggests their suitability under high density planting system. Rakonjac *et al*. (2014) reported growth habit to be as upright, semi-upright and drooping in different cherry cultivars. This is also in agreement with the results of Matteo *et al.* (2017).

The variation in leaf characters is considered as distinguishing features for description and identification of fruit species and cultivars (Upshall, 1924). In the present study huge variation was observed in leaf shape, leaf: angle of apex, leaf: shape of base, leaf: length of petiole and nectaries colour except for leaf length, leaf width, leaf length/width ratio and leaf: presence of nectaries, in which no marked variation was observed. In the present study, leaf shape was found as obovate and lanceolate, whereas, leaf: shape of base as acute and obtuse, which were similar to the findings of Ljubojevic *et al*. (2016). Leaf: angle of apex was observed as acute and right angled in the present study. The nectaries colour was observed as orange yellow, light red, dark red and purple in the sweet cherry varieties under study. Similar variation in nectaries colour has been reported earlier by Olmstead *et al*. (2011). Leaf: length of petiole reported as short and medium in the present study, whereas, Matteo *et al.* (2017) found short, medium and long classes of leaf petiole length in their study.

Similar to foliage characters, some floral characters also varied considerably among sweet cherry varieties, whereas, flower: arrangement of petals and flower: shape of petals did not show any variation. However, Gjamovski *et al*. (2016) reported variation in petals shape as circular, medium obovate and broad obovate, whereas, flower: arrangement of petals as free, intermediate and overlapping. In the present study, most of the varieties had medium flower diameter except for the varieties Durone Nero-II and Lambert, which had small flower diameter. Most of the varieties were late in maturity (DFFH), whereas, some of them were medium and some of them were early. This is in accordance with the findings of Karlidag *et al*. (2009) i.e., early, late and very late.

Huge variation in fruit characters like fruit weight, fruit length, fruit width, fruit shape, fruit skin colour, fruit flesh colour, fruit juice colour, fruit firmness, fruit stalk length, fruit juiciness, and eating quality were observed except for fruit pistil end, which was observed as flat in all the studied varieties. However, Gjamovski *et al.* (2016) recorded pointed, flat and depressed type of fruit pistil end. Considerable variation in fruit skin colour, flesh colour and colour of fruit juice was found with appreciable variation in fruit shape *viz*; reniform elliptic and cordate type of fruit shape among all varieties under consideration. However, Gjamovski *et al*. (2016) found cordate, reniform, oblate, circular and elliptic type of fruit shape in different cherry cultivars.

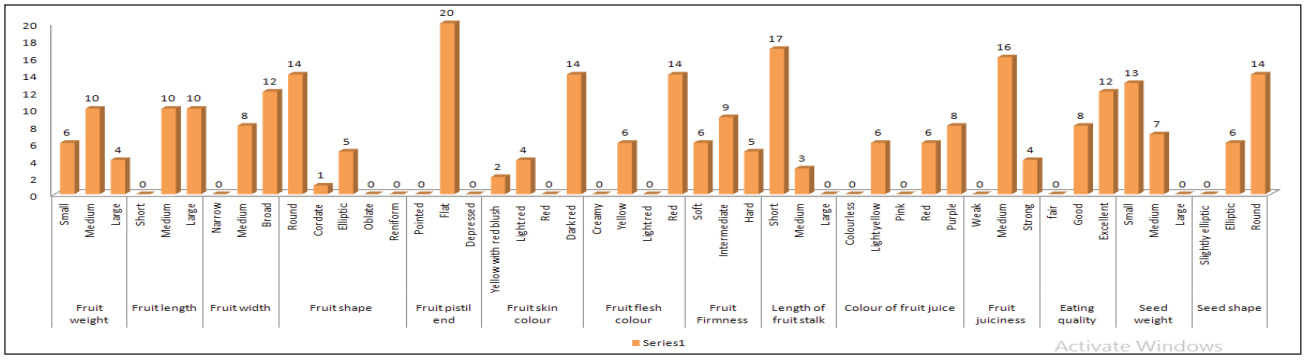

Fig. 3. Frequency distribution of 20 sweet cherry varieties based on fruit and stone characters

Sweet cherry fruits are mainly used for fresh consumption, hence appearance (shape, shiny fruit skin, dark red fruit skin color, length of the fruit stalk and eating quality) is really important in order to define good quality. In the present study considerable variation in fruit skin colour (yellow with red blush, red and dark red), fruit flesh colour (yellow and red), fruit juice colour (light yellow, red and purple) was observed. Similar type of variation in fruit skin colour (yellow, orange red, vermilion, wine red, mahagony and black), fruit flesh colour (cream white, pink, red, dark red and black red), and fruit juice colour (colourless, pink, red, purple and black red) were also noticed by Rakonjac *et al*. (2014). Dark skin and flesh colour are important considerations for fresh fruit marketing. The findings show that appealing taste accompanied by skin colour are the most important characteristics for sweet cherry consumers.

Fruit juiciness was observed as medium and strong in the present study which is similar to the findings of Matteo *et al*. (2017) i.e., extremely weak, weak, medium and strong. Fruit firmness was found to be as soft, intermediate and hard type, which is in accordance with the findings of Iurea *et al.* (2019) as average and firm in their study. Greater fruit firmness is an important trait from the marketing and consumer preference angles. Fruit stalk length was found to be short to medium in the present study, whereas, Matteo *et al.* (2017) reported short, medium and long type of fruit stalk length in their studies. The fruit stalk is one of the important markers of freshness; this is a reason for marketing cherry fruits with stalk. Medium to long type of fruit stalk length is mostly preferred by the consumers and breeders for easy hand picking of fruits (Bujdoso *et al*., 2020). The eating quality in the present study was classified as Excellent and Good. However, Corneanu *et al.* (2020) reported eating quality (taste) of sweet cherry as average sweet to very sweet in their study. Sweet taste is the most important characteristic for the sweet cherry consumers, but fruits with less sweet taste are also preferred in many countries (Bujdoso *et al.*, 2020).

Most of the varieties had low (Black Heart, Durone Nero - II, Durone Nero - III, Early Rivers, Lambert, Lapins, Roundel Heart, Sam, Seneca, Stella, Triumph Domini, Van and Vega) stone weight, whereas, some of the varieties had medium (Bing, Bradbourne Black, Merton Glory, Noir De Guben, Rainier, Red Heart and Sunburst) stone weight. The stone shape among all the twenty varieties under study was observed as elliptic (Early Rivers, Lapins, Noir De Guben, Rainier, Seneca and Triumph Domini) and round (Bing, Black Heart, Bradbourne Black, Durone Nero - II, Durone Nero - III, Lambert, Merton Glory, Red Heart, Roundel Heart, Sam, Stella, Sunburst, Van and Vega). Such type of variation in stone shape was reported by Matteo *et al.* (2017).

Conclusion

On the basis of present study, conclusion may be drawn that morphological descriptors developed through characterization of sweet cherry varieties alone may not meet the DUS criteria for establishment of distinctness among them. So, there is a need to employ some biochemical tools and molecular markers in addition to morphological DUS descriptors for the establishment of distinctness of the morphologically allied varieties. However, the qualitative characterization of sweet cherry varieties revealed that some of these do possess one or more horticulturally desirable characteristics enlisted below.

Sweet cherry varieties	Distinguishing character(s)
i) Black Heart	Early maturity, dark red coloured, small stone
ii) Sam	Large fruits, dark red coloured, small stone
iii) Bing	Upright tree habit, large fruits, dark red coloured
iv) Rainier	Upright tree habit, firm fleshed, dark red coloured
v) Merton Glory	Large fruits, dark red coloured

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SHORT COMMUNICATION

Nutraceutical Profile for Genetic Diversity Assessment in Leafy Mustard (*Brassica juncea* var. *rugosa*) Genotypes

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Mustard greens are an excellent source of many vitamins, dietary fiber, phosphorus, protein and iron as well as a good source of a potassium and magnesium. All genotypes showed variability in nutraceutical property. Highest content of protein was found in FS-13-17 (32.68%). Genotype FS-13-15 has high content of P, S and K Genotypes PRHC-12-14, FS-13-12 and FS-13-1 recorded highest value for S content whereas, EEC-10 had maximum K content. Iron and Manganese content was found maximum in genotype FS-13-10 (37.52mg/100g) and PRHC-12-6 (7.97 mg/100g) respectively. Highest content of Zinc was found in MGVAR-2 (5.83 mg/100g). These genotypes were promising and can be utilized for further improvement programme in leafy mustard. The genotypes which are rich in nutraceutical properties can be used for plant bio-fortification and such bio-fortified plant/varieties are safe for human consumption.

Key Words: Genotypes, Leaf, Mustard, Nutrient, Protein

Introduction

Mustard or hill mustard is popularly known as Rai, Raya, Lahi, Laha, Sarson etc.Lahi (*Brassica juncea*. var. *rugosa*) is well known in hills as green vegetable during the winter season. Leafy Mustard is a rich source of vitamins and minerals (Rawat *et al.,* 1978). Its tender leaves and stalk in early stages are used as green vegetable in the plains and hills of Northern India. In addition to providing these wondrously nutritious greens, this plant also produces the acrid tasting brown seeds that are used to extract vegetable oil. Mustard greens add a pungent and peppery flavour to recipes in which they are featured. Mustard (*Brassica juncea* (L.) Czern.) is an important crop both agriculturally and economically, which is widely cultivated in Asia and Europe (Chen and Chen, 1992), which belongs to family *Brassicaceae*. *Brassica* crops harbor an enormous diversity and had adapted to cultivation in almost every part of the world.Mustard greens seem to originated in the Himalayan region of India and have been grown and consumed for more than 5,000 years (Vavilov, 1926; Singh, 1958). However, the exact origin is unknown, but as an amphidiploid it seems logical that it originated in an area where the parental species *Brassica nigra* (L.) Koch (2n=16) and *Brassica rapa* L. (2n=20) overlap in their distribution (e.g. central Asia). It is generally agreed that the primary centre of diversity of *Brassica juncea* (2n=36) is Central Asia with secondary centres in Central and Western China, Hindustan and Asia Minor. In India, a great diversity exists in *B. juncea* for plant type, seed size, siliqua length, oil content and maturity period (Rana and Singh, 1992; Mishra *et al.* 2012; Semwal *et al*., 2013). It is largely self-pollinated crop with an average of 7.5–30% outcrossing does occur under natural conditions (Rabbani *et al.* 1998). *Brassica juncea* (2n =36) is an erect annual to biennial herb, 300-1600 mm tall, normally unbranched, sometimes with long ascending branches in upper parts; in appearance it is sub-glabrous and sub-glaucose. Mustard green is very nutritious and high in vitamin A, C, and iron. The leaf contain 24 calories, 2.4 gram protein, 0.4 gram fat, 4.3 gram total carbohydrate, 1.0 gram fibre, 1.1 gram ash, 160 mg calcium, 48 mg phosphorus, 2.7 mg iron, 24 mg sodium, 297 mg potassium, 0.06 mg thiamine, 0.14 mg riboflavin, 0.8 mg niacin, and 73 mg ascorbic acid per 100g. Both seed and leaves contain the glucosinolate-sinigrin (USDA, 2020).Genetic diversity plays a significant role in plant improvement because a hybrid between the lines of diverse origin usually display a greater heterosis than those between closely related ones (Singh and Chowdhury, 1983; Naznin *et al.,* 2015) which permit the selection of genetically

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divergent plants to obtain the desirable recombination of segregating generation.

Mustard greens are an excellent source of many vitamins including vitamin K, vitamin A, vitamin C and vitamin E. They are a very good source of dietary fiber, phosphorus, protein and iron as well as a good source of a potassium and magnesium. The iso-thiocyanates like compounds have been identified in mustard greens plants (Hirai *et al*., 2007). These compounds are known for their fungicidal, bactericidal, nematocidal and allelopathic properties (Moreno *et al.,* 2006) and are recently gaining popularity as cancer chemo-preventive and chemotherapeutic agents.

For bio-fortification and to mark nutrient rich germplasm, it is necessary to estimate the nutritional value of leafy green mustard. Present experiment was conducted to determine the nutrient content of thirty two genotypes. The final goal of research is to mark those genotypes which are rich in nutrient content and use these genotypes in development of nutrient rich varieties through bio-fortification and biotechnology.

Material and Methods

The experimental material consisted of 32 leafy mustard genotypes out of which 27 were obtained from the Pantnagar Centre for Plant Genetic Resources of G.B. Pant University of Agriculture and Technology, 4 genotypes from IET, AVT and 1 prominent check, PUSA SAG-1 was received from IARI (Table 1). The research was carried out at Vegetable Research Centre (VRC), G.B. Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar (Uttarakhand) in *rabi* season of 2015-2016. The crop was raised in the field in Randomized Block Design with one check. The recommended package of practices was followed and the significance of difference among treatment means will tested by F-test. Wherever, the F-test found to be significant, critical difference (CD) at 5 per cent level of significance was calculated. D^2 statistic was used for accessing the genetic diversity among the genotypes **(**Mahalanobis, 1936**).** The data recorded during the course of experiment were subjected to analysis through computer by using Windostat version 9.2 from Indostat services, Hydrabad Licensed to Plant Breeding Division Sugarcane Breeding Institute Coimbatore.

Nutrient Analysis

For nutrient analysis, leaves of leafy mustard were collected, dried and used for further analysis of nutrient i.e., protein by rapid N-cube analyser, P and S by spectrophotometer, K by flame photometer and Fe, Zn, Cu, Mn by atomic absorption spectrophotometer. Diacid method was followed for plant nutrient analysis of Zn, Fe, Mn, Cu, P, S and K. Fresh leaf samples were taken and dried first at 60^{o}C and then at 75^{o}C till weight became constant. Dried leaf samples were ground in a Wiley Mill. 1g of finely powdered leaves were taken into 150 ml conical flask and 10 ml concentrated HNO_3 were added to each flask and kept overnight while covering the mouth. The flasks were heated on a hot plate for 30 minutes. After cooling, 10 ml 4:1 of nitric and perchloric acids were added and heated at 40^{o}C till completion of digestion. Brown fumes of nitric acids evolve first and

Table 1. List of genotypes of leafy mustard used in the study

Genotypes	Source	Genotype	Source
2014/MGVAR-1	IET, AVT	FS-13-4	PCPGR, Pantnagar
2014/MGVAR-2	IET, AVT	FS-13-5	PCPGR, Pantnagar
2014/MGVAR-3	IET, AVT	FS-13-7	PCPGR, Pantnagar
2014/MGVAR-4	IET, AVT	FS-13-8	PCPGR, Pantnagar
PRHC-12-6	PCPGR, Pantnagar	FS-13-9	PCPGR, Pantnagar
PRHC-12-7-2	PCPGR, Pantnagar	FS-13-10	PCPGR, Pantnagar
PRHC-12-9-1	PCPGR, Pantnagar	FS-13-11	PCPGR, Pantnagar
PRHC-12-9-2	PCPGR, Pantnagar	FS-13-12	PCPGR, Pantnagar
PRHC-12-11	PCPGR, Pantnagar	FS-13-13	PCPGR, Pantnagar
PRHC-12-12	PCPGR, Pantnagar	FS-13-14	PCPGR, Pantnagar
PRHC-12-13	PCPGR, Pantnagar	FS-13-15	PCPGR, Pantnagar
PRHC-12-14	PCPGR, Pantnagar	FS-13-16	PCPGR, Pantnagar
EEC-10	PCPGR, Pantnagar	FS-13-17	PCPGR, Pantnagar
FS-13-1	PCPGR, Pantnagar	FS-13-18	PCPGR, Pantnagar
FS-13-2	PCPGR, Pantnagar	FS-13-20	PCPGR, Pantnagar
FS-13-3	PCPGR, Pantnagar	PUSA SAG 1	IARI, New Delhi

Table 2. Analysis of Variance for different nutrient characters in leafy mustard

Source	d.f.	Protein (%)	P (mg/100g)	S (mg/100g)	K (mg/100g)	Fe (mg/100g)	Mn (mg/100g)	Zn (mg/100g)
Replication	2	0.14836	524.63	3728.52	1813.01	0.51532	0.06126	0.00195
Treatment	31	26.64**	72279.8**	1073231**	600070**	115.67**	5.43**	2.36**
Error	62	0.50883	1039.62	928.302	3708.42	0.21579	0.02235	0.01275

** Highly significant at 1% level

towards end of digestion evolution of white fumes of perchloric acids. A semi solid viscous material of light brownish colour gets reduced to traces of whitish residue at the bottom of the flask towards the end of digestion. The process completes in a period of 1-2 hrs. In no case full drying should be allowed as there may be chances of volatilization loss of some nutrients. If the samples show charring then an extra 10 ml of HNO_3 is added to the flask and digested again. When the digestion is successfully over, the conical flask is removed from hot plate and cooled and 5ml of 6 N HCL along with few ml of water were added. The contents were boiled gently and transferred to a 100 ml volumetric flask and the volume was maintained by using distilled water. The diluted sample were filtered and stored for further analysis. Macronutrients i.e., Phosphorus and sulphur was analyzed by spectrophotometer and potassium by flame photometer. For the determination of phosphorus yellow colour method was followed. 10ml sample prepared by following diacid method was taken in 50 ml volumetric flask and 10 ml distilled water and 10 ml ammonium molybedate reagents were added to it. It was diluted to 50 ml and mixed well. After 20-25 minutes, when yellow colour was fully developed, Transmittance (%) or Absorbance at 420 nm was recorded. Standard curve in the range of 0 to 15 ppm phosphorus in the final solution were prepared. For estimation of sulphur, 5-10 ml sample prepared by following diacid method was taken in 50 ml volumetric flask and 1 ml 6N HCl and 1 ml of gum acacia solutions were added to it. The contents were mixed by swirling. 0.5g barium chloride crystals were added and the volume was made up to 50 ml using distilled water. The flask was allowed to stand for one minute and then swirled gently until the barium chloride crystals were dissolved. The absorbance for diluted plant digest was recorded on spectrophotometer at 420 nm. Standard curve in the range of 0, 4, 6, 12 and 20 ppm sulphur in the final solution were prepared. The plant sample for potassium was prepared in the same method like that for micronutrient analysis. 5 ml of digested sample was taken in 25 ml volumetric flask and diluted up to the mark using distilled water. Standard curve of K was prepared by aspirating standard K solutions (0-10 µg/ml) in flame photometer and readings were noted for each solution. The concentration of K in diluted plant sample digest was computed with the help of standard curve.

Micronutrient like Zinc, Iron, Manganese and Copper was analyzed by atomic absorption spectrophotometer. Sample prepared by following diacid method is taken for micronutrient estimation. A volumetric flask (100 ml) containing samples were filtered through Whatman No.42 filter paper placed over plastic bottle of volume 100 ml. These samples were fed to atomic absorption spectrophotometer and readings were noted in µg/ml. This reading was multiplied by dilution factor 100 and converted into mg/kg or multiplied by 10 to convert into mg/100gm (Pathak and Agrawal, 2014).

Result and Discussion

The analysis of variance different characters is presented in Table 2. Among all the genotypes highly significant differences were obtained for all the characters namely; protein, P, S, K, Fe, Mn and Zn contents which indicate that variation was due to genetic effects. The significance of genotype difference indicates the presence of variability for each of the characters among the tested genotypes. The exploitation of diversity is of much importance for an effective breeding programme and is a prerequisite for effective screening of superior genotypes.

Proteins are essential nutrients for the human body**.** It perform a vast array of functions within organisms, including catalysing metabolic reactions, DNA replication, responding to stimuli, and transporting molecules from one location to another. Highly significant differences among all the genotypes were observed for protein content (Table 2).Protein content ranges from 32.68% to 20.12% (Table 3). FS-13-17 has the highest protein content (32.68%) followed by FS-13-16 (31.61%) and FS-13-15 (30.11 %) whereas minimum protein content was found in EEC-10

Table 3. Nutrient content in different genotypes of leafy mustard

Genotype	Protein (%)	P (mg/100g)	S (mg/100g)	K (mg/100g)	Fe (mg/100g)	Mn (mg/100g)	Zn (mg/100g)
2014/MGVAR-1	25.41 ± 0.17	1083 ± 0.001	695 ± 0.001	2100 ± 0.07	8.96 ± 0.26	3.59 ± 0.02	3.75 ± 0.05
2014/MGVAR-2	23.06 ± 0.57	1156 ± 0.001	1010 ± 0.006	1750 ± 0.02	26.46 ± 0.02	4.47 ± 0.04	5.83 ± 0.04
2014/MGVAR-3	24.27 ± 0.31	1034 ± 0.001	720 ± 0.009	2080 ± 0.05	14.89 ± 0.02	7.33 ± 0.01	4.41 ± 0.18
2014/MGVAR-4	27.63 ± 0.01	1287 ± 0.001	280 ± 0.006	2300 ± 0.06	24.68 ± 0.28	6.96 ± 0.02	5.24 ± 0.02
PRHC-12-6	26.25 ± 0.07	1239 ± 0.001	990 ± 0.012	2080 ± 0.02	16.94 ± 0.27	7.97 ± 0.02	5.19 ± 0.02
PRHC-12-7-2	22.53 ± 0.42	1395 ± 0.001	670 ± 0.019	2680 ± 0.02	6.49 ± 0.11	3.60 ± 0.01	3.58 ± 0.18
PRHC-12-9-1	27.84 ± 0.26	1451 ± 0.001	740 ± 0.015	3030 ± 0.17	11.96 ± 0.46	4.78 ± 0.06	4.01 ± 0.12
PRHC-12-9-2	24.55 ± 0.14	948 ± 0.001	870 ± 0.015	1900 ± 0.08	15.87 ± 0.63	5.29 ± 0.06	4.42 ± 0.04
PRHC-12-11	23.51 ± 0.42	1348 ± 0.001	1020 ± 0.023	3050 ± 0.05	13.49 ± 0.34	6.74 ± 0.06	4.86 ± 0.31
PRHC-12-12	28.16 ± 0.29	983 ± 0.001	960 ± 0.015	1700 ± 0.11	13.20 ± 0.16	4.64 ± 0.08	4.09 ± 0.10
PRHC-12-13	20.31 ± 0.32	1249 ± 0.001	470± 0.009	1980 ± 0.10	21.87 ± 0.03	3.30 ± 0.02	2.66 ± 0.16
PRHC-12-14	26.51 ± 0.16	1358 ± 0.001	2150 ± 0.02	2650 ± 0.11	8.78 ± 0.06	4.27 ± 0.04	4.32 ± 0.12
EEC-10	20.12 ± 0.31	903 ± 0.001	1080 ± 0.01	3150 ± 0.01	16.13 ± 0.33	4.96 ± 0.07	3.73 ± 0.06
FS-13-1	25.96 ± 0.12	1284 ± 0.001	2150 ± 0.02	1700 ± 0.14	13.44 ± 0.14	2.31 ± 0.03	2.42 ± 0.09
FS-13-2	22.22 ± 0.09	1027 ± 0.001	1550 ± 0.02	2750 ± 0.05	13.92 ± 0.17	3.73 ± 0.02	3.47 ± 0.09
FS-13-3	23.58 ± 0.22	1187 ± 0.001	920 ± 0.04	2280 ± 0.12	16.72 ± 0.09	6.00 ± 0.22	3.62 ± 0.04
FS-13-4	25.94 ± 0.33	1344 ± 0.001	1190 ± 0.006	2320 ± 0.13	13.39 ± 0.17	4.40 ± 0.28	4.57 ± 0.02
FS-13-5	26.60 ± 0.38	1402 ± 0.001	690± 0.006	2830 ± 0.01	19.07 ± 0.05	4.41 ± 0.04	2.93 ± 0.15
FS-13-7	23.66 ± 0.03	1272 ± 0.001	950 ± 0.01	2950 ± 0.02	20.25 ± 0.02	4.92 ± 0.02	5.76 ± 0.01
FS-13-8	25.49 ± 0.43	1159 ± 0.001	500 ± 0.09	2380 ± 0.03	22.09 ± 0.04	3.90 ± 0.08	5.78 ± 0.03
FS-13-9	23.27 ± 0.26	1210 ± 0.001	990 ± 0.01	1700 ± 0.15	17.08 ± 0.09	6.28 ± 0.03	3.53 ± 0.04
FS-13-10	21.43 ± 0.18	1328 ± 0.001	2030 ± 0.009	2320 ± 0.01	37.52 ± 0.48	4.91 ± 0.01	4.64 ± 0.04
FS-13-11	26.55 ± 0.52	1190 ± 0.001	1020 ± 0.01	2530 ± 0.01	11.42 ± 0.03	4.14 ± 0.03	5.22 ± 0.02
FS-13-12	25.41 ± 0.13	1030 ± 0.001	2150± 0.01	2100 ± 0.02	12.57 ± 0.03	4.94 ± 0.01	4.31 ± 0.03
FS-13-13	22.28 ± 0.23	1173 ± 0.001	1400± 0.009	2080 ± 0.03	24.83 ± 0.03	6.04 ± 0.08	3.58 ± 0.04
FS-13-14	21.57 ± 0.05	1399 ± 0.001	2120 ± 0.02	2280 ± 0.02	17.06 ± 0.01	6.30 ± 0.02	4.71 ± 0.02
FS-13-15	30.11 ± 0.42	1471 ± 0.001	150 ± 0.003	2950 ± 0.10	13.15 ± 0.39	4.44 ± 0.25	4.54 ± 0.04
FS-13-16	31.61 ± 0.36	1029 ± 0.001	1800 ± 0.012	3030 ± 0.08	15.93 ± 0.47	6.15 ± 0.02	3.57 ± 0.02
FS-13-17	32.68 ± 0.43	1058 ± 0.001	830 ±0.10	2000 ± 0.15	22.70 ± 0.04	7.05 ± 0.06	4.63 ± 0.03
FS-13-18	26.45 ± 0.36	1146 ± 0.001	90 ±0.02	2200 ± 0.03	19.67 ± 0.01	6.92 ± 0.08	5.48 ± 0.01
FS-13-20	23.81 ± 0.42	1042 ± 0.001	370 ±0.02	1980 ± 0.18	11.00 ± 0.03	6.19 ± 0.08	5.14 ± 0.04
Pusa Sag 1	26.62 ± 0.52	1140 ± 0.001	1550 ± 0.08	2800 ± 0.05	21.58 ± 0.04	4.63 ± 0.01	4.63 ± 0.03

(20.12 %). Rest of genotypes showed protein content between the genotypes mentioned above (Table 3). Gupta and Wagle (1988) also reported high protein value in mustard i.e. 29.82%. Manchali *et al.* (2012) also reported high protein content in cruciferous vegetables. Similar results were reported by Aletor (1995), Fasuyi (2006), Gupta *et al.* (2005) and Meena *et al.* (2020).

Phosphorus is the second most abundant mineral in the body, after calcium. Phosphorus is an essential mineral primarily used for growth and repair of body cells and tissues. Data revealed that there was a significant difference among all the genotypes for phosphorus content (Table 2). Phosphorus content ranged from 903 to 1471 mg/100g. FS-13-15 has the highest phosphorus content (1471mg/100g) followed by PRHC-12-9-1 (1451 mg/100g) and FS-13-5 (1402 mg/100g) whereas minimum phosphorus content was found in EEC-10 (903 mg/100g). Other genotypes give intermediate phosphorus content (Table 2).The results were in agreement with findings of Gupta and Wagle (1988). Aletor(1995) also find the similar results.

Sulphur is one of the core chemical elements needed for biochemical functioning and is an elemental macronutrient for all organisms. Mustard greens are perhaps most famous as a group for their unusual sulphur content and especially their sulphur containing glucosinolates. Sulphur content of all the genotypes is given in Table 3. Data showed that the range of sulphur content was from 90 to 2150 mg/100g. PRHC-12-14, FS-13-12 and FS-13-1 has the maximum sulphur content (2150 mg/100g) followed by FS-13-14 (2120mg/100g) and FS-13-10 (2030mg/100g) while minimum in FS-

13-18 (90mg/100g). Ifon and Bassir (1979) also found high amount of sulphur content in some Nigerian leafy vegetables.

Potassium ions are necessary for the function of all living cells. The transfer of potassium ions through nerve cell membranes is necessary for normal nerve transmission. Potassium is pivotal to heart function and plays a majorpart in skeletal and smooth muscle contraction, so is crucial for normal digestive and muscular function. The data displayed in Table 3 showed highly significant differences for potassium content among all the genotypes. Potassium content ranged from 1700 to 3150 mg/100g (Table 3).EEC-10 has the highest potassium content (3150 mg/100g) followed by PRHC-12-11 (3050 mg/100g), PRHC-12-9-1 and FS-13-16 (3030 mg/100g) whereas minimum potassium content was found in PRHC-12-12, FS-13-1 and FS-13-9 (1700 mg/100g). Other genotype showed in between values of potassium content. The similar results were also observed by Gupta and Wagle (1988), Ifon and Bassir (1979) and Fasuyi (2006).

Data revealed that iron content ranged from 6.49 to 37.52mg/100g (Table 3). Highly significant differences among the genotypes for iron content were observed (Table 3). FS-13-10had highest content of iron (37.52mg/100g) followed by MGVAR-2(26.46mg/100g), whereas minimum iron content was found in PRHC-12-7-2 (6.49mg/100g) followed by PRHC-12-14 (8.78mg/100g). Rest genotypes showed intermediate iron content. Gupta and Wagle (1988) found iron content as high as 45mg/100g for mustard leaves. The findings are in accordance with the findings of Bhatt and Singh, 2015 in fenugreek.

Data presented in Table 3 depicted that there was a significant difference for manganese content among all the genotypes. The manganese content ranged from 2.31 to 7.97 mg/100g (Table 3). PRHC-12-6 has highest content of manganese (7.97 mg/100g) followed by MGVAR-3 (7.33 mg/100g). The minimum manganese content was found in FS-13-1 (2.31 mg/100g) followed by PRHC-12-13 (3.30 mg/100g). Rest genotypes showed intermediate manganese content. The results are in consonance with Gupta and Wagle (1988) and Singh *et al.* (2001).

The perusal of results in Table 3 showed that genotypes differ significantly for this parameter. Zinc content ranges from 2.42 to 5.83 mg/100g (Table 3). Highest content of zinc was found in MGVAR-2 (5.83 mg/100g) followed by FS-13-8 (5.78 mg/100g).Whereas minimum zinc content was in FS-13-1 (2.42 mg/100g) followed by PRHC-12-13 (2.66 mg/100g). Rest genotypes had intermediate zinc content. Zinc is vital for the immune system and zinc also prevents night blindness and prevents development of cataract. Manchali *et al*. (2012), Singh *et al*. (2001) and Aletor (2002) also have the similar results for zinc content.

In present study the copper content in dry leaves was found below detection limit during analysis. The similar results found by Gupta *et al*. (2005), Aletor (1995) and Aletor (2002).

MGVAR-2 is source of iron and zinc, FS-13-10 is rich source of sulphur and iron, FS-13-17 is rich source of protein and manganese, FS-13-15 is rich source of protein and phosphorous and PRHC-12-9-1 is rich source of phosphorous and potassium among all the genotypes. These results are in conformity with the findings of Gupta and Wagle (1988) and also found variation among genotypes for micronutrient contents. They found nutrient content ranges iron from 25 to 72 mg/100g, zinc from 2.2 to 4.2 mg/100g, manganese from 4.3 to 14.0 mg/100g, potassium from 58 to 3802 mg/100g and phosphorous from 740 to 1210 mg/100g, respectively. The results indicate that mustard genotypes cultivated at different locations exhibited variation in the content of mineral elements.

All thirty two genotypes had a wide range of variation for most of the characters. The traits varied in terms of their behaviours and extent of genetic variability. All genotypes were rich in protein content, macronutrient content (P, S and K) and micronutrient content therefore, these genotypes can be considered longevity promoter that will boost the overall health status on consumption meet out the daily need of nutrition.

Conclusion

The nutrient composition of mustard leaves revealed them to be good sources of many nutrients that could help in overcoming micronutrient malnutrition at a negligible cost.The comparatively high content of sulphur in some of the leafy mustard genotypes is important as sulphur has recently been implicated in the detoxification of cyanide in local foodstuffs. This investigation can serve as a basis for selecting promising genotypes for further, more detailed, multi-year, multi-plot studies on leafy mustard to meet the nutritional requirements.

Because of their high nutrient content, greens can be recommended to alleviate micronutrient malnutrition in developing countries. FS-13-15, PRHC-12-14, FS-13-12, FS-13-1, EEC-10, FS-13-10, PRHC-12-6 and MGVAR-2 genotypes can be used in the breeding program for crop improvement as a donor for many nutritional traits and they can be safely utilized for human consumption.

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SHORT COMMUNICATION

Genetic Diversity in Edible Podded Pea (*Pisum sativum* var. *saccharatum*)

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Thirty-six genotypes of snap pea were evaluated during winter 2016-17. D^2 analysis dispersed genotypes in seven polygenotypic clusters with maximum in cluster VI. Genotypes from clusters I and VII followed by II and VII would be paying preposition in hybridization programme with higher inter-cluster divergence. Cluster III showed the highest means for most of economic traits. Genotypes 'DPEPP-15-1', 'DPEPP-10-1', 'DPEPP-2', 'DPEPP-12-2', 'Arka Apoorva' and 'DPEPP-4-2' showed promise either directly as varieties or as potential parents in future breeding program.

Key Words: Cluster analysis, Edible podded pea *(Pisum sativum* var. *saccharatum)*, Genetic diversity, Genotypes, Hybridization, Selection

Edible podded pea is one of the popular, cool-season oriental vegetables that share the cultivation pattern with the garden pea. These are grown for their tender fresh pods that lack the parchment layer inside the pod. Edible-podded peas consist of snow pea (*Pisum sativum* var. *macrocarpon*) and sugar snaps/snap peas (*Pisum sativum* var. *saccharatum*) which can be eaten as whole pods. The combinations of two or three recessive genes contribute to make the whole pod suitable for consumption in the fresh stage (Myers *et al*., 2001). They are an excellent source of dietary fibre, folic acid, and vitamin C, rich in iron and manganese and a decent source of riboflavin, vitamin B_6, pantothenic acid, magnesium, phosphorus, potassium, vitamin A and vitamin K.

Since it is a recently introduced crop, and therefore, the most important task in edible pod pea breeding involves the development of high yielding varieties with stable productivity carrying resistance to diseases and unfavourable environmental conditions. Knowledge about levels and patterns of genetic diversity can be an invaluable source and introgression of desirable genes from variable germplasm into the existing genetic base, indicating thereby that the success in crop improvement through selection ultimately depend upon the genetic variability (Sharma *et al*., 2020). Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts on a smaller number of hybrid combinations (Fuzzato *et al*., 2002), providing better scope to isolate superior recombinants. Therefore, the breeder needs to identify the appropriate genotypes based on genetic divergence for the hybridization purpose. Keeping these points in view, the present investigation was undertaken to gather information on the genetic divergence in edible pod pea.

The experimental material comprised of 36 genotypes of which 29 are advanced breeding lines (F_7) and seven varieties from different institutes (Table 1). They were laid out in Randomized Complete Block Design with three replications in first week of November 2016 with inter and intra-row spacing of 45 cm and 10 cm, respectively. Observations were recorded on randomly selected ten plants of each genotype over the three replications for yield and related horticultural traits besides, quality parameters such as moisture content in seeds (%), total soluble solids for fresh seed (Brix), total soluble solids for whole pod (Brix), ascorbic acid (mg/100g), protein content (%) and total sugars (%) were also estimated by following standard procedures.

The analysis of variance revealed that mean squares due to genotypes were significant for all the traits. Thus, it highlighted the presence of sufficient genetic variability among the genotypes. The multivariate analysis (D^2) illustrated different clustering patterns by arranging 36 genotypes into seven clusters following Tocher's procedure (Fig. 1), and all of them were

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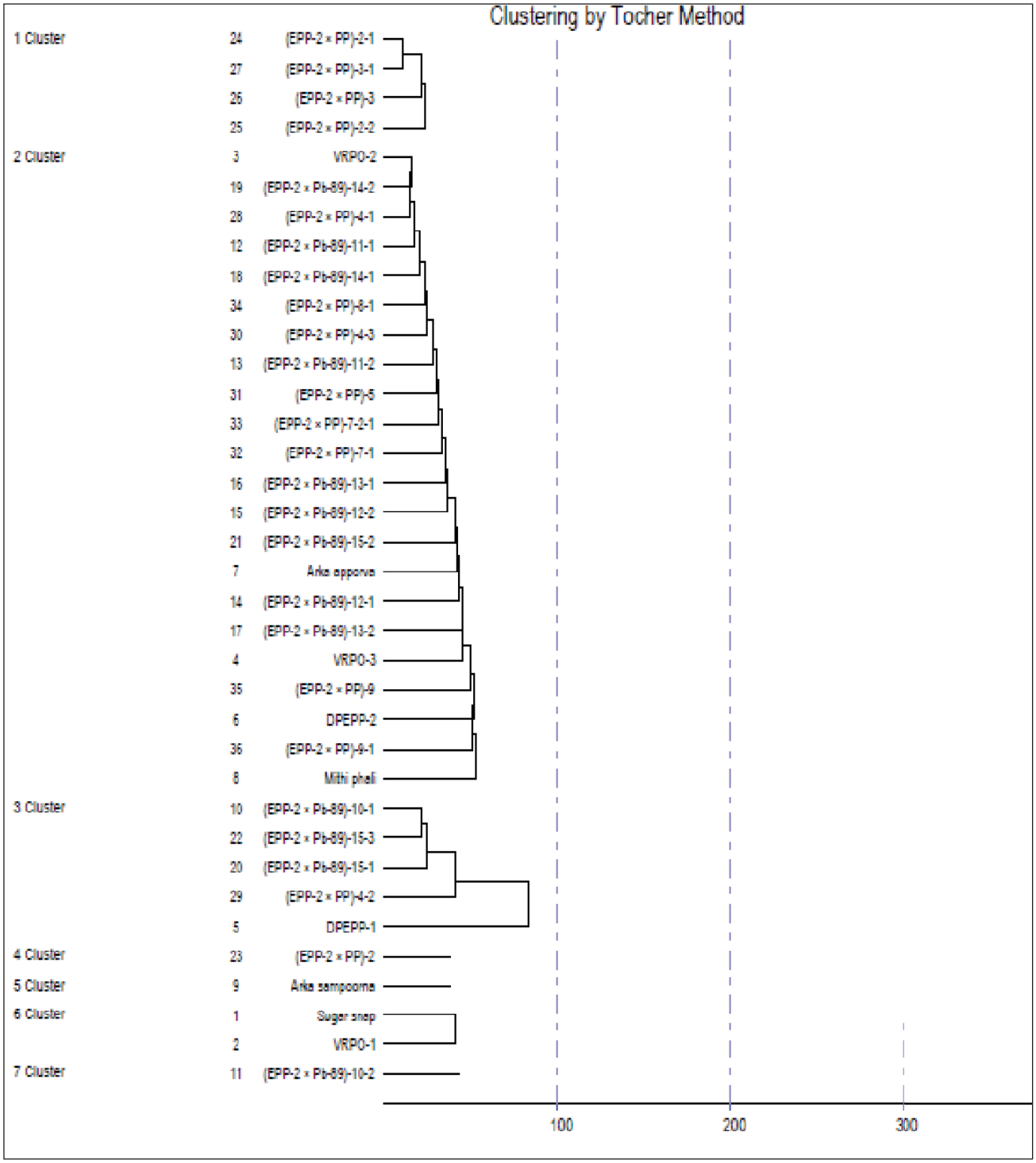

Fig. 1. Dendrogram showing grouping of 36 edible-podded pea genotypes based on D^2 statistics using Tocher's method

polygenotypic. Cluster VI was the largest, with nine genotypes constituting ¼th of the total genotypes. Similarly, clusters I, II and III contained six genotypes each while cluster VII contained five genotypes and clusters IV and V each contained only two genotypes suggesting the diverse origin of these genotypes. This suggests that genetic diversity is not always related to geographical diversity (Sekhon *et al.*, 2019).

The intra-cluster distance varied from 9.844 to 11.321, respectively highest in cluster VII, followed by

Table 1. Plant characteristic and source of genetic material

Genotype	Plant Characteristics	Source
DPEPP-2, DPEPP-10-1, DPEPP-10-2, DPEPP-11-1, DPEPP-11-2, DPEPP-12-1, DPEPP-12-2, DPEPP-13-1, DPEPP-13-2, DPEPP-14-1, DPEPP-14-2, DPEPP-P-2, DPEPP-P-2-1, DPEPP-P-2-2, DPEPP-P-3, DPEPP-P-3-1, DPEPP-P-4-1, DPEPP-P-4-2, DPEPP-P-4-3, DPEPP-P-5	Afilla type	Department of Vegetable Science & Floriculture, CSKHPKV, Palampur
DPEPP-15-1, DPEPP-15-2, DPEPP-15-3, DPEPP-P-7-1, DPEPP-P-7-2-1, DPEPP-P-8-1, DPEPP-P-9, DPEPP-P-9-1, DPDPEPP-1	Non-afilla plant, normal plant like garden pea	Department of Vegetable Science & Floriculture, CSKHPKV, Palampur
Arka Sampoorna, Arka Apoorva,	Non-afilla	Indian Institute of Horticultural Research, Hessarghata, Karnatka
Mithi Phali	Non-afilla	Punjab Agricultural University, Ludhiana, Punjab
Sugar Snap, VRPO-1, VRPO-2, VRPO-3	Non-afilla	Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh

cluster V, I, IV, VI, III and II. Since the intra-cluster distance was low, the chances of developing good segregants by hybridization among parents within-cluster would be low. Consequently, it is logical to attempt crosses between genotypes falling in different clusters based on inter-cluster distance. The inter-cluster distance ranged from 148.266 to 801.751. The highest inter-cluster level genetic divergence was recorded between clusters I and VII followed by II and VII, IV and VII, V and VII and VI and VII. This specifies that the genotypes included in the clusters with high inter-cluster distance showed sufficient genetic diversity, and selection of parents from these diverse clusters would be helpful in hybridization programme (Sharma *et al*., 2013).

The cluster means of different traits revealed substantial distinctions among the clusters for each trait (Table 2). Cluster III seemed to be the most important with the highest cluster means for most economic traits, namely, pod yield/plant, average pod weight,

Table 2. Cluster means for different characters in edible podded pea

Clusters/ Characters	C1	C2	C3	C4	C5	C6	C7	Mean
First flowering node	13.38	13.09	12.85	12.47	**11.53**	13.10	11.87	12.61
Days to Flowering	104.75	101.08	98.40	100.33	95.00	93.67	**91.67**	97.84
Days to First Picking	136.50	134.09	131.60	134.00	130.00	**128.00**	132.00	132.31
Number of branches/ plant	1.55	1.72	**1.96**	1.73	1.73	1.57	1.27	1.65
Internodal Length (cm)	8.03	5.98	6.25	8.64	**5.41**	9.92	5.57	7.11
Nodes/ plant	20.97	19.92	19.79	**21.93**	20.47	21.90	16.53	20.22
Plant Height (cm)	95.95	78.43	78.59	106.60	75.13	127.43	**67.40**	89.93
Pod Length (cm)	8.96	9.34	**10.00**	9.26	7.58	7.21	9.74	8.87
Pod Breadth (cm)	1.94	1.89	1.93	**2.02**	1.74	1.51	1.72	1.82
Seeds per Pod	5.76	6.16	**6.35**	5.50	4.60	5.70	6.30	5.77
Pods per Plant	19.70	16.24	18.33	15.72	**22.43**	19.14	8.58	17.16
Average Pod Weight (g)	4.51	4.49	**5.51**	4.71	2.85	3.33	5.13	4.36
Harvest Duration (days)	16.67	17.76	19.27	**21.00**	20.33	17.83	17.67	18.65
Moisture Content (%)	79.05	77.43	78.80	79.10	73.32	**80.20**	79.85	78.25
Total soluble solids (^{o}Brix) Seed	14.11	15.03	15.32	14.13	**15.47**	14.87	15.00	14.85
Total soluble solids (^{o}Brix) Pod	9.58	10.43	10.33	10.13	11.07	**11.67**	9.93	10.45
Ascorbic Acid (mg/100g)	24.18	24.72	24.61	23.87	22.94	23.87	**27.90**	24.58
Protein Content (%)	25.46	23.60	23.08	23.10	21.93	24.09	**28.23**	24.22
Total Sugars (%)	**8.83**	6.57	7.20	6.40	7.13	6.50	6.40	7.00
Pod Yield/ Plant (g)	88.67	72.81	**101.13**	74.00	62.67	64.67	44.00	72.56
Straw Yield/ plant (g)	14.04	26.10	26.96	21.50	**35.61**	20.38	19.17	23.39
100 Seed Weight (g)	25.33	23.29	23.07	20.00	22.67	22.33	**26.67**	23.34
Dry Pods/plant (g)	19.61	**23.49**	20.44	22.61	22.03	19.89	21.71	21.40
Harvest Index (%)	52.56	44.30	43.44	49.09	38.15	46.02	**55.87**	47.06
Seed Yield/ plant (g)	23.31	**26.49**	23.72	19.84	19.48	24.55	23.37	22.97

Where, C1 to C7 represents different clusters; bold values indicate highest mean

pod length, seeds/pod and branches/plant. On the other hand, cluster VII with five genotypes recorded maximum cluster means for the quality traits, *i.e.* ascorbic acid and protein content and 100 seed weight and harvest index. Different clusters of genotypes based on means revealed divergence for other characters and thereby can be utilized as indicators for selecting diverse parents for a specific trait in hybridization programmes (Sekhon *et al*., 2019). Apart from selecting genotypes from the clusters that have higher inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence regarding a character of interest (Gemechu *et al*., 2005). Straw yield per plant contributed a maximum (22.06%) towards total genetic divergence followed by average pod weight (16.19), total sugars (12.86) and pod yield per plant (12.06).

The selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters. Therefore, it could be suggested that crossing should be made between genotypes belonging to distance clusters. Accordingly, genotypes viz.,'DEPP-15-1', and 'DEPP-15-3' from the cluster II along with other top performing genotypes namely, 'DEPP-10-1', 'DPEPP-2'and 'DEPP-14-2'offer promise for their direct use as varieties and as potential parents in future breeding programmes to isolate transgressive segregants.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXXIst meeting held on September 29th, 2020 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 78 germplasm lines out of 80 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer (s) / author (s) is / are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. GQ-25 (IC0599273; INGR20001), a Rice (*Oryza sativa*) Germplasm with High Temperature Tolerance

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GQ-25 (Samba Mahsuri/SC5126-3-2-4) is a restorer line developed by Hybrid rice division, ICAR-Indian Institute of Rice Research. as Under NICRA project (http://www.icar-iirr.org:8000/), GQ-25 is identified as one of the promising genotypes under low nitrogen (N) field condition as expressed in terms of grain yield (filled grain weight per hill) and also for terminal high temperature stress tolerance (in terms of stable grain yield under high temperature stress). GQ-25 is a medium duration restorer line with 103-105 days to 50% flowering and medium slender grain type.

Morpho-agronomic characteristics:

Traits under Low N condition	
Plant Height (cm)	105
Tiller Number	11.33
Productive Tiller Number	8.33
Single Plant Yield#(grams) (year 1 and 2)	14.8; 15.4
1000 grain weight (grams)	19.97
Harvest Index	44.72
N% in Straw	0.35
N% in Grain	1.15
N% in Biomass	1.50
Agronomic Efficiency (AE) (kg/kg)	-47.45
Physiological Efficiency (PE) (kg/kg)	120.71
Agro Physiological Efficiency (APE) (kg/kg)	96.44
Apparent Recovery Efficiency (ARE) (%)	-50.49
Utilization Efficiency (UE) (kg/kg)	-61.46
Grain Yield Efficiency Index (GYEI)	0.79

Table 2. Agro-morphological and yield characters of GQ-25 under ambient and high temperature stress condition across the locations under AICRIP Plant Physiology trial

Trait	Grand Mean across the locations			
	2015a		2016b	
	Control	HTS	Control	HTS
Days to 50% Flowering	104	103	96	96
Days to Maturity	132	133	129	128
Grain Yield (grams/m^2)	487	361	489.50	366.25
Total dry matter (grams /m^2)	1182.75	1081	1192	1143.25
1000 grain weight (grams)	20.9	20.8	22	20

a - (CHN, IIRR, MTU, REWA, TTB); b - (IIRR, MTU, REWA, PTB)

Associated Characters and cultivation Practices: NUE: GQ-25 is found to be promising across the seasons and years since 2011(DRR Newsletter, 2013; Venkateswarlu, 2013; DRR Annual report, 2013) under low N field condition in terms of yield, yield related components, and Nitrogen Use Efficiency (NUE) indicators among the evaluated genotypes.

N metabolism genes expression analysis in GQ-25: Up regulation of OsAMT1;1 gene was observed in shoot (86%) and root of GQ-25 (63%) under hydroponics (Srikanth, 2015) and down regulation of OsNIA2gene in GQ-25 in root (64.5%) and up-regulation by 11.13% in shoot (11%) under field condition (Srikanth, 2016) were observed in low N in comparison to recommended N.

Compiled and edited by: Anjali Kak and Veena Gupta, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

High Temperature Stress: GQ-25 was evaluated for terminal high temperature stress tolerance in AICRIP Plant Physiology trials during 2015 and 2016 across the locations (Chinsurah, Hyderabad (IIRR), Maruteru, Pantnagar, Pattambi, Rewa and Titabar). During 2015, GQ-25 yielded 361 g/m2 under high temperature stress (CHN, IIRR, MTU, REWA, TTB) with 25% reduction over the ambient temperature (IIRR, 2016). Similar trend of yield reduction (25%) was also observed during 2016 for GQ-25 with the mean yield of 366.25 g/m2 under high temperature stress (IIRR, MTU, REWA, PTB (IIRR, 2017). Based on the Yield Stability Index (YSI) values, GQ-25 was selected as heat tolerant and showed non-significant stability variance (σi2) (IIRR, 2017).

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2. AD (Bio) 09518 (IC0635011; INGR20002), a Rice (*Oryza sativa*) Germplasm Carrying *xa5*, *xa13* and *Xa21* Genes for BB Resistance

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Evolving high yielding rice genotypes with durable resistance to bacterial blight (BB) is pertinent considering the extensive damage caused by the disease in most of the rice growing regions. AD (Bio) 09518, a new short duration bacterial blight resistance rice culture was developed through marker assisted selection. None of the popular varieties, ADT 43, ADT (R) 45, ASD 16 are resistant to this important disease. Pyramiding different resistance genes into a rice cultivar would make it an easier genetic resource for breeders to introgress the genes into their local adaptive cultivars. AD (Bio) 09518 is cross derivative of ADT 43 × IRBB60 harboring xa5, xa13 and xa21 with the yield potential of 5965 kg/ha, short duration and high resistance to bacterial blight has been developed through marker-assisted pedigree breeding (Perumalsamy *et al.*, 2010 and Sakthivel *et al.*, 2017). Marker assisted selection for BB resistance genes (xa5, xa13 and Xa21) using functional markers in F2, F3 and F4 generations of ADT43 x IRBB60 and selection of phenotypically superior genotypes with high resistance reaction against bacterial leaf blight leads to identification of this line. Under artificial screening in green house condition both at TNAU, Coimbatore and Indian Institute of Rice Research, Hyderabad, this genotype shows high resistance to bacterial blight. Out of the 12 pathogenic races tested, the culture is resistant to almost all (11) races of the BB pathogen. The culture also showed moderate resistance to blast, sheath rot and leaf folder. It has medium slender grains with high head rice recovery. The culture, AD (Bio) 09518 has amylose content of 25.48 per cent, soft gel consistency and good volume expansion.

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3. IET23814 (RPBIO5478-185M) (IC0635010; INGR20003), a Rice (*Oryza sativa*) Germplasm with High Zinc in Grains. Purple Leaves and Panicles

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RPBio5478-185M is an elite rice line with high grain zinc concentration in both brown (33.5 ppm Zn) and polished (31 ppm Zn) grain. It is a recombinant inbred line identified from the cross Madhukar × Swarna at IIRR, Hyderabad as part of project 3019 of ICAR-Network Project on Functional Genomics and Genetic Modification of crops (NPFGGM, previously NPTC). 185 M showed 102 ppm Zn in F7 unpolished rice using AAS method (Anuradha *et al.*, 2012) and 30 ppm since then consistently using XRF method (AICRIP 2013, 2014, Naik *et al.*, 2020). It showed the highest overall grain zinc concentration of 27.38 ppm in brown rice out of 12 entries in 2013 and 31.69 ppm in polished rice among 45 entries across 17 locations in 2014 in AICRIP-Bio fortification trials of 2013 and 2014 (AICRIP 2013, 2014; Agarwal *et al.*, 2018) (Table 1). It showed the highest overall grain zinc concentration (30.62 mg/Kg) in brown rice among the 68 lines tested in a combined analysis of 15 trials in 3 years and a mean grain yield of 3.08t/ha at 6 other locations with high and low soil zinc (Naik *et al.*, 2020).

It has purple basal leaf sheath, leaves and panicles. It is 129 cm tall, shows 50% flowering in 98 days to 107 days (Naik *et al.*, 2020) and has long bold grains with white pericarp. The range of Fe in this high zinc line was 7.64 to 14.73 mg/Kg in brown rice across 15 locations in 3 years and was considered among the 5 best breeding lines with high Zn or high Fe or both (Naik *et al.*, 2020). In the presence of ascorbic acid, 185M showed higher bioavailability of Fe (2 times) and Zn (3 times) than in Swarna (Raghu *et al.*, 2019). It shows 62% head rice recovery and good cooking quality traits such as alkali spreading value 4, amylose content 24.48% and gel consistency 50 mm (AICRIP 2013). It showed moderate resistance to sheath blight, blast, neck blast, sheath rot and tungro diseases (AICRIP, 2013).

Table 1. Mean Iron and Zinc concentration in unpolished / polished rice of 185M in AICRIP Biofortification trials 2013, 2014 and as reported by Naik *et al*. (2020).

Identity	AICRIP Biofortification trial-2013 (polished rice)*			AICRIP Biofortification trial-2014 (polished rice)*			Naik *et al.* (2020) mean of 15 trials in 3 years (2014, 2015, 2016) in unpolished rice*		
	Zn (ppm)	DFF (days)	Yield (t/ha)	Zn (ppm)	DFF (days)	Yield (t/ha)	Zn (ppm)	*dff* (days)	Yield (t/ha)
185M (IET23814 RPBio5478-185M)	20.56	99	2.45	31.69	98	2.72	30.62	107	3.08
Kalanamak micronutrient check	16.23	105	3.08	18.29	103	3.01	-----	-----	-----
Chittimuthyalu micronutrient check	15.78	109	2.38	21.49	104	3.29	-----	-----	-----
BPT5204 yield check	15.29	109	3.95	15.51	112	4.19	22.8	114	3.24

DFF- days to 50% flowering; dff- days to 40% flowering, *In 2013, Out of 12 entries across 5 zones in 17 locations 185M showed overall mean value of highest zinc 27.38 ppm in brown and 20.56 ppm in polished rice (AICRIP annual report 2013 vol.1 – 1.465). In 2014, out of 45 entries in 17 locations 185M showed overall mean value

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4. Rice Tetra 5-40 (IC0635009; INGR20004), a Tetraploid Cytotype (2n=4x=48) of Rice (*Oryza sativa*)

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Rice, (*Oryza sativa* L.) is one of the major cereals catering to the food needs of the worlds' population. It is a diploid with 2n=2x=24 chromosomes and designated with AA genome. One of the major breeding strategies had been to gain heterosis in this crop is utilizing indica and japonica subspecies. In order to overcome the yield plateau, rice polyploidization is suggested as one of the approaches (Cai *et al.*, 2005, Tu *et al.*, 2007, Liu *et al.*, 2009). Rice polyploidization also have the potential to improve yield, enhancing fertility of inter-subspecific hybrids (indica x japonica) (Guo *et al.*, 2017, Tu *et al.*, 2007), enhanced vegetative growth, increased protein and total amino acid content (Song and Zhang, 1992), and enhanced resistance and epigenetic elements (Guo *et al.*, 2017). Rice tetraploids also offer new germplasm for polyploid rice breeding, understanding complex regulatory mechanisms associated with heterosis and fertility, as well as understanding ploidy-induced traits expression and as a source material for interspecific hybridisation utilising alien polyploid Oryza species (Kaushal and Ravi, 1998).

In an effort to generate tetraploidy in rice, anther-culture derived regenerants were utilized from a diploid rice line CR5-40. The regenerants were screened for their ploidy utilizing meiotic and flow-cytometry analysis (Mishra *et al.*, 2015). Amongst the tetraploid lines, a line viz. Rice Tetra 5-40 was selected and stabilized through eight generations of self-pollination, eliminating diploid revertants in each generation. There were no revertants since last four generations and the line got fixed for its tetraploid cytotype.

The line Rice Tetra 5-40 contained 2n=4x=48 chromosomes and possessed 1.8 pg sporophytic DNA content, representing double the content in diploid lines. These plants were believed to have originate from endo-polyploidized cells during tissue-culture cycle. Rice Tetra 5-40 line was also characterised for morphological traits such as pollen fertility (70%), spikelet fertility (55-60%) number of tillers/plant (16.0), plant height (95.7 cm), leaf length (57.6 cm) and width (2.0 cm), number of leaves/plant (5.5), panicles/plant (15.6), panicle length (21.5 cm), 100 seed weight (2.4 g) etc. The flowering initiated in 100 days, the seeds had awns, with total seed weight of 32.5 g per plant.

The line (Rice Tetra 5-40), thus represented a stabilized tetraploid line with potential for polyploidy research and interspecific hybridization with alien polyploid *Oryza* species. To the best of our knowledge, this is the first tetraploid rice registered in India.

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5. HI 8791 (IC0635014; INGR20005), a Wheat (*Triticum turgidum* subsp. durum) Germplasm with Resistance to Stem Leaf and Stripe Rusts. Resistance to Flag Smut. High Yield Potential.

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Globally, durum wheat occupies nearly 13 million hectares with production of 30 million tons (Kadkol and Sissons 2016) and a productivity of ~2.3 tons/ha. In India, Central and Peninsular zones are the major durum wheat growing regions. Rusts and other diseases affect durum wheat production in these regions. Developing new varieties having broader genetic base with resistance to multiple disease resistance along with high yield potential is the need of the day as these pathogens keeps on evolving leading to new virulent races. Identifying and utilizing multiple disease resistant along with high yielding genotypes is important in durum wheat improvement.

HI 8791 (HI1531/HI8498//HI8627), durum wheat genotype was developed, which is an erect genotype having strong waxiness on leaf sheath, peduncle and spikes. It is a dwarf genotype (85-90 cm) exhibiting medium late maturity (110-120 days). The grains are hard, amber coloured weighing 42-45 gm/1000 seeds. HI 8791 is a very high yielding genotype, with an average yield of 43.0 and 38.4 q/ha in National Initial Varietal Trials (NIVT) and Advanced Varietal Trials-I (AVT-I) respectively. It showed significant superiority of 16% to 2.6% in NIVT and AVT-I, respectively in comparison to check variety HI 8627 in Central Zone.

HI 8791 was found to be resistant to stem, leaf and stripe rusts; and flag smut in multi-location testing viz., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2016 to 2019 (Table 1). The average co efficient of infection was below 7 for all three rusts over the years of testing. It showed high levels of adult-plant resistance to most prevalent and virulent pathotypes like 77-5 and 77-9 of leaf rust, 40A and 117-6 of stem rust, and 46S119 and 110S119 of stripe rust in isolated nurseries. It also showed immune response to flag smut (Table 2) over two years of testing at different locations. As the availability of multiple disease resistant high yielding genotypes is rare, HI 8791 can be used as potential resistance donor to breed varieties against these multiple pathogens (stem, leaf & stripe rusts; and flag smut) and also a source for high grain yield.

Table 1. Disease data of HI 8791 in comparison with check varieties over years

Year	Trial	Genotype	Stem rust		Leaf rust				Stripe rust	
			South		South		North		North	
			HS	ACI	HS	ACI	HS	ACI	HS	ACI
2015-16	NIVT 5B	HI 8791	TR	0.1	10MS	1.5	20MR	1.1	5MS	0.5
		HI 8627 (c)	5MR	0.5	10MS	1.3	20MR	1.3	40S	4.7
2016-17	AVT I	HI 8791	10MR	1.0	20MR	1.5	TMR	0.1	20MR	4.6
		HI 8627 (c)	10MR	0.8	20S	3.7	0	0	20MR	3.5
2017-18	EPPSN	HI 8791	5MR	1.0	40R	4.1	5S	1.0	10MS	2.3
2018-19	MDSN	HI 8791	30MS	6.6	20S	5.2	TR	0.1	20MS	5.2

(HS-Highest score, ACI-Average Coefficient of Infection)

Table 2. Disease score of Flag smut

Year	Trial	Genotype	Flag smut (%)					
			Ludhiana	Hisar	Durgapura	Karnal	HS	Average
2016-17	AVT I	HI 8791	0.0	0.0	0.0	0.0	0.0	0.0
		HI 8627 (C)	0.0	0.0	0.0	8.8	8.8	2.2
2018-19	MDSN	HI 8791	-	-	-		0.0	0.0

Source: ICAR-IIWBR – Crop Protection Report (2016-19).

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6. HI 1619 (IC0635015; INGR20006), a Wheat (*Triticum aestivum*) Germplasm with Resistance to Leaf and Stripe Rusts, Karnal Bunt and Flag Smut. High Yield Potential.

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HI 1619 (W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1), a bread wheat genotype with semi erect growth habit, having strong waxiness on leaf sheath, flag leaf, peduncle and spike. It is a medium tall (100-105 cm), medium late maturing (140-145 days) genotype. HI 1619 showed significant superiority in grain yield (46.9 q/ha) of 0.2- 5.9% over checks (WH 1142 - 44.3q/ha, HD 3043-44.7q/ha, PBW 644- 46.3q/ha and WH 1080-46.8q/ha) in NIVT and AVT-I restricted irrigation conditions of North Western Plains Zone trials.

HI 1619 was found to be resistant to leaf and stripe rusts, Karnal bunt and flag smut in multi-location testing from 2016 to 2019 (Table 1). It showed ACI values of below 7 for both leaf and stripe rusts. It showed high levels of adult-plant resistance to most prevalent and virulent pathotypes like 77-5 and 77-9 of leaf rust and 46S119 and 110S119 of stripe rust in isolated nurseries. It also showed resistance to other diseases like flag smut (Table 2) and Karnal bunt (Table 3). As the availability of multiple disease resistant high yielding genotypes is

rare, HI 1619 can be used as potential resistance donor to breed varieties against these multiple pathogens and also a source of high grain yield.

Table 1. Field responses of HI 1619 to leaf and stripe rusts along with check varieties

Year	Trial	Genotype	Leaf rust				Stripe rust	
			South		North		North	
			HS	ACI	HS	ACI	HS	ACI
2015-16	NIVT 5A	HI 1619	10S	2.7	10S	2.5	20S	2.0
		DBW 110(c)	10S	1.8	10S	1.5	60S	15.6
2016-17	PPSN AVT	HI 1619	40S*	6.1	TMR	2.1	15S	1.8
		PBW 644 (c)	10S	3.8	10S	2.2	40S	17.6
		WH 1142 (c)	40S	8.1	40S*	8.1	5S	1.4
		HD 3043 (C)	20S	7.9	60S	16.9	60S	28.2
2017-18	EPPSN	HI 1619	30R	2.1	TS	0.2	10S	3.1
2018-19	MDSN	HI 1619	5MS	1.0	5S	1.7	40S	7.5

(HS-Highest score, ACI-Average Coefficient of Infection)

Table 2. Disease score of Flag smut

Year of testing	Trial		Flag smut (%)					
			Ludhiana	Hisar	Durgapura	Karnal	Highest Score	Average
2016-17	AVT I	HI 1619	0.0	2.0	10.5	2.1	10.5	3.7
		CHECK	15.0	36.6	28.6	23.5	36.6	25.9
2017-18	MDSN		-	-	-	-	3.5	-

Table 3. Disease score of Karnal bunt

Year of testing	Trial		Karnal bunt (%)					
			Jammu	Hisar	Delhi	Ludhiana	HS	Avg
2014-15	NIVT 5A	HI 1619	-	-	-	1.2	1.2	
		DBW 110 (C)	-	-	-	5.83	5.83	
2016-17	AVT I	HI 1619	0.0	0.0	0.0	1.0	1.0	0.3
		HD 2967 (C)	19.6	25	14.3	9.0	25	17.0
2018-19	MDSN	HI 1619	-	-	-	-	0.0	
		UP 2338					12.3	

Source: AICW&BIP – Crop Protection Report (2016-19)

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7. DBW 278 (IC0635016; INGR20007), a Wheat (*Triticum aestivum*) Germplasm with High Sedimentation Value under Very Late (January) Sown Conditions of Northern Plains. Additional Feature of Multiple Disease Resistance (Leaf Rust, Karnal Bunt and Flag Smut).

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The northern plains follow sugarcane-wheat, vegetable pea- wheat, potato-wheat crop rotations for which a wheat genotype is needed which can be sown under very late sown conditions especially in the month of January. In order to realise the higher yield levels in very little crop period, the early maturing habit coupled with bolder seeds is needed. The grain quality in this regard has immense value especially the product and nutritional quality. The wheat improvement programme for warmer area has focus of development of early maturing wheat genotypes that can withstand terminal heat stress during grain growth period and yield more than the other traditional cultivars. A bread wheat genotype DBW 278 has been developed in this programme and has been evaluated under Special trial on Very late (January) sown conditions (Spl-VLS) of the North western plains zone and north eastern plains zone for yield, disease resistance and quality traits. DBW 278 was identified as a promising high yielding and disease resistant genotype possessing high sedimentation value along with better grain protein content, grain appearance score as well as test weight.

The proposed genetic stock DBW 278 (PHS 714/UP 2425) was developed through modified pedigree method. The female parental line PHS 714 was germplasm line evaluated in IIWBR station trial during 2007-08 and UP 2425 was high yielding bold seeded variety for north western plains zone. The line DBW 278 was evaluated in preliminary yield trials and based on its performance, it was contributed in coordinated trials under AICRP on Wheat & Barley in Special trial under very late sown (January) conditions meant for NWPZ and NEPZ during 2017-18. The trial was conducted at 15 locations along with three check varieties DBW 14, DBW 71 and WR 544 and data from 13 locations namely Pantnagar, Ludhiana, Karnal, Hisar, Delhi, Bulandshahar and Nagina of NWPZ and Coochbehar, Varanasi, Kanpur, Barabanki, Sabaur and Pusa of NEPZ were pooled for analysis. The seed from Pantnagar, Ludhiana, Hisar, Delhi, Sabaur and Pusa were analysed for quality traits to estimate various quality parameters as per standard procedures adopted under AICRP on Wheat & Barley.

Yield improvement is the prime objective and the farmers require genotypes suitable to January sown conditions that can fit in crop rotation after potato, sugarcane, green pea, etc. The pooled results of north western plains zone and north eastern plains zone together indicated significant yield superiority of DBW 278 (32.5q/ha) over all the check varieties with highest yield potential of 43.8q/ha in January sown conditions as compared to all the check varieties (ICAR-IIWBR, 2018a). It also showed earliness, tall plant stature and bolder seeds. Tall plant height is desirable to get more straw yield for less time span and bolder seed s enhance the consumers' preference.

In addition to yielding ability, the quality parameters are becoming important due to consumer's preference for product making and value addition. For making good quality chapatti, the key quality traits are grain protein content (11-13%), grain hardness (40-75) and sedimentation value (30-60 ml). DBW 278 showed higher values of these key determinants while pooled the data of centres from NWPZ and NEPZ (ICAR-IIWBR, 2018b). It has mean sedimentation value of 67 ml with range of 66-70 ml which is >30.0% higher than the best check DBW 71 (51.1ml) indicating better gluten strength in DBW 278. It also possesses high grain protein content of 13.2% and desired level of test weight (77.5kg/hl), grain hardness index (75) and grain appearance score of 6.6 out of 10.0.

The entry DBW 278 also showed better resistance to leaf rust, leaf blight, powdery mildew, Karnal bunt, and flag smut diseases as compared to check varieties in multilocational evaluation under PPSN (ICAR-IIWBR, 2018c). It was categorised as resistant to leaf rust (ACI upto 10.0), Karnal bunt (Av upto 5.0) and flag smut (Av upto 10%) as per the AICRP on Wheat & Barley standards.

From the results, it is concluded that DBW 278 has high yield potential under January sown very late conditions alongwith better quality traits for chapatti and multiple disease resistance and thus, it can be used as potential donor for wheat improvement programmes for yielding ability and quality traits with special emphasis on adaptability to very late sown conditions.

Performance of DBW 278 and checks for yield traits, quality and disease resistance under very late sown conditions of northern plains

Traits	DBW 278	DBW 71 (C)	WR 544 (C)	DBW 14 (C)	CD (10%)
	Mean (Range)	Mean (Range)	Mean (Range)	Mean (Range)	
Yield & ancillary traits					
Grain yield (q/ha)	32.5 (17.2-43.8)	31.1(20.8-42.8)	27.7(16.2-40.0)	31.0 (20.4-40.5)	0.7
Days to maturity	97 (83-107)	99 (87-108)	95 (77-105)	97 (80-107)	
Plant height	90 (71-102)	80 (67-87)	85 (65-98)	76 (59-89)	
1000-grains weight	37.5 (28-43)	32.5 (24-44)	34.5 (24-39)	36.0(24-44)	
Quality					
Sedimentation (ml)	67.0 (65.6-69.7)	51.1 (47.9-54.1)	47.9 (41.7-50.7)	51.1 (46.8-54.4)	
Protein content (%)	13.2 (11.9-14.1)	12.8 (11.3-13.7)	13.3 (11.8-14.1)	12.9 (11.6-13.6)	
Grain appearance (GAS)	6.6 (5.5-8.0)	6.5(5.5-7.5)	3.4 (2.0-6.5)	5.6 (5.0-6.0)	
Test weight (Kg/hl)	77.5 (74.0-80.5)	76.3(72.0-78.5)	79.2 (74.0-83.0)	75.6 (70.2-79.0)	
Grain hardness index	75	83	83	86	
Disease resistance					
Brown rust (ACI/HS)	5.7(30S)	11.3(40S)	7.8 (30S)	14.0 (60S)	
Powdery mildew (Av/HS)	3(6)	4(8)	5(9)	3(7)	
Karnal Bunt (Av/HS)	4.0(7.1)	14.8(41.3)	4.5(11.4)	4.5(9.2)	
Flag smut (Av/HS)	1.4(5.7)	14.4(54.6)	10.8(37.5)	7.3(25.0)	

HS- Highest score ; ACI- Average coefficient of infection for rust diseases; Av- Average score for other diseases

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8. DBW 166 (IC0635017; INGR20008), a Wheat (*Triticum aestivum* subsp. *aestivum*) Germplasm with High Water Use Efficiency. Low Drought Susceptibility Index. Heat Tolerance with Lower Grain Yield Reduction under Heat Stress.

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Wheat being a primary staple food of India is cultivated in 30 m ha area (GOI, 2017; I. Sharma *et al.*, 2015). Wheat depends extensively on groundwater for irrigation. Recent decades have experienced a steady increase in the depth of the groundwater table in wheat growing regions of Indo Gangetic plains (Hira, 2009; Rodell *et al.*, 2009). The current water productivity of wheat is estimated to be about 0.8 - 1.06 kg m−3 in India (Meena *et al.*, 2015; Zwart *et al.*, 2010). Uncontrolled irrigation supported by subsidized/free electricity clubbed with low water productivity is leading to unsustainability of the traditional wheat cultivation (Humphreys *et al.*, 2010; Meena *et al.*, 2019).

The situation therefore calls for development of improved agronomic management options as well as identification of water use efficient genotypes with better yield. Looking at the necessity for wheat genotypes with high water productivity which can be readily adoptable at farmer's field, the present study has been undertaken aiming at identifying high WUE wheat genotypes under limited moisture conditions.

Seventy-one genetically diverse wheat genotypes were screened for high water use efficiency (WUE) under limited soil moisture level at 60 % of Cumulative Pan Evaporation (CPE) during 2015-16. Out of these best performing sixteen high WUE genotypes were shortlisted

for a detailed field study during 2016-17 and 2017-18.

The proposed genotype (DBW166) had shown the high water use efficiency 2.00 kg m^{-3} during the two years of testing at 60and80% CPE and it was better than the check varieties HD2967, PBW550, WH1105 and DBW88 (Table1 and 2). The genotype was also higher yielding as compared to check varieties at 60% and 80% CPE treatment during both years.

DBW166 genotype was evaluated at multiple locations (total 17) in drought tolerance screening nursery (DTSN) for two years i.e 2015-16 to 2016-17. Based on drought sensitivity index (0.64) it has shown tolerance against the drought (Table-3) and was comparable with the tolerant check C-306 (0.55).

Table 1. Average Wheat WUE, of wheat genotype DBW166 in comparison on the basis of experiment during 2016-17and 2017-18

Genotypes	WUE 60%		WUE 80%		WUE Avg
	16-17	17-18	16-17	17-18	
	kg m^{-3}		kg m^{-3}		kg m^{-3}
DBW166	2.33	2.04	2.00	1.61	2.00
HD2967 (C)	2.19	1.78	2.15	1.42	1.89
PBW 550 (C)	2.03	1.43	1.65	1.26	1.59
WH1105 (C)	2.22	1.69	1.91	1.54	1.84
DBW 88 (C)	2.42	1.69	2.00	1.59	1.93

Table 2. Average Wheat grain yield, of wheat genotype DBW166 in comparison on the basis of experiment during 2016-17 and 2017-18

Genotypes	GY at 60%CPE		GY at 80% CPE		Avg GY
	16-17	17-18	16-17	17-18	
	kg ha^{-1}		kg ha^{-1}		
DBW166	4139	5128	4770	4931	4742
HD2967 (C)	3899	4467	5104	4350	4455
PBW 550 (C)	3619	3579	3919	3875	3748
WH1105 (C)	3945	4241	4519	4719	4356
DBW 88 (C)	4315	4255	4731	4869	4542

Table 3. Drought Sensitivity Index (DSI) of DBW166 tested in Drought Tolerance Screening Nursery (DTSN) during 2015-16 and 2016-17 (avg. values of 17 centres)

Genotype	2015-16	2016-17	Avg.
DBW166	0.99	0.29	0.64
C-306 (C)	0.61	0.49	0.55

9. RWP-2017-21 (IC0635018; INGR20009), a Wheat (*Triticum aestivum*) Germplasm with Heat Tolerance and Lower Grain Yield Reduction under Heat Stress.

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Wheat, a major staple crop of the world as well as of India, provides food and nutritional security to millions of the global population. It provides 55% of carbohydrates, and 21% of protein needs of daily human requirements at the global level. Wheat crop is exposed to many abiotic stresses like drought, heat, salinity etc. According to a special report on global warming, by the Intergovernmental Panel on Climate Change (IPCC), global temperatures are expected to continue to increase by a further 1.5°C between 2030 and 2052. The whole wheat-cropped area in India experiences heat, while the central and peninsular parts experience heat stress all through the crop season, significant parts of north-western and north-eastern plains experience terminal heat. Under controlled experiments, grain yield of wheat per spike was reduced by 3–4% per 1°C increase in temperature above 15°C. Hence, it is very much required to identify the genotypes tolerant to heat stress condition, further to develop heat tolerant varieties for cultivation to cope up with future climate change and global warming scenario.

RWP-2017-21 was selected at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) in 15th Heat Tolerance wheat yield international trial (15th HTWYT-5) during 2016-17 crop season. The HTWYT trial from CIMMYT was constituted mainly by considering the entries having traits for heat tolerance. RWP-2017-21 was one of the highest yielding entry in the 2016-17 HTWYT trial with 107 cm plant height and 43gm thousand grain weight. This promising entry was further used for evaluation in our national multi location heat tolerance trial (MLHT1) during the year 2017-18 crop season and was evaluated in Pune, Niphad, Parbhani

and Junagadh centres which are found to be hot spot locations for heat stress. RWP-2017-21 was found to be promising and has showed HSI lower than checks, DBW150 and WH730 which are registered genetic stocks for heat stress and HD2932 which is a promising heat tolerant variety for late sown conditions. Further, the entry was again validated for the second year also in the MLHT trial in the same hot spot locations. The two years data was pooled and the pooled analysis showed that RWP-2017-21 was found be highly promising with lower heat sensitivity index (HSI) (0.93) and also recorded with lower yield reduction of 18% compared to checks (Table 1). Lower yield reduction under heat stress is the important character of a heat tolerant genotype. Thus, RWP-2017-21 will serve as a potential source to be utilized in future breeding programs to develop heat tolerant wheat varieties.

Table 1. The HSI of genotypes pooled over two years (2017-18 & 2018-19)

Genotype	HSI	Yield Reduction %
RWP-2017-21	0.93	18
DBW150(C)	1.01	19.4
HD2932(C)	0.98	18.8
WH730(C)	1.25	24

10. RW 5 (IC0635019; INGR20010), a Wheat (*Triticum aestivum*) Germplasm with Drought Stress and Heat Stress Tolerance.

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World-wide, climate change and shrinking water resources have identified drought as the most important abiotic stress affecting the productivity of field crops. Wheat is an important food crop in India often seriously affected by high temperature and water stress. In India, even though 90% of the wheat is grown under irrigated conditions, only one-third receives full irrigation while the rest is cultivated under partial irrigation. It is likely that water will become a limiting factor for sustained production of wheat in India. Wheat yields have been projected to reduce by an amount of 2292.6 (1000 metric ton) under irrigated conditions due to the impact of climate change and associated water scarcity by the year 2030. The whole wheat-cropped area in India experiences heat, while the central and peninsular part experience heat stress all through the crop season and significant parts of north-western and north-eastern plains experience terminal heat. Hence, it is needed to develop both drought and heat stress tolerant genotype to combat the climate change.

A recombinant inbreed line (RIL) RW 5 developed from the cross of RAJ 4014/WH 730 was tested in drought tolerance screening nursery (DTSN) of AICRP programme, under moisture stress during 2015-16 and 2016-17 crop seasons. The nursery was conducted across eight locations (Akola, Pune, Indore, Sagar, Kanpur, Ranchi, Karnal and Hisar). Phenotypic data such as, days to heading, days to maturity, plant height, productive tillers, grain yield and thousand grain weight were recorded. Based on the pooled analysis of two years data it was found that RW 5 showed lesser reduction (9.6%) in number of productive tillers and biomass (21.7%) as compared to check (C 306) under drought stress in comparision to irrigated condition. RW 5 is an early flowering genotype with a plant height of 73 cm. Harvest Index and grain yield reduction under moisture stress was at par with C 306(C), Test weight of RW 5 (40.4g) was numerically higher than C 306 (39.9g) with a spike length of 11 cm having 53 grains per spike. RW 5 showed a DSI value of 0.51 which is lower than popular drought tolerant variety C 306 (0.55). Since RW 5 was found drought tolerant across all four zones of the country, this depicts its wider adaptability as well. Hence, this genotype can be used as a potential donor in drought stress wheat breeding programme with an added advantage of reduced height compared to C 306.

The RW5 was also tested under MLHT trial during 2017-18 & 2018-19 crop seasons across 10 locations accounting for all 4 major wheat growing zones of India. It has showed lower HSI compared to the check WH730 with lower reduction in grain yield across zones. Hence, RW5 can serve as a potential donor parent simultaneously both for drought and heat tolerance in wheat hybridization programme.

Table 1. Mean drought susceptibility index (DSI) of RW 5 and C 306 (Pooled over years centre wise)

Genotype	DSI	Test Weight (g)	Harvest Index	Plant Height (cm)
RW 5 (RAJ4014/WH 730)	0.51	40.4	0.34	73
C 306 (C)	0.55	39.9	0.33	101

Table 2. The Pooled HSI of RW5 during MLHT 2017-18 &2018-19 crop seasons across zones

Genotype	HSI pooled CZ&PZ	HSI pooled NWPZ &NEPZ
RW5	1.07	1.02
WH730(C)	1.25	1.15

11. Karan Poshan 1 (33/2/1) (IC0635020; INGR20011), a Wheat (*Triticum aestivum*) Germplasm with High Grain Zinc Content (78.4 ppm).

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Worldwide over 2 billion people suffer from iron (Fe), zinc (Zn) and/or other (multiple) micronutrient deficiencies. In India, 48% of children under the age of 5-10 years have zinc/iron or some other micronutrient deficiency. Zinc is one of the important micronutrient for normal growth and development.

A set of 21 Amphidiploids with 4 international checks received from the University of Nottingham, United Kingdom under DBT-BBSRC project and 4 Indian checks (2 aestivum + 2 durum) were evaluated for zinc, iron, protein content, agronomic traits and disease resistance. They were planted continuously for 3 years in simple randomized block design with 4 rows of 2.5 meter plots in replication at IIWBR-Hisar farm and IIWBR-Karnal.

Agronomic traits like days to heading (DTH), days to maturity (DTM), plant height, (PHT), thousand grain weight (TKW), and chlorophyll content index were recorded. Zinc and iron estimations were performed using an Oxford instruments X-Supreme 8000. Karan Poshan 1 (33/2/1) was recorded highest grain zinc concentration (78.4 ppm) as compared to all the tested genotypes and both national and international check varieties. Percent superiority ranges from 58-118 over check variety.

Thus, Karan Poshan 1 (33/2/1) would be a potential source to be utilized in future breeding programs to develop bread wheat varieties with high grain zinc concentration.

Genotypes	Grain Zinc (ppm)	Percent Superiority Over Checks
Karan Poshan 1 (33/2/1)	78.4	-
T. aestivum cv. Paragon (C)	49.6	58
T. aestivum cv. High bury (C)	46.6	68
T. aestivum cv. Chinese spring (C)	43.6	80
T. aestivum cv. Pavon 76 (C)	47.7	64
MACS 6222 (C)	40.9	92
HI 8498 (C)	40.2	95
KRL 210 (C)	36.2	117
HD 2967 (C)	35.9	118

12. Karan Poshan 2 (98/3) (IC0635021; INGR20012), a Wheat (*Triticum aestivum*) Germplasm with High Grain Iron Content (62.9 ppm).

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Worldwide over 2 billion people suffer from iron (Fe), zinc (Zn) and/or other (multiple) micronutrient deficiencies. In India, 48% of children under the age of 5-10 years have zinc/iron or some other micronutrient deficiency. Iron is one of the important micronutrient for normal growth and development.

A set of 21 Amphidiploids with 4 international checks received from the University of Nottingham, United Kingdom under DBT-BBSRC project and 4 Indian checks (2 aestivum + 2 durum) were evaluated for zinc, iron, protein content, agronomic traits and disease resistance. They were planted continuously for

3 years in simple randomized block design with 4 rows of 2.5 meter plots in replication at IIWBR-Hisar farm and IIWBR-Karnal.

Agronomic traits like days to heading (DTH), days to maturity (DTM), plant height, (PHT), thousand grain weight (TKW), and chlorophyll content index were recorded. Zinc and iron estimations were performed using an Oxford instruments X-Supreme 8000. Karna Poshan 2 (98/3) was recorded highest grain iron concentration (62.9 ppm) as compared to all the tested genotypes and both national and international check varieties. Percent superiority ranges from 40-55 over check variety.

Thus Karna Poshan 2 (98/3) would be a potential source to be utilized in future breeding programs to develop bread wheat varieties with high grain iron concentration.

Genotypes	Grain Iron (ppm)	Percent Superiority Over Checks
Karna Poshan 2 (98/3)	62.9	-
T. aestivum cv. Paragon (C)	44.8	40
T. aestivum cv. High bury (C)	42.9	47
T. aestivum cv. Chinese spring (C)	41.4	52
T. aestivum cv. Pavon 76 (C)	41.7	51
MACS 6222 (C)	45.0	40
HI 8498 (C)	43.3	45
KRL 210 (C)	42.8	47
HD 2967 (C)	40.6	55

13. HS628 (IC0635022; INGR20013), a Wheat (*Triticum aestivum* subsp. *aestivum*) Germplasm with Resistance to all Pathotypes of Brown Rust except 77-8.

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Leaf rust, also known as brown rust, is caused by fungus Puccinia triticina Eriks, (Pt). It occurs worldwide wherever wheat is grown and probably causes more damage than any other wheat rust. The South Asian countries viz., India, Pakistan, Bangladesh and Nepal grow wheat in nearly 37million hectares (mha), of which 30mha are at risk of losses due to leaf/brown rust infestation (Huerta-Espino *et al.* 2011). Therefore, it is imperative to develop rust resistant plant genetic resources effective against brown rust in India. HS628, was developed from a cross HS240*2/FLW20(Lr19)// HS240*2/FLW13(Yr15) using Bulk-Pedigree method of breeding at Indian Agricultural Research Institute, Regional Station, Shimla. HS628 has shown resistance to all the pathotypes of brown rust except 77-8 (Table1). HS628 has shown adult plant resistance under epiphytotic conditions to brown rust (AC1=0.1 to 0.6) (Singh *et al.*, 2016). The field population of Pt pathotype in Northern India, lacks virulence for Lr19 (Bhardwaj and Singh 2019). HS628 has been postulated and validated to carry Lr19/Sr25 using STS markers PSY1-E1 and Gb (Pal *et al.*, 2018). HS628 has semi-erect growth habit, coleoptile pigmentation absents, semi-erect flag leaf attitude, auricle pigmentation absent, rudimentary hairs on auricle, waxy leaf sheath, non-waxy flag leaf, weak ear waxiness, weak waxiness of peduncle, tapering ear shape, medium ear length (11.0 cm), awns present, outer glume pubescence absent, medium shoulder width, medium beak length, ear colour white, plant height (89.5 cm), peduncle length (38.2 cm), takes 189 days to mature. It has lustrous semi-hard ovate shaped amber grains with 38g thousand grain weight. The rust resistance gene pool present in HS628 would prove useful gene source for developing potential rust resistant genotypes and/ or serve as potent donor for creating new usable variability against wheat rusts in India.

Table 1. Response of HS628 against brown rust pathotypes under Seedling Resistance Test during 2017-18.

77-5	77-9	77-7	77-10	104-2	12-5	77-8	16-1	77-2	12-2	12-7	11
0;	0;	0;	0;	0;	0;	3+	;	0;	0;	0;	0;

0; (naught fleck) / ; (fleck) / ;1 (fleck1)=Resistant, 3+=Susceptible

Table 2. Detection of Lr19/Sr25 using molecular markers in HS628

Genotype	Response to STS molecular marker	
	Gb	*PSY1-E1*
HS240	-ve	-ve
FLW20+*Lr19/Sr25*	+ve	+ve
HS628	+ve	+ve
FLW13	-ve	-ve

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14. GW 2014-596 (IC0633422; INGR20014), a Wheat (*Triticum sativum*) Germplasm with High Grain Protein content.

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Wheat is the second most important crop after rice both in terms of area and production in India. India produced a record 101.20 million tonnes of wheat from 29.55 million hectares with a productivity of 34.24 q/ha in the year 2018-19 (ICAR-IIWBR, 2019). There is growing concern to export wheat to have remunerative prices, this situation now calls for diversifying wheat breeding towards quality particularly bread and biscuit making. In this context grain protein content assumes significance as high protein is suitable for bread making and low protein content for biscuit-making (Hehn and Barmore 1965). Looking to this need breeding work for high protein content started at Wheat Research Station, Vijapur. Considering this aspect, cross was made using diverse genotypes (GIANT3//HW 921/CPAN 1934) and generation advancement was made using pedigree selection method (Allard, 1960). This genotype has been developed at Wheat Research Station, SD Agricultural University at Vijapur for high protein content.

Morpho-agronomic characteristics: GW 2014-596 has semi-erect growth habit with broad leaves. During the period of testing, it was tested at national level under quality component screening nursery (QCSN) during the 2015-16 to 2017-18 (ICAR-IIWBR. 2016, 2017 and 2018) across the zones, in which GW2014-596 found to be superior with 14.4% protein content over the years and locations to the check variety UP 2672 (13.7%).

Table 1. Performance of GW 2014-596 genotype during 2015-16 to 2017-18

	Grain protein content at 14% moisture			
Genotypes	2015-16	2016-17	2017-18	Average
GW 2014-596	14.8	14.04	14.3	14.4
UP 2672 (C)	14.4	13.7	13.1	13.7

Associated characters and cultivation practices: GW 2014-596 has very broad leaves and flag leaf attitude drooping type. Grain has bold, amber colour and oblong shape. Ear is having clavate shape and strong waxiness on ear and peduncle. It matures within 110 days the package of practices to be followed as per normal sown irrigated condition and standard agronomic practices is recommended for the cultivation of this genotype. This genotype is adapted to all over the country and resistant to black and brown rust.

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15. GW 2010 288 (IC0623434; INGR20015), a Wheat (*Triticum aestivum*) Germplasm with Number of grains per spike >60. Thousand grain weight > 45 g. Iron content >42 ppm.

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Genetic diversity is crucial for a breeder to create the variability (Johnson *et al.*, 1955) considering this aspect, cross was made using diverse genotypes (WR 196 / CMH83-2578) and generation advancement was made using pedigree selection method (Allard, 1960). This genotype has been developed at Wheat Research Station, S.D. Agricultural University at Vijapur for thousand grain weight, number of grains per spike and high iron content.

Morpho-agronomic characteristics: It has semi-erect growth habit with strong waxiness on peduncle. Ear of this genotype is white at maturity with parallel shape. Grains are hard, amber colour with oval shape. During the period of testing, it was tested at national level under yield component screening nursery during the 2011-12 to 2013-14 (Gyanendra Singh *et al.*, 2012, 2013 and 2014) across the zones, in which it was found promising for multiple traits viz., grains per spike, thousand grain weight and spike length. After found promising consecutively for three years of testing, it was identified for grains per spike, thousand grain weight and spike length and included in National Genetic Stock Nursery for two years of testing in 2014-15 and 2015-16 across the zones. (Singh *et al.*, 2015 and 2016).

Associated characters and cultivation practices: For biotic stress, it was found moderately resistant to black and brown rust in National Genetic Stock Nursery. As it matures within 120 days the package of practices to be followed as per normal sown irrigated condition and standard agronomic practices is recommended for the cultivation of this genotype.

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16. UP 2994 (IC0635426; INGR20016), a Wheat (*Triticum aestivum*) Germplasm for High Protein Content (Av. 14.33%). High Iron (Fe) Content (49 ppm) and Zinc Content (43.5 ppm). Hectolitre weight 80.7kg/kl and Sedimentaion value: 59.5ml.

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Improving the nutritional quality of staple food crops is now getting attention for combating the prevailing malnutrition in a very large population in developing countries. Since wheat is one of the major staple foods around the world and is the major source of nutrients such as protein and micronutrients, wheat and its nutrients are the target traits for improvement whenever strategies to improve nutrient deficiencies are addressed. UP 2994 was evaluated in quality component screening nursery (QCSN/QCWBN) continuously for three years (2016-

17, 2017-18 & 2018-19) and it possessed/showed high protein content consistently for three years, i.e. 15.1% in 2016-17, 14.0% in 2017-18 and 13.9% in 2018-19, with a mean protein content of 14.33%. In addition to high protein content, it also possesses high iron content of 49.0 ppm, which is higher by 4.20 ppm in comparison the best check, WB 2 (44.8 ppm). It is also rich in another important micronutrient i.e. zinc, with 43.5 ppm. This material was developed at GBPUA&T, Pantnagar by pedigree breeding method. The parentage of this material is HUW 636/PBW 651. UP 2994 has been observed possessing other desirable quality traits in national nurseries during 2016-17 and 2018-19 viz., the grain appearance score (6.7), hectolitre weight (80.7 kg/hl) and sedimentation value (59.5 ml) averaged over 3 years. High protein content along with high sedimentation value makes this germplasm will help in the production of wheat varieties with enhanced bread making quality.

Morpho-agronomic characteristics of UP 2994: Foliage colour of UP 2994 is dark green with intermediate growth habit and there is no anthocyanin pigmentation of auricle. Its flag leaf attitude is semi erect type with medium length and width of flag leaves. It possesses medium length ears and has tapering ear shape in profile. It takes an average of 81 days for 75% flowering. It is superior in tillers numbers (107 tillers/meter), 1000 grain weight (41g) and grain yield (433g/m^2) to all the checks viz., UP 2672, C 306, NIAW 1415 and HS 490.

Associated characters and cultivated practices: UP 2994 has been observed possessing other desirable quality traits in QCSN/QCWBN during 2016-17 and 2018-19 viz. the grain appearance score (6.7), hectolitre weight (80.7 kg/hl) and sedimentation value (59.5 ml) averaged over 3 years. UP 2994 is developed using pedigree selection method and hence it is ready to use genetic stock in hynbridization programme without any linkage drag in developing high yielding wheat varieties with enhanced nutritional status.

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17. QST1910 (IC0635697; INGR20017), a Wheat (*Triticum aestivum*) Germplasm with Drought Tolerance and Low Drought Sensitivity Index.

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Recurrent drought associated with climate change is one of the important constraints to global wheat productivity. Efforts to mitigate drought through breeding resilient wheat varieties are underway across the globe. However, progress is hampered because of complexity of the trait, as the trait is controlled by many genes with significant environmental influence. Drought stress affects wheat yield, particularly in central and peninsular India. Therefore, identification and development of drought tolerant wheat germplasm lines is of prime importance in recent past. In this direction under the AICRP on wheat and Barley, 32nd Drought Tolerance Screening Nursery (DTSN) comprising 25 wheat genotypes including 5 checks (C306, MP3288, DBW110, K1317, and NI5439) was conducted at 15 centres to identify wheat genotypes having tolerance to drought stress. The nursery was sown in 5 × 5 simple lattice design both under drought and irrigated conditions on the same date. Except pre-sowing irrigation, no irrigation was given under drought treatment, while recommended numbers of irrigations were provided under irrigated treatment.

QST1910 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing HD2967/WH1080. QST1910 recorded the lowest Drought Sensitivity Index (DSI) in all the tested centers compared to the drought tolerant check varieties. QST1910 found to be superior with DSI of 0.65 compared to drought tolerant check varieties viz., DBW 110 (0.81),

C 306 (0.83), K1317 (1.36), MP 3288 (1.36), and NI 5439 (1.44). The percent DSI superiority of QST1910 over check varieties was 19.8% (DBW 110), 21.7% (C 306), 31.6% (K1317), 52.2% (MP 3288), 54.9% (NI 5439). QST1910 was also superior to all the 5 check varieties for percent yield reduction, plant height, grain filling duration, productive tillers, and days to heading

Thus, QST1910 would be a potential source to be utilized in breeding programs to develop drought tolerant bread wheat varieties.

Table 1. Pooled analysis of DSI and agro-morphological traits of DTSN genotypes during 2019-20.

Trait/ Component	Test Genotype	Checks				
	QST1910	DBW110	C306	K1317	MP 3288	NI 5439
Pooled DSI	0.65	0.81	0.83	0.95	1.36	1.44
% DSI superiority of QST1910 over checks	-	19.8	21.7	31.6	52.2	54.9
% Yield reduction	16.3	20.4	20.9	23.9	34.0	36.2
Plant height (cm)	80	93	81	89	84	85
Grain filling duration	48	44	40	44	44	44
Productive tillers	73	66	69	71	70	66
Days to heading	67	71	74	69	68	71
Days to maturity	115	115	114	113	112	115
Thousand grain weight (g)	36	36	35	40	38	34
Grain number per spike	42	41	46	51	46	45
Grain weight per spike (g)	1.7	1.6	1.7	2.3	1.9	1.6

18. BHS 474 (BBM 777) (IC0635023; INGR20018), a Barley (*Hordeum vulgare*) Germplasm with Resistance to all Pathotypes of Yellow Rust and Brown Rust in Seedling and Adult Plant Stage. Seedling Resistance against all Pathotypes of Black Rust except for Pathotype 11.

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BHS 474 (BBM 777) is barley (*Hordeum vulgare* L.) line resistant against stripe, leaf and stem rust. It has shown highest degree of resistance against all the prevailing pathotypes of stripe and leaf rust at seedling stage and is resistant to both the rust at adult plant stage. BHS 474 (BBM 777) also possesses seedling resistance against all the pathotype of stem rust except for pathotype 11. This line is developed following pedigree method of breeding involving crosses between barley local germplasm line BLG132 and barley genetic stock BHS369 at ICAR-IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Center, Shimla (H.P.)

BHS 474 (BBM 777) has semi erect growth habit with medium maturity (172 days) under Northern Hill condition. The average yield is 2.3 t/ha under rainfed condition of Northern Hill Zone of All India Co-ordinated trials. The distinguish features of BHS474 (BBM 777) are six-rowed; hulled; semi-erect growth habit; semi-erect flag leaf attitude; green leaves; white colour of ear at maturity and thousand grain weight of 39 grams.

Table 1. Reaction to major diseases

Diseases	Condition	Year	Response of Proposed Genetic stock 474 (BBM777)
Stripe Rust (Resistant to yellow rust)	IBDSN (APR)	2017-18	ACI= 0
			HS= 0
	NBDSN (APR)	2018-19	ACI=0.9
			HS=5S
	NBDSN (Seedling)	2018-19	R (Resistant)
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2018-19	HS= 5S
	NBDSN (Seedling)	2018-19	R (Resistant)
Stem Rust (Seedling Resistant to black rust)	NBDSN (Seedling)	2018-19	MR - R (Moderately Resistant to Resistant) except for pathotype *11*

ACI= Average Coefficient of incidence; HS= Highest Score; IBDSN= Initial Barley Disease Screening Nursery; NBDSN= National Barley Disease Screening Nursery

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19. DWRB207 (DWRFB19) (IC0635698; INGR20019), a Barley (*Hordeum vulgare*) Germplasm Highly Resistant to Stripe Rust. High 1000 Grain Weight (47.5g). Low Protein Content (9.5).

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Resistance to yellow rust and high thousand grain weight (TGW) are important traits for improvement of grain yield in barley. Yellow rust caused by *Puccinia striiformis* Westend. f.sp. hordei Erikss. & Hen. (Psh) is an important foliar disease in barley which causes yield loss in the range of 5% to 25%. In addition to yield, yellow rust also affects the grain quality under severe incidence. Early incidence of yellow rust can cause severe losses to the crop in Indian conditions and sometimes, it prevents the emergence of the ear head or grain formation (Prakash and Verma, 2009). Disease can be controlled by fungicides; however, it is costly approach for a low input crop like barley and hazardous to the environment. Use of resistant varieties against yellow rust is an economical and environment friendly approach to minimize the yield losses. Hence, it becomes imperative to develop yellow rust resistant germplasm for barley improvement.

Thousand grain weight (TGW) is an important contributing trait for improvement of grain yield. It is widely used as a standard indicator for grain development and quality (Kumar *et al.,* 2017). At ICAR-IIWBR, Karnal, DWRB207, has been identified having high resistance to yellow rust coupled with higher thousand grain weight during crop season over diverse conditions.

DWRB207 (IC0635698) evaluated as DWRFB19 is hulled barley developed by hybridizing exotic (CDC Manley) and indigenous (BCU2881) barley genotypes following pedigree method making selection of individual plant from F2 to F5 generations. Selection was made for yellow rust resistance under artificial inoculated conditions during course of its development. DWRB207 was tested as DWRFB19 in coordinated screening nurseries (IBDSN) during 2016-17 and 2017-18 and it revealed highly resistance against yellow rust. In field conditions, this genotype had highly resistant response at all locations in IBDSN testing under artificial rust epiphytotic conditions (Singh *et al.*, 2019), while, infector showed highly susceptible reactions against yellow rust in both consecutive years (Table 1A). The Seedling Resistance Test (SRT) was conducted at IIWBR-RS Flowerdale, Shimla during 2017-18 and 2018-19. DWRB207 exhibited resistant reactions against all the yellow rust races viz., 6S0, 7S0, G, M, 24, 57 and Q in the present study.

Table 1A. Rust reaction of DWRB207 in IBDSN under artificially inoculated conditions

Genotype	Year of testing	Durgapura	Ludhiana	Bajaura	Jammu	Karnal	HS	ACI
DWRB207 (DWRFB19)	2016-17	0	0	0	0	0	0	0.0
	2017-18	TR	TR	TR	0	0	0.12	TR
Infector	2016-17	100S	60S	80S	60S	80S	100S	76.0
	2017-18	100S	60S	60S	80S	60S	100S	72.0
Seedling resistance test		Pathotypes						
Genotype	Year	6S0	7S0	G	M	24	57	Q
DWRFB19	2017-18	0;	0;	0;	0;	0;	0;	0;
	2018-19	0;	0;	0;	0;	0;	0;	0;

HS= highest score, ACI= average coefficient of infection, 3+ =susceptible, 3, 3- = moderately susceptible, 2, 2+ = moderately resistant, 0;/;/1/2- = Resistant

Table 1B. Thousand grain weight (g) under multi location ICW&BIP trial during 2018-19

Character	Genotype	Hisar	Kanpur	Faizabad	Mean
1000-grain weight (g)	DWRB 207	47.5	53.6	41.26	47.5
	NDB 1173(C)	43.1	38.0	34.76	38.6
	NDB1445(C)	41.1	34.0	36.6	37.2
	RD2552(C)	41.8	37.8	40.84	40.2
	RD2794(C)	44.7	40.6	38.74	41.3
	RD2907(C)	44.9	47.0	38.16	43.3

In addition to the stripe rust resistance the genotype is also having higher thousand grain weight (47.5 g) averaged under multi-location AICW&BIP trial during 2018-19 (Table 1B).

Agro-morphological characteristics: DWRB207 flowers in 92 days and matures in 130 days on an average. Its average plant height is 100 cm, spike length (7.3 cm), containing 68 grains per spike. It is moderate tillering type genotype with 88 tillers/meter.

Therefore, this genotype, identified on the basis of field and SRT analysis, may be used as donor parent in resistance breeding for yellow rust as well as for higher thousand grain weight.

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20. UPB 1070 (IC0635430; INGR20020), a Barley (*Hordeum vulgare*) Germplasm Resistant to Yellow Rust (ACI0.0). High Yield Potential in NHZ (29.2 q/ha). High Bold Grain Percentage (89.4%) and other Good Agronomic Traits.

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Barley is an important crop also adapted in the marginal and stressed affected environments. Yellow rust is a devastating foliar disease of barley, caused by *P. striiformis* f. sp. *hordei*. It causes severe yield losses particularly in Northern hills and adjoining plains. Due to multicyclic nature of the disease and marginal status of the crop chemical control is not feasible, resistance breeding is highly required for combating this disease. The durability of genetic resistance is under constant threat by the natural variation and novel mutation in the pathogen, resulting in the ongoing erosion of resistance genes in cultivation. For combating the threat of yellow rust, identification and deployment of novel sources of resistance is required in the existing breeding programs. UPB 1070 is recognized as a confirmed source of yellow rust resistance with an ACI of 0.04 in National Barley Disease Screening Nursery, 2017-18 and ACI of 0.0 in Elite Barley Disease Screening Nursery in 2018-19. with a sound agronomic background. It was developed at G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand through pedigree breeding method utilizing hybridization between two parental lines viz; Dolma and BH 947 followed by selection.

Morpho-agronomic characters: UPB 1070 was tested in Co-Ordinated Trials (AVT-RF-NHZ) in North Hills Zone under timely sown rainfed conditions during 2017-18 with an average yield of 29.2 quintals per hectare. UPB 1070 showed superiority in yield over the checks, BHS 352, BHS 400 and VLB 118 in AVT-RF-NHZ during 2017-18. It is a six rowed yellow grain colour barley with 103-154 days to heading, 140-197 days to maturity with a plant height of 47-100 cm, 44-238 tillers per meter and 33-46 gm 1000 grain weight.

Associated characters and cultivation practices: In addition to yellow rust resistance, UPB 1070 showed moderate level of resistance against leaf blight and it also exhibited highest bold grain percentage (89.4 %) in Co-Ordinated Trials (AVT-RF-NHZ) 2017-18, a trait which determines the overall grain plumpness,

an associated trait of malt quality. It is adaptable for hilly areas.

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21. LMDR-2 (IC0635024; INGR20021), Maize (*Zea mays*) Germplasm Resistant to Maydis Leaf Blight and Moderately Resistant to Charcoal Rot of Maize.

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Maize (*Zea mays* L.) an important cereal crop is subjected to extensive yield losses due to fungal diseases at different growth stages. Among them, maydis leaf blight caused by Drechslera maydis occurring at pre flowering stage and charcoal rot caused by Macrophomina phaseolina occurring at post flowering stage of the crop are the major factors threatening maize production in Northern India (Kaur *et al.*, 2010). Thus, it is essential to identify useful sources possessing multiple disease resistance in maize as selection and breeding for resistance is the most economical method of delivering control for farmers.

LMDR-2 inbred line was developed through pedigree selection and inbreeding for six generations. At the end of six selfing and evaluation, uniform progenies were identified and their selfed seeds were bulked which were multiplied in isolation. This inbred line has been developed at Punjab Agricultural University, Ludhiana. This is late maturing line. The plant length is short with low ear placement. Its tassel is light with curved branches and sparse spikelets. Silks are green. Leaves are narrow and straight. Ears are small conical. Grains are orange, round flint with straight kernel rows. 1000 kernel weight is small. Under artificial inoculation conditions, its mean disease score to maydis leaf blight is 3.0 following 1-9 scale of Hooda *et al.* (2018) as given in Table 1A. This line has been found resistant to this disease. Regarding its reaction to charcoal rot, under artificial conditions its mean disease score is 3.7 on 1-9 scale (Hooda *et al.*, 2018) found to be moderately resistant to this disease Table 1B. This genotype has been found highly promising possessing multiple disease resistance to maydis leaf blight and charcoal rot of maize.

Table 1A. Disease reaction of promising germplasm against Maydis Leaf Blight of Maize during *Kharif* 2017 and 2018

Proposed Name	Inbred	Maydis Leaf Blight (1-9)*						Mean over the years (4 Expts)
		2017			2018			
		Karnal	Ludhiana	Mean (2 Expts)	Karnal	Ludhiana	Mean (2 Expts)	
LMDR-2	LL-49	1.0	3.5	2.2	3.8	4.0	3.9	3.0
Susceptible check	CM 600	8.0	8.0	8.0	8.0	8.8	8.4	8.2

*1-3-Resistant; 3.1-5.0- Moderately resistant; 5.1-7.0-Moderately Susceptible; 7.1-9.0-Susceptible

Table 1B. Disease reaction of promising germplasm against charcoal rot of maize during *Kharif* 2017 and 2018

Proposed Name	Inbred	Charcoal Rot (1-9)*						Mean over the years (4 Expts)
		2017			2018			
		Delhi	Ludhiana	Mean (2 Expts)	Hyd	Lud	Mean (2 Expts)	
LMDR-2	LL-49	3.3	3.0	3.1	4.6	3.8	4.2	3.7
Susceptible check#		7.0	6.6	6.8	3.8	5.9	4.8	5.8

*1-3-Resistant; 3.1-5.0- Moderately resistant; 5.1-7.0-Moderately Susceptible; 7.1-9.0-Susceptible
#Sus check: 2017- CM 501 (Delhi); CM 140 (Ludhiana); 2018- CM 600

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22. VR 1081 (IC0635027; INGR20022), a Finger Millet (*Eleusine coracana*) Germplasm Resistant to Finger Blast.

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Finger millet, VR 1081 is finger blast resistant line developed by crossing blast resistant variety GPU 28 with blast resistant germplasm GE 4931. The cross was performed in 2005 for developing blast resistant high yielding variety and subsequent selections were made through pedegree method from F2 to F6. It was promoted at F8 stage to Preliminary Yield Trial in 2013. It belongs to medium maturity with medium plant height medium number of productive tillers/plant. It is comparable with the check, Sri Chaitanya (VR 847) for grain and fodder yield.

The entry, VR 1081 along with other test entries and two checks were tested under high disease pressure under field conditions for consecutive five years from 2014 to 2018. It recorded NIL incidence of Finger blast among all the 3000 entries tested for finger blast resistance and also showed resistance to neck blast (8.2 % Pooled data). VR 1082 has recorded. -100% (less incidence) of finger blast over resistant check, Sri Chaitanya (VR 847) & susceptible check, Champavathi (VR 708) while it recorded -91.5% (less incidence) of neck blast over susceptible check, Champavathi (VR 708). Hence, VR 1081 is unique in terms of finger blast resistance and moreover it also recorded higher grain and fodder yield and hence can be used directly as a source for development of high yielding, finger blast resistant varieties.

23. IPAC 79 (IC0626208; INGR20023), a Pigeon Pea (*Cajanus cajan*) Germplasm Tolerant to Waterlogging Stress and Resistant to Phytophthora Stem Blight Disease.

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Pigeonpea [*Cajanus cajan* (L.) Millisp.] often encounters over-flooding at seedling stage, especially in low-lying areas. Upon exposure to submergence for 3 to 4 days, the crop experiences hypoxia with considerable injury to roots, eventually causing death of the plant (Sultana *et al.*, 2012). Further, the weather conditions during seedling stage, such as intermittent rains and moderate temperatures of 25±1^{o}C favor occurrence of Phytophthora stem blight (PSB) and the ensuing diseases causes' significant loss in crop yield (Kannaiyan *et al.*, 1984; Pande *et al.*, 2011). To the best of our knowledge, no registered pigeonpea genotype is available for water-logging tolerance and PSB resistance. In view of this, we have identified a pigeonpea genotype (IPAC 79) showing remarkable tolerance against both water logging and PSB on the basis of observations recorded over four years (2011-12, 2012-13, 2013-14 and 2017-18) at IIPR, Kanpur. The genotype IPAC 79 is an advance line derived from the cross 'Bennur local/ BRG 1'. It was found to be tolerant up to 96 hours of waterlogging, when the screening conducted after 20 days seedling stage. Under water-logged conditions, the genotype showed 53.8% survival as compared to only 0.6 % survival in sensitive line (ICPL 7035), and 11.2% &18.6% survival in national check varieties viz. Bahar and NDA 1, respectively. It is important to note that IPAC 79 was also resistant to PSB.

Morpho-agronomic characteristics of IPAC 79: The genotype is a tall (210 cm), compact and late maturing (261 days) with purple pigmentation on the stem. It bears streaked and diffused red flowers, purple sticky pods with black seed coat and test weight of about 12.3g/100 seed. The average yield of IPAC 79 is 21.3 quintals/ha in replicated trials conducted at IIPR Kanpur.

Associated physiological characters and cultivation practices: After multiple cycles of waterlogging, the chlorophyll content of IPAC79 remained less affected (18% reduction) even after 4th cycle of stress as compared to ICPL 7035 (50% reduction). Leaf nitrogen balance index (NBI) reduced by 50% in ICPL 7035, whereas only 20% reduction was found in IPAC 79. The root capacitance decreased from 0.86 nf to 0.61 nf in IPAC 79, the extent of reduction was greater in ICPL 7035 (from 1.02 to 0.2 nf), implying an irreversible damage in roots due to higher absorption of minerals and other nutrients from soil. No accumulation of anthocyanin was observed in the leaves of IPAC 79 as opposed to sensitive genotype that accumulated significant anthocynin on exposure to waterlogging. The pigeonpea is sown with the onset of monsoon. The field should be prepared with required tillage practices by adding 5 tons of FYM and NPK of 20:40:40 kg/ha. The seed rate of 12-15 kg/ha is required for sowing with spacing 75×30 cm. This genotype has good worth as a donor of waterlogging tolerance and PSB resistance along with superior yield attributing traits. IPAC 79 will have good utility in crossing programmes of pigeonpea breeding. This genotype has immense commercial value in the ecological niches of terai region of Uttar Pradesh where there is high rainfall and high incidence of Phytophthora stem blight.

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24. RCEA 14-5 (IC0635029; INGR20024), a Pigeonpea (*Cajanus cajan*) Germplasm with No Natural Outcrossing. Twisted Standard Petal Wrapped over Wings. Free Stamens (Non-Diadelphous Condition).

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Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a partially allogamous pulse crop with natural out-crossing varying from 5 to 70 percent. Natural out-crossing is the major source of varietal contamination in pigeonpea and, in order to maintain genetic purity of cultivars, seed multiplication in isolated blocks/poly net house is necessary. This consumes a lot of resources, eventually increasing the cost of seed production. However, genetic purity of a variety can also be maintained through incorporation of 'selfing' traits into desirable cultivars (Choudhary and Nadarajan, 2011). The genotype 'RCEA 14-5', which was derived from a cross IPA 203 × ICPL 87154 by pedigree method, holds high promise as it has shown zero percent natural out-crossing. It combines several unique features such as twisted flowers having the standard tightly wrapped with wings, significantly enlarged keels partly surrounding the standard enfolding the two wing petals and free stamens (non-diadelphous condition), making it highly unattractive to both pollinivore and/or nectarivore insects (Choudhary *et al.*, 2015; Saxena *et al.*, 2016).

Morpho-agronomic characteristics: The developed genotype bears similarity with one of its parents 'IPA 203' which is a leading variety of long-duration pigeonpea for the north-east plain zone. However, it differs from 'IPA 203' for various morpho-agronomic traits (Table 1).

Table 1. Morpho-agronomic Characteristics of 'RCEA 14-5'.

Characters	RCEA 14-5	IPA 203
Stem Colour	Green	Green
Leaf shape	Lanceolate	Lanceolate
Growth habit	Indeterminate	Indeterminate
Plant type	Compact	Semi-compact
Plant height*	Medium (1.75 m)	Tall (2.0 m)
Standard petal colour	Golden yellow	Yellow
Keel petals	Large	Relatively small

Characters	RCEA 14-5	IPA 203
Stamen configuration	Free (non-diadelphous)	Diadelphous (9+1)
Flower configuration	Twisted, tightly wrapped standard with wings	Normal
Natural outcrossing*	Zero	> 15%
Pod colour	Light green with dark streaks	Dark green with black streaks
Seed strophiole	Absent	Present
100 seed wt (g)*	9.10	12.20
Yield (t/ha)*	1.75	1.74

*Mean value based on data of station trials conducted at Darbhanga (2014-15) and Ranchi (2016-17 & 2017-18).

Associated characters and cultivation practices: The unique combination of selfing traits (twisted flowers due to wrapping of standard and keel with wings, and free stamens) considerably delay opening of flower buds and provide many-fold barriers to foraging insects including honeybees, thereby ensuring cent per cent seed set through self-pollination in 'RCEA 14-5'. The cultivation of this genotype will preclude the necessity of seed replacement at regular intervals. The general cultural practices recommended for 'IPA 203' (Choudhary, 2016) may be adopted for cultivation of this genotype too. Alternatively, the genotype 'RCEA 14-5' may be utilized as the donor for "cleisto" traits in future pigeonpea improvement programme.

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25. IPAV 16-1 (IC0635030; INGR20025), a Pigeonpea (*Cajanus cajan*) Germplasm with High 100 Green Seed Weight of 50-52 g. High 100 Dry Seed Weight of 22.5-23.04 g. Compact Plant Type with Green Colour Stem, Yellow Colour Flowers, Brown Colour Pods of 9.5 to 10.25 cm Length Packed with 5-6 Seeds/Pod.

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Pigeonpea [*Cajanus cajan* (L.) Millisp.] is an important grain legume in the semi-arid tropics of Asia and Africa due to its climate adoptability and high dietary protein (20-22%) content. India is world's largest producer (3.59 mt) and consumer of pigeonpea (http://agricoop.gov.in/2018-19). Pigeonpea is consumed in the form of vegetable during green seed stage in the southern and northeastren states like Karnataka, Telangana, Andhra Pradesh, Tamilnadu, Maharashtra, Gujarat, Tripura and Nagaland and matured dry grains in the form of dehulled cotyledons (dal) after essential postharvest milling process in the whole country.

Seed weight being an important yield attributing trait in pigeonpea plays vital role in the final harvest and economic gain for farmers (Satheesh *et al.*, 2013). Pigeonpea green pods are harvested for different purposes like for direct use as vegetable or canning. Near cities where they can be readily marketed are harvested as vegetable. Fully developed seed having 100 green seed weight of >45 grams are mostly preferred by consumers for vegetable purpose (Saxena *et al.*, 2010). However, the most of the released varieties having the 100 green seed weight of 20-30 grams therefore they are less desired by the consumers. Narayanan *et al.* (1981) proved that the large dry seeded pigeonpea varieties (100 dry seed weight >15g) produces larger and more vigorous seedlings, which will have an advantage in crop establishment under adverse conditions. Keeping this in view the present line IPAV 16-1 would be the potential donor for future line of breeding for high 100 seed weight and vegetable purpose.

Morpho-agronomic characteristics: The line IPAV16-1 was a pure line selection from JBP 13. Initially a set of 15 genotypes were selected based on the vegetable traits (pod and seed size and weight) and allowed the natural inter mating among the genotypes, then after

each genotype was selected for high 100 seed weight and advanced generations through plant to progeny row till the line became stable. Subsequently, during 2014 and 2015 cropping season all the advanced pure lines were characterised for wilt resistance, seed nutritional quality and agronomic traits. The line IPAV 1 recorded higher mean values for number of pods/harvest (161.30), pod length (9.81 cm) and number of seeds/pod (5.73) (Satheesh *et al.*, 2016). In 2016 cropping season the line IPAV 1 was tested under ICAR-IIPR, Kanpur station trial as IPAV 16-1 along with the dual purpose (vegetable and grain) released variety BRG 1 and reported high 100 seed weight line ICP 12746 (Upadhyaya *et al.*, 2010) as checks and recorded the data on yield and yield attributes. The results on 100 seed dry and green weight was high in IPAV 16-1 i.e., 23.04g and 52.00g respectively while the better check ICP 12746 recorded 18.03 and 44.8 g/100 dry and green seed weight respectively. Based on the accumulated data over the seasons, IPAV 16-1 was subjected to evaluation for 100 seed weight during 2018-19 cropping season by the germplasm identification committee of ICAR-IIPR, Kanpur. The committee recommended the registration of the line as donor for high 100 seed weight.

IPAV 16-1 is a compact branching semi determinate plant produces 13-15 numbers of primary branches with plant height ranging from 200-215 cm. The plant has green colour stem and absence of leaf pubescence on both the surfaces. IPAV 16-1 produces 9.5-10.5 cm long uniform dark brown colour pods packed with 5-6 seeds per pod. Presence of pod surface wax and stickiness helps in less attack by the pod borer and pod fly complex. IPAV 16-1 produces 1.8-2.0 cm long yellow coloured flowers with no streaks on its standard petal (Fig. 1). The 100 green seed weight ranged from 50-52 grams while the dry seed weight is 22.5-23.04 grams. The dry seeds are oval shaped, having mosaic brown colour seed coat. The genotype IPAV 16-1 attains its 50 % flowering in 120 to 125 days and matures in 180-185 days.

Associated characters and cultivation practices: Pigeonpea is sown with the onset of monsoon. The field should be prepared well with recommended tillage practices by adding 5 tonnes of FYM and NPK of 20:40:40 kg/ha. The seed rate of 12-15 kg/ha is required for sowing with the spacing of 75×30 cm. The line IPAV 16-1 holds great promise for use as donor of high 100 seed weight (50-52g & 22.5-23.04g for green and dry seeds respectively) in pigeonpea breeding programme. The line IPAV 16-1 has immense commercial value as donor for vegetable breeding programme.

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26. GFB-3 (IC0635031; INGR20026), a French Bean (*Phaseolus vulgaris*) Germplasm with Anthracnose Resistance.

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Anthracnose is considered most common bean diseases (*Phaseolus vulgaris* L.) caused by *Colletotrichum lindemuthianum* (Sacc. & Magnus) Scrib. Diseases causing massive loss in crop yield worldwide, preferably in the regions with prevailing high humidity and moderate temperature (13 to 27ºC). Uttarakhand has rich biodiversity for French bean. 100 accessions of French bean germplasm were collected from six district of Garhwal regions and screened for resistance to anthracnose disease.

On screening with SCAR markers GFB-3 accession

amplified with three primers SF-10, SAS-13 and SZ-04 and was found having three genes (Co-10, Co-42, Co-6) for anthracnose resistance. For in vitro screening three weeks old plants were inoculated with spore suspension (106 conidia/ml) of the pathogen *C. lindemuthianum* to check resistance against *C. lindemuthianum* (Fig. 1). Disease reactions were rated visually using a scale from 1 to 9. The plants scored from 1 to 3 were considered resistant.

Four field trials were conducted to test the anthracnose disease incidence. No disease was observed in three field trials. In one trial the disease incidence was very low that was 1.00 (Prabha *et al.*, 2020). Out of the germplasm screened, Accession GFB-3 has multiple genes for anthracnose resistance with good qualitative and quantitative characters (Table 1).

Table 1. Qualitative and quantitative characters of the French bean accessions GFB-3

Accession	Seed colour	Flower colour	Seed length (mm)	Seed diameter (mm)	Pod length (cm)	Number of seed per pod	Pod colour at physiological maturity	Days to 50 % maturity	100 seed weight (gm)
GFB-3	White with light green spot	White	10.1	3.6	11.72	6.4	Green	69	29.10

Reference

Prabha D, N Chamoli, YK Negi and JS Chauhan (2020) Newly Identified Anthracnose Resistant French Bean (*Phaseolus vulgaris*) Accessions from Garhwal Hills of Uttarakhand. *Int. J. Curr. Microbiol. App. Sci.* **9(02)**: 2748-2751. doi: https://doi.org/10.20546/ij cmas.2020.902.31

27. GFB-30 (IC0635032; INGR20027), a French Bean (*Phaseolus vulgaris*) Germplasm with Anthracnose Resistance

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Uttarakhand has rich biodiversity for French bean which is unexplored. Anthracnose disease is a serious constraint to the French bean growth and yield. 100 accessions of French bean germplasm were collected from six district of Garhwal regions and screened for resistance to anthracnose disease.

Accession GFB-30 was amplified with four primers SF-10, SAS-13, SH-18 and SZ-04 was found having three genes (Co-10, Co-42, Co-6) related to anthracnose resistance. Accessions were screened under controlled conditions. For *in vitro* screening three weeks old plants were inoculated with spore suspension of the pathogen *C. lindemuthianum* to check resistance against *C. lindemuthianum*. Disease reactions were rated visually using a scale from 1 to 9.

Four field trials were conducted to test the anthracnose disease incidence. No disease was observed in three field trials. In one trial the disease incidence was very low that was 1.25 (Prabha *et al.*, 2020). Accession GFB-30 has multiple genes for anthracnose resistance with good qualitative and quantitative characters (Table 1).

Table 1. Qualitative and quantitative characters of the French bean accession GFB-30

Accession	Seed Colour	Flower colour	Seed length (mm)	Seed diameter (mm)	Pod length (cm)	Number of seed per pod	Pod colour at physiological maturity	Days to 50 % maturity	100 seed weight (gm)
GFB-30	White with black spot	Purple	8.4	4.2	10.94	7.6	Yellowish green with red spots	62	25.34

Reference

Prabha D, N Chamoli, YK Negi and JS Chauhan (2020) Newly Identified Anthracnose Resistant French Bean (*Phaseolus vulgaris*) Accessions from Garhwal Hills of Uttarakhand. *Int. J. Curr. Microbiol. App. Sci.* **9**(02): 2748-2751. doi: https://doi.org/10.20546/ij cmas.2020.902.31

28. GJG 0922 (IC0635033; INGR20028), a Chickpea (*Cicer arietinum*) Germplasm with Wilt Resistance.

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Chickpea (*Cicer arietinum* L.) is an important pulse crop grown during *rabi* season in tropics and spring in the temperate region of the world. Chickpea is grown on about 10.56 million ha producing 11.37 million tonnes of seed with productivity of 1077 kg/ha in India (Anonymous, 2019). Chickpea attacked by numerous root pathogens, of which the most destructive is *Fusarium oxysporum* f. sp. *ciceri* causing vascular wilt. The disease is soil borne in nature. Chickpea yield is affected by several diseases but wilt caused by *Fusarium oxysporum* f. sp. *ciceri* is a very serious disease and causes losses occurred up to 10 percent in yield (Dubey *et al.*, 2007). This genotype was found to be resistant in wilt sick plot at ICRISAT, Kanpur, Jabalpur, Rahuri and Junagadh during different years (2012-13, 2014-15, 2016-17, and 2018-19) of testing.

The line GJG 0922, was developed at Pulses Research Station, Junagadh Agricultural University, Junagadh using wilt resistant source by pedigree method of selection in a segregating population of a cross (GJG 9920 × FG 703).

Morpho-agronomic characteristics of GJG 0922

Entry	Year	Yield (Kg/ ha)	Maturity days	100 seed wt. (g)
GJG 0922	2011-12	1699	106	29.9
	2012-13	1920	103	23.1
Mean		1809	104	26.5

(Source: AICRP report of Chickpea: 2011-12 and 2012-13)

Associated characters and cultivated practices: GJG 0922 is resistant to Fusarium wilt disease and has semi spreading growth habit. It has a single flower per peduncle. The seeds are brown in colour and angular in shape. Large seed size (26.5 g/100 seeds). It falls in medium maturity group (104 days) and has an average yield 1809 kg/ha.

Recommended cultivation practices: Seed rate: 70 Kg/ ha; Spacing: 45×10 cm; Fertilizer dose: 20:40:00 N:P:K

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29. PMF-1 (IC0635701; INGR20029), a Lentil (*Lens culinaris*) Germplasm with Five Flowers (Penta-Flowering) and Pods Per Peduncle in a Few Flowering Nodes.

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In lentil, with very limited variation, mostly three or occasionally four flowers per peduncle (FPP) bearing habit is commonly observed in the cultivated lentil. However, as reported for various legumes, development of five or more FPP, while maintaining the seed size, looks an attractive option for yield manipulation (Mishra *et al.*, 2020). Penta-flowering was never considered a trait to study, due to unstable expression through generations, environmental influence, and poor conversion to penta-pods. At global level, ICAR-IARI, New Delhi is pioneer for the identification of first stable penta-podded cultivated lentil genotype PMF-1 during *rabi* 2017-18. The flowering expression was again validated at IARI, N. Delhi and ICARDA, Amlaha (Bhopal) in *rabi* 2018-19, and also under partially controlled glasshouse of Phytotron at IARI, New Delhi (2018-19). The PMF-1 was identified from an ICARDA nursery genotype (2011S 56104-5) received from Lebanon which was derived

from a cross 'ILL1005 × ILL7012'. The identified genotype will help in the genetic studies pertaining to the expression of flowers per peduncle in cultivated lentil.

Morpho-agronomic characteristics: PMF-1 is an early maturing genotype, requiring nearly 105-110 days for the seed maturity. Lentil normally bears one to three flowers per peduncle, while PMF-1 recorded sequential appearance of penta-flowering peduncles at multiple flowering nodes. The 9th node was the first node expressing four FPP while expression of five FPP was observed between 12th to 17th nodes. In 2018, the expression of five and six FPP was recorded from 13th to 23rd February; whereas in 2019 this was observed from 25th February to 5th of March when the mean environmental temperature was mostly in the range of 12–18 °C. Thus, besides genetic factors, temperature was also found influencing the MF expression.

Associated characters and cultivation practices: PMF-1 is an early maturing (105-110 days) and bold seeded (100 seed weight 3.1-3.2 g) genotype. The seed-coat is grey coloured while cotyledons are red coloured. The optimum temperature for seed germination is about 22±2oC, while spacing of 30×10 cm is optimum when planted in rows. Due to its erect plant habit, prolific branching and first flowering node not before 9th node, this can be used as a genotype for mechanical harvesting too. Standard cultivation practises can be adopted to raise a healthy crop.

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30. DC 8441-5 & DC 41-5B (IC0632603 & IC0632604; INGR20030), an Ogura Based Cytoplasmic Male Sterile Line of Cauliflower (*Brassica oleracea* var. *botrytis*) in Early Maturity Group (25-30ºC) of Indian Cauliflower. Dwarf Plant Type and Good Combiner for Earliness and Curd Yield.

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Cauliflower (*Brassica oleracea* var. *botrytis* L.; 2n= 2x=18) is an important widely grown vegetable crop in India. The cytoplasmic male sterility system (CMS) introgressed in cauliflower (Sharma *et al.*, 2005) has been found to be stable, easy to maintain and economically viable genetic mechanism compared to that of self incompatibility system. The CMS lines of inter- (early, mid or late) and even intragroup maturity can't be used across the group or even within the group across weekly maturity for hybrid breeding as it leads to genetic drift. The 'DC 8441-5' line is an indigenously developed CMS line of early maturity group of Indian cauliflower. It has refined Ogura male sterile cytoplasm and free from any floral deformities. This CMS line was developed by transferring refined Ogura cytoplasm (male sterile) into nuclear background of an elite inbred line 'DC 41-5' after 10 generations of backcrossing.

Morpho-agronomic characteristics of CMS line 'DC 8441-5': The CMS line 'DC 8441-5' is the second CMS line of early maturity group (October first fortnight) of Indian cauliflower with refined Ogura male sterile cytoplasm (Table 1). It reaches marketable stage in a period of 65 – 75 days after transplanting in North Indian plains. It produces light yellow small to medium size normal flowers with good nectar volume. It bears normal sepals, petals and stigma. In 'DC 8441-5', anthers are shriveled and devoid of pollen mass indicating complete male sterility. Flower opening is proper and have well developed nectaries which enhance honey bees visit. Seed yield of CMS line is 17.82 g/plant in 1:1 ratio (CMS line: fertile maintainer line) which was at par with the fertile maintainer. The CMS line 'DC 8441-5' produces cream white compact and solid curds of medium size (net curd weight = 510.8 g) like its maintainer line 'DC 41-5' (452.5 g). The marketable curd yield of CMS line (24.8 t/ha) is at par with its maintainer line DC-41-5 (22.6 t/ha) (Table 1). It has shown potential for curd yield, earliness, curd compactness in early maturity group of Indian cauliflower (Verma and Kalia, 2011). Hence, it can be useful in commercial hybrid seed production.

DC 41-5: male fertile maintainer line of CMS line 'DC 8441-5': The 'DC 41-5' is a promising genotype of early maturity group of Indian cauliflower. It is suitable for sowing in June first week and transplanting in July second fortnight. It starts curd formation during last week of September which gets ready for harvest in mid of the October month in plains (Delhi condition). Plants are dwarf, spreading type, low spreading type and leaves are dark green. It produces cream white compact and solid curds (Table 1).

Table 1. Important horticultural traits and seed yield of 'DC 8441-5' CMS line and its maintainer

Traits	8441-5 (CMS line)	DC-41-5 (fertile line)
Maturity group	Early	Early
Days to 50% maturity	1st Fortnight of October	1st Fortnight of October
Marketable curd weight (g)	670.6 g	643.4 g
No. of pods/plant	863.0	993.4
Seed yield/plant (g)	17.82	20.50
Curd length (cm)	9.1	9.4
Curd width (cm)	11.8	13.5
Plant height (cm)	41.0	38.1
Plant spread (cm)	46.7	41.4
Gross plant weight (g)	1101.8	1006.0
Net curd weight (g)	510.8	452.5
Marketable curd yield (t/ha)	24.8	22.6

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31. DC 8498 & DC 98-10B (IC0632601 & IC0632602; INGR20031), a Cytoplasmic Male Sterile Line of Cauliflower (*Brassica oleracea* var. *botrytis*) in the Early Maturity Group (25-30°C) of Indian Cauliflower. Carry Ogura Sterile Cytoplasm. Good Combiner for Earliness and Curd Yield.

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Cauliflower (*Brassica oleracea* var. botrytis L.; 2n= 2x=18) is an important Cole crop in India grown almost all the year round in every nook and corner of the country. In early maturity group of Indian cauliflower, the curd initiation and development takes place at a temperature range of 25-30 °C. In order to encash intragroup maturity variability of this heat tolerant group, hybrid breeding is important. For facilitating affordable hybrid seed production, genetic mechanisms, such as self-incompatibility (SI) and cytoplasmic male sterility (CMS) have been exploited Major share of demand of hybrid seeds in India is being met through imports (Sharma *et al.*, 2005) as there is only one SI based hybrid 'Pusa Kartik Sankar' in early group so far from public sector developed indigenously. Since SI system is vulnerable to temperature fluctuations, therefore in the era of climate change chances of occurrence of natural sibs in F1 hybrids get increased forfeiting purpose of hybrid breeding. Alternatively, cytoplasmic male sterility system (CMS) introgressed in cauliflower (Sharma *et al.*, 2005) has been found to have high potential in hybrid breeding. Hence, conversion of elite adapted inbred lines into CMS lines will be instrumental in developing indigenous hybrid seed industry for cauliflower. The CMS line DC 8498-10 is such indigenously developed early maturity group CMS line of Indian cauliflower with refined Ogura male sterile cytoplasm introgressed into nuclear background of an elite inbred line 'DC 98-10' after 10 generations of backcrossing, which is free from any floral deformities.

Morpho-agronomic characteristics of CMS line DC 8498-10: The CMS line DC 8498-10 is the first CMS line with refined Ogura male sterile cytoplasm in Early maturity group (September end –mid November) of Indian cauliflower (Table 1 & Fig.1). It matures in a

period of 60–70 days after transplanting in north Indian plains. It produces light yellow medium size normal flowers with good nectar volume. It bears normal sepals but size of petals is less than its fertile counterpart 'DC 98-10'. It has shrivelled anthers and no pollen mass seen in anthers indicating complete sterility. Good honey bee visit was observed in ' CMS-8498-10'. Seed yield of CMS line is 22.7 g/plant in 1:1 ratio (CMS line: fertile maintainer line) which was at par with the fertile maintainer. Like its maintainer 'DC 98-10', the ' CMS 8498-10' also produced cream white compact and solid narrow elliptic curds of small to medium size (net curd weight = 549.4 g) which is at par with early group. The marketable curd yield of CMS line (25.8 t/ha) is at par with its maintainer line DC-98-10 (23.3 t/ha) (Table 1). The CMS line showed potential in hybrid breeding of early cauliflower (Verma and Kalia, 2011). Hence, it can be used in commercial hybrid seed production.

DC 98-10: male fertile maintainer line of CMS line DC 8498-10: The 'DC-98-10' is a promising genotype of early maturity group of Indian cauliflower. It is suitable for sowing in June first week and transplanting during second fortnight of July under north Indian conditions. It starts curd formation during first week of October and ready to harvest last week of October to first fortnight of November. Plants are medium dwarf, semi-erect, medium in spread and leaves are bluish green. It produces cream white compact and solid curds (Table 1).

Table 1. Important horticultural traits and seed yield of CMS line DC 8498-10 in comparison to the fertile maintainer line DC 98-10

Traits	DC 8498-10	DC 98-10
Maturity group	Early	Early
Days to 50% maturity	September end – October mid	September end – October mid
Gross plant weight (g)	1118.9	1085.3
Marketable curd weight (g)	705.2	607.7
Net curd weight (g)	459.4	453.6
Marketable curd yield (t/ha)	25.8	23.3
Curd length (cm)	9.1	10.2
Curd width (cm)	12.0	11.9
Plant height (cm)	48.6	47.2
No. of pods/plant	883.5	974.2
Seed yield/plant (g)	22.7	24.5

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32. VRRAD-201 (IC625064) & VRRAD-202 (IC625065) KS/BS-37/ (IC0625064 & IC0625065; INGR20032), a Cytoplasmic Male Sterile (CMS) Line Radish (*Raphanus sativus*). Good Combiner and Higher Heterosis for Yield, Root Length and Root Weight.

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Radish (*Raphanus sativus* L.) belonging to Brassicaceae family is a most reliable year-round vegetable crop grown worldwide for fleshy edible roots and soft leaves. It has various category, broadly varying in leaf shape or leaf division incision (lyrate, sinuate, entire), root colour (white, red, purple), root shape (triangular, cylindrical, apically bulbous, elliptic), and vernalization requirement (temperate, tropical). Coloured radishes make salad decorative and nutritious, and good source of polyphenols and anti-oxidative properties (Singh *et al.*, 2017). Globally, the uses of F1 hybrids of many vegetables have increased manifold during last few decades, including India. Heterosis (hybrid vigour) is of direct interest for development and commercialization of F1 hybrids in various vegetable crops which is being facilitated by cytoplasmic male sterility (CMS) and self-incompatibility (SI) in radish. But, SI system in most of the radish genotypes is very weak and unstable and there is always chance to get undesirable number of sibs in hybrid seeds; hence CMS system is mostly preferred.

CMS was first identified in a cultivar of Japanese radish by Ogura (1968) popularly known as Ogura-CMS, and thereafter it has been transferred into various backgrounds of different Brassica vegetable. Although it is the most important salad crop in India because of availability of roots round the year, yet it is unfortunate

that none of the radish CMS lines by Public Sector Institutes is available on public domain in our country till date because of less priority for research in this crop. Keeping in view of the importance and advantage of CMS lines especially in easy maintenance of female parent, harnessing heterotic vigour for economic traits, and cheaper & quality seed production of F1 hybrids; ICAR-IIVR, Varanasi, UP has been developed CMS lines by back cross method. The Ogura- CMS line 'VRRAD-201 or A Line' (IC0625064), First Ogura-CMS line from Public Sector in India, was developed by crossing CMS plants from open population with an elite line 'VRRAD-202 or B Line or Maintainer Line' (IC0625065) which is having better combining ability and higher heterosis for economic traits (Singh *et al.*, 2018). Significant heterotic hybrids for yield, longer roots, earliness, vigour consistency and uniformity have also been reported by many researchers (Kutty and Sirohi 2003, Kochetov and Sinyavina 2019).

VRRAD-201 possesses desirable leaf shape i.e. sinuate type of leaf morphology (leaf division incision), develops root during winter, spring and summer seasons, having white and triangular root, bears whitish-purple flower, and ready to seed harvest in about 4 months after transplanting of stecklings. The quantitative traits of economic importance of CMS line 'VRRAD-201' during winter season of 2016-2019 were observed such as gross plant weight 258.5-275.0 g, root weight 181.2-190.0 g, root length 24.8-26.0 cm, shoot length 35.9-38.4 cm, root diameter 3.3-3.6 cm, number of leaf 9.9-10.7, 40.2-52.4 days to first root harvest, marketable yield 53.9-60.2 t/ha, 34.2-38.1 days to 50% flowering, 381-410 number of pods/plant, 4.2-4.5 number of seeds/pod and 1000 seed weight of 12.8-13.5 g. Moreover, economic parameters of its maintainer 'VRRAD-202' during 2016-19 were realized as 252.1-270.0 g gross plant weight, 171.3-182.5 g root weight, 22.5-24.3 cm root length, 35.1-37.1 cm shoot length, 3.2-3.7 cm root diameter, 10.5-11.1 number of leaf, 41.8-52.9 days to first root harvest, 50.6-59.1 t/ha marketable yield, 30.1-33.5 days to 50% flowering, 360-382 pods/plant, 4.0-4.5 number of seed/pod, and 11.8-12.2 g of 1000 seed weight.

In conclusion, newly developed robust CMS line 'VRRAD-201' would be very effective in harnessing heterotic potential, developing F1 hybrids, and cost-effective commercial hybrid seed production in radish.

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33. BIL-53 (IC0631247; INGR20033), a Pre Breeding Line Watermelon (*Citrullus lanatus* var. *citroides*) Derived from the Cross *C. lanatus* var. *citroides* × Arka Manik Possessing Resistance to WBNV Disease.

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In India, watermelon is a major cucurbit and an important crop cultivated in an area of 82 thousand hectares with a production of 20.38 lakh tonnes (NHB) (http:/www.nhb.gov.in). The productivity levels are constrained by the occurrence of various diseases. Important among them, is a thrips transmitted Watermelon Bud Necrosis disease caused by a Tospovirus (Family: Bunyaviridae). It was first recorded during 1991 infecting watermelon at Indian Institute of Horticultural Research (IIHR) Bangalore, India (Singh and Krishnareddy, 1996) and thereafter it has been characterized as a new tospovirus species belonging to serogroup IV that infects several other cucurbits, such as cucumber, ridge gourd and muskmelon (Jain *et al.*, 1998; Mandal *et al.*, 2003; Jain

et al., 2007; Kumar *et al.*, 2010). The incidence ranges between 39-100% with yield loss of 60-100 % (Krishna Reddy and Singh, 1993). The field symptoms of WBNV in watermelon initially develop as chlorotic mottling, yellow spots or patches, and mild crinkling of leaves. Subsequently, necrosis of buds in the growing tips results in dieback of vines. In the young crop, rapid dieback and wilting of plant happens causing a total yield loss. Since, WBNV is prevalent in major watermelon growing areas in India, there is an immediate need to develop varieties/hybrids possessing resistance to this disease. In this direction, efforts are underway at Indian Institute of Horticultural Research, Bengaluru to develop varieties resistant to WBNV. During 2011-13, we established a natural screening protocol for WBNV and identified *C. lanatus* var. *citroides* (Citron) as a source of resistance. It was crossed to Arka Manik to develop RIL and BIL populations. These were evaluated under natural epiphytotic conditions for WBNV incidence during summer seasons of 2016, 2017 and 2018. Among them, BIL-53 (31% PDI@48DAS, 761 AUDPC and 96.67% survival) was found to be on par with the resistant parent 'Citron' (36.95% PDI@48DAS, 797.54 AUDPC and 83.33% survival) and recorded significantly lower WBNV incidence compared to susceptible parent Arka Manik (59.76% PDI@48DAS, 1278.89 AUDPC and 30.00% survival) and commercial check NS-295 (75.12% PDI@48DAS, 1711.83 AUDPC and 11.90% survival) in terms of PDI, AUDPC and survival over three years of screening. Thus, BIL-53 can be used as a prebred line for breeding resistance to WBNV.

34. VMB-16-10-Non Spiny Brinjal (IC0635040; INGR20034), a Brinjal (*Solanum melongena*) Germplasm with Purple Colour and Green Tinge at Distal End of the Fruit. Non-spiny Nature.

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Brinjal (*Solanum melongena* L.) is an important and widely consumed solanceous vegetable of Indian grown round the year. The spines in the all parts of the plant are a major constraint during picking and highly difficult to harvest of brinjal (VRM-1 Mullukathiri). It is a pure line selection from Elavambadi village of Vellore District. Spines are present in the leaf, stem and calyx of the fruit VRM -1 is high yielding (30-35 t/ha) and most suitable for Northern zone of Tamil Nadu. For developing non spiny brinjal the crossing work was attempted between non spiny (Senur local) × local type spiny (VRM 1) during 2008 to develop non-spiny fruits. The fruit set was ranged from 80-90 percent. Direct and reciprocal crosses (ie. Spiny × non-spiny and Non-spiny × spiny) were attempted to study the inheritance of non-spiny character from spiny brinjal. In both crosses non-spiny character was obtained. Even spiny × non-spiny crosses expressed more number of non-spiny plants. Non spiny types were forwarded to further generation and obtained homozygocity.

Morpho-agronomic characteristics: Non-spiny brinjal is a cross derivative of Spiny × non Spiny brinjal (Senur local type). Spines are absent in the leaf, stem and calyx of the fruit but the quality of the fruit remains same as VRM-1 Spiny Brinjal. Yield is about 40-45t/ha and performs well under wide range of soil with good drainage facility and suitable to cultivate in all three seasons (*Kharif*, *Rabi* and summer) It is of medium duration (140-150 days) and is cluster bearing in nature. Fruits are oval in shape, glossy pink in colour with green tinge in the distal end. Single fruit weigh about 120-150g and the flesh content is more and seed content is less. Suitable for all types of culinary preparations, especially highly suitable for preparations of side dish to biryani. Tolerant to drought conditions and high temperature prevailing during summer months. It is found to be highly resistant to Little leaf incidence and moderately resistant to Tobacco mosaic virus (TMV) and fruit and shootborer.

Associated characters and cultivation practices: Out of the best performing crosses, the cross consecutively performed well over generations for growth, yield

and non-spiny nature. It can be used as donor in the appropriate breeding programme for developing non spiny brinjal types with retaining spiny brinjal taste in terms of quality.

35. Kashi Kale-1 (VRKALE-1 or IC0632940) (IC0632940; INGR20035), a tropical type Collard Green (*Brassica oleracea* var. *acephala*) Germplasm that Bolts, Flowers and Sets Seeds in Spring Season at Varanasi, Uttar Pradesh. No Vernalization Requirement to Stimulate/Induce Bolting and Flowering. Fast Growing and High Leaf Yield Potential i.e. 45-50 t/ha.

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Kale (*Brassica oleracea* L. var. *virdis* L.; formerly *B. oleracea* L. var. *acephala* DC.) is typically a temperate cole crop, classified as a biennial vegetable because of vernalization requirement, grown for its soft and tender leaves, and named as Gobhi Sag in Hindi (Singh *et al.*, 2017). Smooth leafed kale, popularly known as Karam Sag, is commonly grown by amateur kitchen gardeners of Kashmir and Himachal Pradesh. Kale is one of the most nutritious vegetables containing high levels of vitamin A, omega-3 fatty acids, lutein & zeaxanthin, vitamin C, and is a good source of vitamin B complex and minerals. Kale has a higher bio-availability of Ca than milk; and lower content of fat and oxalic acid. Like all Cole crops, except tropical cauliflower, kale requires vernalization (5-10 °C for 30-65 days) to stimulate/ induce bolting (Verma and Sharma, 2000; Myers 2003). In contrast to low temperature requirement, ICAR-IIVR, Varanasi, UP has developed an unique genotype named as Kashi Kale-1 (VRKALE-1 or IC 0632940) which is tropical type–first of its kind in the world that bolts, flowers and sets seeds during spring season of Varanasi, UP having 11-24 °C temperature, 54-91% RH and 5.5 h day light during January-February i.e. 60 days before flowering. Nevertheless, two national check varieties, namely Siberian Kale and Kanyari Local did not flower during 2013-14 and 2014-15. However, seeds of Kashi Kale-1 could be easily produced in non-traditional areas i.e. sub-tropical conditions.

The uniqueness of this genotype 'Kashi Kale-1' could explicitly be classified as tropical annual kale. It is very easy to grow, sprouts quickly, grows fast and produces smooth leaves profoundly. The fresh, soft, tender and crispy leaves are cooked to make saag and soups. Kashi Kale-1 is ready for first leaf picking in 24-27 days after transplanting. The leaves are glossy green, smooth, petiolate, and have profuse axillary buds, and its leaf yield potential is very high i.e. 45-50 t/ha. Newly identified novel genotype 'Kashi Kale-1' initiates flowering in mid-February i.e. 130-135 days after transplanting and continue for next 30-40 days. The inflorescence is racemose type, and flowers borne on the main stem and its branches with long pedicel of 2.91 cm. Flowers are typically cruciferous, having 4 sepals (light green, 0.92 cm long), 4 petals (bright yellow, 1.55×0.65 cm size), 6 stamens (0.98 & 0.65 cm), 1.30 cm long style and 2 carpels along with superior ovary, septum and 2 rows of campylotropous ovules. Pod maturity starts from 3rd week of April and ready to harvest in next 12-15 days depending on the climatic conditions. Seeds are small, globular, smooth and dark brown in colour, and 1000 seed weight is 2.45 g. Like tropical of Indian cauliflower which evolved in India and being grown commercially in tropical and subtropical conditions; in future, it is expected that tropical kale will certainly play a pivotal role in expanding the adoption, popularity and genetic base of kale.

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36. RS-11 (IC0523059) (IC0523059; INGR20036), a Watermelon (*Citrullus lanatus*) Germplasm with Resistance to *Fusarium oxysporum* f. sp. *niveum* race 1 and race 2 Performed Good as a Rootstock

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Fruit rind colour: medium green with dark green mosaic, indistinct stripes. Flesh colour: reddish pink. Seed colour: brown with dark brown pitting. Resistant to *Fusarium oxysporum* f. sp. *niveum* race 1 [recorded a mean survival of 82.14% at 28 days' post-inoculation with 5 ml spore suspension (@ 1×105 conidia per ml)] and race 2 [recorded a mean survival of 79.76% at 28 days' post-inoculation with 5 ml spore suspension (@ 1×105 conidia per ml)]. Root fresh weight 2.73 gm, root dry weight 432.50 gm, root depth 48 cm, hypocotyl length 9.08 cm, hypocotyl diameter 4.25 mm, number of secondary roots 4.75. Vine length of the commercial scion when RS-11 used as rootstock is 383.4 cm (33.06% increase) as compared to the non-grafted control (288.15 cm). Yield per plant of commercial scion when RS-11 used as a rootstock is 6.71 kg (89.54% increase) as compared to non-grafted control (3.54 kg).

37. IC096496 (IC096496; INGR20037), an Early Flowering Linseed (*Linum usitatissimum*) Germplasm

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Linseed or flaxseed (*Linum usitatissimum* L.) is multipurpose crop grown mainly for seed oil and stem fiber. Linseed is gaining popularity over the years owing to high content of health promoting compounds such as high lignan and omega-3 fatty acid. In India, linseed is grown as Rabi crop mainly in rain-fed soils, with limited input and in utera cultivation by resource poor farmers. Linseed being a long day plant requires longer day length for initiation of flowering which often delays the maturity time. In this context, early flowering trait is important in linseed as in other long day plants to facilitate early maturity. Early flowering is also a desirable trait to escape linseed bud fly, a major insect pest of linseed in central India causing losses up to 90%. In this perspective, germplasm accession IC0096496 has been identified for early flowering. In IC0096496, 50% flowering and completion (95% flowering) occurred at 58.6 and 64.2 days, respectively, which is significantly earlier than the early maturing check variety RLC76 (Table 1). This accession also possesses additional agronomically important traits such short height (<50 cm) (desirable for seed type linseed varieties) and higher thousand seed weight (7.9 g) compared to RLC76. Yield per plant was 5.5 g and seed oil content was found to be 39.6% for IC0096496. This accession has bushy growth habit, blue colored tubular flowers with twisted aestivation. The capsules were non-dehiscent with lustrous brown seeds.

Table 1. Flowering time data of linseed accession IC0096496 over five years

Year	Location	Days to 50% flowering		Days to 95% flowering	
		IC0096496	RLC76 (Check)	IC0096496	RLC76 (Check)
2014-15	NBPGR, New Delhi	58.0	77.2	66.0	96.7
2015-16	NBPGR, New Delhi	61.0	78.3	68.0	100.5
2016-17	NBPGR, New Delhi	60.0	83.7	65.0	94.0
2017-18	NBPGR, New Delhi	62.0	85.0	66.0	90.7
2018-19	NBPGR, RS- Akola,	52.0	67.0	56.0	73.0
Mean		58.6**	78.2	64.2**	90.9

** Statistical significance according to t-test (**P < 0.01)

38. DRMRTJ 2016 (IC0635042; INGR20038), an Indian mustard (*Brassica juncea*) Germplasm for Tetralocular Siliquae. Long Main Shoot (119.67 cm). High Siliqua Density (1.09).

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Indian mustard (*Brassica juncea* L.) is an important oilseed crop of India. In spite, impressive productivity gains; there is compelling need to further increase the productivity of the crop to meet the growing needs. This can be achieved through creation of novel genetic variability and effective utilization of germplasm resources. Indian mustard generally has bilocular siliquae, composed of two carpels with a partition. Therefore, it is highly desirable to have germplasm lines with tetralocular siliquae for enriching the present gene pool.

The genotype DRMRTJ 2016 having tetra-locular siliquae (composed of four carpels) was derived through interspecific hybridization between *B. juncea* (NRCDR 2) and *B. napus* (NRCGS-1) at ICAR-DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising for long main shoot and high siliqua density. DRMRTJ 2016 was tested for successive three years (ICAR-DRMR Annual Report, 2017-19) at ICAR-DRMR, Bharatpur. Pooled summary over the years indicates that proposed genotype DRMRTJ 2016 has long main shoot (119.6 cm), more number of siliquae on main shoot (130.4) and high siliqua density (1.09) along with more number of seeds / siliqua (22.3) compared to tetralocular check Geeta (Table 1). Tetralocular siliquae is a rare trait in Indian mustard which we are lacking in germplasm repository. Hence, genotypes with this unique trait will be a very good addition to existing gene pool to understand the genetics of the trait in order to increase more number of seeds per siliquae as this will further act as sink for increasing number of seeds per siliquae. Furthermore, the seed yield is a complex trait depends on various component traits like no. of siliquae/plant, siliquae on main shoot and siliquae density. Since, the proposed genetic stock is having long main shoot and high siliqua density over check. Therefore, this genotype with a combination of useful traits (tetralocular siliquae, long main shoot and high siliquae density) can be used as a donor in Indian mustard yield improvement programmes.

Table 1. Mean performance of proposed genetic stock DRMRTJ 2016 and check for different agro-morphological traits during 2016-17 to 2018-19.

Characters	Mean	
	DRMRTJ 2016	Geeta
Main shoot length (cm)	119.67	83.00
Siliqua density	1.09	0.89
Siliquae on main shoot	130.40	73.60
Plant height (cm)	257.93	216.40
Primary branches	13.07	10.47
Siliqua length (cm)	4.28	3.89
Seeds / siliqua	22.37	18.70
1000-Seed weight (g)	5.37	5.16
Oil content (%)	38.92	39.44
Seed yield/plant (g)	31.93	24.13
Days to maturity	149.67	147.33

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Annual Report (2017) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.11-12.

Annual Report (2018) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.11.

Annual Report (2019) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.12.

39. DRMR-WFYSM 15 (IC0635041; INGR20039), an Indian Mustard (*Brassica juncea*) Germplasm for White Flower. Yellow Seed Coat Colour. Appressed Siliqua Orientation.

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Indian mustard (*B. juncea* L.) is an important oilseed crop of India, contributes nearly 1/3rd of the total edible oil pool of the country. There is limited genetic variation especially for flower colour and seed coat colour in B. juncea. It generally has yellow flower and brown seed colour. Therefore, development of genotypes with new variability for these specific traits will be highly useful in breeding programmes for crop improvement and genetic studies. Thus, the genotype (DRMR-WFYSM 15) with a combination of three important traits viz., white flower, yellow seed coat colour and appressed siliqua orientation has been developed at ICAR-DRMR, Bharatpur. The proposed genotype DRMR-WFYSM 15 was derived through physical mutagenesis of Indian mustard cultivar Kranti by irradiation (at BARC, Mumbai) with gamma rays (100kr). Genotype DRMR-WFYSM 15 was tested at ICAR-DRMR for three successive years during 2016-17 to 2018-19 (ICAR-DRMR Annual Report, 2017-19). The pooled data over the years presented in Table 1. The genotype matures in 124 days and has average seed yield/plant is 21.3g, 1000 seed weight 4.28g, oil content 42.28%, number of seeds per siliqua 16.02 and plant height 175.5 cm.

Maintenance of genetic purity of varieties in Indian mustard is a problem due to often cross-pollinated nature, insect pollination mainly due to honeybee and large number of off-types. The white flower trait when transferred in a high yielding variety than it can be used as a visual marker during seed production programme to rouge out the off-types. Since, there is limited genetic variability for flower colour and seed coat colour in *B. juncea*, the proposed genetic stock DRMR-WFYSM 15 will add a new germplasm source in the repository for these traits. This genotype will be highly useful in breeding programmes and genetic studies since three very specific traits are present in a single genetic background. Apart from this, it has high oil content (42.28%) and matures early in 124 days.

Table 1. Mean performance of proposed genetic stock DRMR-WFYSM 15 for different agro-morphological traits during 2016-17 to 2018-19

Character	Mean of three years
Plant height (cm)	175.53
Primary branches (no.)	6.07
Main shoot length (cm)	73.83
Siliquae on main shoot (no.)	45.23
Siliqua length (cm)	4.50
Seeds / siliqua	16.02
1000-seed weight (g)	4.28
Oil content (%)	42.28
Seed yield / plant (g)	21.32
Days to maturity	124.00
Petal colour	White
Seed colour	Yellow
Siliqua orientation	Appressed

References

Annual Report (2017) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.11.

Annual Report (2018) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.40-41.

Annual Report (2019) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.12.

40. DRMR-C-16-6 (IC0635043; INGR20040), an Extra Dwarf (85 cm height) African Mustard (*Brassica carinata*) Germplasm with High Oil Content (41.3%) and Early Maturity (127 days).

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Brassica carinata A. Braun (BBCC, 2n = 4x = 34), Ethiopian mustard or Karan Rai, is resistant to a wide range of diseases like Altenaria blight, white rust, stem rot and pests and is tolerant to many abiotic stresses particularly moisture stress. Besides having several agronomically important traits such as non-dehiscent siliquae and a much more developed and aggressive root system it could not find favour with farmers largely due to tall plant type, long duration, small seed size and low oil content as compared to popularly grown species i.e. Indian mustard (*B. juncea*). Hence, the high yielding genotypes with dwarf stature, short duration, high content and bold seed size are highly needed in this crop. Therefore, Inter-specific hybridization was initiated at ICAR-DRMR in 2010-11 for widening of gene pool in Brassicas to tap genetic diversity and develop desirable lines of lines of Karan rai. Indian mustard variety NRCDR-2 was crossed with B. carinata genotype NRCKR 304. A desirable segregant with an extra dwarf (< 100 cm) plant type, long siliquae length, high test weight, early maturing (<130 days) and high oil content (>41%) was selected from segregating generation and was further advanced and maintained through progeny selection till stabilization of traits of interest (Kumar *et al.*, 2019). Further this line was evaluated for important traits in four environments (ICAR-DRMR Annual Report, 2019) along with parents and popular cultivar of Karan rai (Kiran) (Table 1).The salient features of DRMR-C-16-6 are plant height (85 cm), maturity (127.8 days) and oil content (41.3%) compared to NRCKR 304 (159 cm, 134.5 days, 40.5%), Kiran (234 cm, 162.7 days, 39.0%) and NRCDR-2 (206 cm, 143.5 days, 41.4%).This line can be utilized as a donor in breeding programmes for development of early maturing dwarf genotypes of Karan rai and it can be used in molecular breeding programme for development of mapping population for plant height.

Table 1. Average performance of DRMR-C-16-6, over four environments during 2016-17 to 2018-19.

Traits	Pooled (4 Environment)			
	DRMR-C-16-6	NRCKR304	Kiran	NRCDR-2
Days to maturity	127.8	134.5	162.7	143.5
Plant height	84.8	158.8	234.0	206.0
Primary branches	9.4	5.5	9.2	6.5
Secondary branches	21.9	13.9	21.3	15.5
Main shoot length	60.0	88.9	38.3	89.1
Siliqua length	3.7	3.8	3.4	5.3
Seeds per siliqua	15.5	16.3	12.7	16.1
1000 seed weight (g)	4.7	5.2	3.2	5.3
Oil content (%)	41.3	40.5	39.00	41.4

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Annual Report (2019) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur-321303 (Rajasthan) p.6.

Kumar A, HS Meena, B Ram, Priyamedha, VV Singh and PK Rai (2019) Development of dwarf B. carinata genotype employing inter-specific hybridization between *B. juncea* and *B. carinata* and cyto-morphological studies for patterns of variation. *Journal of Oilseed Brassica* **10(2)**: 149-155.

41. RDV 29 (IC0589658) (IC589658; INGR20041), an Indian Mustard (*Brassica juncea*) Germplasm with Resistance to Powdery Mildew Disease

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Among various biotic stresses, particularly the fungal diseases, powdery mildew of Indian mustard, caused by *Erysiphe cruciferarum* Opiz. Ex. Junell., has been reported to cause significant yield losses, sporadically, depending on the prevailing agro-ecological conditions. This disease was once considered to be of minor importance, but in the recent years, it became widespread throughout the mustard growing regions of India particularly in the states like Uttar Pradesh, Rajasthan, Jammu & Kashmir, Haryana and Gujarat and in other non-traditional mustard growing areas such as Maharashtra, Karnataka and Andhra Pradesh. All the Indian mustard cultivars currently being cultivated in different states of India are highly susceptible to this disease. This fungus can infect any above-ground plant parts and can cause heavy yield losses by reducing plant growth and consequently, the quantity and quality of seeds (Kumar and Saharan, 2002; Meena *et al.*, 2014). In India, earlier attempts to identify resistant source to powdery mildew of Indian mustard were failed as all the *B. juncea* genotypes evaluated were found to be highly susceptible to this important pathogen and whatever the resistant sources reported belonged to other related species and allied genera with no reports available about its resistance in *B. juncea*, which is an important oil yielding species in Indian context. Keeping in view the economic importance of powdery mildew disease in Indian mustard, research initiatives have begun at ICAR-Indian Agricultural Research Institute, Regional Station, Wellington, which is a hot spot for this disease inter alia many other crop diseases.

With an aim to identify resistant source, 1,020 Indian mustard accessions were evaluated against *E. cruciferarum* PMN isolate, at Wellington, The Nilgiris, Tamil Nadu, India under natural hot spot conditions. The study identified one accession (RDV 29) with complete resistance against *E. cruciferarum* PMN isolate for the first time, which was consistent in five independent evaluations (Table 1). Genetic analysis of F1, F2 and backcross populations obtained from the cross RSEJ 775 (highly susceptible) × RDV 29 (highly resistant) for two season revealed that the resistance is governed by two genes with semi-dominant and gene dosage effect (Nanjundan *et al.*, 2020). The outcome of this study viz. newly identified powdery mildew-resistant Indian mustard accession (RDV 29) and information

Table 1. Reaction of Indian mustard accession RDV 29 and four check varieties to *Erysiphe cruciferarum* during five independent evaluations at ICAR-IARI, Regional Station, Wellington.

Entry/Checks tested	Disease reaction at 80 DAS*				
	Evaluation I	Evaluation II	Evaluation III	Evaluation IV	Evaluation V
	(*Kharif* 2016)		(*Rabi* 2016-17)		(*Rabi* 2017-18)
	(DOS:10-06-2016)	(DOS:11-11-2016)	(DOS:07-12-2016)	(DOS:01-02-2017)	(DOS:18-12-2017)
RDV 29	Highly resistant	HR	HR	HR	HR
KLM 4	Partially resistant	PR	PR	PR	PR
RSEJ 775	Highly susceptible	HS	HS	HS	HS
RH 0704	Highly susceptible	HS	HS	HS	HS
NRCDR 02 (Check 1)	Moderately susceptible	MS	MS	MS	MS
NRCDR 601 (Check 2)	Moderately susceptible	MS	MS	MS	MS
GIRIRAJ (Check 3)	Moderately susceptible	MS	MS	MS	MS
ROHINI (Check 4)	Moderately susceptible	MS	MS	MS	MS

Note: *Disease scoring as per Nanjundan *et al.*, (2020). Plant Pathology Journal, Vol. 36(2), Page 115.

on inheritance of resistance will provide the base for development of powdery mildew-resistant cultivars of Indian mustard.

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42. Palm No. 47 (IC0635046; INGR20042), an Oil Palm (*Elaeis guineensis*) Germplasm for Medium Height Increment.

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There is no source of high yielding and short stature mother palms in India. Productivity and harvesting are the two major gaps in oil palm production in India. After eight years of palm age it is very difficult to harvest bunches manually by climbing palm due to its tall in stature. The present identified palm has a highest yield (221.30 kg) and medium height increment (33.00 cm) in comparison to other progenies by taking moving average (Yield: 103.77 kg, Height increment: 31.81 cm) of the same cross.

The utilization of high-yielding genetic base as a planting material has been proven to be the most efficient and sustainable means of increasing the yield output of existing oil palm genetic base (Arolu *et al.*, 2017). This genetic stock recorded highest yield and short stature compared with other progenies. However, it can be used as a mother parent for the development of high yielding and dwarf oil palm hybrids.

The uniqueness and novelty of this accession of *Elaeis guineensis* Jacq. is confirmed on the basis of its yielding behavior and dwarf stature which are a desirable traits to the farmers. Fruit form of this palm is also confirmed through molecular markers. This accession can further be used for oil palm improvement programmes. The seeds of the accession (Palm number: 47) obtained from the institute exotic germplasm block in research farm of ICAR-Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh.

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Arolu IW, MY Rafii, MM Hanafi, Z Sulaiman, HA Rahim, M Marjuni, MD Amiruddin, MIZ Abidin and R Nookiah (2017) Breeding of high yielding and dwarf oil palm planting materials using *Deli dura* × *Nigerian pisifera* population. *Euphytica*, 213:154.

43. Palm No. 33 (IC0635047; INGR20043), an Oil Palm (*Elaeis guineensis*) Germplasm with More Number of Bunches and Slow Vertical Growth

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Till date there is no source of high yielding and dwarf mother palms in India. The breeding efforts to improve the varieties with high fresh fruit bunches (FFB) yields is major concern to increase palm oil productivity. Reduced height increment, superior oil quality as well as more number of bunches are also important considerations. Productivity and harvesting are the two major gaps in oil palm production in India. After eight years of palm age it is very difficult to harvest bunches manually by climbing palm due to its tall in stature. The present

identified palm has a highest yield (181.70 kg), more number of bunches (20.50) and less height increment (18 cm) in comparison to other progenies by taking moving average (Yield: 98.13 kg, No. of bunches: 13.38, Height increment: 32.48 cm) of the same cross. The mesocarp content of this accession also more (72.20%) when compared with the standard duras.

The utilization of high-yielding genetic base as a planting material has been proven to be the most efficient and sustainable means of increasing the yield output of existing oil palm genetic base (Arolu *et al.*, 2017). This genetic stock recorded highest yield and short stature compared with other progenies. However, it can be used as a mother parent for the development of high yielding and dwarf oil palm hybrids.

The uniqueness and novelty of this accession of *Elaeis guineensis* Jacq. is confirmed on the basis of its yielding behavior and dwarf stature which are a desirable trait to the farmers. Fruit form of this palm is also confirmed through molecular markers. This accession can further be used for oil palm improvement programmes. The seeds of the accession (Palm number: 33) obtained from the institute exotic germplasm block in research farm of ICAR-Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh.

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44. Palm No.72 (IC0635048; INGR20044), a Dura Type Oil Palm (*Elaeis guineensis*) Germplasm with Medium Height Increment.

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Till date there is no source of more number of bunches and medium height dura mother palms in India. Productivity and harvesting are the two major gaps in oil palm production in India. After eight years of palm age it is very difficult to harvest bunches manually by climbing palm due to its tall in stature. The present identified palm having more number of bunches (22.00) with medium height increment (30 cm) in comparison to other progenies by taking moving average (No. of bunches: 15.40, Height increment: 31.56 cm) of the same cross. The details morphological traits are given in Table 1.

The utilization of high-yielding genetic base as a planting material has been proven to be the most efficient and sustainable means of increasing the yield output of existing oil palm genetic base (Arolu *et al.,* 2017). This genetic stock recorded highest yield and short stature compared with other progenies. However, it can be used as a mother parent for the development of high yielding and dwarf oil palm hybrids.

The uniqueness and novelty of this accession of *Elaeis guineensis* Jacq. is confirmed on the basis of its yielding behavior and dwarf stature which are a desirable traits to the farmers. This accession can further be used for oil palm improvement programmes. The seeds of the accession (Palm number: 72) obtained from the institute exotic germplasm block in research farm of ICAR-Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh.

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45. Palm No. 542 (IC635049; INGR20045), a Sterile Dura Type Oil Palm (*Elaeis guineensis*) Germplasm with Virescence.

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The sterility in dura is may be due to crossing over and recombination of genes. The problem of gene flow is particularly important to the genetic improvement of perennial crop like oil palm. By using female sterile lines there is a possibility to create sterile hybrid plants to control gene flow. The ovule of female sterile plants is aborted but the phenotype of most of the plant is otherwise normal. The inflorescence and flowers of sterile plants are normal and had a high pollen fertility.

Development of superior variety by accumulation of beneficial alleles from vast plant genetic resources is a major challenge. Fertility in the oil palm is shown to be controlled by a single gene which is linked to the gene controlling fruit form. The sterile dura's are very rare and can be used as a male parent in selected crosses.

Sterile female plants sometimes can be used to identify regulatory genes that influence ovule and female gametophyte development. These regulatory genes are involved in nucellar and integument cell development (Balasubramanian and Schneitz, 2002).

The uniqueness and novelty of this genetic stock of *Elaeis guineensis* Jacq. is confirmed on the basis of its fruit form and its 100% sterility as well through molecular markers.

This accession can further be used for oil palm improvement programmes. This accession (Palm number: 542) obtained from the institute field gene bank in research farm of ICAR-Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh.

Research on female sterility in plants can have several applications. The selection against sterility for seed production improvement could be made easier. Female-sterile plants could be used as pollen parents for hybrid seed production.

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John R Pannell and Marie Voillemot (2015) Plant Mating Systems: Female Sterility in the Driver's Seat. *Current Biology* **25**: 490–514.

46. Palm No. 482 (IC635050; INGR20046), a Sterile Dura Type Oil Palm (*Elaeis guineensis*) Germplasm with Broad Leaf Sheath.

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Wild traits are the reservoir of many useful genes/ alleles which can be used to survive climate extremes. Wild traits have very high level of resistance/tolerance to various stresses. Due to climate change, several areas are now becoming unsuitable for cultivation of traditional crops. To cope with this situation, there is a need to breed new crop cultivars with a broad genetic base capable of withstanding frequent climatic fluctuations and wider adaptability due to adapted gene complex.

The sterility in dura is may be due to crossing over and recombination of genes. The problem of gene flow is particularly important to the genetic improvement of perennial crop like oil palm. By using female sterile lines there is a possibility to create sterile hybrid plants to control gene flow. The ovule of female sterile plants is aborted but the phenotype of most of the plant is otherwise normal. The inflorescence and flowers of sterile plants are normal and had a high pollen fertility.

Fertility in the oil palm is shown to be controlled by a single gene which is linked to the gene controlling fruit form. The sterile dura's are very rare and can be used as a male parent in selected crosses. Sterile female plants sometimes can be used to identify regulatory genes that influence ovule and female gametophyte development. These regulatory genes are involved in nucellar and integument cell development, 2002).

The uniqueness and novelty of this genetic stock of *Elaeis guineensis* Jacq. is confirmed on the basis of its fruit form, broad leaf sheath and its 100 % sterility. This accession can further be used for oil palm improvement programmes. This accession (Palm number: 482) obtained from the institute field gene bank in research farm of ICAR-Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh. Research on female sterility in plants can have several applications. The selection against sterility for seed production improvement could be made easier (Rosellini *et al.*, 1998). Female-sterile plants could be used as pollen parents for hybrid seed production.

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John R Pannell and Marie Voillemot (2015) Plant Mating Systems: Female Sterility in the Driver's Seat. *Current Biology* **25**: 490–514.

47. IC0610027-20 (IC0610027; INGR20047), a Pisifera Oil Palm (*Elaeis guineensis*) Germplasm with 98.5% Sterility. Nigrescence Fruit Form.

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Oil palm is very important crop for fulfils the edible oil requirement of our country. As compared to other annual oil yielding crop this is giving more oil yield (5-6 t/ha). Oil palm breeding programme mainly depending male (sterile pisifera) and female parent (fertile dura) for hybrid seed production. Commercial material for farmer cultivation is tenera, this can be obtained by crossing of fertile Dura and sterile pisifera. Pisifera population is rare and in that also getting sterile pisifera is very scarce. Male parent (Sterile pisifera) should be having 100% sterility. In breeding programme dwarf dura material as female parent is already available but we are not having sterile pisifera. Pisifera palms available are usually with more trunk girth, high vegetative growth and less fruit set or no fruit set. But this palm will be having more sterility (98.55%). So this pisifera with high sterility needed in breeding programme as a male parent and this pollen can be used for hybrid seed production of oil palm.

Trait description (Accession: IC0610027-20)

Traits	2016-17	2017-18	2018-19	Average
Number of bunches per year	8	10	7	8.33
FFB yield (kg/palm/year)	117.21	147.30	106.65	123.72
Bunch weight (kg)	18.25	14.37	10.64	15.38
Total number of fruits	1200	1405	1035	1275.66
Number of sterile fruits	1181	1399	1011	860
Sterility %	98.41	99.57	97.68	98.55

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48. IC0610024-47 (IC0610024; INGR20048), a Parthenocarpic Pisifera Oil Palm (*Elaeis guineensis*) with Good Fruit Set (68.62%).

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Oil palm (*Elaeis guineensis* Jacq.) is monocious crop, male and female inflorescence will be bearing separately on the same palm. Oil palm is cross pollinated crop and it is mainly pollinated by weevil (*Elaeidobius kamerunicus*) and if pollinator is not available, poor fruit set or no fruit set can be happened. Parthenocarpy is the natural or artificially induced production of fruit without fertilization of ovules, which makes the fruit seedless. In oil palm parthenocarpy is not common. In oil palm induced parthenocarpy was done and it was given poor fruit set. Identified palm is natural parthenocarpic and fruit set is good and this palm can be directly used in breeding programme and If this palm performs better in yield and oil content, directly this palm can be multiplied clonally used for commercial plantation. So this will reduce the problem of pollination. Where ever pollinator is a problem or pollinator not able survive in that areas this material will be useful. Cultivated variety of oil palm is Tenera and this is having high mesocarp, less shell and kernel. Our main objective is to get a more oil from the mesocarp for edible purpose and this will be obtained from this fruit and here no kernel and shell. Here we are having an advantage of whole fruit can be processed for oil extraction and will be getting more oil to bunch ratio as compared to normal fruits and Parthenocarpic pisifera palms could be use in molecular breeding programme aim to develop linkage mapping and further evaluation.

Trait description

Traits	2016-17	2017-18	2018-19	Average (2016-19)
Number of bunches per year	14	26	8	16
FFB yield (kg/palm/ year)	111.66	220.23	77.19	136.36
Bunch weight (kg)	9	10.42	7.22	8.88
Total number of fruits	632	788	805	741.66
Number of Parthenocarpic fruits	347	578	625	516.66
Sterile fruits	285	210	180	225
Parthenocarpic fruit set %	54.90	73.35	77.63	68.62

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49. NRCGCS 636 (HOS-89) (IC635044; INGR20049), a Groundnut (*Arachis hypogaea*) Germplasm with High Oil Content (56%).

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Groundnut (*Arachis hypogaea* L.) is an improtant oilseed crop worldwide. About 47.09 million tonnes of peanut are produced from 27.94 million hectares worldwide (FAOSTAT 2017). In general, oil content in groundnut varied from 48% to 53%. It is estimated that 1% increase in the seed oil content increases the groundnut processer's benefit by 7% (Liao, 2003), indicating greater impact of oil content trait for farmers and traders. Hence, breeding groundnut for enhanced oil content is a major objective worldwide.

A high oil content (53%) breeding line ICGV 06100 was crossed with Sunoleic 95R in 2011 and 104

advanced lines were developed using SSD method. Of which four lines were found with very high oil content (~55%). Oil content of these lines was confirmed over five seasons. Oil content was estimated using both Soxhlet method and Gas Chromatography. Of which a very high oil content breeding line, NRCGCS-636 was characterized for morpho-physiological and yield traits.

NRCGCS-636 is a Spanish bunch, very high oil content groundnut germplasm developed at ICAR-Directorate of Groundnut Research, Junagadh, Gujarat. It was bred from a cross between ICGV 06100 × Sunoleic95R using pedigree selections. It has moderate plant height, alternate branching and small dark green ovate leaves. It bears compound inflorescence with yellow coloured standard petal and takes about 24 days after sowing for 50% flowering in kharif season. It yielded 154 g of pod/m2 with ~35% Harvest Index, ~68% shelling out-turn and ~38 g of 100-kernel weight. Kernels of NRCGCS-636 are monochrome with rose colour testa. NRCGCS-636 is tolerant to Rust (scored 1 in 1-9 scale) and susceptible to Late leaf spot disease (scored 7 in 1-9 scale). Oil content of NRCGCS-636 over five years varied from 55% to 58% with a mean of 57%. NRCGCS-636 matures in 115 days after sowing during kharif season. NRCGCS-636 can be grown directly as very high oil content genotype or used as donor in future breeding program.

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50. NRCGCS-635 (HOS-30) (IC635045; INGR20050), a Groundnut (*Arachis hypogaea*) Germplasm with High Oil (56%).

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Groundnut (*Arachis hypogaea* L.) is an improtant oilseed crop worldwide. About 47.09 million tonnes of peanut are produced from 27.94 million hectares worldwide (FAOSTAT 2017). In general, oil content in groundnut varied from 48% to 53%. It is estimated that 1% increase in the seed oil content increases the groundnut processer's benefit by 7% (Liao, 2003), indicating greater impact of oil content trait for farmers and traders. Hence, breeding groundnut for enhanced oil content is a major objective worldwide.

A high oil content (53%) breeding line ICGV 06100 was crossed with Sunoleic95R in 2011 and 104 advanced lines were developed using SSD method. Of which four lines were found with very high oil content (~55%). Oil content of these lines was confirmed over five seasons. Oil content was estimated using both Soxhlet method and Gas Chromatography. Of which a very high oil content breeding line, NRCGCS-635 was characterized for morpho-physiological and yield traits.

NRCGCS-635 is a Spanish bunch, very high oil content groundnut germplasm developed at ICAR-Directorate of Groundnut Research, Junagadh, Gujarat. It was bred from a cross between ICGV 06100 × Sunoleic95R using pedigree selections. It has moderate plant height, alternate branching and small dark green ovate leaves. It bears compound inflorescence with yellow coloured standard petal and takes about 25 days after sowing for 50% flowering in kharif season.

It yielded 150 g of pod/m^2 with ~36% Harvest Index, ~67% shelling out-turn and ~40 g of 100-kernel weight. Kernels of NRCGCS-635 are monochrome with rose colour testa. NRCGCS-635 is tolerant to Rust (scored 1 in 1-9 scale) and susceptible to Late leaf spot disease (scored 7 in 1-9 scale). Oil content of NRCGCS-635 over five years varied from 55% to 58% with a mean of 56%. NRCGCS-635 matures in 120 days after sowing during kharif season. NRCGCS-635 can be grown directly as very high oil content genotype or used as donor in future breeding program.

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51. ACC. No. 52 (IC632088; INGR20051), a Cumin (*Cuminum cyminum*) Germplasm with White Flower and Compact Plant Type.

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Cumin with white flower is unique character, generally all cultivated, released varieties and genetic stock are having pink flowers. Seed Spices Research Station, S.D. Agricultural University, Jagudan, Gujarat has explored cumin with white flower. Cumin with pink flower is having anthocynanin pigmentation in their flower.

52. 52. Acc. No. 53 (IC632089; INGR20052), a Cumin (*Cuminum cyminum*) Germplasm with Hairy Seed and Spreading Plant Type

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Hairiness on seeds of cumin is rare occurrence; moreover, it is heritable character. Hairy cumin is maintained at Seed Spices Research Station, S.D. Agricultural University, Jagudan, Gujarat. In the past, hairy cumin was considered as a weed but after continuous selection now it is germplasm. To study various agronomical advantages for commercial cumin cultivation, this was identified and maintained.

According to morphological description, hairiness found on seeds till maturity, and after harvesting it will disappear which does not affect quality of cumin seed.

53. Jor Lab L-11 (IC635431; INGR20053), a Lemon Grass (*Cymbopogan flexuosus*) Germplasm Rich in Methyl Isoeugenol (48%) and Myrcene (39%) in Essential Oil.

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Cymbopogon flexuosus L of the family Poaceae is a highly valued grass known throughout the world for its aromatic properties. It belongs to the family Poaceae and consists of 140 species, of which 45 species reported from India and tropical Asia (Lal *et al.*, 2016). The essential oil from this species is widely used in flavours, fragrances, perfumery, soaps and detergents owing to its lemon like odour (Dutta *et al.*, 2017, Ganjewala 2009). The compounds present in C. flexuosus essential oil viz- citral, geraniol, geranyl acetate, methyl eugenol, citronellol, beta-myrcene, methyl iso-eugenol, limonene, piperitone, citronellal, alpha-terpineole, pinene etc are known to posses insecticidal, antibacterial, antifungal and insect repellent properties and recently gained importance for its biological and pharmacological applications (Lal *et al.*, 2018, Ganjewala 2009, Baruah *et al.*, 2017). Besides citral rich there are some species which contains geraniol (*Cymbopogon martini),* elemicin (*Cymbopogon khasianus, Lal et al., 2018*), and methyl eugenol (*Cymbopogon khasianus)* as their main component. The objective of the study is to identify novel myrcene and methyl iso-eugenol rich variety of lemongrass available in North East India. Myrcene has an earthy, spicy, clove fragrance commonly used in culinary and perfume industry while methyl iso-eugenol has typical sweet-warm, spicy-clove, woody, floral odour mostly used in perfume industries. In the present study total 230 lemongrass accessions collected from different regions of North East India were planted in Randomized Block Design (RBD) with three replications at experimental farm CSIR-NEIST, Jorhat, during the year 2014. Morphological and essential oil quality data were recorded during the year 2015-16 and 2016-17 and based on two years selection trial data a high myrcene

and methyl iso-eugenol rich line was identified and named as Jor Lab L-11. The identified line was planted along with two checked variety at four locations during the year 2017-18. The average essential oil yield of Jor Lab L-11 for multilocation trial was 0.58% and contains 48% and 39% myrcene and methyl iso-eugenol as major component in the essential oil respectively (Table 1). Myrcene and methyl iso-eugenol percentage, essential oil percentage, tillers/plant were significantly higher as compared to check varieties. Besides these, the essential oil of Jor Lab L-11 also contain limonene, elemicin, β-pinene, α –pinene, citronellol, neryl acetate, linalool, geranyl acetate, methyl eugenol, geraniol, citral b, citronellal, citral a, α–terpineol and nerol as minor compounds.

Table 1. Average multilocation trial data of Jor Lab L-11 planted in four different locations (Jorhat, Imphal, Pasighat, Lakhimijan) of North East India during 2017-18

Variety	Plant height (cm)	Tillers/plant	Herbage yield/ tons/ha/yr	Essential oil % v/w	Myrcene %	Methyl isoeugenol%	Major oil constituent
Jor Lab L-11	109.25	48.5	20.68	0.58	48	39	Myrcene, Methyl iso-eugenol
RRLJM-622(Check-1)	109	43	19.21	0.42	12	20	Myrcene, Methyl iso-eugenol
Jor Lab L-2 (Check-2)	118	38.25	21.25	0.38	2.3	0.67	Citral

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54. Jor Lab AC-1 (IC635433; INGR20054), a Sweet flag (*Achorus calmus*) Germplasm with Essential Oil Yield more than 1.2% on Dry Weight Basis. Cis Asarone is more than 80% of the Essential Oil.

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Acorus calamus L. (sweet flag) is an aromatic medicinal plant, generally found in the temperate and subtropical regions of the world (Nigam *et al.*, 1990). It is abundantly found in the northern temperate and subtropical regions of Europe, North America and East Asia (Nigam *et al.*, 1990). It is used in various commercial and pharmaceutical industries for its medicinal and aromatic properties; and used since ages in traditional medicines (Van *et al.*, 1997, Lal *et al.*, 2016). The essential oils obtained from the rhizome are used medicinally, as flavourings in alcoholic beverages, as fragrant essences in perfumes and sacred oils, and for insecticidal properties (Mazza, 1985). The aim of the present study was to identify a high essential oil yielding variety of A. calamus. In this study, forty germplasm were collected from different parts of India and planted in RBD during the year 2014. All agronomical and oil quality data were recorded. The major compound in the essential oil was β-asarone (Table 1). After evaluation of two season data, a high essential oil genotype was identified and was named as "Jor Lab AC-01". The newly identified line is superior to the check variety as the yield of essential

Table 1. GC/MS data of components present in the essential oil of *Acorus calamus* (Jor Lab AC-1)

S.No.	Compound name	RT	Area (%)
1	methyl 2-methylbutyrate	03.22	0.05
2	ocimene	05.77	0.17
3	camphene	06.24	0.01
4	*l*-linalool	06.49	0.14
5	terpineol	07.05	0.09
6	*α*-citronellol	08.13	0.04
7	nerol	09.01	0.05
8	linalyl acetate	10.39	0.03
9	neric acid	10.40	0.04
10	2-methoxy-3-allylphenol	11.95	1.91
11	calarene	12.18	2.41
12	*α*-maaliene	13.20	0.22
13	methyl isoeugenol	13.67	1.51
14	sulcatol	14.16	0.03
15	germacrene-*D*	14.85	0.17
16	epiglobulol	15.35	0.12
17	euasarone	15.64	1.90
18	spathulenol	15.79	0.14
19	*cis*-asarone	16.53	80.42
20	dieoicedren-1-oxide	16.89	1.52
21	isolongifolenone	16.89	0.13
22	acorenone	18.51	0.45
23	*iso*-calamendiol	18.93	0.75
24	paroxetine	20.82	0.25

oil is much higher (1.20%) in comparison to the check variety (0.62%). Moreover, in this new line, in addition to high essential oil yield, the total dry rhizome yield/ tones/ha/year (2.18) is much higher as compared to the check variety (1.89) (Table 2). Data recorded from the five locations across Northeast India gave satisfactory and stable results. High essential oil varieties have wide range of use across several industries like pharmaceutical, perfumery, cosmetic and many others (Lal *et al.*., 2018). As the market demand is increasing for high essential oil yielding varieties day by day along with the market price of essential oils, farmers will be benefitted by selling the essential oil of this high yielding variety and cultivation of this crop seems to be a profitable venture.

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Table 2. Average morphological and oil constituent of *A. calamus* with check variety at five different locations in the year 2017-18

Variety	Location	Plant height (cm)	No. of tillers/ plant	No. of leaf/ plant	No. of primary rhizome	Dry rhizome recovery	Fresh rhizome yield/tones/ha	Essential Oil%	Essential oil yield tonnes/ ha/season	Total dry rhizome yield/tones/ ha/season
Jor Lab AC-1		88	8	12	1	32	6.80	1.20	2.63	2.18
Check variety (CIM-Balya)		92	10	11	1	31	5.60	0.62	1.19	1.89

55. Jor Lab B-2 (IC635434; INGR20055), a Annato (*Bixa orellana*) Germplasm with Bixin Content More than 1.1%. Normal Range of Bixin Content is 0.3 to 1.3% in the Germplasm.

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Bixa orellana commonly known as Sinduri plant is a natural source of bixin. This perennial, rapidly growing tree is of great agro-industrial interest as the seeds of the plant are rich in carotenoid content, mainly bixin which is a source of natural dye (Madrid *et al.*, 2006; Franco *et al.*, 2008). Annatto colorants have several uses due to which it is a popular agro-industrial crop (Franco, 2007). it is used extensively in food industry, particularly in cheese and dairy products cereal-derived products, sweets, beverages, sauces, sausages and meat

products (Barcelos *et al.*, 2012; Giriwono *et al.*, 2013; Pierpaoli, 2013; Vilar, 2014; Kang *et al.*, 2010; Galindo-Cuspinera *et al.*, 2003; Shibata, 2008; Matuo *et al.*, 2013). In this experiment a total of 52 genotypes were collected and planted in the CSIR-NEIST Experimental farm during 2008. After screening five-year data all the genotypes were screened for agronomical, qualitative and quantitative characters out of which 5 genotypes were selected for high bixin content and high seed yield and were planted again in RBD during 2013. After study of six years from the studied genotype the genotype 2 was found the best variety of Bixa orellena possessing high bixin content. The genotype 2 has an average plant height of 209 cm, average number of branch per plant is 23 and the average plant diameter is 70 cm. The average number of capsule per clump is 12.75; the average capsule clump per plant is 58, and the average number of seeds per capsule is 32.50. Among the studied varieties the genotype 2 was found to have an average yield of 554.50 gm of bixin yield per plant and the average bixin content was found 1.1%. While the average yield of bixin content per plant of the check variety was found 541.00 gm and the bixin content of the check variety was found 0.60%. The genotype was named as 'Jor Lab B-2'. Till date none of the variety of *B. orellena* has been reported to have high bixin content. Cultivation of this variety will be much beneficial economically as it has a high bixin content which is a source of natural dye that has various applications in numerous fields. Presently there is no variety of *Bixa orellena*, so the identified variety is novel as it has high bixin content and higher yield than the check variety.

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56. Jor Lab L-15 (IC635702; INGR20056), a Lemon Grass (*Cymbopogon khasianus*) Germplasm with High Geraniol Content (83%) in Essential Oil.

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Cymbopogon species, which belongs to the family Poaceae, is an important genus of medicinal and aromatic plants. *C. khasianus* is a perennial crop which grows by vegetative propagation (Lal *et al.*, 2018; Dutta *et al.*, 2017). It is commonly found in Khasi Hills, Jaintia Hills, Naga Hills and lower Assam of NE India (Dutta *et al.*, 2016). The essential oil of this species is rich in various valuable chemical compounds, which are useful for industrial and commercial purposes (Dutta *et al.*, 2016, Lal *et al*., 2016, Baruah *et al.*, 2017). In this present study, a total of 425 germplasm of *Cymbopogon* species which were collected from different regions of India, and was analyzed for its agronomical, essential oil yield and quality data, for two year 2014-15 and 2015-16. To identify the constituents, extraction of essential oil was done using hydro-distillation and GC/MS analysis. The

major constituent was geraniol (Table 1). On the basis of two consecutive year data, a geraniol rich line was identified and the results were confirmed by planting as multi-location trial, along with the standard check (IIMJ (CK) – 10) during the year 2016-17 and 2017-18. The average essential oil yield of the newly developed variety in the five different locations was 0.54% and average geranial content of the multi-location trial was 83%; which is much higher as compared to the check variety that showed essential oil yield of 0.40% and geraniol content of 46.8% This selected germplasm also showed better agronomical traits in comparison to the check variety (Table 2).. This new identified line was named as "Jor Lab L –15". The high essential oil yielding varieties meet the needs of various pharmaceutical, cosmetics and food industries,

Table 1. GC/MS analysis of the compounds identified in the essential oil of Jor Lab L-15

Compound Name	Retention time	Area%
O- cymene	8.445	0.23
2- Carene	9.565	0.12
D-limonene	10.683	0.14
trans-β-Ocimene	11.071	3.70
1,3,6-Octatriene	11.502	1.87
4-Nonanone	12.550	0.13
Linalool	13.728	0.39
γ-Terpinene	14.660	1.17
3-Carene	15.463	0.56
p-Mentha-1,5-dien-8-ol	16.707	0.11
α-Phellandrene	17.983	0.32
γ-Terpinene	18.540	0.33
Citral	20.049	0.24
Geraniol	20.826	83.58
Citral	21.396	0.59
β-myrcene	26.310	4.74
trans-Isoeugenol	28.966	0.14
Copaene	31.668	0.16
Hedycaryol	32.997	0.10
Elemicin	33.317	1.00
3-Carene	33.456	0.37

across the world (Lal *et al*., 2018). Therefore it can be concluded that the farmers would be benefited by adopting this superior variety having high geraniol content. The societal status of the farmers will become better, as they can sell the essential oil at higher rates. This in turn will help in raising the economic status of the farmers as well as the whole society.

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Table 2. Average agronomical and essential oil data of multi-location trials, along with check variety for two years (2016-17 and 2017-18)

Plant variety	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Tiller/ plant	Herbage yield (tons/ha/year)	Essential Oil%	Essential oil yield/ha/year	Major oil constituent (% geraniol)
Jor Lab L-15	109.00	86.00	1.10	56.00	22.8	0.54	12.31	83.00
IIMJ (CK) - 10	79.00	84.00	0.78	76.00	16.8	0.37	6.74	46.8

57. CSIR-IHBT-VJ-08 (IC0630605; INGR20057), a Tagar (Indian_Valeriana) (*Valeriana jatamansi*) Germplasm with High Essential Oil Content: 0.331% (3.31 g/kg).

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Valeriana jatamansi Jones is popularly known as Indian valerian, Mushkbala (Kashmiri/ Hindi), Sugandhwala or Tagar (Sanskrit) and is a native plant of Himalayan origin. Valeriana jatamansi, a perennial medicinal herb, is now endangered and at the edge of becoming extinct in India (Mahajan and Pal, 2016). It is therefore a pressing need to conserve and maintain this species in their natural habitat. The species is extensively utilized for its roots and rhizomes which contain essential oil. In order to improve productivity and essential oil content of the roots, a breeding programme has been undertaken to identify promising selection for commercial cultivation.

Using progeny selection approach nine accessions of Indian valerian were initially shortlisted based on root biomass accumulation and essential oil content over two years. The progeny plants of these nine accessions were evaluated in multi-location trials for root biomass and essential oil content at four locations in mid- and high-altitude regions over a period of two years along with check variety 'Himbala'. Overall, CSIR-IHBT-VJ-08 performed better than check at all the four locations with high essential oil content of 0.331% (3.31g/kg). The genotype CSIR-IHBT-VJ-08 was developed at CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh (Latitude: 32.0934° N, Longitude: 76.5439° E and at an altitude of 1300m amsl).

Morpho-agronomic characteristics: The characteristic features of CSIR-IHBT-VJ-08 are large leaf size with slightly serrated margins and pointed apex. The selection CSIR-IHBT-VJ-08 is vigorous in growth and has a potential to be utilized as aromatic plant on commercial basis for high essential oil content.

Associated characters and cultivation Practices: *Valeriana jatamansi*, a perennial medicinal herb of the Valerianaceae family, is widely found in the temperate zone of the western Himalaya at an altitude of 1300–3300 m amsl. In India, the species is now endangered and at the edge of becoming extinct (Nayar and Sastry, 1998) due to over-exploitation from its natural habitat to meet the burgeoning demand and there is need to cultivate the plant species for production of essential oil.

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Table 1. Essential oil content (g/kg) in Indian valerian accessions CSIR-IHBT-VJ-08 in comparison to check

Plant No.	Essential oil content (g/kg)				
	Palampur	Mukteshwar	Kukumseri	Ribling	Mean
CSIR-IHBT-VJ-08	3.81	3.66	3.59	4.12	3.80
Himbala (check)	3.02	2.88	2.82	3.19	2.98

58. TNGsy-55-Mettupalayam Local 4 (IC0630558; INGR20058), a Gymnema (*Gymnema sylvestre*) Germplasm with Elliptic Leaf Shape and Obtuse Base.

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Gymnema sylvestre is one of the important medicinal plants that holds a unique position among the sweetness modifying materials of natural origin. Various poly herbal formulations with *Gymnema sylvestre* extract

are being used for the treatment of Diabetes mellitus. Several clinical trials and experimental studies have indicated that the plant is an invaluable source of bioactive compounds for the treatment of diabetes. The plant is source of gymnemicacid. Gymnemic acids have been used as molecular targets in drug development. Besides having pharmacological importance, the gymnema extract possesses valuable dietary applications to combat diabetes. Although the plant has immense prospects in drug development, it faces threat of extinction due to continuous deforestration and indiscriminate collection.

Under natural habitat, considerable variations exist among the morphological traits in this species. However detailed information on the extent of variability is not available. At present no descriptors as well as varieties are available in Gymnema sylvestre. Identification of morphological marker will help for DUS descriptor development which is important for protecting IPR. Moreover, morphological marker will help for varietal identification.

Research at the Department of Medicinal and Aromatic Crops of Tamil Nadu Agricultural University, Coimbatore has led to the establishment of a germplasm of Gymnema comprising of sixty-six accessions collected from various parts of Tamil Nadu. At present no descriptors as well as varieties are available in *Gymnema sylvestre*. The characterization of germplasm was made based on the Kew Plant Glossary (Henk Beentje, 2010). Based on the characterization, variations were observed for leaf characters viz., leaf shape, leaf base leaf tip and leaf pubescence.

Morpho-agronomic characteristics: Leaf shape varied from ovate, elliptic and lanceolate. 24 % of the germplasm had ovate shaped leaves; 15% of the germplasm had elliptic shape and 12% had lanceolate shape. The shape in other entries ie 48% of the germplasm had shape which varied from ovate-elliptic, elliptic-ovate, ovate- lanceolate and ovate-oblanceolate. Of the varied leaf shapes observed, ovate is the most common and considered as reference or check. The accession TNGSy 33–IC-0630536 which is collected from Palani, Dindigul district of Tamil Nadu is the reference genotype which has ovate shaped leaves with round base and acute tip. Pubescence is present in the leaves. The accession TNGSy55-IC-0630558 is an elite genotype which has elliptic shape with obtuse base and acute tip. Pubescence is absent in the leaves. Compared to the reference genotype, the elite genotype TNGSy-55–IC-0630558 varied for leaf shape and leaf base and leaf pubescence.

Morphological, yield and quality traits: Observations on morphological and yield characters were recorded for the 66 accessions and the per seperformance of the genotypes ranged from 2.40-4.58 cmfor leaf length; 1.57-2.90 cm for leaf breadth; 0.47-1.37 cmfor petiole length and 1.07-2.74 cm for intermodal length. The per se performance for leaf dry weight ranged from 0.08 -0.75 kg and 0.48-1.54 % for gymnemagenin content. The elite genotype recorded leaf length 2.57 cm; leaf breadth-2.17 cm; petiole length-1.14 cm; intermodal length-1.69 cm and leaf dry weight of 0.26 kg/plant with gymnemagenin content of 1.07%.

Associated characters and cultivation practices: Pubescence was absent in leaves present in midrib, petiole and stem. Commercial propagation is done through cuttings; Planting season: June to August; Spacing: 1 × 1m; Training: Being a climber, support has to be provided for training the vine; Intercultural operations: Based on the prevailing climate and intensity of weeds, weeding has to be carried out; Plant Protection: Need based control measures has to be followed; Harvesting: One year after planting.

Table 1. Characteristics features of elite genotype TNGSy-55–IC-0630558

Particulars	
Leaf shape	Elliptic
Leaf base	Obtuse
Leaf tip	Acute
Leaf pubescence	Absent
Mid rib pubescence	Present
Leaf length (cm)	2.57 cm
Leaf breadth(cm)	2.17 cm
Petiole length (cm)	1.14 cm
Internodal length (cm)	1.69 cm
Leaf dry weight (kg/plant)	0.26 kg/plant
Gymnemagenin content (%)	1.07%

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59. CSIR-IHBT-DH-04 (IC635704; INGR20059), a White Dragonhead (*Dracocephalum heterophyllum*) with High Biomass Yield 3.11 kg/plot (6 sqm). Essential Oil Content 0.22%.

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White dragonhead (*Dracocephalum heterophyllum*) is perennial, aromatic herb of high altitude region in Himalayas which has characteristic aroma in the aerial parts of the plant. The plant is native of Western Himalayas (Stappena *et al.*, 2015; Zeng *et al.*, 2010) and has been reported growing wild in the northern part of India, including Jammu and Kashmir, Himachal Pradesh, Uttarakhand and Sikkim at an altitude of 3000–5200 m amsl (Mahmood *et al.* 2005; Agarwal *et al.*, 2005). Leaf extract of white dragonhead is reported to be used in treating eye ailments like redness of eyes, irritation and conjunctivitis by the native people of Spiti valley in Himachal Pradesh and in Laddakh region of trans-Himalaya (Singh *et al.*,. 2008; Mahmood *et al.* 2005). Its essential oil has antiasthamatic, anticoughing and disinfectant properties. It is known to contain flavones and essential oil content (Zhang *et al.*, 2008). The essential oil of Dracocephalum heterophyllum contains mainly citronellol (74.2%) of total 40 compounds. Only small amounts of cis-rose oxide (2.2%), citronellyl acetate (1.7%) and trans-rose oxide (1.1%) contribute to the oil (Stappena *et al.* 2015).

In this context, with an aim to improve aerial biomass and essential oil content, breeding of white dragonhead was done using progeny selection approach. One hundred eighty-two accessions representing populations of diverse origin were screened for morphological traits viz., leaf lamina size, leaf number, number of branches and inflorescence length were measured at the time of flowering. Multivariate clustering approach was used to identify six accessions with significantly high values for all the parameters which were shortlisted by retaining their seeds. Progeny plants of these six breeding lines were evaluated in multi-location trials at four locations over two years along with 'Him surabh' variety of white dragonhead as the check variety. CSIR-IHBT-DH-04 performed better than the check variety with high biomass yield of 3.11 kg/plot

Morpho-agronomic characteristics: The characteristic features of CSIR-IHBT-DH-04 are large mature leaf size (leaf lamina length more than 6 cm and width more than 2.5 cm). The plants are vigorous in growth and flower in the months of June and July.

Associated characters and cultivation practices: Propagation of white dragonhead is through seed in the month of March-April.

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Table 1. Mean of two years for aerial biomass yield (kg/plot) of CSIR-IHBT-DH-04 in white dragonhead accessions in comparison to check

Plant No.	Aerial biomass (kg/plot)				
	Location-1	Location-2	Location-3	Location-4	Mean
CSIR-IHBT-DH-04	3.11	2.96	3.19	3.18	3.11
Him surabh (check)	2.75	2.64	2.62	2.78	2.69

60. 60. CSIR-IHBT-AM-02 (IC635705; INGR20060), a Wormwood (*Artemisia maritima*) Germplasm with High Biomass Yield 8.175 kg/plot (24sqm).

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Sea wormwood (*Artemisia maritima*; family Asteraceae) indigenous to high altitudes of western Himalayan region is an endangered perennial shrub with localized distribution and being highly habitat specific (Parihar *et al.*, 2012; Watson *et al.*, 2002; Mehrdad *et al.*, 2007). It is called Chhara, Jantunashava in sanskrit, Darmanah in urdu, Kirmaniova, Surabandi in Marathi, Chhuvaria-Jamoda in Gujarati. It has strong aroma. The essential oil is used as a deodorant, anthelmintic, antiseptic (Parihar *et al.*, 2010), antisplasmodic, carminative, vermifuge and has insecticidal properties (Kumar *et al.*, 2011). It is also used to cure arthritis (Nawchoo and Buth, 1995). Locally, people in Himalayas use the leaves of the plants for preparation of dhoop. The main compounds analyzed by simultaneous GC/MS and GC/FID were camphor and 1,8-cineole from *A. maritima* (Stappen, 2014). Aqueous methanol extract of *Artemisia maritima* (L.) at a dose of 500 mg/kg has been reported to exhibit hepatoprotective activity against acetaminophen and carbon tetrachloride-induced hepatic damage (Janbaz & Gilani, 1995). Plant has erect woody stems arising from the base with woody rootstock. Leaves are simple, sessile to sub-sessile 2 - 5 cm long, highly lacerate, alternate and obtuse. Capitulum is terminal with 0.3-0.4 cm diameter, ovoid-globose, involucral bracts (Bora and Sharma, 2011; Heywood and Humphries, 1997; Mucciarelli and Maffel, 2002; Polyakov and Shishkin, 1995; Anonymous, 2021).

In order to improve biomass production and essential oil, breeding of sea wormwood was undertaken using progeny selection approach. One hundred fifty accessions of diverse origin were screened for above ground biomass at the time of maturity and eight accessions with high biomass were shortlisted by retaining their seeds. The progeny plants of eight breeding lines were selected for further evaluation in multi-location trials at four locations over two years. Population mean of Artemisia breeding lines being evaluated was used as control. CSIR-IHBT-AM-02 is a selection from AU-11 (collection from Udaipur, Lahaul & Spiti, HP) which performed well with average biomass yield 8.175 kg/plot (24 sqm plot).

Morpho-agronomic characteristics: The characteristic features of CSIR-IHBT-AM-02 are plant height of approximately 70 cm and secondary branches more than 40. The plants are vigorous in growth and secondary branches attain a length of 60-65 cm.

Associated characters and cultivation practices: Artemisia maritima is a shrub with much branched stem up to 1m high. Leaves are whitish in colour. Artemisia maritima is found naturally in the Western Himalayas between altitude range of 2500m to 3500m. It can be grown in degraded poor dry soil pH range 6.0-7.6. under temperate conditions but requires adequate sunlight for growth.

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61. IIHR-12 (IC0630783; INGR20061), a Tuberose (*Polianthes tuberosa*) Germplasm. Open Pollinated Seedling Selection from Arka Shringar.

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Tuberose (*Polianthes tuberosa* L.) belongs to the family Asparagaceae is a tropical bulbous fragrant ornamental plant, native to Mexico (Trueblood, 1973). It occupies a prime position in Indian floriculture industry for loose flower, cut flower and floral concrete. Tuberose genetic stock IIHR-12 is derived from open pollinated seedling selection from Arka Shringar. It was developed at ICAR-Indian Institute of Horticultural Research (ICAR-IIHR), Bengaluru, Karnataka, India which is situated at an altitude of 930 meter above mean sea level and latitude 120 58′ North latitude, 780 45′ East longitude, respectively. The genetic stock IIHR-12 is unique for medium tall upright spike, attractive star shaped floret, compactly arranged on spike with shorter internodes.

Table 1. Morpho-agronomic description of tuberose genetic stock IIHR-12

Traits	Two years pooled data
Days to spike appearance	148.30
Days to opening of 1st floret	19.77
Spike Length (cm)	72.64
Rachis length (cm)	28.06
Number of florets per spike	42.53
Length of floret (cm)	6.02
Diameter of the floret (cm)	3.67
Bud length (cm)	6.06
Matured bud weight (g)	1.40
Single flower weight (g)	1.71
Flowering duration (days)	190.80
No. of spikes per clump	3.89
Weight of spike (g)	54.87
Internodal length (cm)	3.39
No. of matured bud in spike	5.31
Flower type	Single
Flower bud tinge	Pinkish tinge
Nature of spike	Straight
Colour/tinge of unopened bud	RHS Red Purple group 58 D
Colour of floet	RHS White group 155 C

Morpho-agronomic characteristics: IIHR-12 produces medium tall spike (72.64 cm), longest rachis (28.06 cm) with more number of matured bud on spike (5.31) and shorter intermodal length (3.39 cm)

Associated characters and cultivation practices: Tuberose require moderate climate with temperature ranging from 20-35 ºC. Tuberose is suited to a wide range of soils from loamy to sandy loam having a pH in the range of 6.5 to 7.5 with good aeration and drainage. It is a day neutral plant and full sunlight is essential for flowering. Tuberose is sensitive to water logging and hence proper drainage is essential. The medium size bulbs of 2.5 cm in diameter are planted on the sides of the ridges with a spacing of 30 × 30 cm at 2.5 cm depth during June-July. The genetic stock IIHR-12 is suitable for cut flower and flower arrangement.

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62. 62. IIHR15-7 (IC0632114; INGR20062), a Gerbera (*Gerbera jasmeonii*) Germplasm. Flower Form: Semi-Double. Flower Colour: NN155A, White Group.

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Gerbera, family Asteraceae, is one of the important cut-flowers grown for domestic and export markets. Gerbera grown under 870 ha with productivity of 21300 t/ha, and stands fourth most important cut flower in India. Highest production of gerbera comes from Uttarakand with 7.80 (000' MT), while share of Karnataka is 6.2 (000, MT) (Anon., 2017). The Gerbera germplasm IIHR15-7 was developed through half-sib method of breeding with IIHR9 as parent, at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13º 58' N Latitude, 78oE Longitude and at an altitude of 890 meter above mean sea level), India. The germplasm IIHR15-7 along with its parent and commercial check was evaluated for flower quality traits under polyhouse in Completely Randomized Block Design, during 2016-17 to 2018-19. The germplasm IIHR15-7 is unique for its white flower colour (NN155A, White group) and semi-double flower form. It is suitable for cut-flower and flower arrangement purposes.

Morpho-agronomic characteristics: The Gerbera germplasm IIHR15-7 is having white flower (RHS colour chart, NN155A White group) with semi-double flower form. On an average, it produces 2.87 flowers per plant per month with flower stalk length (61.39 cm).

Associated characters and cultivated practices: The germplasm IIHR15-7 has average flower head diameter (11.89 cm), flower stalk diameter (5.79 mm) and vase life (7.74 days). The Gerbera is generally grown under polyhouse with shade net. It grows best in well drained loamy soil, rich in organic matter, having adequate moisture holding capacity with soil pH (5.5-6.5) and EC less than 1 dS/cm^2. The tissue cultured plug plants (4-5 leaves) to be planted on raised beds at a spacing of 40 cm between rows and 30 cm between plants accommodating 6-7 plants/m^2. The water requirement during the peak summer is 4-6 litres/m^2/day and 2 to 3 litres/m^2/day during the winter.

During bed preparation, a basal dose of FYM @ 20 kg/m^2, and first three months of planting apply 10:15:20 g NPK/m^2 and 15:10:30g NPK/month/m^2 from fourth month onwards (when flowering starts) in two splits at 15 days interval is good for establishment.

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Table 1. Morpho-agronomic description of Gerbera germplasm IIHR15-7 with parent and commercial check (pooled data of three years)

Genotype	Flower diameter (cm)	Flower stalk length (cm)	Flower stalk diameter (mm)	No. of flowers/ plant/ month	Vase life (days)	Flower colour (RHS colour chart)	Flower form
IIHR15-7	11.89	61.39	5.79	2.87	7.74	White group NN155A	Semi-double
IIHR9 (parent)	11.46	61.19	5.80	2.43	7.29	Red purple group 69A	Semi-double
Arka Ashwa (check)	11.86	61.10	6.64	2.56	7.42	Red purple group 68D	Semi-double
Susan (commercial check)	12.04	62.81	6.62	2.69	7.59	White group NN155C	Semi-double
SEm±	0.47	0.44	0.38	0.49	0.51	-	-
C.D. at 5%	NS	NS	NS	NS	NS	-	-

63. IIHR16-8 (IC0632115; INGR20063), a Gerbera (*Gerbera jasmeonii*) Germplasm with Flower Colour: 65A, Red Purple Group. Flower Form: Double

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Gerbera, family Asteraceae, is one of the important cut-flowers grown for domestic and export markets. Gerbera grown under 870 ha with productivity of 21300 t/ha, and stands fourth most important cut flower in India. Highest production of gerbera comes from Uttarakand with 7.80 (000' MT), while share of Karnataka is 6.2 (000, MT) (Anon., 2017). The Gerbera germplasm IIHR16-8 was developed through half-sib method of breeding with Arka Ashwa as parent, at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13º 58' N Latitude, 78º E Longitude and at an altitude of 890 meter above mean sea level), India. The germplasm IIHR16-8 along with its parent and commercial check was evaluated for flower quality traits under polyhouse in Completely Randomized Block Design, during 2016-17 to 2018-19. The germplasm IIHR16-8 is unique for its flower colour (65A, Red Purple Group) and double flower form. It is suitable for cut-flower and flower arrangement purposes.

Morpho-agronomic characteristics: The Gerbera germplasm IIHR16-8 is having red-purple flower colour (RHS colour chart, 65A Red Purple Group) with double flower form. On an average, it produces 2.85 flowers per plant per month with flower stalk length (65.64 cm).

Associated characters and cultivation practices: The germplasm IIHR16-8 has average flower head diameter (12.89 cm), flower stalk diameter (5.77 mm) and vase life (7.00 days). The Gerbera is generally grown under polyhouse with shade net. It grows best in well drained loamy soil, rich in organic matter, having adequate moisture holding capacity with soil pH (5.5-6.5) and EC less than 1 dS/ cm^2. The tissue cultured plug plants (4-5 leaves) to be planted on raised beds at a spacing of 40 cm between rows and 30 cm between plants accommodating 6-7 plants/m^2. The water requirement during the peak summer is 4-6 litres/m^2/day and 2 to 3 litres/m^2/day during the winter.

During bed preparation, a basal dose of FYM @ 20 kg/m^2, and first three months of planting apply 10:15:20 g NPK/m^2 and 15:10:30g NPK/month/m^2 from fourth month onwards (when flowering starts) in two splits at 15 days' interval is good for establishment.

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Table 1. Morpho-agronomic description of Gerbera germplasm IIHR16-8 with parent and commercial check (pooled data of three years)

Genotype	Flower diameter (cm)	Flower stalk length (cm)	Flower stalk diameter (mm)	No. of flowers/ plant/ month	Vase life (days)	Flower colour (RHS colour chart)	Flower form
IIHR16-8	12.89	65.64	5.77	2.85	7.00	Red purple group 65A	Double
Arka Ashwa (parent and check)	11.86	61.10	6.64	2.56	7.42	Red purple group 68D	Semi-double
Bismark (commercial check)	12.12	62.93	6.21	2.73	7.26	Red group 45B	Semi-double
SEm±	0.50	0.47	0.43	0.41	0.52	-	-
C.D. at 5%	NS	NS	NS	NS	NS	-	-

64. CSIR-IHBT-Gr-29-1 (IC0630599; INGR20064), a Gerbera (*Gerbera jasmeonii*) Germplasm with Double Flower Shape and Red Flower Colour.

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Gerbera (*Gerbera jamesonii* Bolus ex. Hooker F.) is an important cut-flower with extensive demand throughout the world due to its numerous shapes, colours and extended vase-life. It belongs to family Asteraceae and ranks fifth among the top ten cut flowers in the global market. Apart from its use in beds, borders, pots and rock gardens, it also has considerable export potential (Tija, 2001). It is a perennial plant which can be grown under wide range of climatic conditions. Based on its floral biology, gerbera is an out-cross in breeding behaviour and clonal propagation through tissue culture has resulted in development of large number of gerbera cultivars. New variations in gerbera can be developed through hybridization program involving diverse parents which will widen the range of floral variations and facilitate selection of desirable genotypes that can be clonally multiplied through vegetative propagation. With an objective to develop unique selections of gerbera, hybridization program was undertaken involving elite and diverse parental lines differing for flower color (Singh *et al.*, 2013), shapes and size at CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh, India (Singh *et al.*, 2009 & 2011).

F1 seeds of gerbera developed through manual crossing among selected parental lines were used for establishment of in vitro gerbera cultures. Germination of seeds was done on MS basal medium and the shoots obtained from seeds were cultured on MS media supplemented with different doses of growth regulators for shoot proliferation. maximum micro-shoot formation, number of leaves and leaf size were obtained in MS medium supplemented with 1 mg/L BAP + 0.03mg/L IBA + 0.025 mg/L NAA. Root induction was achieved by using half strength MS medium supplemented with 0.4 mg/L IBA. Primary hardening of rooted plantlets was done in trays filled with moist sand which was maintained under growth room conditions for about 15 days. Hardened plantlets were subsequently transferred to soil in sleeves for further hardening under nursery conditions. Morphological characterization of gerbera F1 genotypes with respect to floral traits was done under polyhouse conditions and evaluated for agronomic performance in comparison to parents over a period of four years. On the basis of mean performance of gerbera hybrids compared to respective parents, gerbera selection CSIR-IHBT-Gr-29-1 was found promising having double flower shape of standard size (flower diameter of 10.28 cm) and is red in color. The genotype CSIR-IHBT-Gr-29-1 has been developed at CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh (Latitude: 32.0934° N, Longitude: 76.5439° E and at an altitude of 1300m amsl).

Morpho-agronomic characteristics: CSIR-IHBT-Gr-29-1 was found promising having double flower shape of standard size (flower diameter of 10.28 cm) and is red in color.

Associated characters and cultivation practices: Commercially, gerbera is grown under controlled environmental conditions. Day temperature of 22o-25oC and night temperature of 12-16oC is ideal for growth and flower production. (Aswath *et al.*, 2015)

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65. No. 18 (IC635707; INGR20065), a Lily (*Lilium* sp.) Germplasm with Multiple Shoots/Sprouting, 100% Flowering and Larger Bud Size. Low Juvenile Period. No Vernalization Requirement.

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Lilium is an important ornamental bulbous crop worldwide. It is grown almost throughout the year in India. In India, bulbs of Lilium sourced from Holland, are planted for production of cut flower. At present, commercial cultivation of lilium is centered in and around Himachal Pradesh, Uttrakhand, J&K, Bangaloru and Haryana, from where flowers are being sent to local and international market. Commercially, lilium is propagated vegetatively through scaling, which usually takes 2-3 years to reach the flowering size bulb. Propagation of lilium through seeds took 5-6 years to start flowering. A short juvenile period and early flowering are the most important traits in lily breeding. Hence, introgression of precocious flowering traits from the species (Lilium formosanum) is the only method to minimize the juvenile period and produce flowering plants from smaller bulb in a short period of time (McRae, 1998 and Hiramastsu *et al.*, 2002).

Generally, for early sprouting and flowering, lilium bulbs require a cold treatment at 2-7 ºC for 6-8 weeks. Hence, low juvenility and precocious flowering are advantageous specially to reduce the cost of bulb storage, production of flowers from small bulbs and advance the breeding cycle. However, the contribution of indigenous hybrids/varieties in lilium is negligible and the bulbs are imported every time from the Netherlands (Dhiman *et al.*, 2014). Development of indigenous hybrids in flower crop like lilium is the need of the hour. It will not only save revenues spent in import of their bulbs but will also create several employments in India. Development of indigenous low juvenility line with no vernalization requirements holds the key for indigenous bulb production. The lilium line, No.18 is one indigenously developed breeding line with low juvenile period and ability to flower precociously, no vernalization requirement and multiple sprouting of flower stalk. This white flower coloured pure breeding line selected from a cross between *Lilium formosanum* Wallace × *Lilium longiflorum*.

Morpho-agronomic characteristics: This is one of the first Low juvenile line with precocious flowering ability. This line took 335 days to flowering from seed sowing. This line has white coloured trumpet shaped flower, bearing 2-3 flowers from seed with mild fragrance and good flower size. This line produced 1.2 shoots per bulb was at par with female parental line. The bulb has no vernalization requirement and re-sprouting under open as well as protected conditions.

Table 1. Salient growth and flowering traits of No.18 seed propagated line over the parents

Traits	No. 18	*Lilium formosanum*	*Lilium Longiflorum*
Days to bud formation (days)	299.9	279.13	343.0
Number of leaves/plant	57.3	27.13	26.0
Days to flowering (days)	335.6	300.3	385.0
Leaf length (cm)	12.6	8.33	11.0
Leaf width (cm)	1.9	2.08	2.8
Bud length (cm)	14.2	10.73	12.2
No. of shoots /plant	1.2	1.3	1.0
Flower size (cm^2)	11.0	9.62	8.5
% age first year flowering	100.0	65.0	35.0
Vernalization requirement	No	No	Yes (2 ºC for 6-8 weeks)

Associated characters and cultivation practices: The line No.18 belongs to the Lilium and flower during the month of July-August. This line has white coloured trumpet shaped side facing flowers with mild fragrance. Because of low juvenile period and precocious flowering, multiple sprouting and no vernalization requirement of bulbs, this line can be used in hybrid development programme.

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66. IIHRG-7 (IC620379; INGR20066), a Gladiolus (*Gladiolus hybridus* Hort) Germplasm with Variegated Florets on the Spike. Floret Colour [Red-Purple (65.B) having Red-Purple (62.A) Streaks with Red-Purple (67.B) Splash].

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Gladiolus is one of the most important bulbous flowering plant commercially grown for cut flowers, garden display and floral arrangements. It belongs to the family Iridaceae. The gladiolus hybrid selection IIHRG-7 is derived from a cross Meera × Picardy followed by selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13o 58' N Latitude, 78oE Longitude and at an altitude of 890 meter above mean sea level), India. The hybrid selection IIHRG-7 is unique for its floret colour [Red-Purple (65.B) having Red-Purple (62.A) streaks with Red-Purple (67.B) splash] and spike with variegated florets.

Morpho-agronomic characteristics: The plants are tall (142.06 cm) and on an average produces florets in 72.25 days. Its average spike length is 123.11 cm and rachis length (46.77 cm) which bears 12.66 florets per spike. On an average, it also produces 1.43 number of marketable spikes per corm, 1.46 number of corm and 26.63 number of cormels per mother corm.

Associated characters and cultivation practices: In and around Bengaluru, planting of gladiolus corms during the June, October and November months found to be the best considering the quality of the spike. Planting can be done during August to November in plains of northern India and March-April in hilly regions.

Gladiolus is generally planted in ridges and furrows system of planting with varying distance of 30 cm × 20 cm, 30 cm × 15 cm and 30 cm x 10 cm between rows and plants within the rows depending on size of the corms and the variety. For getting good quality of flowers, healthy corms of above 3 cm diameter should be selected and treated with Carbendizim (2 g/Litre) and Captan (2 g/Litre) for 20 minutes.

Table 1. Morpho-agronomic description of Gladiolus hybrid Selection IIHRG-7

Character	IIHRG-7
Days to spike emergence	63.95
Days to flower	72.25
Plant height (cm)	142.06
Spike length (cm)	123.11
Rachis length (cm)	46.77
Floret diameter (cm)	10.66
No. of florets per spike	12.66
Florets remain open at a time	5.55
Total spikes per corm (No.)	1.66
Marketable spikes per corm (No.)	1.43
Flowering duration (Days)	9.61
Corms produced per corm (No.)	1.46
Cormels produced per corm (No.)	26.63
Diameter of corm (cm)	6.75
Diameter of cormel (cm)	1.17
Weight of corm (g)	72.44
Weight of cormel (g)	0.57
Vase life (Days)	9.33
Spike weight (g)	78.33
Floret Type	Open-faced
Floret texture	Medium
Floret structure	Wavy
Floret placement	Good
Floret colour	Red-Purple (65.B) having Red-Purple (62.A) streaks with Red-Purple (67.B) splash

Apply 10 tons FYM per hectare if soil organic carbon levels are 0.5% to 0.75%. The dose of manure and fertilizer depends upon the soil health and nutrients content. In gladiolus, the major nutrient requirement is 250 kg N, 50 kg P_2O_5 and 200 kg K_2O per ha based on nutrient removal pattern of different cultivars raised from corms as planting material. Half dose of phosphorus and potash are applied at the time of land preparation

as basal dose. Remaining half dose of phosphorus and potash is top-dressed at 3-leaf stage of the crop along with half dose of Nitrogen fertilizer. Remaining half dose of Nitrogen is applied at 6-leaf stage to get quality flowering. At the time of top dressing, earthing up to be done. The residual leaf biomass and other waste biomass can be ploughed back.

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67. IIHRG-11 (IC620380; INGR20067), a Gladiolus (*Gladiolus hybridus* Hort) Germplasm for Resistant to Fusarium Wilt Disease. Floret Colour [Red (41.C) having Red (41.A) Margin. Blotch Red (46.B) with Yellow (13.C) border].

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Gladiolus is one of the most important bulbous flowering plant commercially grown for cut flowers, garden display and floral arrangements. It belongs to the family Iridaceae. The gladiolus hybrid selection IIHRG-11 is derived from the cross Gold Medal 412 × Poonam followed by selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13º58' N Latitude, 78º E Longitude and at an altitude of 890 meter above mean sea level), India. The hybrid selection IIHRG-11 is unique for its floret colour [Red (41 ºC) having Red (41ºA) margin. Blotch Red (46.B) with yellow (13 ºC) border] and resistant to Fusarium wilt disease.

Morpho-agronomic characteristics: The plants are tall (120.72 cm) and on an average produces florets in 76.65 days. Its average spike length is 95.18 cm and rachis length (48.81 cm) which bears 17.54 florets per spike. On an average, it also produces 1.70 number of marketable spikes per corm, 1.91 number of corms and 10.14 number of cormels per mother corm.

Associated characters and cultivation practices: In and around Bengaluru, planting of gladiolus corms during the June, October and November months found to be the best considering the quality of the spike. Planting can be done during August to November in plains of northern India and March-April in hilly regions.

Gladiolus is generally planted in ridges and furrows system of planting with varying distance of 30 cm × 20 cm, 30 cm × 15 cm and 30 cm × 10 cm between rows and plants within the rows depending on size of the corms and the variety. For getting good quality of flowers, healthy corms of above 3 cm diameter should

Table 1. Morpho-agronomic description of Gladiolus hybrid Selection IIHRG-11

Character	IIHRG-11
Days to spike emergence	66.66
Days to flower	76.65
Plant height (cm)	120.72
Spike length (cm)	95.18
Rachis length (cm)	48.81
Floret diameter (cm)	9.46
No. of florets per spike	17.54
Florets remain open at a time	6.86
Total spikes per corm (No.)	1.92
Marketable spikes per corm (No.)	1.70
Flowering duration (Days)	11.70
Corms produced per corm (No.)	1.91
Cormels produced per corm (No.)	10.14
Diameter of corm (cm)	6.64
Diameter of cormel (cm)	1.53
Weight of corm (g)	64.44
Weight of cormel (g)	1.08
Vase life (Days)	7.12
Spike weight (g)	73.15
Floret Type	Open-faced
Floret texture	Thick
Floret structure	Slightly ruffled
Floret placement	Double row
Floret colour	Red (41.C) having Red (41.A) margin. Blotch Red (46.B) with yellow (13.C) border

be selected and treated with Carbendizim (2 g/Litre) and Captan (2 g/Litre) for 20 minutes.

Apply 10 tons FYM per hectare if soil organic carbon levels are 0.5% to 0.75%. The dose of manure and fertilizer depends upon the soil health and nutrients content. In gladiolus, the major nutrient requirement is 250 kg N, 50 kg P2O5 and 200 kg K2O per ha based on nutrient removal pattern of different cultivars raised from corms as planting material. Half dose of phosphorus and potash are applied at the time of land preparation as basal dose. Remaining half dose of phosphorus and potash is top-dressed at 3-leaf stage of the crop along with half dose of Nitrogen fertilizer. Remaining half dose of Nitrogen is applied at 6-leaf stage to get quality flowering. At the time of top dressing, earthing up to be done. The residual leaf biomass and other waste biomass can be ploughed back.

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68. Co 13001 (IC635051; INGR20068), a Sugarcane (*Saccharum* sp.) Germplasm with High Sucrose at 240 days. Short Duration Clone (Maturing @ 240 days). Sucrose % 19.40.

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Sugarcane cultivation in the Southern states of India is in declining trend on account of continued monsoon failures and dip in water table. Similarly, sugar factories record low sugar recovery. This situation has necessitated development of short duration sugarcane varieties which can mature in 240 months instead of the normal maturity time of 360 days. Germplasm sources to serve as parents in breeding for earliness are needed to breed suitable varieties which can be harvested in 8-9 months as a way to tide over the harsh summer months in places where water is a scarce input. The identified germplasm Co 13001 is a typical short duration clone with a juice sucrose of 19.40 % at 240 days, which is a rare feature in sugarcane.

Co 13001 was developed through crossing two proven parents Co 740 x CoT 8201 and was selected from the ground nursery when it was assigned the number 2007-228. Based on its better performance of juice sucrose and on par performance of cane yield this clone was promoted to Pre Zonal Varietal trial where it was tested in the name 2011-17 and was elevated to Co cane status in 2013 as Co 13001 at ICAR Sugarcane Breeding Institute, Coimbatore. The clone recorded a remarkable performance for juice quality with sucrose of 19.40 % at 240 days, and fitted very well as a short duration maturing clones satisfying the norm of a minimum of 18% sucrose at 240 days. The juice sucrose content increased to 20.39% at 300 days and combined with yield levels on par with the standards, showing its merit as a potential clone for sugar richness.

Encouraged by its high early accumulation potential, Co 13001 was included in the multilocation trials in different sugar factory areas of Tamil Nadu along with 19 other elite clones with maturity ranging from 240 to 360 days, with an objective of enhancing sugar productivity in Tamil Nadu. The programme was started during 2016 through Institute- Industry Participatory Approach with the collaboration of South India Sugar Mills Association (SISMA), Chennai, Tamil Nadu. The trials were conducted during 2017-19 for two plant and one ratoon crops.

The superiority of the clones was assessed by comparing its performance in relation to a germplasm material registered for earliness (based on sucrose at 240 days) with ICAR NBPGR viz 2007-291, also known as Co 16001 and with the popular ruling variety of Peninsular zone of India viz Co 86032. Co 13001 was superior at five test locations viz., at ICAR-Sugarcane Breeding Institute, Coimbatore, Bannari Amman Sugars Ltd., Alathukombai, EID Parry (India) Ltd., Nellikuppam, Kothari Sugars and Chemicals Ltd., Sathamangalam and Sakthi Sugars Ltd., Sivaganga in first plant crop trials (2017-18) and second plant crop trial during 2018-19. Co 13001 performed better than Co 16001 at 240 days in both plant crops (2017-18 and 2018-19) and registered an improvement of 4.82% over Co 16001 and 5.21%

over Co 86032 (Hemaprabha *et al.* 2019). Hence Co 13001 qualified as a clone with short duration maturity. Genetic gain for juice sucrose content can be achieved byselecting parents like Co 13001 in breeding programme on account of the high heritability of the character. Number of such high parents with extra-earliness is very limited in sugarcane and hence this clone owes potential as a new source for developing short duration maturity genotypes. Co 13001 regularly flowers early in the crossing season (October-November) to facilitate its utilization in breeding programmes

Reference

Hemaprabha G, C Appunu, K Mohanraj and Bakshi Ram (2019) Promising genetic stocks identified from multi location varietal trials of institute-industry collaborative programme in Tamil Nadu. *Journal of Sugarcane research* **9**: 184-186

69. Co 14016 (IC635052; INGR20069), a Sugarcane (*Saccharum* sp.) Germplasm for High Cane Population (Number of Millable Canes 1,07,670/ha). Donor for Ratoonability.

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Sugarcane farmers' acceptance of a sugarcane variety rests in its ratooning potential, as a good ratoon crop adds productivity and profitability with substantially less input costs. Hence f armers tend to take multiple ratoons and choose varieties according to their ratooning potential. Trait specific enhancement of the character necessitates identification of suitable parents to be used in hybridization programmes.

Co 14016 was developed through biparental mating between two proven parents namely Co 86032 and Co 86011. The clone was advanced from early generations through selection by virtue of its robust growth and more number of millable canes (NMC) and was promoted to the Pre Zonal varietal trial, where it was tested in the name 2012-17. In this trial conducted at ICAR Sugarcane Breeding Institute, Coimbatore, the clone exhibited excellent crop stand with high cane population and cane yield and was elevated to Co cane status as Co 14016. Its cane yield was 143.52 t/ha, sugar yield was 20.44 t/ha and sucrose content was 21.91% at 360 days of crop age.

The encouraging performance of 14016 in the station trials promoted its testing in All India Co-ordinated research trials of Peninsular zone as well as multilocation trials in different sugar factory areas of Tamil Nadu aimed at identifying promising varieties. The multilocation testing of this clone along with 19 other elite clones through Institute-Industry Participatory Approach with the collaboration of South India Sugar Mills Association (SISMA), Chennai, Tamil Nadu was conducted during 2017-19 for two plant and one ratoon crops. Co 14016 was remarkable for its cane yield and enhanced cane population in plant as well as ratoon crops with synchronous tillering.

The performance of Co 14016 in plant crop and its ratoon crop at four centres in Tamil Nadu is considered for assessing its yield and ratoonability potential. In the plant crop (2017-18) at four locations viz. Bannari Amman Sugars Ltd., Sathyamangalam, Dharani Sugars and Chemicals Ltd. Polur, EID Parry (India) Ltd., Nellikuppam and Rajshree Sugars and Chemicals Ltd., Mundiambakkam, mean cane yield of Co 14016 was 155.26 t/ha against 127.60 t/ha of the best standard and the ruling variety Co 86032, with an improvement of 21.67%. The high cane yield of Co 14016 was contributed mainly by increase in NMC of 1,07,670/ha in comparison with 84,620/ha of Co 86032. NMC has been identified as an effective selection criterion for selecting better ratooning and high yielding clones in sugarcane under different environments and under abiotic stresses for its high genotypic coefficient of variation and high inter-environmental correlations. The high cane yield was translated to high sugar yield of 19.90 t/ha in Co 14016 over 16.76 t/ha in Co 86032 registering an improvement of 18.73% at these test locations. In the ratoon crop (2018-19), Co 14016 recorded a mean cane yield of 140.46 t/ha against 110.96 t/ha in Co 86032 with a remarkable improvement of 26.59% thus exhibiting high ratoonability potential (Hemaprabha *et al.*, 2019). In the ratoon crop as well, NMC was the main character for high cane yield with 1,21,640/ha, while Co 86032 recorded 92,590 canes/ha with a notable

improvement of 31.39%. It could be seen that NMC in the ratoon crop registered 12.97% improvement over its plant crop. It is thus evident that Co 14016 has superior ratoonability combined with high cane yield and sugar yield. Hence this clone can be used as potential donor high NMC and ratoonability. The clone regularly flowers at Coimbatore conditions during October- November to facilitate breeding.

Reference

Hemaprabha G, C Appunu, K Mohanraj and Bakshi Ram (2019) Promising genetic stocks identified from multi location varietal trials of institute-industry collaborative programme in Tamil Nadu. *Journal of Sugarcane Research,* **9**: 184-186

70. AS 04-2097 (IC635053; INGR20070), a Sugarcane (*Saccharum officinarum*) Germplasm Tolerant to Drought. Interspecific Hybrid with Broadened Genetic Base.

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Predictions of climate change have indicated an increased variability of rainfall in the next 40 years and an increased risk of high temperature and drought. Sugarcane production and productivity are significantly affected by abiotic stresses. Among the abiotic stresses, drought is an important stress which causes yield loss upto seventy percent (Zhao and Li, 2015). Hence development of varieties for drought tolerance becomes crucial in the current scenario of climate change. Saccharum spontaneum L. has been utilized in sugarcane breeding since 1912 due to its wider adaptability under biotic and abiotic conditions. The proposed genetic stock AS 04-2097 having drought tolerance and good vigour is an interspecific hybrid derived from a cross between sugarcane commercial cultivar (Co 8371) and the wild species *S. spontaneum* (SH 216, 2n=72). The clone distinguished in semi erect habit with curved canes, moderately thick internodes, prominent node swelling and lanceolate auricle.

Fifteen ISH/IGH hybrids with diverse genetic base were tested for climate resilience at four AICRP(S) centres both in tropical (Padegaon, Anakapalle) and subtropical (Karnal, Faridkot) regions with 2 standards for each region in replicated trials (Alpha design) during 2015-2016. Drought was imposed by withdrawing irrigation between 60 and 150 days after planting in all four centres. Data on cane yield, juice quality, physiological and agronomical traits contributing to drought tolerance were recorded. Percentage of increase/ decrease due to imposition of drought for the characters was worked out. The entries which showed less than 15% reduction under drought were identified as tolerant clones.

Performance of AS 04-2097 under normal and drought conditions

Among the agronomic traits, AS 04-2097 showed less reduction for cane thickness, single cane weight and cane yield at 360 days at harvest under drought condition. Cane diameter showed 9.13% reduction with the mean value of 2.19 cm. Less reduction in single cane weight (3.0 %) was observed with mean cane weight of 1.0 kg/cane and 0.93 kg/cane under normal and drought conditions respectively. The complex character cane yield (90.48 t/h) had 13.08% of reduction under drought while the checks exhibited 17.21% reduction.

Table 1. Mean performance of AS 04-2097 under normal and drought conditions at 360 days

Clone	AS 04-2097			Checks*		
	Mean			Mean		
Traits	Normal	Drought	% Change	Normal	Drought	% Change
Cane Diameter (cm)	2.41	2.19	-9.13	2.75	2.28	-17.23
Single Cane weight (kg)	1.0	0.97	-3.0	1.14	0.98	-14.03
Cane yield t/h	104.1	90.48	-13.08	93.41	77.42	-17.21

*CoM 88121, 83 R 23, CoJ 88 (two locations), CoM 0265, CoA 06231, Co 98014 (two locations)

Considering cane yield and yield attributing parameters the clone AS 04-2097 was found to be one of the tolerant clones to drought. It shows 60% flowering hence readily can be utilized in hybridisation programme. The drought tolerant interspecific hybrid AS 04-2097 derived from the interspecific cross involving S. spontaneum with the cytotype 2n=72 is identified as a promising genetic stock for both to develop climate resilient varieties and to broaden the genetic base of modern sugarcane varieties.

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71. CYM 08-922 (IC635054; INGR20071), a Sugarcane (*Saccharum* sp.) Germplasm with Drought Tolerance. Higher Relative Water Content and Lower Malondialdehyde Content under Drought. Second Backcross Progeny of the Cross involving Erianthus arundinaceus and *S. spontaneum* having the Cytoplasm of *E. arundinaneus*.

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Drought is one of the major abiotic stresses that influence sugarcane productivity in all sugarcane growing areas of tropical and subtropical zones in India. Traditionally Saccharum spontaneum has been the donor for many important traits in sugarcane. In recent years, considerable attention has been given to use *Erianthus* spp. which is identified as a valuable source for many traits such as ratoonability, tolerance to biotic and abiotic stresses and vigour. (Piperidis *et al.*, 2000). CYM 08-922 is a BC2 progeny of a novel intergeneric hybrid between Erianthus arundinaceus "IK 76-62" and Saccharum spontaneum "Iritty-2" which was developed at ICAR-Sugarcane Breeding Institute, Coimbatore during 2008. The clone was cytologically characterized using Genomic in situ hybridization (GISH) technique and had a total of 108 chromosomes, out of which 12 chromosomes were from *E. arundinaceus* and 96 chromosomes from Saccharum.

During 2015-17, a set of parental clones were evaluated for drought tolerance along with the susceptible check Co 775 in the field condition for cane yield, juice quality and physiological parameters. The results revealed that, the clone CYM 08-922 recorded the highest cane yield of 113.59 t/ha under drought condition and also recorded the highest Stress tolerance Index (STI) of 1.256. The clone 08-922 also recorded the highest relative water content (68.40%) and significantly lower malondialdehyde (MDA) content (97.34 µg/g) than the drought tolerant commercial varieties Co 86032 (158.78 µg/g) and CoM 0265 (134.23 µg/g) under severe water stress condition. Under glass house condition also the clone CYM 08-922 recorded significantly higher proline content and SOD activity. Among gas exchange parameters, photosynthetic rate and stomatal conductance were significantly higher in CYM 08-922. Based on the results, the clone CYM 08-922 with superior drought tolerance could be used as a potential parent for the breeding of drought-tolerant varieties in sugarcane.

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72. BER57 (IC635057; INGR20072), a Solanum (*Solanum berthaultii*) Germplasm Highly Resistant to Late Blight Disease. Diploid Wild Potato Species with Wider Genetic Base.

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The elite genetic stock BER57 was developed at ICAR-Central Potato Research Institute, Shimla by Clonal Selection method from several clones regenerated from true potato seed (TPS) of wild species (Solanum berthaultii, Accession no. PI265857). BER57 is an important genetic material for fusion parent in somatic hybridization and parental line in diploid breeding programme for introgression of very high resistance to late blight trait with wider genetic base into cultivated potato and also basic research studies on diploid potato breeding. Since potato is native to Lima, Peru (South America) and under the routine germplasm procurement programme of the institute, TPS of this wild species were obtained at the institute from the International gene bank the Potato Introduction Station, NRSP-6, Wisconsin (USA). This shows successful utilization of clonal selection method in development of elite genetic stock BER57 for high resistance to late blight over four seasons under controlled conditions by challenge inoculation. DNA fingerprinting of BER57 revealed SSR alleles (STU: 182, 184, 190, 193, 202 bp, and STIIKA: 188, 192, 195, 203, 218, 240, 243 bp) for genetic fidelity. A few DUS descriptors of BER57 are: purple lightsprout, semi-compact plant foliage, small plant height, green stem colour, intermediate leaf structure, small leaf length, narrow leaf width, ovate lanceolate leaf shape, white flower corolla, small flower size, yellow anther colour, normal anther cone, normal pistil, longer stylar length, late maturity, brown tuber skin colour, rough skin, long oblong tuber shape, shallow eye depth and yellow tuber flesh colour. This wild spcies BER57 with diverse genetic background, having very high resistance to late blight disease has potential to widen the gene pool of the cultivated potato.

73. PLD47 (IC635058; INGR20073), a Potato (*Solanum polyadenium*) Germplasm Highly Resistant to Late Blight Disease. Diploid Wild Potato Species with Wider Genetic Base.

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The elite genetic stock PLD47 was developed at ICAR-Central Potato Research Institute, Shimla by Clonal Selection method from several clones regenerated from true potato seed (TPS) of wild species (Solanum polyadenium, Accession no. CGN17747). PLD47 is an important genetic material for fusion parent in somatic hybridization and parental line in diploid breeding programme for introgression of very high resistance to late blight trait with wider genetic base into cultivated potato and also basic research studies on diploid potato breeding. Since potato is native to Lima, Peru (South America) and under the routine germplasm procurement programme of the institute, TPS of this wild species were obtained at the institute from the International gene bank of the Centre for Genetic Resources, the Netherlands (CGN). This shows successful utilization of clonal selection method in development of elite genetic stock PLD47 for high resistance to late blight over four seasons under controlled conditions by challenge inoculation. DNA fingerprinting of PLD47 revealed SSR alleles (STU: 147, 154, 160, 184, 193, 197, 202, 206, 209 bp, and STIIKA: 188, 192, 195, 203, 209, 214 bp) for genetic fidelity. A few DUS descriptors of PLD47 are: purple lightsprout, open plant foliage, small plant height, green stem colour, poorly developed wings, open leaf structure, large leaf length, medium leaf width, ovate lanceolate leaf shape, white flower corolla, small flower corolla size, yellow anther colour, normal anther cone, normal pistil, longer stylar length, late maturity, yellowish brown tuber skin colour, rough skin, ovoid

tuber shape, shallow eye depth and yellow tuber flesh colour. This diploid wild species PLD47 with diverse genetic background having very high resistance to late blight disease has potential to widen the gene pool of the cultivated potato.

74. JAM07 (IC635059; INGR20074), a Potato (*Solanum jamesii*) Germplasm Highly Resistant to Late Blight Disease. Diploid Wild Potato Species with Wider Genetic Base.

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The elite genetic stock JAM07 was developed at ICAR-Central Potato Research Institute, Shimla by Clonal Selection method from several clones regenerated from true potato seed (TPS) of wild species (Solanum jamesii, Accession no. PI 498407). JAM07 is an important genetic material for fusion parent in somatic hybridization and parental line in diploid breeding programme for introgression of very high resistance to late blight trait with wider genetic base into cultivated potato and also basic research studies on diploid potato breeding. Since potato is native to Lima, Peru (South America) and under the routine germplasm procurement programme of the institute, TPS of this wild species were obtained at the institute from the International gene bank the Potato Introduction Station, NRSP-6, Wisconsin (USA). This shows successful utilization of clonal selection method in development of elite genetic stock JAM07 for high resistance to late blight over four seasons under controlled conditions by challenge inoculation. DNA fingerprinting of JAM07 revealed SSR alleles (STU: 171, 175, 178, 193, 202 bp, and STIIKA: 192, 195, 203, 209 bp) for genetic fidelity. A few DUS descriptors of JAM07 are: red-purple lightsprout, semi-compact plant foliage, small plant height, green stem colour, open leaf structure, small leaf length, narrow leaf width, narrow lanceolate leaf shape, white flower corolla, small flower corolla size, yellow anther colour, normal anther cone, normal pistil, longer stylar length, late maturity, brown tuber skin colour, rough skin, oblong tuber shape, shallow eye depth and white tuber flesh colour. This diploid wild species JAM07 with diverse genetic background having very high resistance to late blight disease has potential to widen the gene pool of the cultivated potato.

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75. CSR 59 (IC627947; INGR20075), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stresses upto ECe 10.0 dS/m with Long Bold Grain.

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A total of 800 million hectares of land are salt-affected, including both saline and alkaline soils, which are more than 6% of the world's total land area (FAO 2014). In India, 6.73 million ha are affected by salt and 3.77 million ha are affected by alkaline soils. Genetic improvement of salt tolerance in rice appears to be economically feasible and a promising strategy for maintaining stable rice production, globally. The rice (*Oryza sativa* L.) line,

CSR 59 (IET 24547), a derivative of the cross CSR 27/ CSR 11 at ICAR-CSSRI, Karnal. The line CSR 59 was developed for saline and alkaline areas where ECe ~ 10.0 dS/m. Of the two parents, CSR 27 is salinity (ECe~ 10.0 dS/m) and another parent CSR11 is tolerant to alkalinity (pH ~ 9.9) with high yield potential.

Morpho-agronomic characteristics: The line CSR 59 was developed from the cross CSR 27/CSR 11 for saline areas ECe = 10 dSm-1 (Krishnamurthy *et al.*, 2018). During 2014, CSR 59 showed superiority yield advantage of 8%, 94%, 10%, 7% and 8% over CSR 36 (National check), Jaya (Yield check), CSR 10, Local Check and CSR 23 respectively under high salinity condition in Panipat and Karnal district of Haryana (Directorate of Rice Research, 2015). During 2015, CSR 59 showed superiority yield advantage of 4%, 174 %, 26%,2% and 28 % over CSR 36 (National check), Jaya (Yield check), CSR 10, Local Check, and KR09003(Qualifying Variety IET 24538) respectively across salt affected locations of Panipat and Karnal in Haryana (Directorate of Rice Research, 2016). During 2016, CSR 59 showed superiority yield advantage of 66%, 722%, 42%, 61%, 75% and 39 over CSR 36 (National check), Jaya (Yield check), CSR 10, Local Check, CSR 23 and KR09003 (Qualifying Variety IET 24538), respectively across salt affected locations of Panipat and Karnal in Haryana (Directorate of Rice Research, 2017). The line CSR 59 was found superior in yield over CSR 36 (National check), Jaya (Yield check), CSR 10, Local Check, CSR 23 and KR09003 (Qualifying Variety IET 24538) by 19%, 185% 23%,17%, 12% and 18%, respectively across the three years (2014, 2015 and 2016) in salt affected locations of Haryana (Panipat and Karnal). The performance of CSR 59 was consistently high under salinity for three successive years in Haryana. It showed yield superiority over CSR 36 (National check), Jaya (Yield check), CSR 10, Local Check, CSR 23 and KR09003 (Qualifying Variety IET 24538).

Associated characters and cultivation practices: This line is medium duration (130-135 days), dwarf culture, with green foliage, long bold grains and complete panicle exertion. This line is moderately tolerant to stem borer, leaf folder and gall midge. This line is moderately tolerant to blast. The performance of CSR59 was consistently high across salinity stress locations for three successive years with other acceptable quality traits. This Germplasm can be used as a genetic stock for future breeding programmes aiming at development of high yielding salt tolerant rice varieties for saline and alkaline soils.

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76. CISG 20 (IC628575; INGR20076), Cotton (*Gossypium arboreum*) is a Spontaneous Mutant GMS Identified from Agronomically Adapted Line CISA 20. One among few GMS lines available in diploid. The line CISG20 (GMS) has Open Red Flower Facilitating Easy Crossing; Red Flower, Red Petal Spot and Red Plant Body.

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Cotton, also known as white gold is the leading commercial cash crop of the world. In India, cotton is grown in area of 12.3 million hectares with total production of 370 lakh bales (1 bale = 170 kg of lint) (ICAR-CICR Annual Report 2017-18). The majority of cotton area (more than 90%) is under G. hirsutum while <10% constitute the other three species (Mehetre, 2015). The identification and registration of first genetic male sterile line DS 5 in G. arboreum by Singh *et al.*, (1993) facilitated male sterility based seed production of intra-arboreum hybrids and their release. The new genetic male sterile line has been identified in the seed multiplication plot of CISG 20 at ICAR-Central Institute for Cotton Research, Regional Station, Sirsa. The GMS line CISG 20 is a spontaneous mutant identified from agronomically adapted line CISG 20 during 2008-09 crop season. It was maintained by sib mating.

Inheritance of male sterility: The male sterile plants were maintained through sib mating with male fertile plants and ratio of 3:1 was observed. The genetic study was performed by the test of goodness of fit to an expected segregation ratio by calculating the probability in Chi square test (Table 1). In F2 and BC1, the fertile-sterile plants ratio of 3:1 and 1:1 showed goodness of fit and non-significant confirming that a single-recessive gene is responsible for male sterility in line CISG 20.

Gene controlling male sterility: The male sterile plants of CISG 20 were crossed with heterozygous male fertile plants of DS 5 (GMS) line, an existing source of GMS in G. arboreum, having genetic constitution of aMs1 ams1 to ascertain whether the gene responsible for male sterility is the same or different as that of DS (GMS) which has ams1 ams1(Singh and Kumar, 1993). If the gene governing the male sterility in new source is same, then the test cross ratio among the male fertile and male sterile plants would have been 1:1, but the segregation was 3:1 ratio. Therefore, the genetic male sterility observed in the present study is governed by a single pair of alleles, which are different from the gene ams1 ams1 governing male sterility in DS5 (GMS) line. The gene for male sterility is designated as ams2 ams2 expressing completely male sterility condition and the heterozygous F1 (male fertile) is designated as aMs^2 ams^2.

Morpho agronomic characteristics: The line CISG 20 (GMS) has complete pigmentation i.e. red flower with red petal spot and red plant body which can be used as a marker trait for male sterility genotype identification and grow out test. The genetic male sterile line CISG 20 is pollen sterile throughout its reproduction stage, no pollen shedders are reported which rules out the selfed seed during hybrid seed production programme thus enhances the boll setting percentage (Patil *et al*., 2018). The line has been observed as good general combiner. Associated characters and cultivation practices: The line CISG 20 (GMS) was evaluated for five years at ICAR-CICR, Regional Station, Sirsa having plant height of 140-150 cm with 5-7 monopodia/plant and 12-17

Table 1. Segregation pattern for male and fertility and sterility in F1, F2 and BC1 generation of GMS - CISG 20

Year	Generation	Ratio	Segregation observed		χ^2	P=0.05
			Fertile	Sterile		
2016-17	F_1	-	38	-	-	-
2017-18	F_1	-	43	-	-	-
2017-18	F_2	3:1	1128	398	1.011	0.31468
2018-19	F_2	3:1	1236	442	1.683	0.19457
2017-18	BC_1	1:1	211	183	1.990	0.15836
2018-19	BC_1	1:1	215	191	1.419	0.23361

sympodia/plant. Greenish red hairs are present on all over stem with dense gossypol glands on the underside of the leaf surface. The line showed a good yield potential of 88.6g seed cotton /plant with an average of 106 bolls/ plant, GOT (Ginning outtrun) of 36.4% with an lint index of 2.63. The line also showed tolerance against sucking pests and having a better adaptation under north western cotton belt of India.

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77. IPC 2010-121 (IC628574; INGR20077), a Desi Type Chickpea (*Cicer arietinum*) Breeding Line Resistant against Race-2 of *Fusarium oxysporum* f. sp. *ciceris*.

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Wilt disease caused by *Fusarium oxysporum* f. sp. *ciceris* (FOC) is a major biotic stress for chickpea crop leading to yield losses ranging from 10-40% worldwide (Nene *et al.*, 1984). It causes 100% loss under specific conditions (Jalali and Chand, 1992). Several elite breeding lines of chickpea were screened against Kanpur race (race 2) in wilt-sick plot of ICAR-Indian institute of Pulses Research, Kanpur. Among several desi type of chickpea lines, IPC 2010-121 was found resistant for four consecutive years. Disease development was very high with 100% mortality in susceptible check (cv. JG 62) and C-104 as late wilt check with WR 315 (JG 315) as resistant check. In each years of evaluation, wilt specific differentials were planted along with test genotypes for monitoring of the racial system (Haware and Nene 1982). Per cent Disease Incidence of Fusarium wilt in IPC 2010-121 was 6.35% (2014-15), 2.10% (2015-16), 6.65% (2016-17) and 7.50% (2017-18).

The parentage (Pedigree) of the line IPC 2010-121 is single cross (one way cross) of genotypes IPC 1997-7 and IPC 1995-1. The pedigree of the parentages used in the development of IPC 2010-121 includes IPC 1997-7 = ICCV 10 / BG 364 and IPC 1995-1= (Avrodhi/ PDG 83-34) / ICCV 95118. Pedigree breeding, accompanied with type selection was followed for the development of IPC 2010-121 at ICAR-Indian Institute of Pulses Research, Kanpur.

The identified genotype IPC 2010-121 is resistant to Race-2 of FOC (Sabale *et al*., 2019). Therefore, this genotype will be useful for the chickpea breeder to include IPC 2010-121 as one of the parent in developing race specific resistant cultivars with high yield nature. Thereby, it prevents losses caused by the chickpea wilt disease.

Morpho-agronomic characteristics: The plant has semi erect type of architecture at maturity. It matures late (143 days) and has a medium seed size (Hundred Seed Weight=18.2 g). The genotype initiates flowering at 71 days after sowing while fifty per cent of the flowering reaches within 86 days after sowing. The pod initiation occurs at 91 days and fifty per cent podding reaches within 104 days after sowing. The plant height is about 65 cm. Number of pods per plant ranges from 64-80. Based on plot yield data, yield of IPC 2010-121 has been observed up to 3249 kg/ha.

Associated characters and cultivation practices: The genotype IPC 2010-121, thrive well under timely sown (first week of November) irrigated fields under Kanpur condition (East zone). Crop requires irrigation at 40-45days after sowing, pod initiation and seed setting or pod filling stages (if subjected to terminal heat/drought stress). This genotype is suitable for the development of resistant cultivars where race-2 is prevalent under irrigated condition.

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78. PM-81 (IC628568; INGR20078), a Sunflower (*Helianthus annuus*) Germplasm with Resistance to Powdery Mildew (PDS<10%).

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Sunflower (*Helianthus annuus* L.) is one of the important edible oilseed crops grown in the world after soybean and groundnut. The full potential of this crop is far from being exploited due to several abiotic and biotic stresses. The crop suffers from many fungal diseases, among them foliar disease takes a heavy toll by reducing the yield to considerable extent. Among the foliar diseases powdery mildew caused by the obligate parasite Golovinomyces orontii DC (formerly known as Erysiphe cichoracearum) is a potential destructive disease in recent years causing severe yield loss. Since decade, disease observed regularly during rabi-summer seasons and under severe conditions disease is found infecting the cotyledonary leaves up to ray florets.

Breeding efforts were initiated to develop powdery mildew resistant sunflower lines in Sunflower Scheme at Main Agricultural Research Station, Raichur during 2011-12. It was aimed to incorporate powdery mildew resistance in some of the elite lines of sunflower through intraspecific and interspecific crosses followed by selections to identify powdery mildew resistant lines. Sunflower line Powdery Mildew-81 (PM-81) was developed from an intraspecific cross between mono-head inbred (CMS-B) having good seed yield and a multi-head medium resistant line RCR-1947/1-1, followed by pedigree selection (Anon., 2016). The PM-81 has been found to be resistant for powdery mildew under artificial screening in greenhouse by spraying spore suspension culture prepared in 1% sucrose solution (Swetha 2016). Further the PM-81 was also screened in ICAR-Indian Institute of Oilseeds Research during 2017-18, wherein it recorded 'score 0' while susceptible check PS 2023 recorded 'score 9' on 0-9 scale (Anon., 2018). Several earlier reports are available for powdery mildew resistant line in wild relatives and pre-breed inter-specific crosses of sunflower (Reddy *et al.*, 2013). However, PM-81 is the first intra-specific cross derivative with cultivated background which can be directly used in line conversion and hybrid development.

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GENERAL

Indian Journal of Plant Genetic Resources (IJPGR) is the official publication of the Indian Society of Plant Genetic Resources. Aim of the Journal is to disseminate knowledge on plant genetic resources (PGR) research and application. Being the only journal in the area of PGR, the journal aims to provide a forum for discussion and debate on current issues of PGR. For publication in the journal, the authors must be a member of the Society. IJPGR publishes full-length papers or short communications of original scientific research in the field of plant genetic resources. Review articles (with prior consent or invitation only) summarizing the existing state of knowledge in topics related to plant genetic resources will also be published.

Contributions should be as concise as possible. The maximum length of the review article, full-length papers and short communications is usually restricted to 12, 6, 3 printed pages including illustrations and tables, respectively.

SCOPE

- Basic research on biosystematics, genetics and genomics related to PGR
- Applied research on field and laboratory evaluation of PGR
- Supportive research in conservation and quarantine of PGR
- Policy research on access and benefit sharing; IPRs
- Status reports on ecology, conservation, traditional knowledge and use of PGR

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ORGANIZATION OF THE MANUSCRIPT

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Name and Address: The name of authors and the address of the institution where the work was carried out should be mentioned below the title. Present address of correspondence, if different, should be given as footnote indicating by asterisk (*) the author to whom the correspondence and reprint requests are to be made. E-mail addresses should also be indicated, if any.

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Introduction should be brief and limited to the statement of the problem and aim of the experiment.

Materials and Methods should include relevant details on the nature of material, experimental design, the techniques employed and the statistical method used. For well-known methods, citation of reference will suffice.

Results and Discussion should be clear to readers in different disciplines. Units of measurement should be SI.

Tables should be typed on separate sheets, each with a heading stating its contents clearly and concisely. Numerical data and calculations should be thoroughly checked.

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WOI (1985) *The Wealth of India – Raw Materials. A Dictionary of Indian Raw Materials and Industrial Products – Raw Material* Vol 1: A (Revised). Publications and Information Directorate, Council of Scientific and Industrial Research, New Delhi, 513 p.

Engels, JMM and V Ramanatha Rao (eds) (1988) *Regeneration of seed crop and their wild relatives.* Proceedings of a Consultation Meeting, 4-7 December 1995. ICRISAT, Hyderabad, India and IPGRI, Rome, Italy, 167 p.

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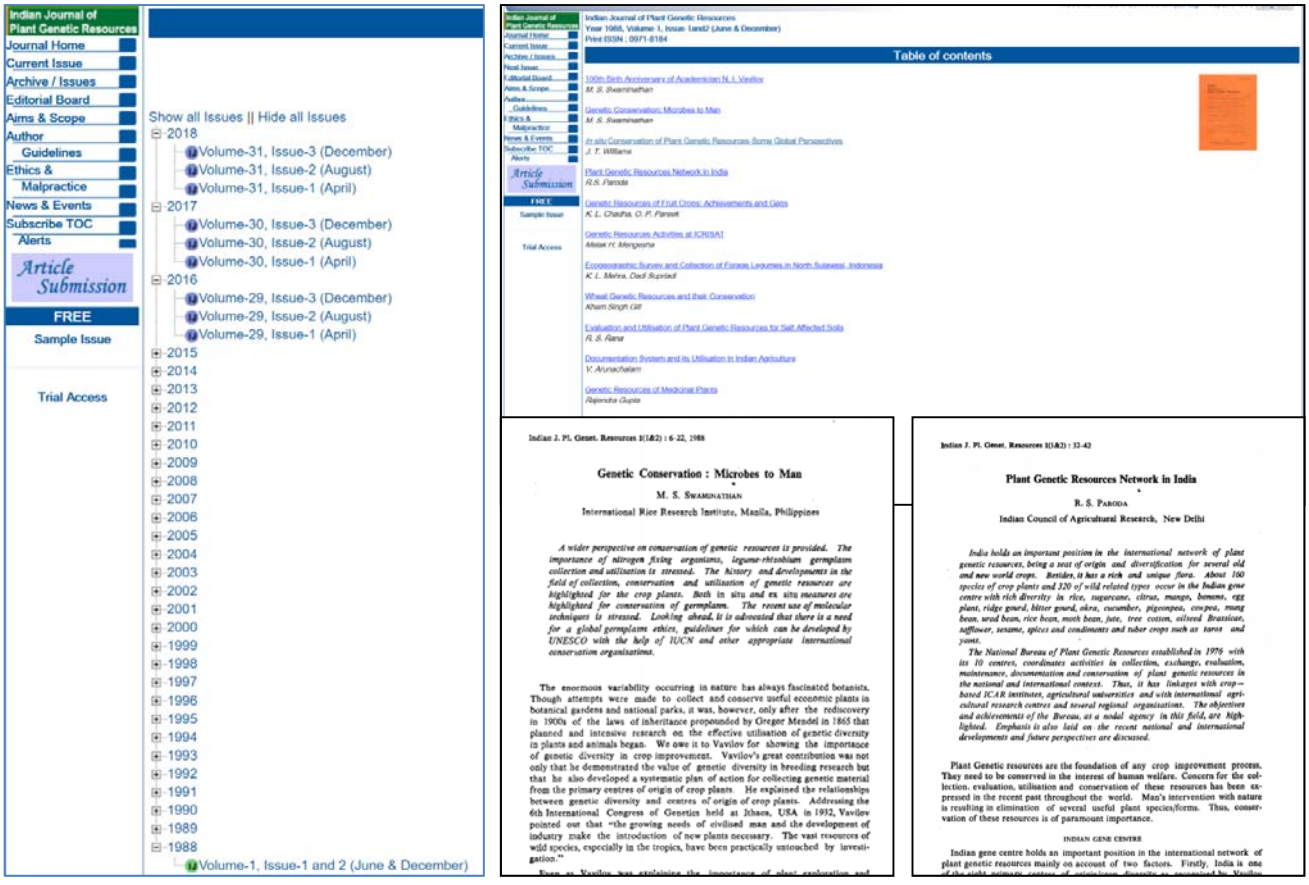

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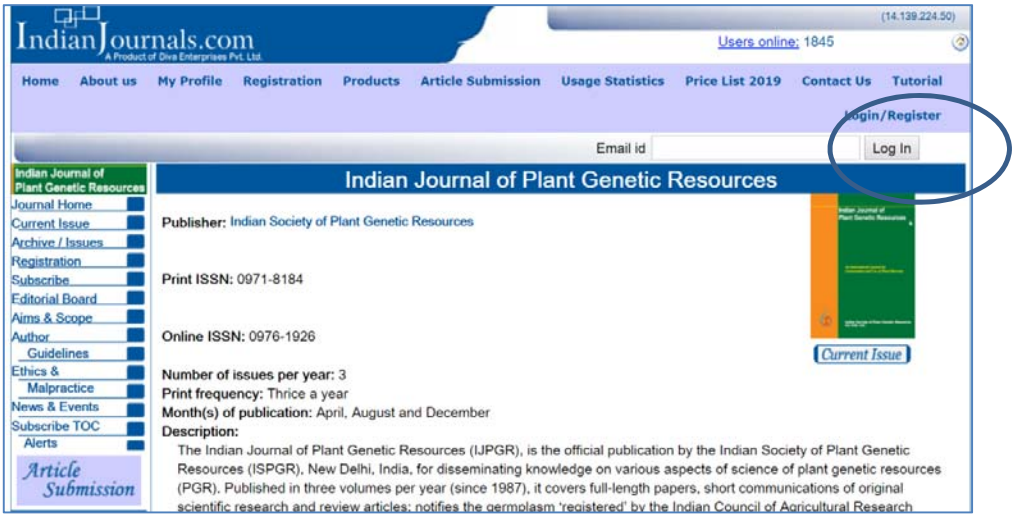

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