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(Registration No. S/18336)

The Society was founded in 1987 with the following objectives:

- To serve and promote the scientific cause and to advance academic interest in the field of plant genetic resources.
- To disseminate knowledge relating to various aspects on plant genetic resources.
- To provide a forum for organizing symposia/conferences with a view to develop close relationship among the scientists engaged and interested in plant genetic resources activities.

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CONTENTS

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RESEARCH ARTICLE

Expression and Stability Studies on Axillary Branching in Novel Grain Sorghum (*Sorghum bicolor* L.) Somaclonal Mutant, SbABM

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Sorghum bicolor axillary branched mutant (SbABM) is the first axillary branched mutant reported in grain sorghum till date with desirable phenotype and stability of expression of axillary branching over generations. However, the trait was expressed at different levels of intensity (for number of axillary branches per plant) within the progenies of a single true breeding plant. The mutant along with its parent A-1 and a local check M 35-1 were analysed in variable environments like variation in plant density and intensive management practices over years to understand the stability and expression of axillary branching. The mutant exhibited significant increase in yield which was in turn attributed to significant increase in yield attributing parameters *viz.,* number of branches per plant, number of panicles per plant, panicle weight per plant and thousand seed weight compared to A-1 and M 35-1 in all the three spacings and at two fertilizer levels. However, the expression of the traits in SbABM under different treatments was at par with each other. Though there was some variation in the degree of expression of characters in SbABM, the expression of the characters was highly stable, genetically controlled and significantly superior over the other two *rabi* varieties.

Key Words: Axillary branching, Lodging resistance, Mutant, Stay green, Variable environment

Introduction

Shoot architecture is largely determined by the number of axillary shoots produced. Axillary shoot development begins with the initiation of a meristem in the axil of a leaf to form a bud (Ward and Leyser, 2004; McSteen and Leyser, 2005). Depending on internal and environmental signals, the bud may continue growing to form an axillary shoot or enter into dormancy. In this context, axillary branching has great relevance to modern agriculture by maintaining an appropriate branching habit that maximizes utilization of resources and production of biomass and/or reproductive structures. This goal may be achieved in part through a better understanding of mechanism of axillary shoot development in plants. In-depth knowledge of the development of branches will help in modifying the shoot architecture of crops to maximize yield. Although environmental signals are key determinants of the development of an axillary shoot, little has been done to understand how these signals regulate branching at the molecular level.

To examine axillary shoot development in plants, axillary meristem mutants have been identified and characterized in maize, pea, petunia, tomato and *Arabidopsis* (Kerstetter and Hake, 1997; Schmitz and Theres, 1999). There are no detailed studies in sorghum except those on the wild type sorghum with axillary branching and its mutant phyB-1 (phytochrome B) by Kebrom *et al.* (2006). Grain sorghum (*Sorghum bicolor* L.) is an important source of food, feed and biofuel, especially in the semi-arid tropics because this cereal is well adapted to harsh, drought prone environments. The cultivated sorghum genotypes are generally uniculm. However, Maralappanavar *et al.* (2000) reported an axillary branched mutant, SbABM (*Sorghum bicolor* Axillary Branched Mutant) in cultivated sorghum obtained through somaclonal mutation, derived from Annigeri-1 (A-1) wherein branching at every node from the lower most node till the top most, was reported (Fig. 1). This is the first axillary branched mutant reported in grain sorghum till date with desirable phenotype and stability of expression over generations. Sorghum is a self- pollinated species and the axillary branched mutant plants were maintained as homozygous, true breeding lines for several generations at Agricultural Research

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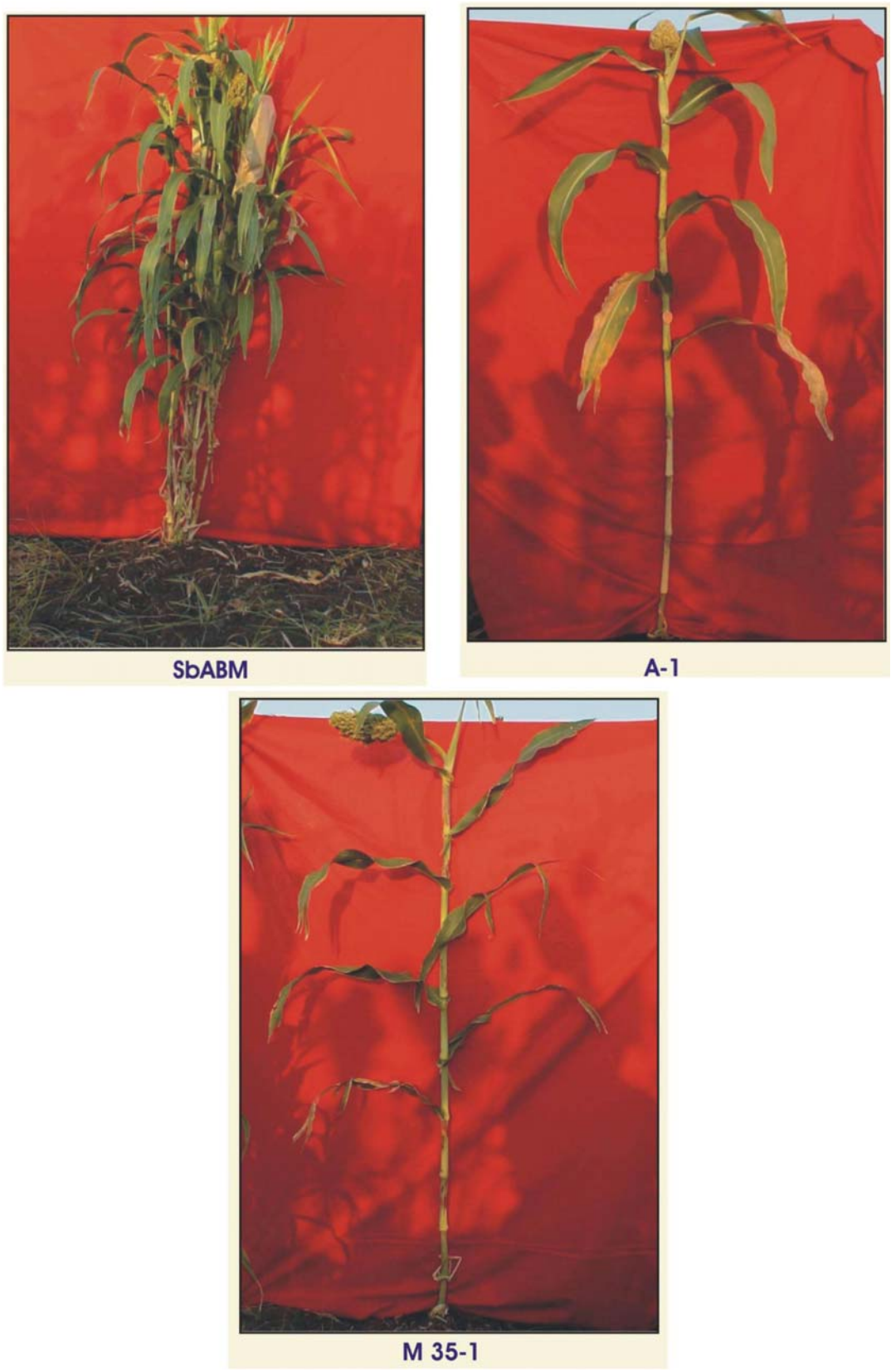

Fig. 1. Phenotypic features of the sorghum mutant, SbABM, parental variety A-1 and the local check M 35-1

Station, University of Agricultural Sciences, Dharwad, India. To understand whether axillary branching in the mutant is genetically controlled or is mainly because of environmental factors, the present study was undertaken to elucidate the stability and expression of axillary branching in variable environments.

Materials and Methods

The experiments on *Sorghum bicolor* were conducted in the experimental field of Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka, India. The experimental site is situated at an altitude of 678 m above the mean sea level at latitude 15°26′ North and at longitude 76°7′ East and has well-drained fertile medium black soil with an average annual rainfall of 735 mm.

The experiment was laid out in a split plot design with three genotypes *viz.*, Annigeri-1 (A-1), SbABM (an axillary branched mutant derived through somaclonal mutation) and a local check M 35-1 (Fig. 1) as main plots, three planting geometries *viz.,* 45 × 15 cm, 60 × 15 cm and 75 × 15 cm as subplots, two fertilizer levels *viz.* 40:20:20 Kg N, P_2O_5, K_2O ha^{-1} and 80:40:40 Kg N, P_2O_5, K_2O ha^{-1} and one protective irrigation at flowering stage *i.e.,* 65 days after sowing as sub subplots with four rows per treatment replicated two times. The same set of experiment was repeated for two years during *rabi* season of 2008-09 and 2009-10.

Fertilizer dose as per the treatments was applied at the time of sowing. Nitrogen, phosphorous and potassium were applied in the form of urea, single super phosphate and nitrate of potash, respectively. Half the dose of nitrogen and, full dose of phosphorus and potassium were applied as basal dose in five cm deep furrows which were opened at five cm away from seed row. The remaining half of nitrogen was top-dressed at 30 days after sowing.

Observations were recorded on ten quantitative traits, *viz.* days to 50% flowering, days to maturity, plant height, number of axillary branches per plant, number of panicles per plant, panicle weight per plant, thousand-grain weight, grain yield per plant, fodder yield per plant and lodging percentage, which are the characteristic idiotypic changes due to somaclonal mutation. Data were recorded on each of the five randomly selected competitive plants tagged in each replication of all the test genotypes.

SPAD Chlorophyll Meter Reading (SCMR)

SPAD (Soil Plant Analytical Development) chlorophyll meter reading (SPAD 502; Minolta company Ltd.) measures the greenness or relative chlorophyll content of leaves. SCMR was taken at an interval of 60 and 90 days after sowing on five random plants. The third leaf from the top was used for measuring SCMR, which was taken on one side of leaf blade, midway between the leaf base and tip. The readings were taken between 10.00 and 12.00 hours of the day. Mean of the readings from five tagged plants was recorded.

The data collected from the experiment were subjected to factorial statistical analysis by Gomez and Gomez (1984). The level of significance in 'F' and 't' tests was P = 0.01. Critical difference values were calculated. Treatment combinations were compared by using the critical difference values. Correlation analysis was carried out to study the nature and degree of relationship between various growth yield components and yield. The statistical analyses was worked out individually for both the years.

Results and Discussion

Multiple shoot branching refers to the ability of a plant to produce an extra number of axillary shoots. This phenotype usually reflects healthy and yield-promising plant because increase in shoot branching can be translated to greater vegetative biomass, fruit and seed production. Historically, multiple shoot branches was a desirable trait in some crop plants, such as rice, in which multiple shoot branches (tillers) are associated with increased yield. In contrast, maize cultivars have been selected for a low number of axillary branches to improve the quality of the ears and kernels by concentrating plant resources.

High-yield production can be achieved by genetically altering the number of shoots per plant and/or by modifying other processes related to plant growth and development, as axillary branch formation is controlled by a complex interaction between genetically regulated developmental processes and the environment. Multiple shoot branching can also be achieved, to some extent, by augmenting the amount of fertilizers used in the field. However, the application of large amount of fertilizer to increase the number of shoot branches per plant would not only enhance input cost to farmers, but also lead to an accumulation of unused fertilizers in the soil which would ultimately pollute the groundwater. Therefore,

the probable solution is to use reasonable amount of supplied nutrition and genetically alter the number of shoot branches to maximize yield in crop plants. This requires an understanding of the mechanism controlling plant architecture.

Performance of Sorghum bicolor Axillary Branched Mutant SbABM

Genotypes play an important role in determining the yield of a crop. The potential yield of genotypes within genetic limits is set by its environment. Genotypes differ in their yield potential depending on many physiological processes which are controlled by both genetic makeup and the environment.

The performance (for two years) of the three genotypes for grain yield per plant and other related traits is depicted in Table 1 and the average performance over two years is depicted in Figure 2. Of the three genotypes (SbABM, A-1 and M 35-1), SbABM recorded significantly higher grain yield than A-1 and M 35-1 which exhibited comparable yield. The increase in grain yield in SbABM over its parent, A-1 and M -35-1, was 57 and 60.6 %, respectively.

The higher grain yield of SbABM over other two genotypes is attributed to improved yield components like number of branches per plant, number of panicles per plant, panicle weight and thousand grain weight. Axillary branching, the characteristic feature of the mutant, was significantly higher than that in A-1 and M 35-1. The average number of branches per plant in the mutant was 7.78 compared to 2.33 in A-1 and 2.12 in M 35-1. The increase in number of branches per plant also resulted in significant increase in fodder yield per plant (109.46 gm) in the mutant. Out of eight branches

Table 1. Expression of different traits in three sorghum genotypes as influenced by different row spacing and fertilizer levels

Treatments	Days to 50% flowering		Days to maturity		Plant height (cm)		Number of axillary branches per plant		Number of panicles per plant	
	2008-09	2009-10	2008-09	2009-10	2008-09	2009-10	2008-09	2009-10	2008-09	2009-10
Genotypes										
A-1	76.8	73.2	135.5	129.5	181.25	174.26	2.41	2.25	1.83	1.83
SbABM	65.0	68.9	149.6	145.1	166.61	164.28	7.66	7.91	5.00	6.08
M35-1	75.8	70.2	134.3	126.8	190.92	152.46	2.25	2.00	1.66	1.67
S.Em ±	0.8	0.9	2.0	1.9	3.40	3.35	0.98	0.74	0.98	0.74
CD (P=0.01)	3.6	3.8	9.5	8.8	14.70	14.47	4.23	3.20	4.23	3.20
Spacing										
45 x 15 cm	72.8	71.9	137.5	126.3	185.45	174.27	3.66	3.25	2.16	2.33
60 x 15 cm	73.4	72.9	139.1	132.2	187.99	164.29	4.16	4.33	2.83	3.41
75 x 15 cm	74.2	72.2	142.9	133.3	165.37	152.46	4.50	4.58	3.50	3.83
S.Em ±	0.9	0.7	1.6	0.3	2.33	3.78	1.12	0.98	0.22	0.23
CD (P=0.01)	5.6	NS	10.2	NS	15.19	24.58	7.29	6.38	NS	NS
Fertilizer (Kg NPK/ha)										
40:20:20	73.4	71.3	138.5	133.8	170.29	151.20	3.77	3.66	2.50	2.83
80:40:40	73.6	73.3	141.2	127.3	188.90	176.13	4.44	4.44	3.16	3.55
S.Em ±	0.4	0.3	1.2	0.2	14.57	2.49	0.54	0.35	0.24	0.04
CD (P=0.01)	31.8	NS	106.1	NS	311.42	223.89	NS	NS	NS	NS

NS- Not significant

Contd.

Treatments	Panicle weight per plant (g)		Thousand grain weight (g)		Grain yield per plant (g)		Fodder yield per plant (g)		Lodging percentage	
	2008-09	2009-10	2008-09	2009-10	2008-09	2009-10	2008-09	2009-10	2008-09	2009-10
Genotypes										
A-1	64.29	57.91	30.27	30.95	55.10	44.12	61.90	67.07	83.66	80.58
SbABM	96.30	83.33	36.77	35.91	85.67	75.58	102.54	116.38	26.00	34.08
M35-1	65.09	64.75	31.60	30.95	51.92	47.97	58.78	69.43	83.83	79.66
S.Em ±	4.45	1.68	0.74	0.82	3.00	1.96	1.20	1.55	1.03	1.09
CD (P=0.01)	19.22	7.27	3.11	3.54	12.97	8.47	5.19	6.71	4.47	4.71
Spacing										
45 × 15 cm	75.63	67.09	32.30	32.97	64.31	51.41	73.70	77.37	62.74	68.41
60 × 15 cm	74.12	68.64	33.14	32.08	66.56	52.71	72.77	87.31	65.41	62.00
75 × 15 cm	75.93	7078	33.20	32.84	69.97	55.19	76.75	88.21	65.33	63.91
S.Em ±	2.61	3.74	0.37	NS	2.87	0.75	1.04	2.09	2.03	0.79
CD (P=0.01)	16.99	24.35	0.12	NS	18.68	4.88	6.79	13.62	13.19	5.14
Fertilizer (Kg NPK/ha)										
40:20:20	73.64	65.82	33.05	33.14	64.45	53.53	68.25	85.04	63.94	58.88
80:40:40	76.81	71.84	32.72	32.07	64.01	58.24	80.56	83.55	65.05	70.66
S.Em ±	3.80	0.71	0.26	NS	0.76	0.10	0.83	1.65	0.79	0.71
CD (P=0.01)	341.69	63.87	0.34	NS	68.04	10.86	74.45	148.25	70.73	63.66

NS- Not significant

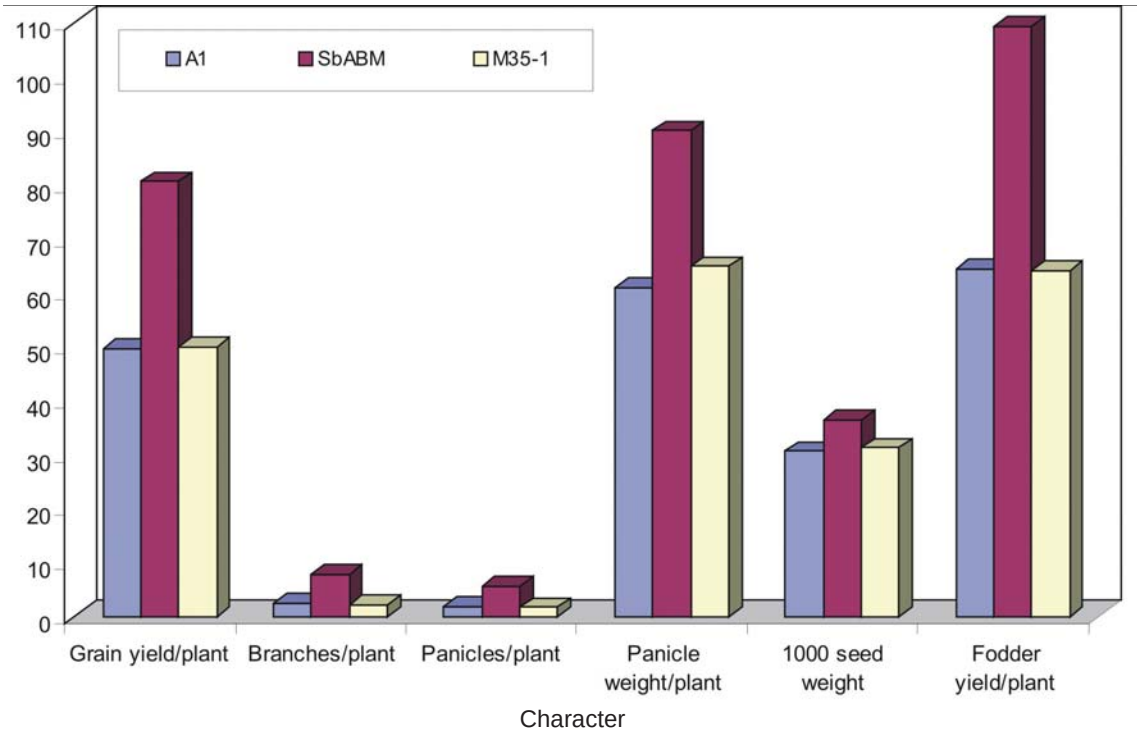

Fig. 2. Average performance of the three sorghum genotypes for important yield characters

per plant, six branches produced fertile inflorescence in SbABM as against 1.83 and 1.66 in A-1 and M 35-1, respectively.

The increase in number of panicles per plant resulted in increased panicle weight of the mutant. The panicle weight/plant in the mutant was 41.21 and 52.94% higher than that in A-1 and M 35-1, respectively. Similarly, per cent increase in thousand seed weight in the mutant compared to its parent and local check was 16.1 and 18.7 %, respectively. The grain size in all the lateral branches was same as in the main head. Owing to this positive feature, it is possible to bulk the seeds from main as well as axillary heads without discriminating between them.

The mutant SbABM, not only exhibited improved yield, but also displayed improvement in some of the growth components. Significant difference was observed between the genotypes for days to 50 % flowering. The mutant took significantly less number of days and flowered 8.25 and 9.79 days earlier than did A-1 and M 35-1, respectively. The mutant displayed reduced plant height compared to that of A-1 and M 35-1. Average plant height of the mutant was 165.44 cm whereas that of A-1 and M 35-1 was 177.73 cm and 171.69 cm, respectively.

There was 63% more lodging in A-1 and M 35-1 compared to that in the mutant (Fig. 3). On an average, only 30% of the plants showed lodging in SbABM, whereas in A-1 and M 35-1, 80 % of the plants showed lodging at the time of harvest. Usually dryness of the stalk is associated with lodging of the plant. In this mutant, at every node, new growth was induced which was similar to the growth in main stem. By virtue of this, the branches as well as the main stem remain juicy. It is because of this reason that the mutant resists lodging.

Leaf greenness, an integrated measure of the stay green phenotype, was analyzed using SPAD meter at 60 and 90 days after sowing (Table 2). The average SPAD values recorded at 90 DAS was less compared to the values recorded at 60 DAS in all the three genotypes At 60 DAS, there was 43.7 and 38.7 % more leaf greenness in the mutant than that in A-1 and M 35-1, respectively. Similarly, the per cent increase at 90 DAS was 58.25 and 54.48 in the mutant compared to that at, in A-1 and M 35-1, respectively. This clearly shows that, when the two genotypes, A-1 and M 35-1 exhibited senescence, the mutant still showed leaf greenness. The SPAD readings clearly indicated increased chlorophyll content in the mutant. This is an indication of additional greenness at different stages of crop growth. Even after maturity, the

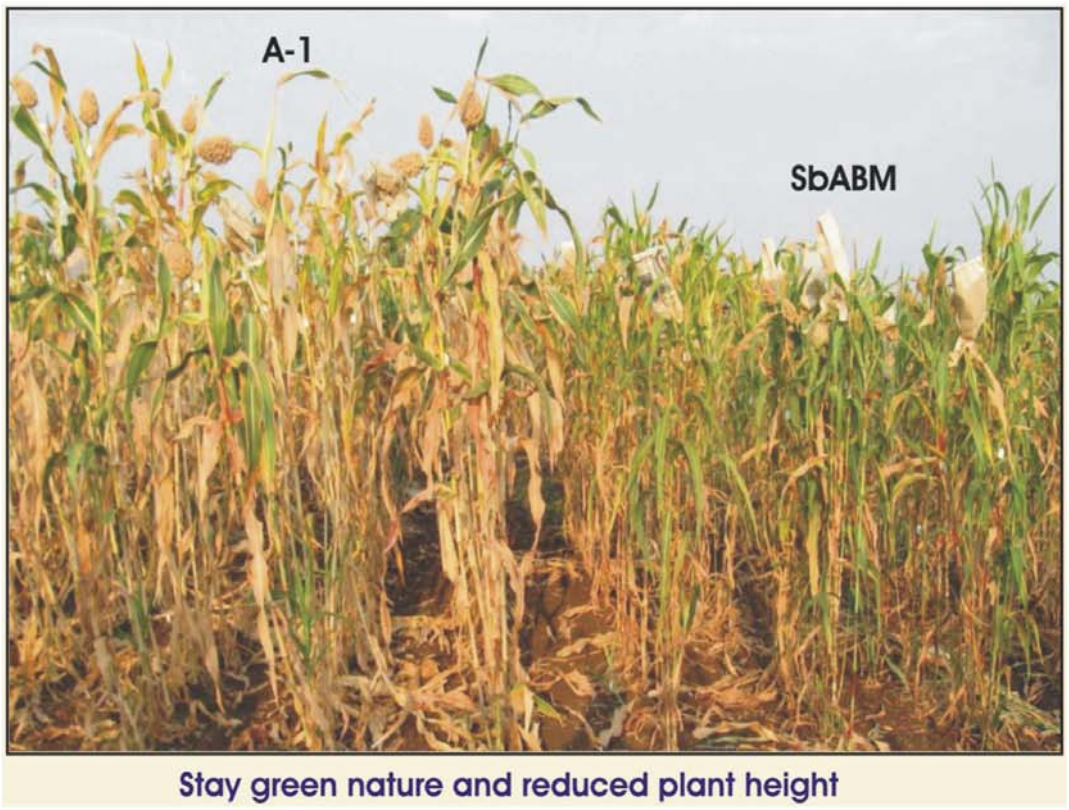

Fig. 3. Plant type features of sorghum mutant, SbABM

Table 2. SPAD chlorophyll meter reading in three sorghum genotypes as influenced by different row spacings and fertilizer levels

Treatments	SPAD chlorophyll meter reading			
	2008-09		2009-10	
	60 DAS	90 DAS	60 DAS	90 DAS
Genotypes				
A-1	30.40	22.56	28.10	21.25
SbABM	43.19	35.33	40.89	34.00
M35-1	31.42	23.65	29.20	22.42
S.Em ±	0.85	0.72	0.77	0.81
CD (P=0.01)	3.67	3.11	3.33	3.50
Spacing				
45 × 15 cm	34.42	26.75	32.12	25.16
60 × 15 cm	34.69	26.55	32.39	25.64
75 × 15 cm	35.90	28.25	33.69	26.86
S.Em ±	0.52	0.47	0.53	0.49
CD (P=0.01)	NS	NS	NS	NS
Fertliser				
40:20:20: Kg NPK/ha	34.51	26.33	32.10	25.44
80:40:40 Kg NPK/ha	35.50	28.03	33.37	26.33
S.Em ±	0.24	0.20	0.24	0.25
CD (P=0.01)	NS	NS	NS	NS

leaves remained lush green pointing to the stay green nature of the genotype. Increased chlorophyll content coupled with stay green nature has led to distinct increase in total photosynthetic output of the leaf. In addition to this, there was a continuous increase in leaf number, contributing to a total increase in green leaf area, finally leading to enhanced source. This, in turn, facilitated increased filling of grains contributing to higher grain weight. Apart from this, the increase in source even in later formed axillary panicles was so evident that the boldness of the grain size was maintained in all the panicles.

The total biomass of SbABM was significantly higher than that of the parent A-1 and M 35-1, contributing to higher fodder value (109.46 g/plant). This is an important requirement for acceptance of *rabi* genotypes.

Effect of Spacing on Genotype

Branching of plants could be modified by altering the plant density. Higher the plant density, lesser is the branching due to increased competition among the plants for light and nutrients. However, lower plant density increases branching of plants. To know the effect of plant density on axillary branching, the mutant along with its parent A-1 and local check M 35-1 were analyzed in three different row spacings.

From Table 1, it is clear that in wider row spacing of 75 × 15 cm, there was increase in yield (83.12 g/plant) of the mutant, SbABM whereas grain yield per plant in closer and medium row spacing was comparable with each other. Compared to A-1 and M 35-1, the mutant displayed significantly higher grain yield in all the three spacings. Average percent increase in grain yield of the mutant was more than 60 compared to that in, of, A-1 and M 35-1, in all the three spacings.

The increased grain yield of the mutant was due to improved yield attributing characters like number of panicles per plant, panicle weight and thousand seed weight exhibited by the mutant. For all the above traits, there were higher values in wider row spacing, though these were at par with closer and medium row spacing.

The mutant exhibited earliness for days to 50% flowering. Among the three spacings, wider row spacing delayed flowering compared to medium and closer row spacing in all the three genotypes. The mutant was 10 days earlier than A-1 and M 35-1 for days to 50 % flowering. This trend was, however, not exhibited for days to maturity. Maturity period of the mutant was delayed by more than 15 days compared to A-1 and M 35-1 in all the three spacings. Closer spacing led to early maturity compared to medium and wider row spacing. Under wider row spacing, the mutant recorded more number of panicles per plant (Table 1) and hence delay in maturity. The mutant produced branches only after the main inflorescence was formed. It took more than a week's time to have inflorescence in the branches,

hence increased number of panicles per plant led to the corresponding delay in maturity of the mutant.

Compared to A-1 and M 35-1, the mutant displayed reduced plant height in all the three spacings. Among the three different spacings, the plant height was more in narrow row spacing compared to medium and wider spacing. The increase in plant height under narrow row spacing was mainly due to competition for light among the plants owing to increased plant density.

Number of branches per plant in medium and wider row spacing was significantly higher than that in narrow row spacing in the mutant, SbABM. In the genotypes A-1 and M 35-1, number of branches per plant was comparable among all the three spacings yet it was significantly lower than those of the mutant. On an average, the mutant recorded eight branches per plant. Out of these eight branches, approximately five branches per plant produced panicles. Similar to number of branches per plant, number of panicles per plant was also high in medium and wider row spacing, which were at par with each other and was significantly higher than A-1 and M 35-1 in all the three spacings.

On an average, the mutant exhibited 40% increased panicle weight/plant in all the three spacings compared to its parent and the local check. No significant difference was observed in SbABM for panicle weight among all the three spacings. The mutant recorded significantly higher seed weight (>36.00 g/1000 seeds) irrespective of the spacings, compared to A-1 and M 35-1.

Similarly, the lodging percentage was significantly less (<30%) in the mutant than that in A-1 and M 35-1, in all the three spacing. The resistance to lodging in the mutant could be mainly due to juicy stem. Resistance to lodging is also one of the important traits for terminal drought-tolerant genotypes.

The increase in number of branches per plant also resulted in significant increase in fodder yield per plant (> 100 gm/plant), in the mutant.

The increase in number of leaves per plant increases the photosynthetic area and hence increase in leaf chlorophyll content. As evident from the SPAD meter reading (Table 2), the mutant exhibited significantly higher SPAD meter values than those exhibited by A-1 and M 35-1, at both 60 (>40.00) and 90 (>30.00) days after sowing, in all the three spacings. These traits are very important due to stay green nature of the genotypes and coupled with increased fodder yield and superior quality, make the genotype highly suitable for both grain and fodder purposes.

Effect of Fertilizer and Irrigation on Genotype

Similar to the effect of spacing on genotypes, with the increase in fertilizer and irrigation, the genotypes displayed improved yield and other yield attributing traits. With the increase in fertilizer, the mutant displayed significantly higher yield and yield attributing traits like number of panicles per plant (>5), panicle weight (>90 g/plant) and thousand seed weight (>36 g) when compared with A-1 and M 35-1. Significant difference was also observed for number of branches per plant, fodder yield per plant and SPAD meter readings. Though the mutant was far superior than other two genotypes for most of the agronomic traits, yet it did not exhibit any significant difference at low and high fertilizer levels.

Correlation Analysis

The nature of relationship between grain yield per plant and other parameters was compared with correlation coefficient (Table 3). Grain yield was positively and significantly correlated with all the parameters except for plant height during 2008-09 and 2009-10.

In the mutant (SbABM), axillary branching was seen at nodal points, therefore, the branches were borne on the main stem in an alternate fashion *i.e.,* on left and right side of the main stem. On an average, it was observed that six branches terminated in fertile inflorescence under normal conditions in this genotype. Figure 4 depicts the average % contribution of seed yield from the panicles born on axillary branches on both left and right side of the plant, to the total seed yield per plant. When the distribution of seed weight contributed by each of the side branches was considered, there was a decline in the contribution from side branches which were away from the main branch. Thus, there was a symmetric increase in contribution while moving from last side branch to the main branch. This is one of the characteristic features of the mutant SbABM.

An attempt was made to know the average contribution from main panicle and panicles from axillary branches to the total seed yield per plant in different treatments (three genotypes, three different spacings and two fertilizer levels) (Table 4). From the Table, it is clear that in the mutant, the contribution from main panicle accounts for 40-50 %, whereas that from the panicles of axillary branches was 50-60 % to the total seed yield per plant. In A-1 and M 35-1 genotypes, the

Table 3. Correlation co-efficient (r) between grain yield per plant and other parameters of sorghum

S.No.	Parameters	'r' values	
		2008-09	2009-10
1	Days to 50 percent flowering	0.685*	0.826*
2	Days to maturity	0.820*	0.896*
3	Plant height	0.055	-0.494
4	Number of branches per plant	0.905*	0.953*
5	Number of productive branches per plant	0.913*	0.902*
6	Percentage of branched plants	0.875*	0.926*
7	Number of leaves per plant	0.818*	0.826*
8	Panicle length	0.554	0.880*
9	Panicle breadth	-0.504	-0.667*
10	Panicle weight/plant	0.782*	0.903*
11	Thousand grain weight	0.801*	0.877*
12	Fodder yield per plant	0.859*	0.821*
13	Lodging percentage	0.748*	0.961*

* - Significant at 5% probability level

main panicle contributed more than 70%, while those from axillary branches contributed less than 30 % to the total seed yield per plant.

When the number of branches per plant increased (in wider row spacing and with higher fertilizer dosage), percent contribution from the main panicle to the total yield decreased slightly, while the contribution from the panicles born on axillary branches increased. However, it was seen that in treatments with higher number of branches (wider spacing and higher fertilizer) actual yield per plant was more than that in treatments with lower number of branches (narrow spacing and low fertilizer). Therefore, it can be concluded that, the plant tries to put forth more branches and this trait is enhanced if the plant is given wider spacing or high dose of fertilizer and irrigation (intensive management). From Table 4, it is clear that the % contribution of main panicles became lesser with widening of spacing and higher dose of fertilizer, whereas that from branched panicles increased.

These results *i.e*., the effect of plant density and increased nutrient supply to the mutant suggested that, even though medium and wider row spacing and increased fertilizer application resulted in the increased expression of different agronomic traits in the mutant, it did not affect the characters studied under different environmental conditions. Therefore, it could be concluded that, even though plastic in nature due to environmental conditions, the mutant characters are genetically controlled and significantly superior to those of the other two *rabi* varieties. A study was also conducted to understand penetrance and expressivity of axillary branching in the mutant and it revealed stable penetrance of more than 85 % for axillary branching (Immadi *et al*., 2014). However, the trait exhibited variable expressivity and the deviation (from mean) among the plants was not heritable. An attempt was also made to understand the nature of inheritance of axillary branching which is of great significance for the genetic modification of plant architecture for improved yield and fodder qualities. The mutant line, SbABM, was crossed with five normal sorghum cultivars both as a male and a female parent, to elucidate the effect of cytoplasm on axillary branching, if any. All the ten F_2 populations showed the same segregation ratio of three mutant to one normal type phenotype based on Chi square test. The results revealed that axillary branching is controlled by a single dominant nuclear gene (Immadi *et al*., 2014).

Considering its developmental significance and phenotypic diversity, this mutant was subjected to detailed genetic analysis (Immadi *et al*., 2016). To

Table 4. Contribution from main panicle and panicles from axillary branches to the total seed yield per plant in different treatments

	Contribution from	45 × 15cm		60 × 15 cm		75 × 15 cm		Low fertilizer		High fertilizer	
		Actual yield (g)	% contribution	Actual yield (g)	% contribution	Actual yield (g)	% contribution	Actual yield (g)	% contribution	Actual yield (g)	% contribution
SbABM	Main panicle	38.35	48.31	36.52	46.06	34.49	41.45	42.34	53.64	38.68	46.99
	Branched panicle	41.04	51.70	42.76	53.94	48.72	58.55	36.59	46.36	43.64	53.01
	Number of panicles	4.13		5.75		6.75		4.92		6.16	
A-1	Main panicle	40.66	79.37	33.58	69.42	38.46	78.11	36.12	71.30	30.25	62.29
	Branched panicle	10.57	20.63	14.79	30.58	10.78	21.89	14.54	28.70	18.31	37.71
	Number of panicles	1.25		2.00		2.25		1.75		1.92	
M 35-1	Main panicle	36.24	75.52	33.58	68.48	37.62	71.22	47.38	100.00	35.29	67.21
	Branched panicle	11.75	24.48	15.45	31.51	15.20	28.78	-	-	17.22	32.79
	Number of panicles	1.38		1.63		2.00		1.33		2.00	

Low fertilizer – 40:20:20 kg NPK/ha High fertilizer – 80:40:40 kg NPK/ha

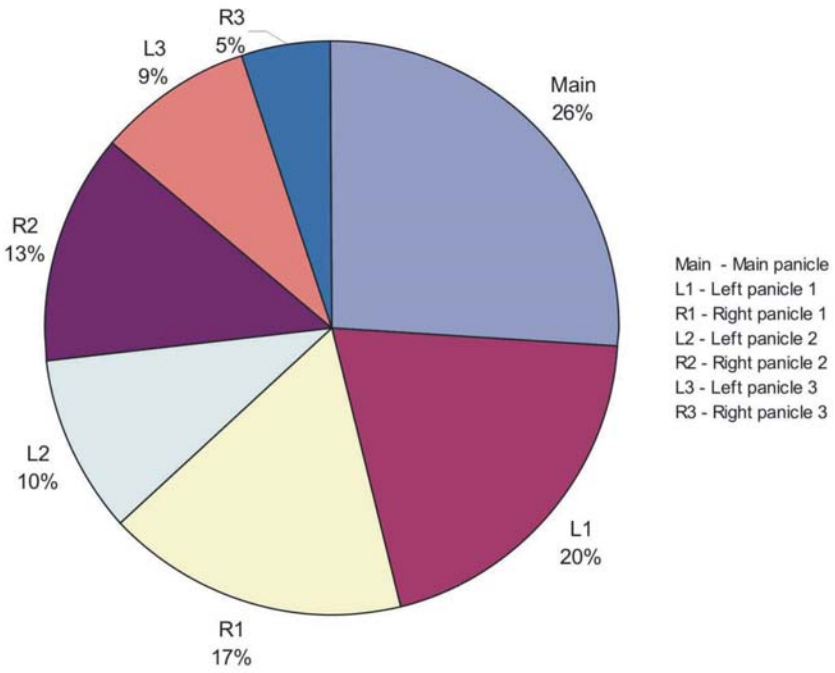

Fig. 4. Average per cent seed yield contribution from panicles born on tight and left side of the sorghum mutant under normal conditions

exploit its genetic potential, the mutant was involved in a full diallele study along with ruling varieties (A-1, M 35-1, 104 B, M 31-2B and CSV 216 R) to assess the combining ability and to quantify the magnitude of heterosis. SbABM performed exceptionally well in hybrid combinations for all the traits. Mean squares due to genotypes were highly significant for all the traits. The results on general combining ability revealed that SbABM was significantly a better general combiner for all the traits. Majority of the hybrids involving SbABM as parental line exhibited high degree of heterosis for most of the traits, finally contributing to overall vigour of the plant. However, SbABM did not restore fertility on both *milo* and *maldandi* cytoplasm.

Conclusion

Apart from being an excellent material for basic studies, the mutant has an immediate value for commercial cultivation. It can serve as an important source for diversification of Maldandi and its relatives in the farmers' field. There is a need for the complete understanding of the regulation of branching, by environmental, hormonal and genetic factors and their interactions. In this direction, emphasis should be given to investigate molecular mechanisms associated with the regulation of branching by environmental and hormonal factors.

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REVIEW ARTICLE

'*Kulagar*' – A Potential System to Conserve the Crop Diversity

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Goa and Konkan region of Maharashtra are parts of Western Ghats with huge diversity of flora and fauna. Hot-humid climate with heavy monsoon makes this area a biodiversity hotspot. Farmers of this region have a conventional, multitier, homestead system of gardening called *kulagar*, inherited from their ancestors, to cultivate and conserve the local crop plants near their household. It is an integrated system with the skeletal component as areca nut palms. Other types of crops included in the system are cash crops, plantation crops, spices, fruits, local vegetables, medicinal and aromatic plants and flower crops. Some of the *kulagars* include animal components to make the system cost effective and holistic. Bioresource conservation, crop diversification, recycling of the resources, value addition and processing and byproduct utilization are important features of a *kulagar*. Advanced crop production technologies are being incorporated in *kulagar* by the new generation farmers to make it sustainable and economically viable.

Key Words: Conservation, Crop diversity, Goa, Konkan, *Kulagar*

Western Ghat is a mountain range covering 1,60,000 sq. m area parallel to the west coast. It is one of the biodiversity hotspots and designated as one of the UNESCO world heritage sites. Goa and Konkan region of Maharashtra are blessed with the diversity of tropical flora and fauna due to the proximity to the Western Ghats. The hot humid climate and the presence of heavy monsoon have made this region a biodiversity hotspot with beautiful landscape. Western Ghat begins from the boarders of Gujarat and Maharashtra and ends in Kanyakumari, Tamil Nadu covering the states of Maharashtra, Goa, Karnataka, Kerala and Tamil Nadu. The region is home to 7,402 species of flowering plants, 1,814 species of non-flowering plants, 139 mammal species, 508 bird species, 179 amphibian species, 6,000 insects species and 290 freshwater fish species (Nayar *et al.* (2014)., Myers *et al.,* (2000), Dahanukar *et al*., (2004). Some of them are facing the threat of extinction and therefore need urgent conservation measures to protect them.

Farmers of Goa and Konkan region have a conventional homestead system of gardening inherited from their ancestors, called *kulagar,* to cultivate and conserve the local crop plants near their household. It is an integrated system which includes cash crops, plantation crops, spices, fruits, local vegetables, medicinal and aromatic plants and flower crops. Some of the *kulagars* include animal components and follow the integrated farming system. *Kulagar* has its own identity and culture. The Konkani word '*kull*' means family and '*aagar*' means store house (Khedekar, 2013).

Kulagar is a system to cultivate horticultural crops in plains, terraces and hill tops. The skeletal tree species are areca nut palms in every *kulagars.* Black pepper vines (*mirvel*) or betel vines (*paanvel*) are trailed on these palms. The interspaces are utilized for the cultivation of different crop species. A few groups of people (Bhat and Kulwadi and a few families of Baman) are maintaining the *kulagar* as heirloom gardens. Some of them belong to the Paddye in Ponda, Kepem, Kankon and parts of Sattari and Bicholim. In Ponda, *kulagars* maintained by the Baaman-Saraswat community are very common. The upper portion of the *kulagar* is known as *visol,* wherein regular watering is not provided (Khedekar, 2008). They are irrigated by the natural flow of the gravitational water. In local language it is called *aapune udak* (*water by summon*). This part is cultivated with plantation crops and fruit trees which require less water for growth. Cashew, bamboo, pineapple, mango, tamarind are some of the plant species grown in this region. The area near to the farm house is called *porsum,* where plants like turmeric, ginger, bread fruit *etc* are grown. The area of each *kulagar* is different from others. Generally a *kulagar* is 1-2 hectares. It is known as *daando* and a

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chain of *kulagars* is called *faall.* The total area under *kulagar* in Goa is approx. 15,000 hectares (Khedekar, 2013).

Features of *Kulagar*

Kulagar system has features of crop diversification, recycling of resources, organic production, water harvesting and soil and water conservation that makes it an exclusive, sustainable system for horticulture crop production. The cash crop component in a *kulagar* can be areca nut, coconut, cashew nut, betel vine *etc*. In Goa, mostly areca nut based (rarely coconut based) *kulagars* are common. Local tall type areca nut palms are nowadays replaced by the improved cultivars like Mangala, Sumangala and Mohit nagar. The landraces of coconut found in Goa are 'Benaulim' of South Goa and 'Calangute' of North Goa. These palms are trailed with black pepper and betel vines. Black pepper varieties commonly grown in Goa are Panniyur varieties, Karimunda and Thevam. 'Kalem' (Black/hard) and 'Dhavem' (white/soft) are the two types of betel vines grown in Goa. 'Kalem' is used for consumption and the 'Dhavem' is used for religious occasions as *vida*. In areca nut plantations, inter culturing with pineapple, banana, shade tolerant vegetables and tuber crops like elephant foot yam is commonly practiced.

'Mankurad' and 'Hilario' are two local goan mango varieties with sweet relishing flavor and enormous diversity in size, shape and quality. Apart from these two, a large number of mango varieties are available in different parts of Goa. Alfonsa, Babio, Baretto, Bemcorada, Bishop, Ball, Brindao, Carreira, Carreira branca, Culas, Colaco blanca, Costa, Dourado, Durbate, Fernandin, Furtad, Godgo, Japao, Jeronimo, Jose, Kapri, Madame, Malgesh, Massarrat Bardez, Mussaret Salcete, Malgoa, Nicolau Afonsa, Olieveria, Papel, Papel Branco, Rebello, Reynold, Rosa, Secretin, St. Antony, Salgada, Tanque, Toranja, Chimut, Udgo and Xavier are the mango varieties grown in Goa (Dhander *et al.,* 1997). Commonly cultivated banana varieties of Goa are Saldatti (AAB), Savarboni (ABB), Amti (AAB), Raspali (AAB), Sakkari (AAB), Velchi (AB), Myndoli (AAB) and Sugandi (AAB). Pineapple varieties Kew, Giant Kew, Queen and Red Spanish are locally grown in *kulagars* of Goa. Spice crops like nutmeg, cinnamon, clove and underutilized fruit crops like kokum, jack fruit (Firm flesh type–kappa and soft flesh type–rasal), acid lime, pummelo (red flesh type and white flesh type), bread fruit, karonda, sapota, flower crops like hibiscus, jasmine, marigold, crossandra (ratan aboli-unique type with dark red petals) and a large number of medicinal and aromatic plants are a part of this system. Multi-tier cropping assures the proper utilization of space and sunlight. The highest tier comprises of palms which are often trailed with betel vines and black pepper. The next tier has fruit trees like guava, banana, papaya, wax apple, kokum, jackfruit, bread fruit and spice crops like nutmeg, cinnamon etc. Lowest tier is pineapple, tuber crops, vegetables, shade loving flower crops, medicinal and aromatic plants. This assures the proper sunlight penetration and distribution inside the system through the canopy of different layers of the crops. The same kind of pattern can be seen in the root distribution also. The fibrous root system of palms spread to a maximum of two meter depth and the surrounding shallow rooted fruit crops like banana, pineapple, vegetables, tuber crops and ornamental crops will not compete with each other for moisture and nutrients.

Water Harvesting and Soil and Water Conservation

Kulagars are green throughout the year. Most of the *kulagars* consist of ponds, wells and canals which are naturally filled by the rains obtained during the abundant monsoons. They can provide water to the system throughout the year by water harvesting. The water is supplied in three different manners in the *kulagars* using the customary methods. Water from tank or *tallem* is used for irrigation during day and stops during night. Another method is from a *baand* created on a tributary also known as *vhall*. It is constructed usually in the middle region and it supplies water to both sides of the *kulagar*. Sometimes water is stored in the mud tank known as *ushen*. It is placed at high altitude and at the lower level; a hollow trunk of the areca nut tree is used as a pipe, which is fixed into the wall. During the night, this pipe is closed with the putrefied banana stem. When the mouth of the trunk pipe is opened, water flows into the *kulagar*. It is splashed onto the roots manually with the help of a curved wooden channel called *kallem*. The main channel of *kulagar* is known as *paat*. It runs from the top of the *kulagar* to the bottom. For the conservation of soil and protection from leaching and erosion, terraces, trenches and contour bunds are made in the *kulagars*. Stone wall parchments are made in the terraces. The pathways are also pitched with stones in some places. For the convenient movement to the higher areas, there are uneven flights of steps made in *kulagars*. At every

Table 1. Crop diversification in *Kulagars*

Name	Scientific name	Family
Plantation crops		
Areca Nut	*Areca catechu*	Arecaceae
Coconut	*Cocos nucifera*	Arecaceae
Spice crops		
Betel vine	*Piper betle*	Piperaceae
Black pepper	*Piper nigrum*	Piperaceae
Cardamom	*Elettaria cardamomum*	Zingiberaceae
Cinnamon	*Cinnamomum zeylanicum, Cinnamomun verum*	Lauraceae
Clove	*Syzygium aromaticum*	Myrtaceae
Curry leaf	*Murraya koenigii*	Rutaceae
Ginger	*Zingiber officinale*	Zingiberaceae
Nut meg	*Myristica fragrans*	Myrsticaceae
Tamarind	*Tamarindus indica*	Fabaceae
Turmeric	*Curcuma longa*	Zingiberaceae
Fruit crops		
Acid lime	*Citrus aurantifolia*	Rutaceae
Ambada	*Spondias pinnata*	Anacardiaceae
Aini	*Artocarpus hirsutus*	Moraceae
Aonla	*Phyllanthus emblica*	Euphorbiaceae
Banana	*Musa* sp.	Musaceae
Ber	*Ziziphus mauritiana*	Rhamnaceae
Bilimbi	*Averrhoa bilimbi*	Oxalidaceae
Bread fruit	*Artocarpus altilis*	Moraceae
Carambola	*Averrhoa carambola*	Oxalidaceae
Custard apple	*Annona squamosa, Annona muricata*	Annonaceae
Fig	*Ficus carica*	Moraceae
Guava	*Psidium guajava*	Myrtaceae
Jack fruit	*Artocarpus heterophyllus*	Moraceae
Jamun	*Syzygium cuminii*	Myrtaceae
Karonda	*Carissa carandas*	Apocynaceae
Kokum	*Garcinia indica*	Clusiaceae
Lemon	*Citrus limon*	Rutaceae
Malabar tamarind	*Garcinia gummigutta*	Clusiaceae
Mango	*Mangifera indica*	Anacardiaceae
Monkey jack	*Artocarpus lakoocha*	Moraceae
Papaya	*Carica papaya*	Caricaceae
Passion fruit	*Passiflora edulis*	Passifloraceae
Pineapple	*Ananas comosus*	Bromiliaceae
Pummello	*Citrus grandis*	Rutaceae
Sapota	*Manilkara achras*	Sapotaceae
Wax apple	*Syzygium samarengense*	Myrtaceae
Vegetable crops		
Chilli	*Capsicum annuum, Capsicum frutescence, Capsicum chinensis, Capsicum baccatum*	Solanaceae
Brinjal	*Solanum melongena*	Solanaceae
Bhindi	*Abelmoschus esculentus*	Malvaceae
Amaranthus	*Amaranthus tricolor, Amaranthus viridis*	Amaranthaceae
Melons	*Cucurbita pepo*	Cucurbitaceae
Pumpkin	*Cucurbita maxima*	Cucurbitaceae
Agathi	*Sesbania grandiflora*	Fabaceae
Tomato	*Lycopersicon esculentum*	Solanaceae
Drumstick	*Moringa oleifera*	Moringaceae
Elephant foot yam	*Amorphophallus paeoniifolius*	Areceae
Basella	*Basella alba, Basella rubra*	Basellaceae

Contd.

Name	Scientific name	Family
Colocasia	*Colocasia esculenta*	Areceae
Tapioca	*Manihot esculenta*	Euphorbiaceae
Chekkurmanis	*Sauropus androgynus*	Euphorbiaceae
Flower crops		
Bougainvillea	*Bougainvillea spectabilis*	Nyctaginaceae
Clitoria	*Clitoria ternatea*	Papilonaceae
Crape jasmine	*Tabernaemontana divaricata*	Apocynaceae
Crossandra	*Crossandra infundibuliformis*	Acanthaceae
Golden champa	*Michelia champaca*	Magnoliaceae
Indian Oleander	*Nerium oleander*	Apocyanaceae
Ixora	*Ixora coccinea*	Rubiaceae
Jasmine	*Jasminum sambac, Jasminum grandiflorum, Jasminu miltiflorum*	Oleaceae
Marigold	*Tagetes erecta*	Asteraceae
Medlar	*Mimusops elengi*	Sapotaceae
Night jasmine	*Nyctanthes arbor-tristis*	Oleaceae
Rangoon creeper	*Quisqualis indica*	Combretaceae
Shoe flower	*Hibiscus rosa-sinensis*	Malvaceae
Trumpet flower	*Tecoma stans*	Bignoniaceae
Medicinal and aromatic plants		
Adhatoda	*Adhatoda vasica*	Acanthaceae
Aloe vera	*Aloe barbadensis*	Liliaceae
Ashoka	*Saraca asoca*	Caesalpiniaceae
Asparagus	*Asparagus racemosus*	Liliaceae
Basil	*Ocimum sanctum* (Holy basil), *Ocimum basilicum* (Sweet basil)	Lamiaceae
Calotropis	*Calotropis gigantea*	Asclepiadaceae
Coleus	*Coleus aromaticus*	Lamiaceae
Costus	*Costus speciosus, Costus igneus* (Insulin plant)	Zingiberaceae
Davana	*Artemisia annua, Artemisia pallens, Artemisia vulgaris*	Asteraceae
Henna	*Lawsonia inermis*	Lythraceae
Insulin Plant	*Costus igneus*	Zingiberaceae
Kalmegh	*Andrographis paniculata*	Acanthaceae
Long pepper	*Piper longum*	Piperaceae
Medicinal yam	*Dioscorea floribunda*	Areceae
Mint	*Mentha arvensis*	Lamiaceae
Periwinkle	*Catharanthus roseus*	Apocynaceae
Red flowered leadwort	*Plumbago indica*	Plumbaginaceae
Serpent wood	*Rauvolfia serpentina*	Apocynaceae
Sweet flag	*Acorus calamus*	Acoraceae
Vetiver	*Vetiveria zizanioides*	Poaceae

terrace, there are cross channels. Each channel has two or three pits called *fondi.* In order to divert the water from main stream to another channel, a *Banne* is placed at different spots. *Bann*e is a decomposed banana stem which act as a water tight arrangement to prevent water leakage. Farmers are well versed to operate the *banne* with their legs. This is practiced till the *ushen is* empty. On every third day plants are watered in the *kulagars* and this is called *pairo* (Khedekar, 2013).

Recycling of the Resources and Organic Production

The resources generated in the *kulagars* are recycled inside the system itself by *in situ* composting. Some farmers have incorporated vermi composting units in the system to utilize the biomass waste. Cows and Buffaloes contribute to the compost and biogas production in the system. The animal manures are mixed with the water source and are diverted to the *paat*. The annual task of *aallem* is performed by removing the roots of areca nut and coconut by clearing the soil. Dried leaves and plant derbies are collected from surrounding regions and mixed with cow manure and mulched on the root portion of the plants. Microclimate created due to the close spacing, diversity and moisture cause the infestation of pests and diseases in the *kulagar*. Some serious issues related to pest and diseases are black pepper wilt, damping off

of vegetables, root rots, cashew stem borer, banana pseudo stem weevil, banana skipper butterflies, mealy bugs, scales, nematodes and viral diseases. In order to overcome this problem, farmers follow eco friendly measures like neem cake application, sprinkling of ash and salt in the field.

Advanced Production Technologies

Advanced crop production technologies like sprinkler and drip irrigation has been established in some of the *kulagars* recently. Some have included shade net houses for the production of quality planting materials and for incorporation of commercial crops. Mechanization for farm activities and storage facilities are other important aspects that can be incorporated in this system to enhance the sustainability. Introduction of modern agro production technologies, exotic plant and animal species, mechanization and irrigation facilities in the *kulagar* helps to improve its productivity.

Future Perspectives of *Kulagar*

The existing *kulagars* can be well utilized for the year round income generation activities which assures financial security to the farmer or the farm family. It is an excellent opportunity for employment generation. Rural youth can be trained for skilled activities and can be engaged in the system for maintenance. Along with this, it can be converted into a system for conservation of local genotypes and traditional crop production strategies. The future perspectives of a *kulagar* system of cultivation are the following.

Value Addition, Processing and Byproduct Utilization

Diversified products and year round production is the potential of each *kulagar*. Farmers can assure income from the direct sales of the produce or the value addition of the available produce. Minimal processing and value addition has lots of scope in the rural areas. Jack fruit, which is often considered as an under exploited fruit can be well utilized for a diverse array of products like papad, halwa, ice cream, chips, seed powder *etc*. Similarly, farmers can produce, squashes, juices, RTSs and other beverages from kokum, bilimbi and carambola. Pickling of mango is another potential area. Most of the mango varieties present in Goa are small, sour type which is suitable for pickle making. Jam, jellies and marmalades are another set of products which can easily prepared at homestead levels with underutilized and underexploited fruit crops.

The fiber extracted from the coconut and coconut shell can be utilized for the production of different types of hand crafts. Coconut fiber mats, mattresses and ropes can also be prepared from this. Areca nut leaf sheath is used for the production of plates, bowls etc. Bags, crafts, mats, saris etc are prepared from the banana fibers. The large quantity of biomass generated in the system can be converted into vermi compost which fetches good price in the market due to popularity of organic farming.

Agro-ecotourism

Goa and Konkan regions are considered as one of the most preferred tourist spots of India. Annually more than 10 lakhs foreign and domestic tourists visit this region. Agro-ecotourism centers (AET) with *kulagars* are one of the hotspots in all tourist packages. Agro-ecotourism is a perfect blend of agriculture and tourism. It helps the visitors to understand the farm, farm related activities and rural life and rural culture. The concept of on-farm conservation also can best fit into this agro-ecotourism models, where the *kulagars* are being converted into the agro-ecotourism units. The basic principles of agro-ecotourism are 'something for the visitors to see, something for the visitors to do and something for the visitors to buy' (Barbuddhe and Singh, 2014). While converting a *kulagar* as an agro eco tourism centre, the basic objectives like harmonious integration of diversified farming activities for sustainable economic returns, local employment generation, aesthetic goods and services, environment protection and management, ecotourism industry development, infrastructure development and socio economic transformation should be considered (Desai, 2016). Foreigners as well as urban tourists and students find it interesting to visit such units. The relevance of these indigenous plants and its traditional uses can be spread to the society through agro ecotourism ventures.

On-farm Conservation of Genetic Resources

Farmer have pivotal role in conservation of genetic resources and there is a need to sensitize them about the effect of genetic erosion and the significance of biodiversity conservation and utilization. They should be encouraged and supported by providing various inputs to continue cultivating and conserving as much plant diversity as possible. An understanding of what and why farmers do, in a two way process would help the researchers and policy makers to help farmers effectively and extend the practice to other farmers

also (Dhillon *et al.,* 2004).The farmers are routinely conserving the local genotypes and landraces in the *kulagars.* Awareness can be provided to them for the relevance of the conservation of these local resources. Appreciation for the plant genetic conservation can be provided to them in the form of awards. In this way, *kulagars* can be considered to be a very effective system to collect, conserve and utilize the local genetic resources and spread awareness to the people regarding the local resources by show casing it.

Conclusion

Kulagar is an ancestral system of cultivation of horticulture crops in Konkan and Maharashtra region. Integrated farming system is one of the peculiar features of the system. It conserves traditional crops and technologies. New generation farmers introduce advanced production technologies to this system and take it to new dimensions like value addition and processing, agro ecotourism and on farm conservation of genetic resources.

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RESEARCH ARTICLE

Assessment of Genetic Diversity in Ajwain (*Trachyspermum ammi* L.) Genotypes using Morphological and Molecular Markers

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Twenty-eight genotypes of ajwain **(***Trachyspermum ammi* L.**)** consisting 25 genotypes and 3 checks were evaluated for genetic diversity using morphological and molecular markers (i.e RAPD markers). Out of 18 decamer RAPD primers, 10 primers were found polymorphic showed an average 5.16 numbers of polymorphic bands per primer. The similarity coefficient for different genotypes was in the range of 0.07 (GP-113 and GP-7) to 0.58 (Gujarat ajwain-1). The average similarity (0.32) across all the genotypes indicating a low level of genetic similarity among the genotypes and a high polymorphism (100%) and variability (78%) by RAPD and morphological analysis, respectively for all the genotypes under study. Though the genotypes *viz.,* GP-7, GP-113, Gujarat ajwain-1 and Pratap ajwain-1 showed moderate divergence in D^2 analysis, but found highly divergent in RAPD analysis and also had high *per se* performance for seed yield and its contributing characters, hence could be selected for the further breeding programme in ajwain.

Key Words: Ajwain, Germplasm, Genetic diversity, Morphological markers, RAPD markers.

Ajwain (*Trachyspermum ammi* L.) 2n=18 belongs to the family Apiaceae, a native of Egypt (Sayre, 2001) also known as Bishop's weed and Carum in English and cultivated mainly for its seed, herb and volatile oil in Iraq, Iran, Afghanistan, and India. In India, it is grown in Gujarat, Rajasthan, Madhya Pradesh, Bihar, Punjab, Tamil Nadu, West Bengal, Andhra Pradesh and Uttar Pradesh covering an area of 27000 ha with a production of 19000 mt and productivity of 703.70 kg/ha (Anonymous, 2014). It is highly valuable and medicinally important seed spice, widely grown in arid and semi-arid regions (Joshi, 2000) where the soil contains a high amount of salts (Munnas, 2002). It is an annual, aromatic and profusely branched herb having an erect straight stem which may grow up to 90-100 cm height. A number of chemical constituents have been reported from the herb. Carbohydrates (24.6%), fat (21.1%), protein (17.1%), fiber (11.9%), glycosides, tannins, saponins, flavones and other components (7.1%) involving iron, iodine, calcium, copper, phosphorous, cobalt, manganese, riboflavin, thiamine, and nicotinic acid are the phytochemical constituents of ajwain reported by Zarshenas *et al.* (2014). The seeds contain essential volatile oil responsible for its odor and taste. The main component of ajwain oil is thymol (~50%) which is a strong germicide and anti-spasmodic. The oil exhibits fungicidal (Singh *et al.,* 2000), antimicrobial (Sivropoulou *et al.,* 1996) and anti-aggregatory (Srivastava, 1988) effects on humans.

Despite the economic importance of ajwain, it is cultivated on marginal lands with poor fertility because of which, productivity is quite low (Meena *et al.,* 2015). Though the crop has domestic, medicinal as well as commercial value, it has altogether been neglected as far as genetic improvement is concerned. As a result, local types have low yield potential and are susceptible to diseases resulting in poor production. In our country improved ajwain varieties with good adaption are available in a limited number. Genetic variability available in the germplasm collection of a species is a basic requirement for its crop improvement programme. Genetic analysis of ajwain is essential to enhance the yield potential and maximum utilization of the desirable characters for development of any ideal genotypes. Detailed information on the genetic divergence in the available germplasm collection is necessary to ascertain the potential of the germplasm as a base material to sustain a varietal improvement programme. As already established, seed yield is the most important character and has complex inheritance, governed by a large number of genes and is greatly affected by environmental factors. Selections made in the field are not likely to be reliable as character, are subjected to large number

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of non-genetic factors. Molecular markers can provide an opportunity to measure genetic variability/genetic relationship among genotypes more precisely because these markers are potentially unlimited in number and are not affected by the environment.

DNA based molecular markers have applications in genetic diversity analysis among naturally occurring populations. Germplasm management could be brought about by conserving a minimum number of plants that show maximum diversity. For genetic relationships among genotypes and detecting and monitoring pedigree breeding record of inbred parents, RAPD is the first PCR-based molecular marker technique (Dongre and Parkhi, 2005) and has proved itself as an efficient method for varietal identification, study of polymorphism, gene mapping, biodiversity, genetic map construction, hybridization and phylogenetic relationships. The aim of the study was to observe the genetic diversity within twenty eight ajwain accessions by using morphological and random amplified polymorphic (RAPD) DNA markers and develop phylogenetic tree of different ajwain accessions by using bioinformatics tools.

Materials and Methods

Germplasm used and Experimental Plan

Twenty-eight genotypes originating from different places were selected for this study (Table 1). These accessions were grown at the Agricultural farm, Rajasthan College of Agriculture, MPUAT, Udaipur, India in RBD with three replications during *rabi* 2014-15. In each replication, the genotype was sown in 2 row plot of 4-meter row length keeping row to row distance of 30 cm. All the recommended agronomical practices and plant protection measures were adopted to raise a healthy crop to attain maturity. Fertilizers were applied @ 20 kg N: 20 kg P_2O_5 at the time of sowing as basal dose while 20 kg N/ha was top-dressed in two split doses in thirty and sixty days, respectively. The crop was irrigated 6 times during the crop season. First irrigation was given immediately after sowing and there after irrigation was given at an interval of 20-25 days.

Morphological Characterization

Observations were taken on each accession along with the checks for 10 morphological and one biochemical trait *viz.,* days to 50 per cent flowering (DF), days to 75 per cent maturity (DM), plant height (PH), primary branches (PB), secondary branches (SB), umbels per plant (UPP), umbellates per umbel (UPU), seed yield per plant (YPP), biological yield per plant (BY), harvest index (HI) and seed oil content (SO), respectively.

Statistical Analysis

For calculating Genetic Divergence for eleven characters, Mahalanobis D^2 Statistics (1936) was used.

DNA Isolation and quantification

Total genomic DNA was isolated from fresh and healthy leaves using the CTAB method (Doyle and Doyle, 1990) with few modifications. Briefly, 2.0 g of leaves were ground in liquid nitrogen to get a fine powder. The powder was added to 3 mL of extraction buffer (100 mM Tris–HCl pH 8.0, 1.4 M NaCl, 20 mM EDTA, 2% (wv-1) CTAB, 2% 2–mercaptoethanol and incubated at 65°C for 30 min. DNA was extracted with C:I (24:1)

Table 1. Twenty eight diverse ajwain (*Trachyspermum ammi* L.) genotypes

S.No.	Name of Genotypes	Origin	State	S. No.	Name of Genotypes	Origin	State
1.	GP-7	Udaipur	Rajasthan	15.	GP-90	Chittorgarh	Rajasthan
2.	GP-28	Chittorgarh	Rajasthan	16.	GP-113	Chittorgarh	Rajasthan
3.	GP-29	Chittorgarh	Rajasthan	17.	GP-125	Chittorgarh	Rajasthan
4.	GP-30	Chittorgarh	Rajasthan	18.	GP-127	Neemauch	Madhya Pradesh
5.	GP-32	Chittorgarh	Rajasthan	19.	GP-131	Neemauch	Madhya Pradesh
6.	GP-41	Chittorgarh	Rajasthan	20.	GP-141	Neemauch	Madhya Pradesh
7.	GP-48	Chittorgarh	Rajasthan	21.	GP-149	Radhapur	Gujarat
8.	GP-53	Chittorgarh	Rajasthan	22.	GP-168	Banaskantha	Gujarat
9.	GP-63	Pratapgarh	Rajasthan	23.	GP-169	Banaskantha	Gujarat
10.	GP-66	Pratapgarh	Rajasthan	24.	GP-175	Banaskantha	Gujarat
11.	GP-70	Bhilwara	Rajasthan	25.	GP-191	Banaskantha	Gujarat
12.	GP-71	Bhilwara	Rajasthan	26.	Gujarat Ajwain-1	Banaskantha	Gujarat
13.	GP-83	Chittorgarh	Rajasthan	27.	Pratap Ajwain-1	Banaskantha	Gujarat
14.	GP-87	Chittorgarh	Rajasthan	28.	Local check	Banaskantha	Gujarat

and precipitated by the addition of equal volume of 70% chilled isopropanol, with step by step centrifugation. After washing with 70% ethanol and dissolved in 100 µl of HPLC water. DNA was quantified by spectrophotometer by using a comparison of the optical density values of the solution at A260/A280 wavelengths. Stock DNA samples were stored at -20°C.

RAPD Analysis

A total of 18 decamer oligonucleotide RAPD primers of arbitrary sequence obtained from Department of Molecular Biology and Biotechnology, Rajasthan College of Agriculture, MPUAT, Udaipur, were tested for PCR amplification. The sequences of these primers were selected from literature and purchased from Banglore Genei Pvt. Ltd. Bengaluru. PCR reaction was performed in a final volume of 20 µl containing 1X reaction buffer, 1 unit of Taq DNA polymerase, 200 mM each dNTPs, 0.5 µM/reaction primer and 50 ng of template DNA. DNA amplification was carried out in advanced Thermal cycler using the following conditions: initial denaturation of 94°C for 4 minutes, followed by 35 cycles comprising 30 sec at 94°C, 1 min at 36°C and 2 min at 72°C. An additional cycle of 7 min at 68°C was used for final extension. Amplified products were separated by electrophoresis at 50 Volts for 3-4 hrs in 1.2 per cent agarose gel prepared in 1X TAE buffer (Sambrook *et. al.,* 1989) containing 0.5 µg/ml of ethidium bromide. Gels were photographed under UV light with the help of gel documentation system (Bio Rad Gel DOC).

Scoring the RAPD Products

RAPD bands were designated on the basis of their molecular size ranging between 100-1000 bp. The molecular size of PCR products was estimated by referencing to a 100 bp DNA ladder. Presence of a band was denoted by score of '1' while its absence was denoted by '0'. Only prominent bands were considered for scoring.

Statistical Analysis for Similarity Coefficient

The pair-wise association coefficients were calculated from data matrix using Jaccard's similarity coefficient (Jaccard, 1908). The equation for calculating Jaccard's similarity coefficients 'F' between two samples A and B is:

f = nxy / (n1 – nz)

nxy = Number of bands common to sample A and sample B.

n1 = Total number of bands present in all samples.

nz = Number of bands not present in sample A or B, but found in other samples.

For genetic distance, cluster analysis was then conducted by using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) clustering method (Sneath and Sokal, 1973). The genetic distances obtained from cluster analysis through UPGMA were used to construct the dendrogram, depicting the relationships of the genotypes using computer program NTSYSpc version 2.02 (Rohlf, 1998).

Result and Discussion

Per se Performance

The present experimental material showed a wide range of variability for almost all the characters including seed yield (Table 2). Days to 50 per cent flowering ranged from 72.33 to 80.00 days with a mean value of 76 days. Values for primary branches and secondary

Table 2. Analysis of variance along with *per se* and coefficient of variation (CV) for eleven characters in ajwain

Characters	Replication	Genotypes	Error	Mean ± SE	Range	CV (%)	Best Genotypes on the basis of per se
	[2]	[27]	[54]				
Days to flowering	12.76	12.32**	5.43	76.76±1.35	72.33-80.00	3.04	GP- 41 (72.33 days)
Days to maturity	14.89	40.18*	23.14	164.14±2.78	156.67-169.33	2.93	GP-87, GP-113 (156 days)
Plant height	43.80	83.73**	15.92	98.02± 2.30	82.00-107.00	4.07	GP-83 (107 cm)
Primary branches	0.90	2.12**	0.45	10.10±0.39	8.67-11.33	6.63	GP-149, GP-169, GP-191 (11)
Secondary branches	35.51*	67.42**	10.78	59.87± 1.90	49.67-71.00	5.49	Local check (71)
Umbels/plant	112.40	676.84**	40.42	116.02±3.67	72.33-160.67	5.48	GP-41 (160.67)
Umbellates/ umbel	1.65	2.11**	0.79	10.19±0.51	8.33-12.00	8.73	GP-191 (12)
Seed yield /plant	1.45	5.32**	0.50	10.33±0.41	8.14-12.39	6.89	GP-191 (12.39 g)
Biological yield/plant	13.16	43.63**	4.54	33.84±1.23	27.68-42.58	6.30	Pratap ajwain-1 (42.58 g)
Harvest index	0.61	22.34**	3.56	30.62±1.09	25.48-36.63	6.17	GP-125 (36.63 %)
Oil content	0.02	0.52**	0.01	3.62±0.06	2.72-4.03	3.01	GP-191 (4.03 %)

branches ranged from 8.67 to 11.33 and 49.67 to 71.00, respectively. Umbels/plant showed a mean value of 116.02 umbels, while each umbel has an average 10.19 umbellates, with a range of 8.33-12.00 umbellates/umbel. Seed yield /plant was ranged from 8.14-12.39 g with the mean of 10.33. Oil content showed a mean value 3.62 % and ranged from 2.72-4.03 %. Similar trends of results for seed oil content were found by Kole *et al.* (2002). Genotypes GP-191, GP-175, Gujarat ajwain-1 and Pratap ajwain-1 displayed high *per se* for both seed yield per plant and seed oil content. Therefore, these entries could be gainfully utilized in breeding programmes.

D^2 Analysis

Twenty-eight varieties were grouped into 5 clusters on the basis of observed similar D^2 values among genotypes within a cluster as compared to genotypes in another cluster (Table 3). Cluster II includes a maximum number of genotypes i.e. 14 followed 9 in cluster V, 3 in cluster I and cluster III, IV were monogenotypic. The clustering pattern revealed that, in general varieties from the same origin showed no tendency to be in the same cluster.

Looking at the pattern of varietal distribution in different clusters, it appeared that geographical distance between the varieties had no relation with the genetic divergence as the varieties from same source had fallen into different clusters as well as the same cluster contained varieties from different sources. These findings are in close agreement to earlier reports of Mathur (1992), Banerjee *et al.* (2004), Jain *et al.* (2006) and Kole and Saha (2009) in fenugreek.

Average inter cluster values were found maximum between cluster III and IV (89.65), whereas maximum intra cluster values were recorded for cluster V (10.12) followed by cluster II (9.18) and cluster I (6.61) (Fig. 2). The inter-cluster distances were greater than intra-cluster distance revealing a considerable amount of genetic diversity among the genotypes (Table 4). Therefore, the genotypes falling in these clusters appeared to be divergent and might have genetic origin hence could be gainfully utilized in ajwain improvement programme. These findings were in agreement with Banerjee *et al.* (2004) and Swami *et al.* (2012).

Table 3. Ajwain genotypes included in each cluster

Clusters	Number of Genotypes	**Genotypes**
I	3	GP-53, GP-87, GP-168
II	14	GP-63, GP-66, GP-70, GP-71, GP-83, GP-90, GP-113, GP-125, GP-127, GP-131, GP-141, GP-149, GP-169 and Gujarat Ajwain-1
III	1	GP-29
IV	1	GP-41
V	9	GP-7, GP-28, GP-30, GP-32, GP-48, GP-175, GP-191, Pratap Ajwain-1 and Local check

Contribution of Different Traits towards Total Genetic Divergence

The importance of genetic divergence and its use in the manifestation of heterosis is obvious. The maximum amount of heterosis and variability will be manifested in a cross involving parent belonging to the most divergent cluster. The perusal of the comparison of contribution of different characters towards genetic diversity was estimated based on ranking method. As evident from Table 5, seed oil content contributed maximum (42.03 %) followed by umbels/plant (14.13 %), and Seed yield/ plant (13.94 %). The characters like days to 50 per cent flowering, days to maturity, umbellates/umbel and harvest index was found to be least contributing traits. These findings are in close agreement with Kole *et al.* (2002), Banerjee *et al.* (2004) and Pathak *et al.* (2014) in other seed spice.

To conclude that seed oil content, seed yield per plant and umbels per plant had high estimates of all variability parameters and were strongly correlated with

Table 4. Average intra and inter-cluster D^2 values in twenty eight genotypes of ajwain

Clusters	I	II	III	**IV**	**V**
I	**6.61**	12.13	39.86	52.50	21.92
II		**9.18**	40.29	50.48	16.42
III			**0.00**	89.65	55.52
IV				**0.00**	37.36
V					**10.12**

Bold number = intra-cluster distance

Table 5. Contribution of characters to divergence

Characters	Contribution percent	Parent I rank	Total rank
Days to 50 per cent flowering	1.92	0.00	2829
Days to maturity	2.05	0.53	2805
Plant height	4.50	6.61	2346
Primary branches/plant	4.26	2.38	2328
Secondary branches/plant	5.78	2.91	2241
Umbels/plant	14.13	15.08	1950
Umbellates/umbel	2.32	0.26	2725
Seed yield/plant	13.94	20.90	1538
Biological yield/plant	6.66	7.14	2065
Harvest index	2.42	1.59	2720
Seed oil content	42.03	42.59	1399

each other having maximum direct effects towards seed yield appeared promising to contribute genetic diversity in ajwain. Further, these genotypes were grouped into 5 clusters and cluster III and IV had maximum inter cluster distance, therefore, the genotypes belonging to these clusters namely GP-29 and GP-41 showed high *per se* performance for oil content, umbels per plant and exhibited earliness and hence, could be utilized in breeding programmes.

RAPD Analysis

RAPD markers are superior in terms of simplicity and cost, and are used for analysis of genetic diversity and reliability in the identification of cultivars due to their high resolution in several types of plant material such as natural population in breeding programme and cultivar collections. RAPD analyses does not require any prior sequence information because arbitrary DNA sequence can be used as primer which target random genomic sequences to generate a genetic profile. RAPD (Random Amplified Polymorphic DNA) markers have the advantage of detecting polymorphism simply and quickly (Demeke *et al.,* 1996). Khan *et al.* (2008) mentioned that RAPD is a simple and fast technique to compare the genetic relationship and pattern of variation among the gene pool in mustard crop.

Genetic Polymorphism among Ajwain Accessions

All the 28 varieties of ajwain cultivars were examined for DNA polymorphism using 18 decamer primers (OPERON) showing high (G+C) content. Out of 18 primers 10 primers were found polymorphic. The RAPD primer OPA-07, OPA-08, OPA-10 generated 9 bands with 100% polymorphism and other primers *viz.,* OPA-14, OPB-03 and OPB-06 gave 11 bands and showed 100% polymorphism (Plate 1). Whereas primer OPB-07, OPA-05, OPA-11 and OPA-09 showed 7, 8, 8, 10 bands respectively with 100% polymorphism (Table 6). The average numbers of polymorphic bands per primer were 5.16. Similar results were observed by Srivastava *et al.* (2011) observed 97.26% polymorphism in black gram (*Vigna mungo*) while, Kameswari *et al.* (2014) in chrysanthemum genotypes obtained 97.4% polymorphism.

Plate-1

RAPD Profile of Ajwain genotypes generated with primers OPB-06 and OPB-07

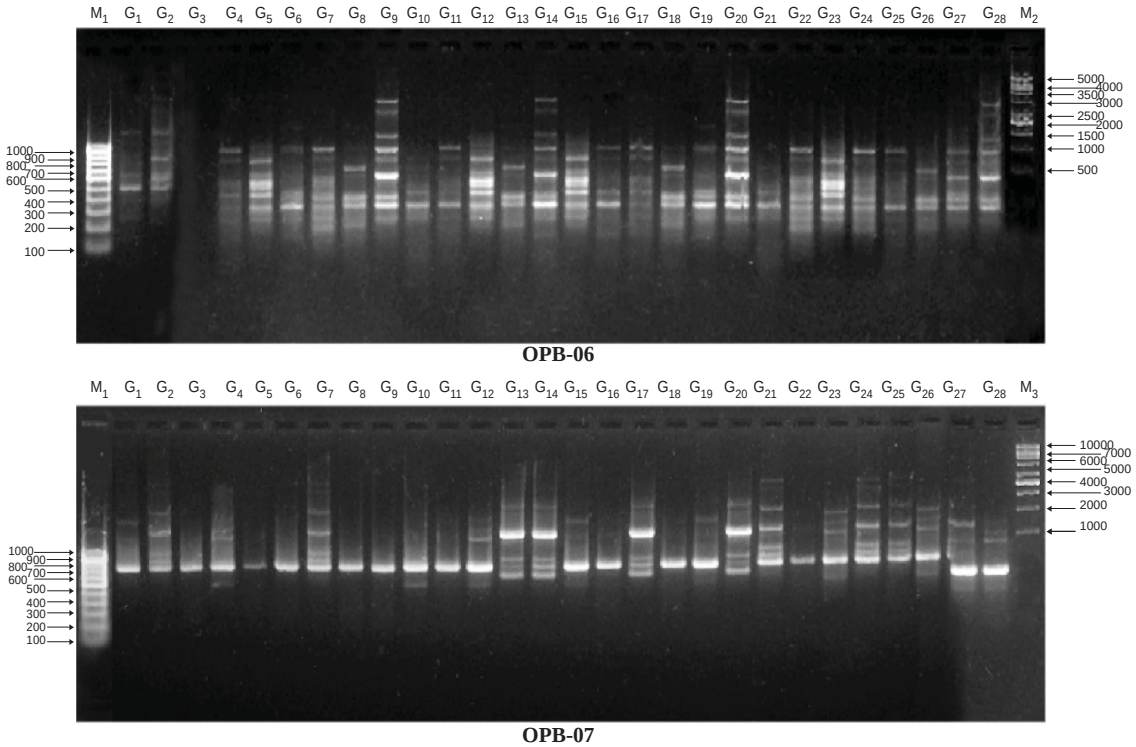

Plate 1. G-1= GP-7, G-2= GP-28, G-3= GP-29, G-4= GP-30, G-5= GP-32, G-6= GP-41, G-7= GP-48, G-8= GP-53, G-9= GP-63, G-10= GP-66, G-11= GP-70, G-12= GP-71, G-13= GP-83, G-14= GP-87, G-15= GP-90, G-16= GP-113, G-17= GP-125, G-18= GP-127, G-19= GP-131, G-20= GP-141, G-21= GP-149, G-22= GP-168, G-23= GP-169, G-24= GP-175, G-25= GP- 191, G-26= Gujarat Ajwain-1, G-27= Pratap Ajwain-1, G-28= Local check.

Table 6. Polymorphism information of RAPD primers analyzed

S. No.	Primers code	Sequence 5' -3'	Base pair	Total No. of bands (a)	Total No. of polymorphic bands (b)	Polymorphism % (b/a × 100)
1.	OPA-05	AGGGGTCTTG	400-2000	8	8	100
2.	OPA-07	GAAACGGGTG	300-3000	9	9	100
3.	OPA-08	GTGACGTAGG	300-4000	9	9	100
4.	OPA-09	GGGTAACGCC	200-2000	10	10	100
5.	OPA-10	GTGATCGCAG	500-3000	9	9	100
6.	OPA-11	CAATCGCCGT	800-7000	8	8	100
7.	OPA-14	TCTGTGCTGG	400-6000	11	11	100
8.	OPA-15	TTCCGAACCC	NA	NA	NA	0
9.	OPA-16	AGCCAGCGAA	NA	NA	NA	0
10.	OPB-02	TGATCCCTGG	NA	NA	NA	0
11.	OPB-03	CATCCCCCTG	200-2500	11	11	100
12.	OPB-04	GGACTGGAGT	NA	NA	NA	0
13.	OPB-05	TGCGCCCTTC	NA	NA	NA	0
14.	OPB-06	TGCTCTGCCC	200-3000	11	11	100
15.	OPB-07	GGTGACGCAG	600-4000	7	7	100
16.	OPB-08	GTCCACACGG	NA	NA	NA	0
17.	OPB-10	CTGCTGGGAC	NA	NA	NA	0
18.	OPB-11	GTAGACCCGT	NA	NA	NA	0
Total				93	93	100
Average				5.16	5.16	–

** NA= Not Amplified

Genetic relationship among Ajwain Genotypes and Cluster Analysis based on RAPD

Genetic similarity estimates based on RAPD banding patterns were calculated using method of Jaccard's coefficient analysis. The similarity coefficient matrix generated for the primers was subjected to algorithm UPGMA (Unweighted Pair Group Method with Arithmetic averages) and dendrogram was generated using NTSYS-pc 2.02 programme (Rohlf, 1997).

The RAPD data were used to obtain a similarity matrix (Table 7). The similarity coefficient for different genotypes was in the range of 0.07 to 0.58. The average similarity across all the genotypes was found to be 0.32 indicating a low level of genetic similarity among the genotypes. This indicated a broad genetic base of tested cultivars.

The maximum similarity coefficient (0.58) was observed between local check and Pratap ajwain-1 followed by GP-149 and GP-131, GP-87 and GP-83 showed similarity of 0.48 and 0.47 respectively. The minimum similarity coefficient (0.07) was observed between GP-113 and GP-7 and Gujarat ajwain-1 and GP-70. The results obtained were in conformity with the earlier report by Javan *et al.,* 2012 who evaluated the genetic variation among eight species of Salvia using the RAPD markers. The pair-wise Jaccard genetic similarity varied from 0.07 to 0.35 for RAPD.

RAPD Dendrogram

The dendrogram generated on the basis of Jaccard's similarity coefficient, clearly indicated two main clusters. The clustering results based on RAPDs did not match with those based on morphological traits. The result suggested the high level of genetic diversity.

Cluster I was the major cluster which included 26 genotypes out of 28 genotypes. This cluster was divided into 2 sub clusters IA and IB at the similarity coefficient of 0.202. Sub-cluster IB included only one genotype *viz.,* GP-29. Sub cluster IA was divided into two sub clusters IA-1 and IA-2. Both had the similarity coefficient of 0.240. The sub clusters IA-1 included two genotypes Pratap ajwain-1 and local at the similarity coefficient of 0.58. Sub cluster IA-2 included 23 genotypes and so on shown in Fig 1. Genotypes Pratap ajwain-1 and local showed highest similarity co-efficient 0.580 for traits like days to 50 % flowering, primary branches per plant, umbels per plant, umbellates per umbel, seed yield per plant, harvest index and seed oil content. Cluster II was the minor cluster which included two genotypes *viz.,* GP-7 and GP-28 at the similarity coefficient of 0.471.

Table 7. Jaccard similarity coefficient for ajwain genotypes based on RAPD analysis

	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27	G28
G1	1																											
G2	0.42	1																										
G3	0.08	0.24	1																									
G4	0.13	0.29	0.37	1																								
G5	0.14	0.25	0.26	0.45	1																							
G6	0.15	0.23	0.20	0.31	0.41	1																						
G7	0.14	0.30	0.20	0.35	0.34	0.39	1																					
G8	0.17	0.27	0.29	0.38	0.40	0.35	0.41	1																				
G9	0.10	0.17	0.17	0.33	0.31	0.33	0.36	0.36	1																			
G10	0.16	0.26	0.36	0.37	0.36	0.38	0.34	0.41	0.26	1																		
G11	0.11	0.15	0.19	0.28	0.34	0.42	0.33	0.40	0.30	0.27	1																	
G12	0.18	0.21	0.12	0.24	0.37	0.27	0.32	0.25	0.23	0.17	0.37	1																
G13	0.13	0.27	0.19	0.31	0.32	0.30	0.46	0.31	0.27	0.39	0.19	0.25	1															
G14	0.15	0.28	0.23	0.40	0.35	0.37	0.37	0.30	0.23	0.39	0.26	0.26	0.48	1														
G15	0.35	0.26	0.18	0.37	0.29	0.27	0.31	0.34	0.22	0.33	0.17	0.27	0.30	0.23	1													
G16	0.07	0.17	0.21	0.30	0.29	0.30	0.37	0.30	0.41	0.27	0.31	0.24	0.30	0.23	0.35	1												
G17	0.13	0.21	0.13	0.34	0.28	0.27	0.39	0.25	0.24	0.27	0.24	0.17	0.33	0.32	0.22	0.36	1											
G18	0.18	0.16	0.19	0.35	0.37	0.28	0.42	0.41	0.41	0.37	0.22	0.22	0.37	0.24	0.31	0.28	0.30	1										
G19	0.22	0.22	0.14	0.32	0.20	0.31	0.42	0.50	0.50	0.30	0.28	0.28	0.26	0.19	0.41	0.33	0.27	0.35	1									
G20	0.25	0.30	0.12	0.31	0.23	0.24	0.37	0.31	0.31	0.22	0.29	0.40	0.39	0.40	0.33	0.26	0.33	0.25	0.37	1								
G21	0.17	0.30	0.20	0.38	0.27	0.35	0.51	0.32	0.32	0.29	0.29	0.28	0.36	0.33	0.29	0.33	0.34	0.38	0.49	0.37	1							
G22	0.10	0.24	0.24	0.44	0.43	0.41	0.47	0.47	0.47	0.32	0.34	0.26	0.32	0.29	0.27	0.35	0.47	0.40	0.41	0.38	0.43	1						
G23	0.18	0.20	0.18	0.22	0.32	0.21	0.32	0.28	0.28	0.33	0.18	0.30	0.36	0.27	0.37	0.30	0.27	0.40	0.22	0.22	0.29	0.33	1					
G24	0.14	0.26	0.15	0.33	0.28	0.23	0.42	0.39	0.39	0.31	0.20	0.29	0.37	0.40	0.27	0.26	0.35	0.33	0.33	0.34	0.41	0.47	0.44	1				
G25	0.17	0.33	0.20	0.33	0.20	0.30	0.33	0.27	0.27	0.38	0.26	0.18	0.32	0.37	0.24	0.26	0.26	0.25	0.36	0.32	0.44	0.31	0.27	0.42	1			
G26	0.10	0.20	0.15	0.35	0.20	0.19	0.32	0.23	0.15	0.25	0.07	0.17	0.26	0.27	0.31	0.25	0.28	0.32	0.23	0.29	0.38	0.33	0.40	0.39	0.24	1		
G27	0.14	0.17	0.11	0.25	0.26	0.18	0.24	0.23	0.14	0.21	0.17	0.21	0.26	0.30	0.22	0.21	0.24	0.29	0.19	0.22	0.26	0.27	0.34	0.30	0.30	0.32	1	
G28	0.11	0.17	0.11	0.27	0.25	0.14	0.20	0.27	0.18	0.24	0.16	0.11	0.20	0.29	0.29	0.21	0.18	0.27	0.24	0.25	0.20	0.25	0.30	0.31	0.31	0.27	0.58	1

G-1= GP-7, G-2= GP-28, G-3= GP-29, G-4= GP-30, G-5= GP-32, G-6= GP-41, G-7= GP-48, G-8= GP-53, G-9= GP-63, G-10= GP-66, G-11= GP-70, G-12= GP-71, G-13= GP-83, G-14= GP-87, G-15= GP-90, G-16= GP-113, G-17= GP-125, G-18= GP-127, G-19= GP-131, G-20= GP-141, G-21= GP-149, G-22= GP-168, G-23= GP-169, G-24= GP-175, G-25= GP- 191, G-26= Gujarat Ajwain-1, G-27= Pratap Ajwain-1, G-28= Local check.

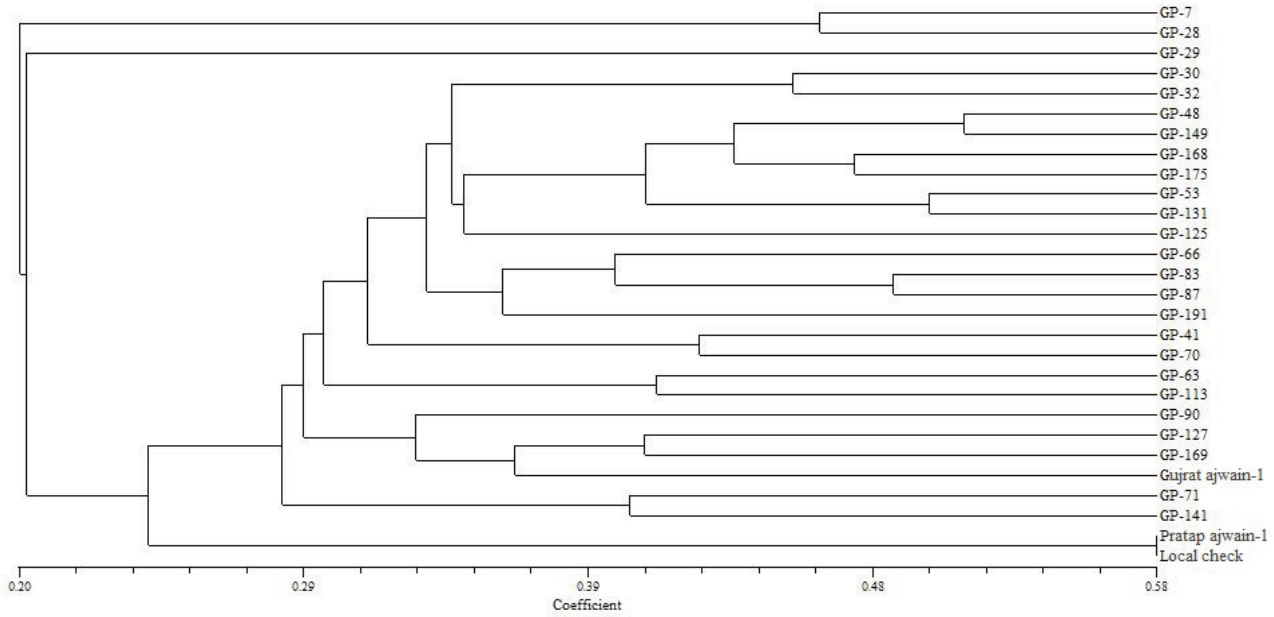

Fig. 1. Dendrogram generated for ajwain genotypes using UPGMA cluster based on Jaccard similarity coefficient (RAPD analysis)

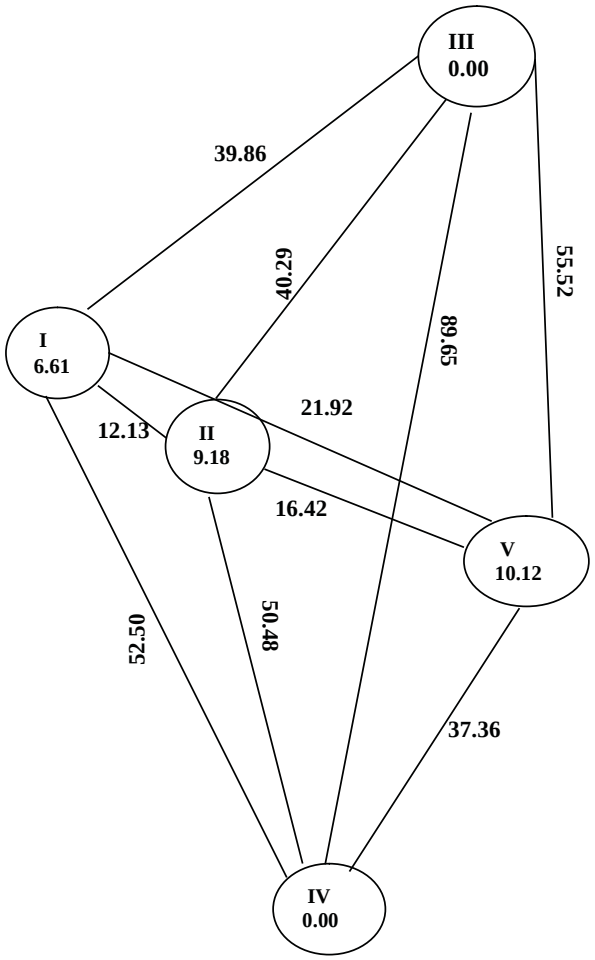

Fig. 2. Cluster diagram for 28 genotypes of ajwain based on Mahalonobis D^2 analysis

The results of the present investigation could also be used as a stepping stone for evolving a well-defined approach based on evaluation and characterization of genetic variation in ajwain, which is one of the important minor seed spices crop.

On the basis of results, it might be concluded that RAPD profile of ajwain genotypes *viz.,* GP-7, GP-28, GP-113, GP-29, GP-70, Gujarat ajwain-1, Pratap ajwain-1 and local can be used for the diversity studies. Further, the groups/clusters obtained by dendrogram could also be distinguished by similarity coefficient. The most dissimilar genotypes GP-113, GP-7, Gujarat ajwain-1 and GP-70. (similarity co-efficient 0.07) could be utilized to breeding programmes.

RAPD analysis revealed that 28 ajwain genotypes had high polymorphism (100%) and morphological analysis also had high variability (78%) and both analyses conclude that high variability could be used for seed yield improvement.

Conclusion

To conclude, characters like umbellates per umbel, secondary branches, and biological yield per plant had high estimates of all variability parameters and were strongly correlated with each other having maximum direct effects towards seed yield appeared promising to contribute genetic diversity in ajwain.

On the basis of D^2 analysis, it was found that genotypes *viz.,* GP-29 and GP-141 were highly divergent whereas these genotypes had low *per se* performance for seed yield and its contributing characters. Genotypes *viz.,* GP-7, GP-113, Gujarat ajwain-1 and Pratap ajwain-1 showing moderate divergence in D^2 analysis, were found high divergent in RAPD analysis and also had high *per se* performance for seed yield and its contributing characters like umbellates per umbel, secondary branches, and biological yield per plant. Results obtained through RAPD analysis appeared highly precise and accurate hence the genotypes identified can be selected for further breeding programme in ajwain.

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RESEARCH ARTICLE

Identification of New Sources for Good Quality High Biomass Yield and other Promising Traits in Mini Core Collection of Forage Sorghum

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Mini core collection of forage sorghum was evaluated for genetic diversity analysis in randomized block design. Observations were taken for total of thirty traits including quantitative and quality traits. Eleven principal components were extracted on the basis of PCA. First to eleventh principal components explained 16.42, 7.70, 6.98, 6.98, 6.83, 6.69, 5.74, 5.10, 4.87, 4.74, 4.31% of the total variance, respectively. The first eleven principal components had eigen values more than one and explained 75.77 % of the total variability of the original data units. On the basis of principal component analysis genotypes IS 651 and IS 23890 were found to be better for green fodder, dry fodder, DDM and mineral content; IS 28614, G 46 and SSG 59-3 recorded better performance and implied their superiority for fodder yield and resistance against stem borer, shoot fly and grey leaf spot; ICSV 700 was found better for fodder yield and IVDMD and low HCN and lignin content. Use of these genotypes is suggested in breeding programme as different sources/parents for further improvement of forage sorghum for green and dry fodder yield, IVDMD, mineral content and disease resistance.

Key Words: Fodder and yield, Forage sorghum, Mini core, PCA

Introduction

Sorghum is a major staple food crop in semi-arid tropics and among most food insecure people across the world. It could be due to crop's xerophilic characteristics, adaptation potential, quick growing habit, good ratoonability, palatability, digestibility and wide range of potential uses as green fodder, dry roughage, hay and silage. It is recognized worldwide as a "4F" crop especially under moderate inputs and water deficit environments.

In India, sorghum accounts for 1% of the total agricultural GDP. The present acreage under multicut fodder sorghum is one lakh hectares. Now increasing demand for livestock suggests that the fodder sorghum area will be 27.0 million hectares by 2050 (Vision IIMR, 2050). Landraces and wild relatives are rich sources of resistance to diseases, insect pests and other stresses such as high temperature, and drought etc. They are also rich sources of traits to improve food and fodder quality, animal feed and industrial products. To prevent the extinction of landraces and wild relatives, collection and conservation of sorghum germplasm has been accelerated in the past four decades. Since then, it has become an integral component of crop improvement programs (Rosenow and Dahlberg, 2000).

A core collection of 2247 accessions of sorghum was developed in 2001 to enable researchers to have access to a smaller set of germplasm. However, this core collection was found to be too large. To overcome this, mini core (10% accessions of the core or 1% of the entire collection) was developed and is being maintained at ICRISAT, Patancheru, India (Grenier *et al.*, 2001).

Most rapid method to step up livestock production is to enhance nutritive value of the forage sorghum by improving IVDMD (Pedersen *et al.,* 1982). When IVDMD is increased, winter hardiness is decreased, prussic acid glycosides may be increased and maturity is extended (Hoveland and Monson, 1980). A comprehensive analysis for importance of the mineral content in forage animal nutrition reveals that most tropical forages have low mineral contents than the temperate species. Screening of forage sorghum germplasm has shown existence of significant genetic variation for toxic constituents like, hydrocyanic acid and tannin, which reduce the quality of forage sorghum. Structural carbohydrates like NDF, ADF, cellulose and

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lignin are resistant to digestive enzyme and are found in cell wall portion of plant.

A major loss of quality and yield of forage sorghum crop is caused by insect pests like stem borer **(***Chilo partellus***)** (Hiremath *et al.,* 1988). It being an internal borer, its frass and fecal matter remain inside the stem lowering the quality of juice. Keeping in view these facts, a study was undertaken to characterize and assess the genetic diversity in sorghum accessions for morphological variability, quality and biotic resistance.

Material and Method

A field experiment was conducted in Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. It is situated in semi-arid sub-tropical region at 29º10ºN latitude and 75º46ºE longitude with-at elevation of 215.52 m above mean sea level. Hisar has semi-arid and sub-tropical climate with hot dry summer and severe cold winter. Average annual rainfall is about 492.7 mm was received in 33 rainy days, out of which 230.7 mm is received in three months, from July to September due to southwest monsoon. The soil of the experimental field was sandy loam in texture, slightly alkaline in reaction (pH 8.0). Sixty one sorghum genotypes were used in the present study. The experiment was laid out in randomized block design in three replications of two rows of 4m each with inter-row distance of 60 cm intra-row plant distance of 15 cm.

All the recommended agronomical practices for sorghum were followed to raise a good crop during the season. Data for all the traits was recorded from five plants in every replication.

Observations were recorded for various morphological traits like plant height, leaf length, leaves per plant, tillers per plant, leaf breadth, stem girth, green fodder yield and dry fodder yield and for three foliar diseases viz., grey leaf spot **(***Crecospora sorghi***),** zonate leaf spot **(***Gloeocercospora sorghi***)** and sooty stripe **(***Ramulispora sorghi***)** at 35 and 55 days after sowing. Scoring for foliar diseases was done using visual standards adopting the following scale:

1= no symptoms;

3= few scattered lesions/spots;

5= typical lesion developed on leaves covering up to 25% leaf area; 7= coalescing spots covering about 26-40% leaf area, and 9= symptoms severe covering more than 40% of leaf area

And the disease intensity was computed using the formula,

$$\text{Disease intensity} = \frac{\text{Sum of all numerical ratings}}{\text{Total number of leaves observed} \times \text{highest rating}} \times 100$$

All the genotypes were also evaluated for insects attack and observation were recorded for shoot fly **(***Atherigona soccata***)** and stem borer **(***Chilo partellus***)** attack as prescribed by Mathur (1991). For shoot fly data were collected at 14 and 28 days after germination and per cent dead hearts were calculated using the following formula:

$$\%\ \text{Dead heart} = \frac{\text{Number of dead heart/ plot}}{\text{Number of plants/plot}} \times 100$$

For quality estimation, samples of green fodder consisting of stalks after removal of heads were collected from the field and 500 g. was dried to constant weight at 60 ºC for dry matter determination. Then dried was passed through a small chopper, mixed thoroughly and sampled for dry matter determination and laboratory analyses. Neutral deteraent fibre (NDF) (%), acid detergent fibre (ADF) (%), Cellulose (%), Lignin (%) by (Goering and Van Soest (1970); Total phenol (mg/g DM) by Swain and Hillis (1959); Tannin (mg/g DM) by Bruns (1971); Mineral content : Zn, Fe, Cu, Mn, Na, K (µg/g DM) by Atomic Absorption Spectrophotometer; HCN content (mg/100g DM) by Gilchrist *et al.,* 1967; Crude Protein (%) by Micro-Kjeldhal's method; IVDMD (%) by Tilley and Terry (1971); Total soluble sugar (%) by Dubois *et al.,* (1956); DDM (Digestible dry matter) (q/ha) by IVDMD (%) X DFY/100 and º Brix by Refractometer were estimated as per the standard procedure.

The data were statistically analyzed for principal component analysis (PCA) and first two principal components were plotted against each other to find out the patterns of variability among genotypes and characters using statistical software packages of SAS 9.2 software.

Results and Discussion

The estimation of descriptive statistics of thirty traits indicated the existence of diversity among the genotypes. Among all the traits investigated, number of tillers, number of leaves, stem girth, green fodder yield, dry

fodder yield, total phenol, DDM, Fe, Mn, Zn, Cu, Na, Brix, HCN content, shoot fly, stem borer, sooty stripe, zonate leaf spot, grey leaf spot, tannin, lignin recorded higher variation in mean, range, variance and standard deviation.

Principal Component Analysis

The principal component analysis of sixty one genotypes based on correlation matrix yielded the eigen roots and vectors. These values and associated cumulative percentage of variation explained by eigen root have been presented in Table 1. Principal components with eigen values greater than one were selected for interpretation (Kaiser 1958 and Jeffers 1967). The first principal component explained 16.42 % of the total variation. The second to eleventh principal components explained 7.70, 6.98, 6.98, 6.83, 6.69, 5.74, 5.10, 4.87, 4.74, 4.31% of the total variance, respectively. The first eleven principal components had eigen values more than one and altogether explained 75.77 % of the total variability of the original data units.

The findings are in agreement with findings of Kang and Lee (1996), Ayana and Bekele (1999); Yadav and Pahuja 2013; Jain *et al.,* 2011; Jain and Patel, 2012 & 2016. Other yield contributing traits were also positively correlated with each other indicated that selection may be done in positive direction based on these traits towards crop improvement program. The PCA grouped the 30 traits in to eleven components which accounted for total (100%) variability among the studied genotypes. According to Chatfield and Collins, (1980) components with an eigenvalue of < 1 should be eliminated so that fewer components are dealt with. Furthermore, Hair *et al.* (1998) suggested that, eigenvalues greater than one are considered significant and component greater than 0.3 were considered to be meaningful.

The first principal factor (PF) showed high loading for plant height, leaf length, dry fodder yield, green fodder yield, DDM and Mn (Table 2). Number of tillers and number leaves per plant were found to have high loading on PF-2. PF-3 enabled high loading for Na, Cu and Fe. PF-4 had high loading for shoot fly dead heart, stem borer and grey leaf spot. The fifth principal factor enabled high positive loading for lignin and HCN and IVDMD and brix had high negative loading. The sign of loading indicates the direction of relationship between the factor and the variables, as correlation study showed IVDMD and brix are negatively correlated with

Table 1. Total variance explained by different principal components in sorghum genotypes

Principal components	Eigen value	Variation explained (%)	Cumulative variation explained (%)
1	4.92	16.42	16.42
2	2.12	7.07	23.48
3	2.09	6.98	30.47
4	2.09	6.98	37.46
5	2.05	6.83	44.29
6	2.01	6.69	50.99
7	1.72	5.74	56.74
8	1.53	5.10	61.85
9	1.46	4.87	66.72
10	1.42	4.74	71.46
11	1.29	4.31	75.77

both lignin and HCN. The sixth principal factor had variables like ADF, cellulose, phenol and Zonate leaf spot incidence whereas, PF-7 showed high loading for stem girth, tannin, crude protein and Zn. The eighth principal factor exhibited high loading for K only. Total soluble sugar showed factor loading on PF-9 while, the tenth principal factor enabled loadings of NDF. The eleventh principal factor had high loading for variable sooty stripe incidence. Genotypes with PF1 score therefore would have high level variability of these quantitative traits. Chozin, 2007, Mujaju and Chakuya, 2008 and Ali *et al.,* (2011) reported important contribution of the PF1 in total variability while studying different traits. The second and third PF explained 2.16 and 1.28 eigenvalues and contributing 24.08% and 14.31% variations, respectively. Overall, the PCA analysis under this study showed that phenotypic markers are useful in genotypes of sorghum and able to identify few key traits that accounted for the largest variability. Ali *et al.,* 2011; Akatwijuka *et al.,* 2016 and Jain & Patel, 2016 too observed similar observations.

Among the principal factors, Factors 1 and 2 can be regarded as fodder yield factors cumulatively, while Factors 3 and 8 can be regarded as mineral factors. The factors 4 and 11 can be regarded as diseases factors. The factors 5, 7 and 9 can be regarded as quality factors. The factors 6 and 10 could be antinutritional factors.

In the present study, principal factor analysis was carried out using principal component method, which does not require assumption of multivariate normal distribution of population in contrast to the other methods like maximum likelihood method (Jaiswal, 2000). Initially the data were analyzed without any rotation but it failed to load all the variables meaning thereby

Table 2. Factor loading of different characters with respect to different principal factor (Varimax rotation)

Characters/PF	PF-1	PF-2	PF-3	PF-4	PF-5	PF-6	PF-7	PF-8	PF-9	PF-10	PF-11
Dry fodder yield (q/ha)	0.9571	0.071	0.005	-0.038	-0.025	0.018	-0.004	-0.089	0.047	-0.036	0.091
Green fodder yield(q/ha)	0.947*	0.1	0.068	-0.025	-0.011	-0.031	-0.16	-0.072	0.025	0.003	0.053
Plant height (cm.)	0.924*	-0.064	0.122	0.014	-0.016	-0.088	-0.068	-0.135	-0.005	0.079	0.009
DDM (q/ha)	0.901*	-0.007	0.03	-0.011	-0.308	0.014	0.018	0.075	0.019	-0.106	-0.063
Leaf length (cm.)	0.640*	-0.02	0.293	-0.076	0.052	-0.079	0.069	0.012	0.299	0.116	0.207
Mn (µg/g DM)	0.456*	-0.254	0.139	0.139	-0.041	-0.095	-0.423	0.276	-0.161	0.073	-0.299
No. of tiller/plant	-0.010	0.927*	-0.133	0.080	0.012	0.028	-0.07	0.048	0.068	-0.005	0.048
No. of leaves/plant	0.097	0.898*	0.029	-0.165	0.210	-0.050	0.096	-0.017	-0.015	-0.011	-0.095
Na (µg/g DM)	0.007	0.014	0.779*	0.032	-0.162	0.004	-0.094	-0.044	0.252	0.154	0.012
Cu (µg/g DM)	0.180	0.001	0.726*	0.263	-0.008	0.024	-0.071	-0.119	-0.222	0.045	-0.266
Fe (µg/g DM)	0.300	-0.285	0.638*	-0.061	-0.117	0.043	-0.06	0.157	-0.134	-0.3	-0.02
Shoot fly dead heart	-0.171	-0.065	0.171	0.827*	-0.006	-0.007	-0.015	-0.002	-0.118	0.027	0.014
Stem borer dead heart	0.276	-0.085	-0.074	0.805*	-0.033	-0.1	-0.098	0.094	0.034	0.001	-0.081
Grey leaf spot	-0.214	0.127	0.06	0.647*	-0.016	0.332	0.211	0.08	0.105	-0.152	-0.087
Lignin (%)	0.137	0.035	-0.149	-0.162	0.702*	0.058	0.214	0.072	-0.085	-0.112	-0.321
IVDMD%	0.184	-0.129	0.007	0.015	-0.619*	0.019	0.016	0.316	0.007	-0.135	-0.24
Brixº	0.284	-0.117	0.404	-0.07	-0.582*	-0.04	0.064	0.045	-0.19	-0.047	0.088
HCN(mg/kg)	-0.123	0.153	-0.01	0.065	0.567*	0.05	0.239	0.324	-0.233	-0.01	0.33
ADF (%)	-0.078	-0.011	-0.019	-0.019	-0.008	0.827*	0.038	-0.105	0.006	0.1	-0.163
Cellulose (%)	-0.016	-0.122	-0.015	0.11	0.171	0.688*	-0.016	0.413	0.129	0.22	0.065
Total phenol (mg/g DM)	-0.141	-0.129	-0.12	0.118	0.327	0.540*	-0.228	0.081	0.405	-0.124	-0.024
Zonate leaf spot	-0.224	0.055	0.082	0.264	0.226	0.499*	-0.066	-0.167	-0.100	-0.327	0.346
Stem girth (mm.)	0.034	-0.130	-0.167	-0.057	0.036	0.130	0.763*	-0.014	0.161	0.035	0.044
Tannin (mg/g DM)	-0.365	0.172	0.065	0.164	0.125	-0.061	0.574*	0.209	-0.137	-0.203	0.043
Zn (µg/g DM)	-0.049	0.168	0.164	0.102	0.243	-0.247	0.419*	-0.364	-0.199	0.38	-0.048
Crude protein (%)	-0.091	0.291	-0.265	-0.018	0.243	-0.040	0.478*	-0.179	0.372	-0.289	0.068
K (%)	-0.176	0.051	-0.02	0.095	-0.038	-0.036	0.006	0.843*	0.040	0.061	0.033
Total soluble sugar %	0.200	0.064	0.028	-0.033	-0.096	0.015	0.109	0.066	0.807*	-0.101	0.017
NDF (%)	0.019	-0.028	0.030	-0.060	0.017	0.235	-0.072	0.075	-0.126	0.864*	-0.001
Sooty stripe	0.322	-0.075	-0.187	-0.156	-0.018	-0.113	0.108	0.07	0.042	-0.013	0.780*

that it could not provide much information regarding the idea of correlation between the variables and the principal factors.

The failure of principal factor analysis without rotation to draw sensible conclusions prompted to go for analysis with rotation. Varimax method of orthogonal rotation (Kaise, 1958) was utilized to rotate the factor axes. This is the most commonly used method and can be placed in a meaningful biological context (Titz, 1983). All the 30 variables showed high loadings on different principal factors and none of them was left after rotation of the principal factor axes. Moreover, it clearly grouped the similar type of variables by loading them together on a common principal factor.

The sign of loading indicates the direction of relationship between the factor and the variables, as correlation study showed IVDMD and brix are negatively correlated with both lignin and HCN. Similar results was observed in rapeseed by Valiollah, 2014 in which PF 1 had high positive loadings for days to flowering and days to maturity and high negative loadings for duration of flowering. These results are in conformity with that of Yadav *et al.,* (2003) who found that principal factor analysis identified nine principal components which explained 79 % variability. Loadings of similar type of variables on a common PC permitting to designate them as fodder yield factor, insect-pests attack factor disease incidence factor etc. as per type of variable loaded with. Abe *et al.***,** (2013) analysed 31 sorghum landrace accessions for chemical analysis. The PCA revealed that the first four PCs contributed 71.77 per cent of the variability among sorghum grain landrace accessions.

Using the principal factor scores (PF scores), four different graphs were plotted to represent the position of genotypes on X and Y-axis taking two most important factors at one time and to chalk out the breeding plan for further improvement by identifying superior parents

for hybridization/-crossing programme. The genotypes HJ 541, ICSV 700, COFS 29, IS 28614, SSG 59-3, S 540-2 and G 46 were found high in dry fodder yield, green fodder yield and DDM and stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had high Na, Cu and Fe clustered towards the positive side of PF 3 axis (Fig. 1) and such genotypes were IS 651 and IS 23890. The genotypes placed towards the positive end of the PF-1 and PF-3 are supposed to be superior collectively both for high yield and mineral content. On the basis of the present investigation, genotypes IS 651, S 540-1 and HJ 541 have been identified superior for both the characters collectively.

The genotypes HJ 541, ICSV 700, COFS 29, IS 28614, SSG 59-3, S 540-2 and G 46 were found having high dry fodder yield, green fodder yield and DDM stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had low stem borer, shoot fly and grey leaf spot incidence clustered towards the negative side of PF4 axis (Fig. 2) and such genotypes were IS 28614, G 46, SSG 59-3, and S 540-2. The genotypes placed towards the positive end of the PF-1 and negative end of PF-4 are supposed to be superior collectively both for high yield and biotic resistance. On the basis of present investigation, genotypes IS 28614, G 46 and SSG 59-3 have been identified superior for both the characters collectively.

The genotypes ICSV 700, COFS 29, IS 28614 and HJ 541 were found having high dry fodder yield, green fodder yield and DDM stood out towards the positive portion of PF1 axis in the plot, whereas the genotypes which had high brix and IVDMD and low lignin and HCN clustered towards the negative side of PF 5 axis (Fig. 3). IVDMD and brix had high negative factor loading so genotype towards negative side are superior and such genotypes were S 473-1, ICSV 700, IS 2205 and S 540-1. The genotypes placed towards the positive end of the PF-1 and negative end of PF-5 are supposed to be superior collectively for high yield, and high brix, IVDMD, low lignin and HCN. On the basis this investigation, genotypes ICSV 700 has been identified superior for these characters collectively.

Similar results were reported by Bucheyeki (2008) while studying morphological characterization of Tanzanian sorghum [*Sorghum bicolor* (L.) Moench]

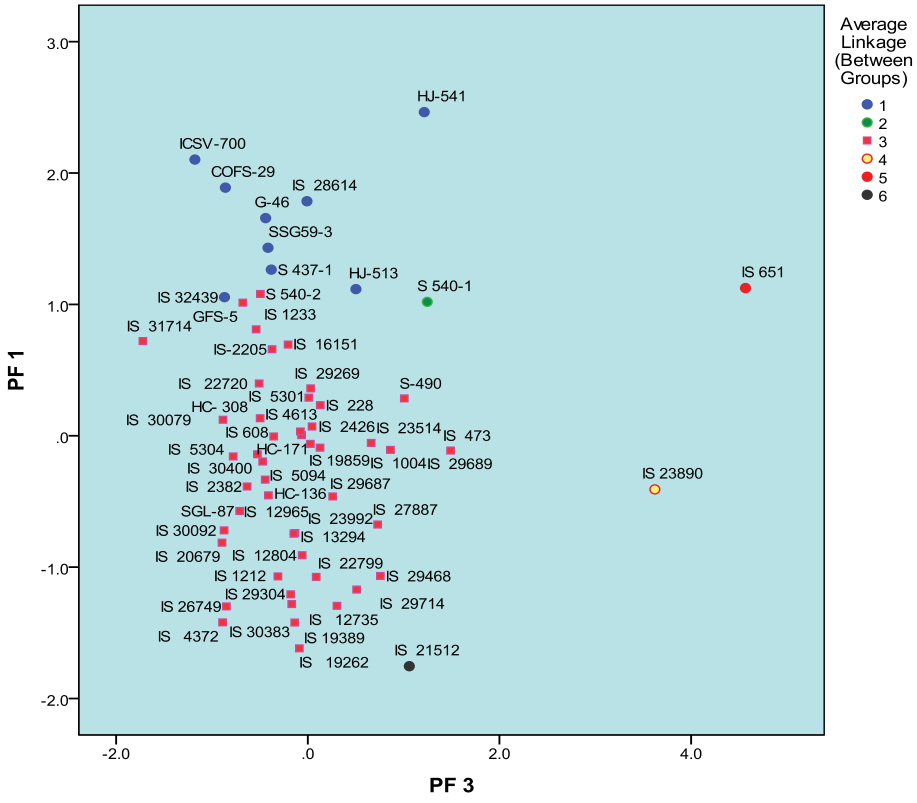

Fig. 1. Distribution of sorghum genotypes based on Principal Factor 1 and 3

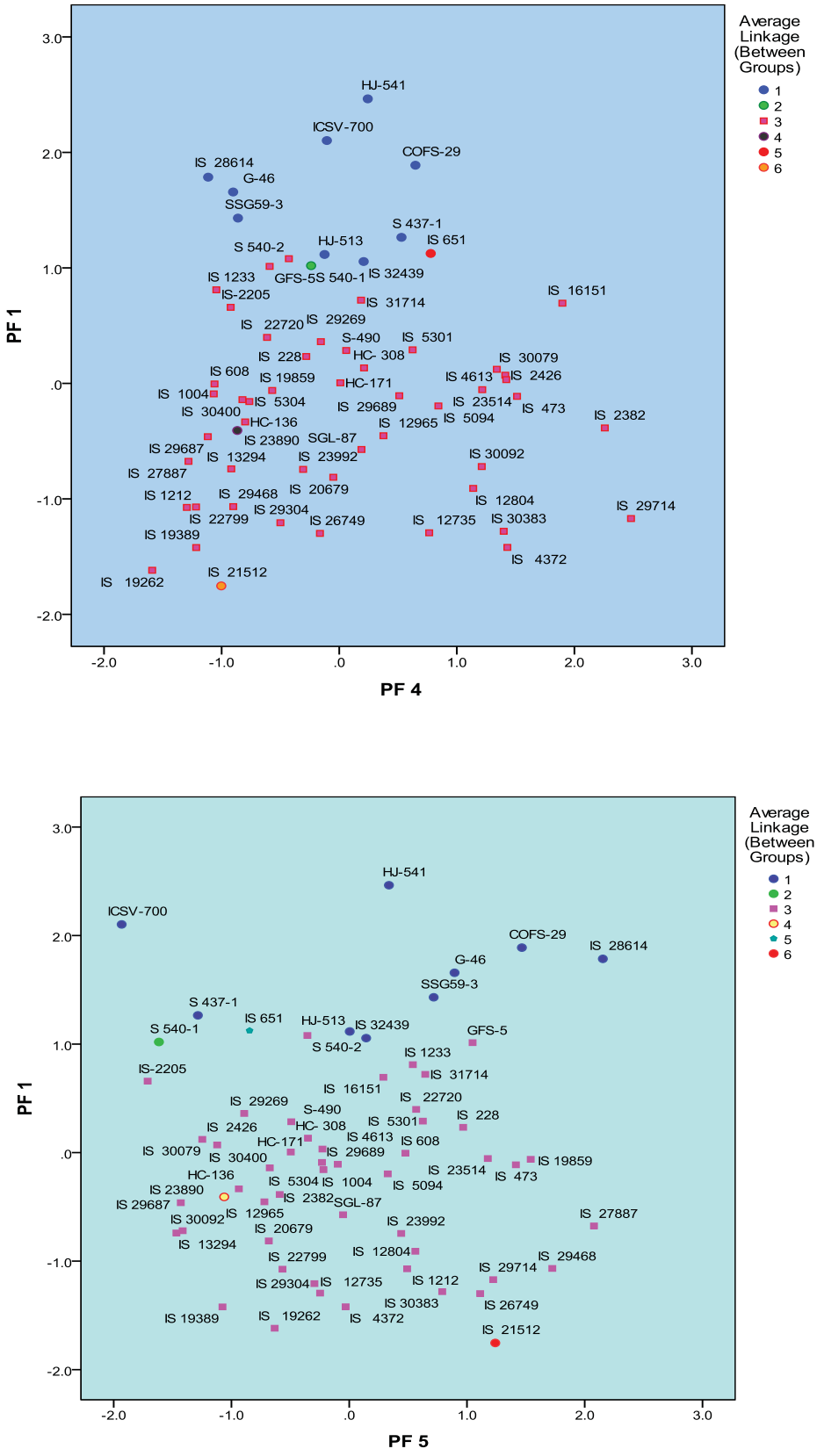

Fig. 3. Distribution of sorghum genotypes based on Principal Factor 1 and 5

landraces. Other researchers too recorded more than 70 % contribution to variability by the first two-to-six principal components (Haussmann *et al.,* 2000). However, Grenier *et al.* (2001) observed 48.8 % of the variance with the two axes of the principal components. Gerrano (2010) reported genetic diversity in sorghum using phenotypic marker in 22 sorghum accessions. The principal component analysis showed that the first five principal components (PC) contributed 87 % of variability among the accession. Leaf number, days to 50 % flowering, number of internodes, plant height and panicle width contributed mainly to PF 1 and leaf width, leaf area, grain yield, leaf sheath length, internodes length and panicle weight to PF 2. Yadav *et al.* (2003) characterized 90 sorghum genotypes on the basis of plant height, leaf length, leaf breadth, stem girth, number of tillers, number of leaves and disease parameters and three, visual fodder quality parameter. Four PC had eigen values greater than one explaining 73.57 % variability. Abe *et al*. (2013) analyzed 31 grain sorghum landrace accession were used for chemical analysis. The PCA revealed that the first four PC contributed 71.77 % of the variability among sorghum landrace accessions.

It is concluded that first eleven principal components had explained 75.77% of the total variability among the sorghum genotypes tested and it indicated the presence of excellent opportunity to bring about improvement through hybridization. Use of these genotypes is suggested in breeding programmes as different sources/parents for further improvement of forage sorghum for green fodder yield, dry fodder yield, IVDMD and mineral content.

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RESEARCH ARTICLE

Diversity in Melon (*Cucumis melo L.*) Landraces of Karnataka State of Southern India for Downy and Powdery Mildew Disease Resistance

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We present here the report on evaluation of melon landraces from the Karnataka state of India for resistance to downy mildew (*Pseudoperonospora cubensis*) and powdery mildew (*Podosphaera xanthii*), the major diseases of melon as well as other cucurbits. Thirty four melon landraces collected from different agro-climatic regions of the state were evaluated for resistance against downy mildew under natural epiphytotic conditions and powdery mildew under artificial conditions. Percent disease index (PDI) was calculated for each entry and based on that accessions were categorised as resistant, moderately resistant and susceptible. A very wide variation was observed among the accessions for resistance to both the diseases. Based on PDI, out of 34 accessions, COHB04, COHB37, COHB38, COHB41 and COHB43 were resistant to downy mildew. Ten genotypes were moderately resistant, fifteen were susceptible and four lines including susceptible check were highly susceptible to disease. Three landraces, COHB12, COHB38 and COHB40 were resistant to powdery mildew disease. Two genotypes were moderately resistant and rest of the lines were susceptible to disease. COHB38, an unexplored and uncultivated genotype was resistant to both the diseases. The highly resistant genotype COHB38 identified within the accessions tested offers an additional source for the development of downy and powdery mildew resistant melon cultivars.

Key Words: *Cucumis melo,* Downy mildew, Landraces, Powdery mildew resistance

Introduction

Melons (*Cucumis melo* L., 2n = 24) of Cucurbitaceae family are one of the global crops of high economic importance and provide health beneficiary nutrients. They are highly polymorphic and include a diverse botanical group. Melons have been divided into two subspecies and different horticultural groups (Jeffrey, 1980; Pitrat, 2008; Pitrat, 2016). East Africa was considered as the probable centre of origin of melon (Pitrat, 2008) but the recent data shows that melons might have originated in Asia (Sebastian *et al*., 2010). In India, depending upon the local market preferences in melon, several landraces have established themselves in different geographical pockets or riverbeds (Nandpuri, 1989; Fergany, 2011; Sudhakara, 2014; Reddy *et al*., 2016). Commercial melon varieties of superior yield and quality bred for bigger markets are being grown in larger areas and are narrowing down the genetic variability. Many of the locally adapted melons may not be very good with respect to yield and quality compared to the improved varieties and hybrids but they may be repositories of useful genes and also contribute to widen the crop genetic diversity. Melons of Karnataka are tailored to different agro-climatic regions and have considerable variability with respect to plant and fruit characters (Sudhakara, 2014). The landraces are being cultivated on river beds and some uncultivated melons are found as weed in rainy season.

Diseases are a limiting factor for profitable melon production. Downy mildew (*Pseudoperonospora cubensis*) and powdery mildew (*Podosphaera xanthii* and *Golovinomyces cichoracearum*) are the most widespread diseases of melon. The powdery mildew causal organism, *G. cichoracearum* is common in temperate and cooler areas (Lebeda *et al*., 2011) whereas *P. xanthii* occurs more frequently in sub-tropical and tropical areas (Kristkova *et al*., 2009). *P. xanthii* is most prevalent species in India (Gupta and Sharma, 2012). Though there are cultural practices employed and fungicides are being used to manage the disease, the most cost effective way of combating diseases is exploring the resistant genes and developing durably resistant varieties by pyramiding race specific genes (McCreight *et al*., 2005). Some melon fruits are usually

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consumed fresh and to avoid the risks of unacceptable levels of chemical residue due to fungicidal application, breeding for disease resistance is the preferred and environmentally safe means of managing disease and successful production of the crop. With emergence of new races, over the time, resistant varieties become susceptible and therefore the search for new resistant sources and introgression of resistant genes from donor parents to the cultivated lines is a continuous process. So, it is pertinent and needful to screen the different local lines of melon against diseases. Sources of resistance to downy and powdery mildew were reported in several Indian landraces (Seshadri and More, 1996; Dhillon *et al*., 2012; Liu *et al*., 2010; Fergany *et al*., 2011 and Reddy *et al*., 2016) and are being used worldwide to develop resistant varieties. The most commonly used sources of resistance were LJ 525, PI 79376, PI 124112, PI 313970, PI 124111, (Thomas *et al*., 1988; Balass *et al*., 1992; Pitrat and Besombes, 2008; Pitrate, 2008), PI 414723 (Epinat and Pitrat, 1989) and PI 134198 (Liu *et al*., 2010). The purpose of this study was to evaluate the unexplored and endemic landraces of Karnataka state for resistance to powdery and downy mildew diseases.

Materials and Methods

Germplasm

This study included thirty four landraces of melon (only the low sweet type melons used for consuming ripen fresh fruits) collected directly from farmer's field in five agro-climatic zones of Karnataka state (Table 1) and check varieties. Kashi Madhu, a popular variety under cultivation (Pandey *et al*., 2008) was used as a susceptible check in both the experiments. Resistant checks were IIHR651 for downy mildew and IIVR231 for powdery mildew. The accessions were selfed for three generations under insect proof shade net and were evaluated for morphological traits and disease resistance in separate experiments.

Screening for downy mildew: The evaluation of landraces for downy mildew resistance was done under natural epiphytotic condition during June-September of 2014 and 2016. Ten plants per genotype were planted with a spacing of 2.5m × 0.45m with two replications. Nine leaves (three top, three middle and three bottom) in each plant were visually assessed for percent leaf area infected using linear 0 to 5 scale and the percent

Table 1. Description of *Cucumis melo* L. landraces from different agro-ecological regions of Karnataka state and reference genotypes included in the study

Source of germplasm	Accession and their local names	Botanical group	Use
Davanagere district–Southern Transition Zone (Three different places)	COHB01 (Mallapur Ganjam), COHB03 (Banaspathre), COHB05, COHB010& COHB11 (Ganjam)	*indicus*	Ripen fruits for slicing and juice making
	COHB02 & COHB07 (Sidoota), COHB04, COHB06 & COHB08 (Karabooja)	*chandalak*	
Shivamogga–Hilly Zone	COHB12 (Kekkarale)	*momordica*	Ripen fruits consumed with jaggery
Chamarajanagar–Southern Dry Zone (Two different places)	COHB13,COHB14, COHB15, COHB35 & COHB36	*chandalak* but monoecious	Ripen fruits for slicing and juice making
	COHB16,COHB17,COHB18,COHB19,COH B22,COHB23,COHB28,COHB30,COHB31& COHB32 (All are called as Minake irrespective of their phenotype)	Intermediate forms of *chandalak* and *momordica*	
Bijapur (Three different villages)–Northern Dry Zone	COHB38 (Puttikaayi)	Intermediate form of *acidulus* and *momordica*	Ripen fruits consumed with jaggery
	COHB37, COHB40, COHB41, COHB41a, COHB 42 & COHB42a (All are called as Puttikaayi but appear different)	*acidulus*	
Tumkur– Central Dry Zone	COHB43 (Budame kaayi)	*kachri*	Only ripen fruits are consumed.
Reference Genotypes			
ICAR-Indian Institute of Horticulture Research, Bengaluru	Kashi Madhu (Susceptible check for downy and powdery mildew)	*chandalak*	Ripen fruits for slicing and juice making
	IIHR651 resistant check for downy mildew	Not known	Ripen fruits for slicing and juice making
ICAR-Indian Institute of Vegetable Research, Varanasi	IIVR231 resistant check for powdery mildew	*momordica*	Semi dessert fruits

disease index (PDI) was calculated (Shashikumar *et al*., 2010). 0 = Healthy and no symptoms, 1=1.1-5 % leaf area covered with chlorotic/necrotic symptom, 2= 5.1-10% leaf area covered with chlorotic/necrotic symptom, 3=10.1-20 % leaf area covered with chlorotic / necrotic symptom, 4=20.1-30 % leaf area covered with chlorotic/necrotic symptom and 5=> 30 % leaf area covered with necrotic symptom. The observations were made four times with seven days interval once the disease was observed on susceptible host. Phenotypic data on plant responses to downy mildew was used to calculate PDI according to Wheeler (1969) where, PDI = (Sum of numerical disease ratings/Number of plants observed) × 100/ Maximum disease rating value. Based on the average PDI, the genotypes were categorized into four groups (Pitchaimuthu *et al*., 2012). 0.1-25 % as resistant, 26-40 % as moderately resistant, 41-60% as susceptible and >60 % as highly susceptible.

Screening for powdery mildew: The germplasm was evaluated for powdery mildew disease resistance during October-December 2015 under shade net conditions through artificial inoculation. The obligatory pathogen was isolated from diseased plants maintained in the greenhouse to inoculate seedlings at two true leaf stage (when all plants have produced two true leaves). Seedlings were evaluated for disease resistance reaction after observing infection on susceptible check Kashi Madhu using 0-5 scale of Zhang *et al*. (2013) where 0 = no evidence of infection, 1 = trace (up to 20 %) infection of cotyledons only, 2 = low infection (21–50 %) of cotyledons or trace infection of hypocotyls, 3 = moderate infection of cotyledons (51–70 %) and low infection of hypocotyls (21–50 %), 4 = severe infection (>71 %) of cotyledons and hypocotyls, slight infection of leaves (20 %), 5 = whole plant infected and/or dead because of disease. Three observations were recorded with four days interval. Calculation of PDI is same as that for downy mildew and genotypes were categorised into three groups based on their PDI. Genotypes having a PDI $\leq$ 40 were considered resistant, between 40 and 60 were partially or moderately resistant and $\geq$ 60 were classified as susceptible. The resistant lines were re-tested in 2016 and 2017 for powdery mildew disease resistance at seedling stage to confirm their resistance.

Results

A wide variation was observed among the landraces for resistance to both downy and powdery mildew diseases (Table 2, Fig.1 and Fig. 2). For downy mildew, landraces COHB04, COHB37, COHB38, COHB41 and COHB43 were resistant with PDI value less than 25 percent. Ten genotypes (including the resistant check IIHR651) were moderately resistant and their PDI ranged from 27.1 to 37.5 percent. Fifteen accessions were susceptible with the PDI ranging from 41.9 to 57.9 percent and five lines including susceptible check were highly susceptible to disease. For powdery mildew disease, COHB12, COHB38 and COHB40 were resistant with low PDI values ranging from 2.5 to 17.6 per cent. Genotypes COHB37, COHB43 and IIVR231 (resistant check) were moderately resistant but COHB43 showed segregation for resistance and susceptibility. All the other accessions were susceptible to disease and the PDI for susceptible genotypes ranged from 46.5 to 100 percent. COHB38, an unexplored, uncultivated and weedy genotype was resistant to both downy and powdery mildew diseases with PDI of 19.2 % and 2.5 %, respectively. COHB37 was resistant to downy mildew and moderately resistant to powdery mildew. COHB12 (snap melon) and COHB40 showed resistance to powdery mildew and moderate resistance to downy mildew.

Discussion

Karnataka state is one of the major melon growing states in southern part of India and has ten different agro-climatic regions which include coastal, hilly area, arid or dry zone and transitional belts between hilly and dry zones. The different botanical types of melons grown traditionally in the state include *acidulous*, *agrestis*, *kachri*, *momordica* (snapmelon or Phut), *chandalak* and *indicus*. *Acidulus* melons are one of the widely grown and used melons for vegetable purpose. *Chandalak* and *indicus* type melons are cultivated on the residual moisture on river beds and wide variability exists among them. *Momordica* and *agrestis* are grown in a small scale whereas *kachri* are not cultivated but grow as weed in finger millet fields. Apart from these melons some intermediate forms are also available. An *acidulous* type of melon also grows in northern part of the state as a weed in sorghum field and the ripen fruits are marketed in local markets. The high yielding commercial varieties are replacing the landraces and narrowing down the genetic diversity which intern makes the crop susceptible to diseases. Downy and powdery mildew are the major foliar diseases of melons that affect yield and fruit quality. We made an attempt to collect the cultivated landraces and uncultivated types directly from farmers (Table 1). A very wide variation was observed among the melons

Table 2. Percent disease index (PDI) and reaction of melon landraces for downy and powdery mildew diseases

Sl. No.	Accession No.	Downy mildew		Powdery mildew	
		PDI (%)	Disease reaction	PDI (%)	Disease reaction
1	COHB01	57.38 ± 3.00	S	67.00 ± 3.46	S
2	COHB02	35.00 ± 0.00	MR	73.25 ± 3.17	S
3	COHB03	29.84 ± 1.33	MR	63.00 ± 3.46	S
4	COHB04	18.05 ± 0.10	R	84.50 ± 5.19	S
5	COHB05	50.88 ± 4.59	S	64.50 ± 5.19	S
6	COHB06	56.88 ± 4.74	S	75.00 ± 3.46	S
7	COHB07	72.77 ± 3.20	HS	100.0 ± 0.00	S
8	COHB08	33.11 ± 1.73	MR	100.0 ± 0.00	S
9	COHB10	41.94 ± 1.92	S	100.0 ± 0.00	S
10	COHB11	37.50 ± 2.50	MR	100.0 ± 0.00	S
11	COHB12	28.33 ± 0.00	MR	17.57 ± 5.62	R
12	COHB13	46.11 ± 2.56	S	100.0 ± 0.00	S
13	COHB14	44.81 ± 3.63	S	84.80 ± 5.54	S
14	COHB15	47.77 ± 3.62	S	100.0 ± 0.00	S
15	COHB16	66.33 ± 6.43	HS	100.0 ± 0.00	S
16	COHB17	51.80 ± 1.76	S	77.55 ± 3.40	S
17	COHB18	47.50 ± 3.84	S	100.0 ± 0.00	S
18	COHB19	66.80 ± 5.99	HS	100.0 ± 0.00	S
19	COHB22	63.88 ± 6.39	HS	66.75 ± 5.48	S
20	COHB23	47.66 ± 4.05	S	100.0 ± 0.00	S
21	COHB28	57.88 ± 4.33	S	100.0 ± 0.00	S
22	COHB30	47.36 ± 1.44	S	77.50 ± 2.88	S
23	COHB31	51.77 ± 0.37	S	68.25 ± 4.90	S
24	COHB32	36.80 ± 0.80	MR	100.0 ± 0.00	S
25	COHB35	34.58 ± 3.33	MR	100.0 ± 0.00	S
26	COHB36	50.44 ± 1.76	S	100.0 ± 0.00	S
27	COHB37	17.47 ± 1.49	R	41.00 ± 1.15	MR
28	COHB38	19.22 ± 0.21	R	2.50 ± 2.88	R
29	COHB40	27.14 ± 1.33	MR	13.00 ± 3.46	R
30	COHB41	17.50 ± 0.10	R	46.50 ± 2.88	S
31	COHB41a	29.00 ± 0.90	MR	53.00 ± 5.77	S
32	COHB42	51.85 ± 1.28	S	64.00 ± 4.61	S
33	COHB42a	28.88 ± 0.64	MR	69.50 ± 2.88	S
34	COHB43	16.00 ± 1.44	R	40.50 ± 2.88	^MR
35	Kashi Madhu*	76.11 ± 4.61	HS	100.0 ± 0.00	S
36	IIHR-651**	31.00 ± 1.73	MR		
37	IIVR231**			42.00 ± 1.15	MR

** Resistant checks & * Susceptible check ^ segregated for resistance
R = Resistant MR =Moderately Resistant S = Susceptible & HS =Highly susceptible

for resistance to downy and powdery mildew diseases. For downy mildew, accessions were screened under natural disease epiphytotic conditions and the reaction of landraces ranged from resistant (five landraces) to high susceptibility (four landraces). Ten genotypes were moderately resistant and fifteen accessions were susceptible to disease. Powdery mildew resistance screening was done under artificial condition. Since the pathogen is an obligatory parasite, disease inoculum was maintained on susceptible host for inoculating accessions. Resistance was noticed for three landraces, moderate resistance was observed for two lines but majority of the accessions (30) were found susceptible to powdery mildew. Some lines showed moderate resistance to downy mildew but were susceptible to powdery mildew (Table 2). Genotypes resistant to both the diseases are more useful in breeding. COHB38 showed resistance to both downy mildew and powdery mildew diseases. COHB38 is a selection from the segregating lines of an uncultivated plant from northern dry Zone. The fruits of original plant look like *acidulous* melon with patches on skin but on selfing, it segregated for disease

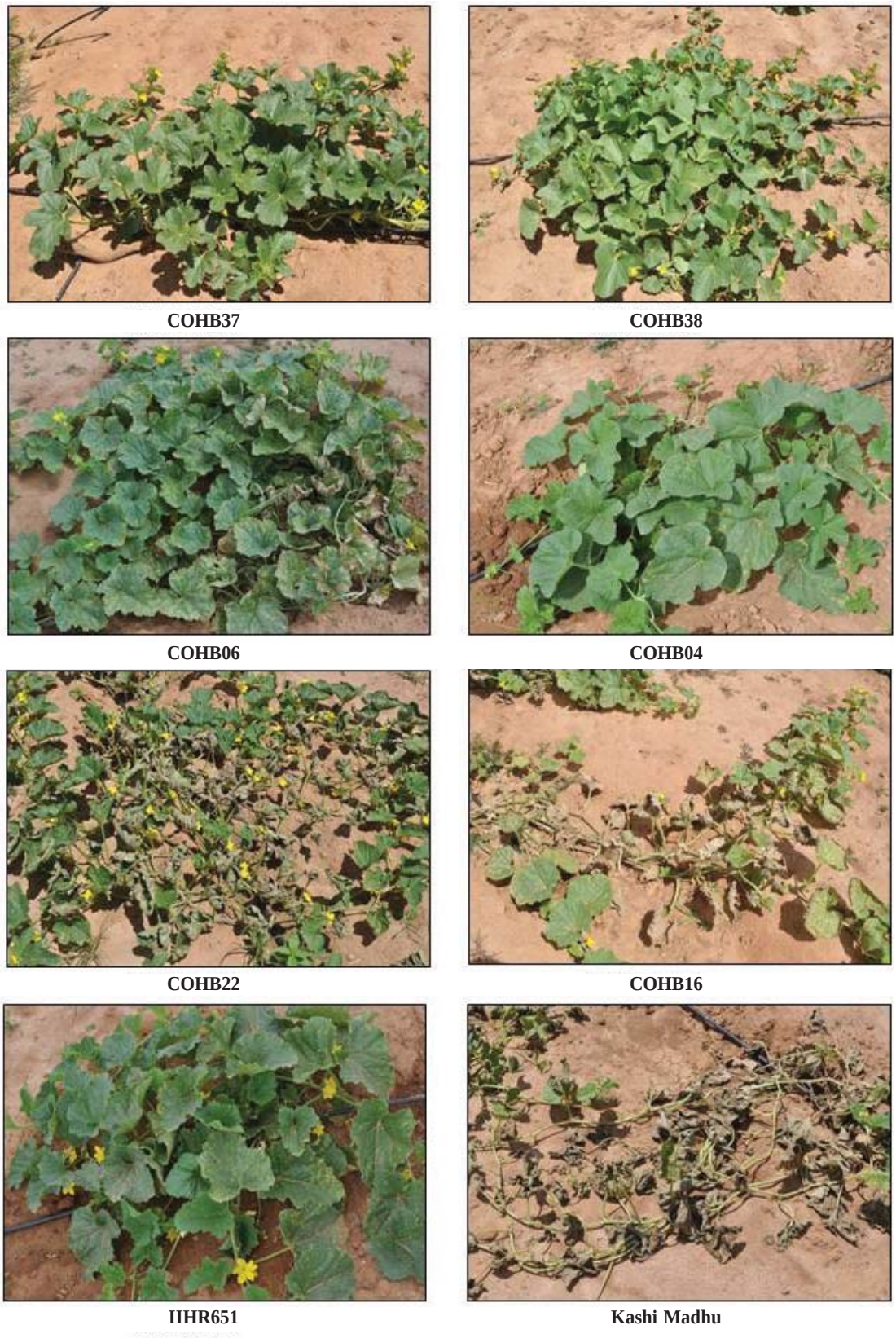

Fig. 1. Reaction of melon landraces for downy mildew disease

Fig. 2. Reaction of melon landraces for powdery mildew disease

resistance as well as fruit characters. It may be an intermediate type between *acidulous* and *momordica* melon but fruit cracking is not observed as in *momordica*. COHB37 (*acidulous*) was resistant to downy mildew but moderately resistant to powdery mildew. COHB12 (*momordica*) and COHB40 (*acidulous*) were resistant to powdery mildew but moderately resistant to downy mildew. The other resistant genotypes in the present study belong to *acidulous, indicus*, *kachri* and some intermediary types between *momordica* and *chandalak*. Variation for disease resistance was also observed among landraces collected from Kerala and Tamilnadu of South India (Fergany *et al*., 2011). Some powdery mildew resistant *acidulus* (AM22, AM67 and AM 90) and *momordica* (AM 86) melons were also identified. The Indian melon line 90625 (PI 313970) belongs to the *acidulus* botanical group was described as resistant to powdery mildew (Dogimont *et al*., 1996). Five unique genes conferring resistance to powdery mildew were identified in 90625 that acted as a potential source of resistance for strains in France (Pitrat and Besombes, 2008).

Germplasm evaluation for identification of new sources of disease resistance for the emerging new races of pathogen and genetic improvement through resistant gene introgression play great role in production and

productivity of crops. The unexplored resistant genotypes of the present study could be used in resistant gene introgression to cultivated varieties and also useful in studying the inheritance of disease resistant genes in a new background. The resistant line has also shown cross compatibility with other botanical groups of melon tested in our experiments. In melon improvement, the landraces especially snap melons of Indian origin have played an important role in providing disease resistance genes for major diseases throughout the world (Thomas *et al*., 1988; Balass *et al*., 1992; Pitrat and Besombes, 2008; Pitrate, 2008). Snapmelon accessions of *momordica* botanical class from North India have served as resistant sources for both powdery mildew and downy mildew diseases (Seshadri and More, 1996; Perchepied *et al*., 2005; Pitrat and Besombes, 2008, Pitrate, 2008; Liu *et al*., 2010; Dhillon *et al*., 2012; Reddy *et al*., 2016). Local types and wild relatives may look inferior but can contribute useful genes especially for biotic stresses (Simpson and Sedjo, 1998).

Breeding powdery mildew resistant melon cultivars started in the 1930 in California with the release of 'PMR 45' (Jagger and Scott 1937) using resistant gene of snap melon from Kathiawar region of Gujarat (Dhillon *et al*., 2012) and since then, many resistant cultivars have been created in different cultigroups of melons. Till now more than 28 putative races of *P. xanthii* have been identified (McCreight, 2006) and 30 different sources of resistance have been found in melon. The most commonly used sources of resistance are K 6205, K 6206, K 5692 and K 5519 (Malinina, 1974), PI 321005 (Zonia *et al*., 1983), PI 414723 (Epinat and Pitrat, 1994), LJ 525 (source for PMR 45), PI 79376 (source for PMR 5, PMR 6), PI 124112, PI 12411 (MR-1), all of them are from India (Perchepied *et al*., 2005; Pitrat and Besombes, 2008 and Pitrate, 2008).

Global genebanks contain Indian melon accessions originating from the north (Rajasthan) and central (Madhya Pradesh) parts of India (Staub and McCreight, 2004). The genetic diversity among the melon landraces of North and central India (McCreight *et al*., 1993 and Reddy *et al*., 2016), Tamilnadu and Kerala states of Southern India has been studied earlier (Fergany *et al*., 2011) but very minimum representation of germplasm of Karnataka state is observed (Reddy *et al*., 2016). The melon landraces of Karnataka state are unexplored for research purpose and literature about their documentation and usage is also very scanty. In this regard, the present study is very much relevant in collecting, evaluating and adding a new source of disease resistance line to melon crop improvement. The identification of highly resistant plants for downy and powdery mildew diseases within the accessions tested offers additional sources for the development of disease resistant melon cultivars and also to study the genetics of resistance in new background. Apart from this, the study also helps in documenting and conserving the endemic germplasm of the Karnataka state which is under-represented at national and world gene pool of melon.

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Ethical Statements

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Conflict of Interest: Nil

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RESEARCH ARTICLE

Status of Rice (*Oryza sativa* L.) Genepool Collected from Western Ghats Region of India: Gap Analysis and Diversity Distribution Mapping using GIS Tools

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This paper analyses the genetic resources of cultivated and wild rice in Western Ghats region (WGR) spread in six states of the country. Landraces and wild relatives of rice (*Oryza sativa* L.) always form a priority germplasm for exploration, collections, conservation, evaluation and utilization. Western Ghats region is one of the 35 biodiversity hot-spots of the world and harbour large diversity of rice under its varied climatic and edaphic conditions. So far, ICAR-NBPGR, New Delhi has collected 2,758 accessions of cultivated and 49 of wild rice germplasm from 42 districts of WGR of India. Germplasm collecting sites linked with geo-coordinates forms geo-referenced map which showed that Kerala had significant representation (2,036 accessions), followed by Karnataka (203), Maharashtra (201), Tamil Nadu (153), Gujarat (116) and Goa (49). Highest numbers of landraces were collected from Kerala (386), followed by Tamil Nadu (92), Karnataka (88), Gujarat (56), Goa (30) and Maharashtra (26). GIS-based grid map shows that highest numbers of landraces were collected from north and central regions of Kerala, validated by the highest Shannon-Weaver diversity index (2.1-2.8). Diverse agro-ecosystems as well as selection by farmers for various uses and traits, coupled with extensive exploration efforts might have lead to the assemblage of such landraces collection from Kerala. Collected wild rice germplasm consists six taxa - *Oryza meyeriana* var. *granulata* (11), *O. nivara* (4), *O. officinalis* (4), *O. rufipogon* (10), *O. sativa* f. *spontanea* (19) and *O. officinalis* subsp. *malampuzhaensis* (1). Literature analysis revealed that, out of 678 rice landraces of this region, 43 have been identified/ used in crop improvement as source of important traits *viz.* early and late maturity, aroma, high iron content, medicinal value, drought/cold/salt tolerance, resistance to brown plant hopper, etc. This analysis identified gaps and priority areas for future explorations.

Key Words: Diversity distribution mapping, GIS, Rice landraces, Western Ghats Region, Wild rice

Introduction

Rice (*Oryza sativa* L.) is one of the three major food crops of the world and forms staple food for more than 1.5 billion people. While 20 per cent calories and 15 per cent protein requirements of world's human population are met out from this cereal (Brar and Khush, 1997). Rice accounts for 35 to 75% of calories consumed by more than 3 billion Asians (Khush, 2005). In South Asia, rice is cultivated over 60 m ha with production of more than 225 m tons, accounting for 37.5% and 32% of global rice area and production, respectively (FAOSTAT, 2015). In India, rice is cultivated in 44.11 m ha and is the major food crop for more than 70% of the population (FAOSTAT, 2015). It is widely recognized that ensuring food and nutritional security in developing countries through increase in rice grain production is a challenge under shrinking land resources and the adversities arisen due to climate change (Aggarwal *et al.,* 2000; Kumar *et al.,* 2011).

In the Western Ghats region (WGR) rice is cultivated in 2.68 lakh ha area, with production of 0.65 m t and productivity of 2,387 kg/ha (Kumar *et al.*, 2011). In Western Ghats rice is grown under different agro-ecosystems influenced by soil, topographic, altitudinal and seasonal variations; this along with diverse use pattern by local people had resulted in rich landraces diversity (Vaughan, 2003). In Kerala, rice landraces diversity offers wide range to adapt to multiple agro-ecologies provides resistance to biotic and abiotic stresses carries special culinary traits and has cultural significance (Gopi and Manjula, 2018). Landraces, also known as local varieties and traditional cultivars (Zeven, 1998), are genetically heterogeneous in nature, often confined to specific agro-ecological niche, and identified by distinct

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vernacular names. These precious genetic resources consisting of large genetic variability are very useful in complementing and broadening the gene pool of advanced genotypes (McCouch *et al.,* 1997). They are the most-sought after germplasm for rice improvement against tolerance to abiotic stresses (drought, cold, salinity) and quality traits (Vanaja *et al.,* 2009).

Western Ghats is one of the 35 biodiversity hotspots of the world and the second most biodiversity rich zone in India, covering about 5% land area (159,000 sq. km) (Mittermeier *et al.,* 2004). 625 wild species related to 78 crops from this region have documented by John *et al*. (2015). In the genus *Oryza* L., richness of species diversity in WGR is evident by the occurrence of five taxa, *viz*., *Oryza meyeriana* (Zoll. & Moritzi) Baill. var. *granulata* (Nees & Arn. ex G. Watt) Duist, *O. nivara* S.D. Sharma & Shastry, *O. officinalis* Wall. ex G. Watt, *O. rufipogon* Griff. (syn. *O. jeyporensis* Krishnasw. & Chandras.) and *O. officinalis* subsp. *malampuzhaensis* Krish. et Chand. (Pradheep *et al.,* 2014). *Porteresia coarctata* (Roxb.) Tateoka, a species often included under *Oryza* and known for salinity tolerance, is reported from mangrove pockets of this region. Forest reserves *viz*., Bhoothathankettu, Parambikulam and Karulai along the Western Ghats have been also identified for *in-situ* conservation of wild rices (Vaughan and Muralidharan, 1989). Tetraploid wild rice (*O. malampuzhaensis*) closely resembling to diploid *O. officinalis* was reported in 1958 from two localities in Malampuzha in Kerala (Krishnaswamy and Chandrasekharan, 1958). This endemic taxon now kept under *O. officinalis,* has a localized distribution along the Western Ghats, particularly in forest reserves (Vaughan, 1994; John and Nizar, 1998).

In present study we have analyzed the status of rice landraces diversity, cultivation and germplasm utilization in WGR through geo-referencing of germplasm collection sites and grid mapping using DIVA-GIS tools (Hijmans *et al*., 2001), and also extent of utilization in breeding programmes, besides identifying gaps in collections and conservation.

Materials and Methods

Study Area and Cclimate Data of the Regions

Western Ghats extends from 8.32° to 21.23°N latitude and 72.91° to 77.15°E longitude, along with coast of the country comprising 42 districts in the state of Gujarat (4), Maharashtra (8), Goa (2), Karnataka (7), Kerala (14) and Tamil Nadu (7) formed the study site (Fig. 1). The WGR starts from the southern districts of Gujarat, south of the Tapti river and runs approximately 1600 km long chain of hills, plateaus, plains in the rainy and rain shadow areas in the above six states ending near Kanyakumari (Gadgil, 1996). While almost all the parts of Goa and Kerala come under WGR, only a few districts of other four states form the part of this region. Altitude varies considerably from sea level (in West Coast) to above 2,694 m in Anamalai of Kerala and Nilgiris of Tamil Nadu and merges with rain shadow areas in eastern slopes and plains in Tamil Nadu and with the Deccan Plateau in Karnataka and Maharashtra. In the Konkan region, hills are comparatively lower and form plateau.

Soils play an important role in vegetation and agriculture. Red soils, lateritic soils, black soils, humic forest soils and coastal alluvial soils are the major soil types found in WGR (Bhattacharyya *et al.* 2013) and played a role in the evolution of distinct, locally adapted landraces. WGR experiences extreme variation in the climate over the annual seasonal cycle. Average annual rainfall of study area is 2,030 mm while maximum rainfall is 2,540 mm. Among states maximum rainfall (3,107 mm) was recorded in Kerala state. Mean temperature (min. & max.) ranged between 24.2-28.3°C and 31.2-35.0°C during last 65 years (Geethalakshmi *et al.,* 2011).

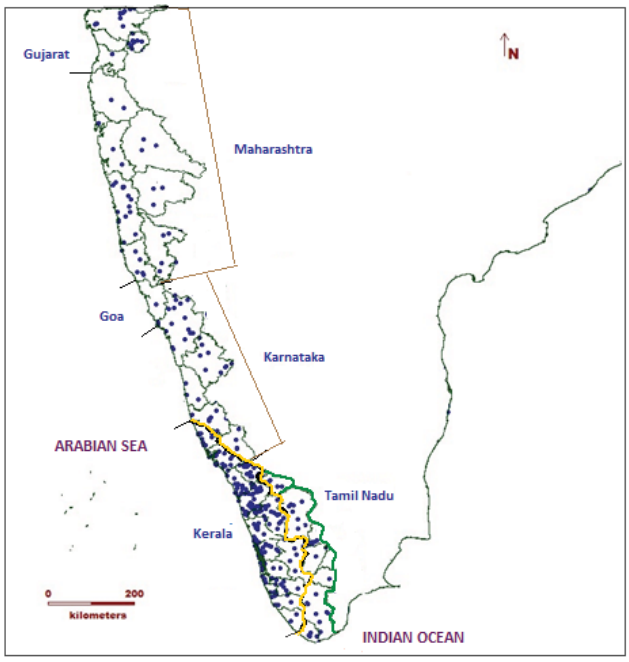

Fig. 1. Rice germplasm collection sites in Western Ghats region of India

In Kerala state rice is grown in widely diverse ecological niches *viz*., from deeply submerged areas below sea level in Kuttanad (-10 m) to upland areas in high altitudes like Anamudi (1200 m) (John and Nizar, 1998; Kumary 2016). Based on altitudinal gradients, the entire rice growing tracts of Kerala are categorized into four distinct regions *viz*., high ranges (>750 m MSL), high lands (75-750 m) midlands (7.5-75 m) and lowlands (up to 7.5 m) (Kumary, 2016; Farm Guide, 2009). In Goa, rice is mostly cultivated in low-lying coastal lands reclaimed from marshy mangroves by construction of dykes, sluice gates and canals etc., known as *khazan* ecosystem (Manohara and Singh, 2013). In Gujarat, rice occupies about 7 to 8% of gross cropped area of the state and accounts for around 14% of the total food grain production. It is grown on an average about 6.5 to 7.25 lakh hectares of land comprising nearly 55 to 60% of low land (transplanted) and 40 to 45% of upland (drilled) rice (Pathak *et al.,* 2011). In Western Ghats region of Maharashtra rice is cultivated on small scale because 85-90% area is rainfed and known as Konkan region in the state (Thaware *et al.,* 2011). In drill sowing of rice under rainfed condition is being practiced in the Western Ghats area of Karnataka (Hanamaratti *et al.,* 2008). In Western Ghats region of Tamil Nadu rice is cultivated on small scale because maximum area is covered under forests. State is severely affected by cyclones, floods and salinity which have led to a decline in rice production (Sathya *et al.,* 2011).

Scrutiny of Passport Data and Diversity Analysis

Since inception in 1976, ICAR-National Bureau of Plant Genetic Resources (NBPGR) has augmented rice germplasm from various parts of the WGR through crop-specific/ multi-crop explorations conducted in collaboration with crop-based institutes and State Agricultural Universities. This resulted in collection of a total of 2,739 accessions from all 42 districts, which were used in this study (http://192.168.1.5 /NBPGR/ Search Passport.aspx; NBPGR Annual Reports 1976-2016; Plant Germplasm Reporters 2002-2015). Passport data of these accessions was checked for botanical names, landraces and geo-coordinates of collection sites (village/block/tehsil, district and state) using GIS tools. GIS-based grid mapping technique is used to analyse species richness, assess variability and occurrence of trait-specific germplasm of crops in different parts of the country (Ramirez-Villegas *et al.,* 2010; Semwal *et al.*, 2013).

Gap Analysis

After comprehensive screening of passport/germplasm data geo-referenced map was prepared using geo-coordinates, WGS84 datum and projection systems. To know spatial distribution and assessment of landraces richness, DIVA-GIS software is useful for point-to-grid analysis using simple-circular neighborhood method (Hijmans *et al.,* 2001). Landraces diversity is calculated using Shannon-Weaver diversity index (Shannon and Weaver, 1963). In view of the diversity assessment *vis-à-vis* germplasm collected/conserved, literature survey/reports (Kumary, 2016; Vanaja *et al.,* 2009) and personal communications with crop experts, the gaps are identified.

Results and Discussions

Rice Germplasm Geo-referencing and Collection vs Conservation Status

The geo-referenced map of collected accessions showed that southern and coastal part of WGR had significant representation (Fig. 1). The states of Kerala (2,036 acc.) followed by Karnataka (203) and Maharashtra (201) account for the highest number of collected accessions. Out of 2,037 accessions from Kerala, maximum accessions were collected from the districts of Palakkad (827) followed by Malappuram (185), Wayanad (172), Ernakulam (164), Kannur (154), Thrissur (152), Kasaragod (110) and Idukki (93). Majority of accessions (539) from Palakkad district was assembled by the Rice Research Station located at Pattambi, which has augmented germplasm from adjoining areas for past two decades. District wise maximum germplasm collections in remaining states include: Uttara Kannada (104), Dakshina Kannada (51) and Shivamoga (40) in Karnataka; Ratnagiri (78) and Kolhapur (20) in Maharashtra; Nilgiris (54), Coimbatore (52) and Tirunelveli (32) in Tamil Nadu; Surat (43) and Dangs (42) in Gujarat; and North Goa (30) and South Goa (19) in Goa (Fig. 1). Germplasm database maintained at ICAR-NBPGR revealed that considerable variability for grain characteristics (e.g. grain shape, size, colour and taste) had been assembled from these districts. Highest collections of wild germplasm (>80%) were made during the execution of World Bank-funded National Agricultural Technology Project on Plant Biodiversity (1999 to 2005), spearheaded by the Bureau.

Out of a total of 2,739 accessions collected, only 1,656 (60.46%) are conserved in the National Gene Bank

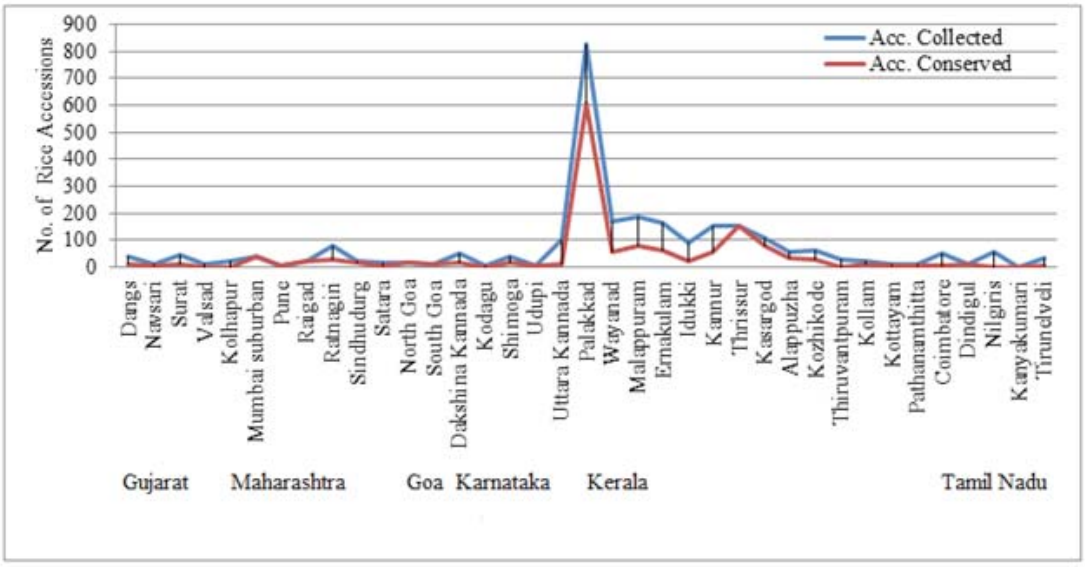

Fig. 2. Rice landraces collected from different districts of Western Ghats

(NGB) of ICAR-NBPGR. All the collected germplasm samples did not qualify for conservation in genebank. Maximum accessions were conserved from Kerala (1,431) followed by WGR districts– in Maharashtra (119), in Karnataka (48), in Goa (30), in Gujarat (28) and in Tamil Nadu (24) (Fig. 2). None of the collected accessions from Tiruppur, Theni and Virudhunagar districts of Tamil Nadu; and Palghar and Thane of Maharashtra could reach NGB indicating the need for revisit on priority. Not all the collected accessions could be preserved in NGB, owing to reasons such as low sample size, requirement of niche-specific habitat for regeneration, seeds often exhibiting post harvest dormancy (Dr. Kalyani Srinivasan, ICAR-NBPGR, Pers. Comm.), besides some accessions are still under seed multiplication/rejuvenation. There are also instances of collaborators often reluctant to return back the multiplied germplasm for deposition in NGB.

Rice Landraces Status and Mapping using GIS Grid Method

Conserved germplasm accessions represent 678 landraces (belonging to 1,440 accessions), of them, highest numbers were from Kerala (386) followed by Tamil Nadu (92), Karnataka (88), Gujarat (56), Goa (49) and Maharashtra (26). Out of 386 landraces from Kerala, maximum were from Palakkad (78, mainly through the efforts of RRS, Pattambi), followed by Malappuram (63), Ernakulam (52), Wayanad (47) and Kannur (41) districts. Other districts with significant number of landraces (≥20) collected were Uttara Kannada (63) in Karnataka; Nilgiris (49) and Tirunelveli (29) in Tamil Nadu; Surat (38) in Gujarat; and Ratnagiri (20) in Maharashtra (Fig. 3). However, there would be possibility of some rice landraces known by different names across the districts/states which needs further study.

Shannon-Weaver diversity index has grouped 678 landraces in four groups namely 0-0.7 (grid no. I),

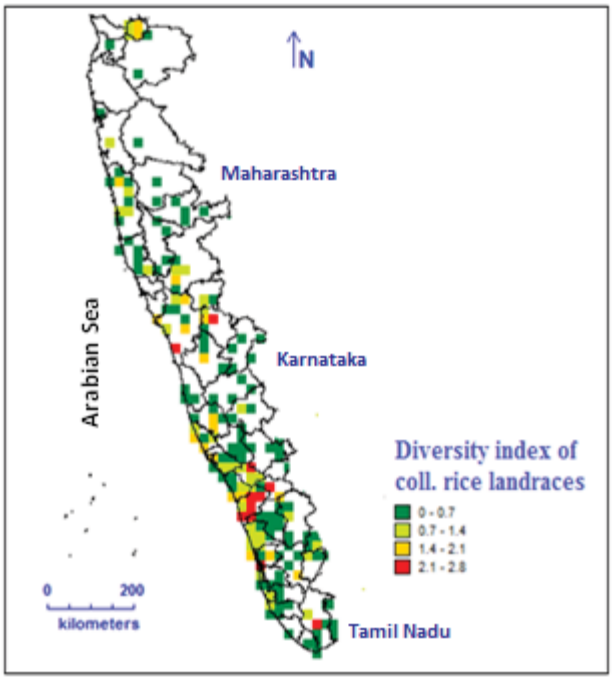

Fig. 3. Variability mapping based on passport information in rice landraces collected from Western Ghats region of India

0.7-1.4 (II), 1.4-2.1 (III) and 2.1-2.8 (IV), which is depicted in GIS-based grid maps (Fig. 3) with different colours according to the extent of diversity and variability in the germplasm accessions. In the map, orange/dark red colour of the grid (nos. III & IV) indicated high diversity areas while dark green/light green (grid nos. I & II) indicated low diversity areas. North and central regions of Kerala, exhibited the highest Shannon-Weaver diversity index (2.1-2.8) indicating the richness of landraces and diversity in these areas.

Cultivation and Use Pattern of Landraces

Besides topographic, soil and climatic factors, farmers have played crucial role in developing, maintaining and conserving rice landraces since time immemorial. In Kerala, there are popular landraces adapted to different habitats, for instance - deep water or floating rice (in submerged localities with 1 to 5 m depth); *pokkali* rice adapted for saline conditions; *Modon* or upland rice grown in dry situations (Latha *et al.,* 2013). *Kaima* is most popular red bold rice of irrigated belt (Latha *et al.,* 2013; John and Nizar, 1998). It is long duration cum photo-period sensitive type having rapidly elongating internodes. Landraces which are adapted to high altitudes are normally referred to as *Malanellu* rice. Within the *Pokkali* varieties, there exists high genetic diversity as represented by different primitive cultivar names *viz*., *Pallippuram Pokkali, Kuzhippalli Pokkali* and *Vettikkal Pokkali. Kuthiruvithu, Kochumundon* and *Mundon* are the saline tolerant varieties of the *Kaipad* system of Kannur District (Kumary, 2016).

Highly heterogeneous land pattern in WGR is conducive for novel genetic diversity in rice through adaptation in different microhabitats; this pattern is attributed to undulating topography, sloppy terrains, high rainfall, deltaic formations of the large network of rivers, large wetland systems and saline water intrusion in pockets of lowland. Kerala has different agro-climatic zones and intentional or natural selections of crop varieties in such agro-climatic zones have resulted in a large number of traditional varities suited to each region (Gopi and Manjula, 2018). In WGR, landraces differ for a range of characters including maturity duration, plant height, tillering, pigmentation in various plant parts, grain characters (grain shape and size, husk and kernel color, aroma) and consumption qualities (puffing, flattening, popping, flour, cooking). Nevertheless, there exists a strong traditional preference among local people of Kerala for coarse varieties with red kernel.

Scented rices mostly grown in the high ranges of Kerala are *Gandhakasala, Jeerakasala,* (grown 750m above msl), *Neycheera, Pookkulathari* and *Rajak* (Kumary *et al*., **2003**). Some important medicinal rices which were in cultivation in Kerala during ancient times like *Chennellu, Chembavu, Erumakkari, Kalamappari, Kunjinellu, Neduvali, Narikar, Poovali, Velvali, Varakan, Tanavala etc.* are believed to be *saali* varieties (group of owned grains) having medicinal value. Local people in Kerala use *Navara (Nijavara)* and *Varinellu* (a weedy relative of rice) as medicine for treatment of small pox. These landraces possess tolerance to drought and resistance to diseases like blast and are adapted to the low light intensity. *"Karanellu"* landrace grown by the tribal people of Attappadi (Palakkad) needs special mention that is highly competitive to weeds through profuse tillering and fast growing nature. Nevertheless, vast conversion of traditional rice growing areas into banana-ginger-coconut over the last 40 years, especially midlands, and replacement of landraces by high yielding varieties (e.g. Kuttanad belt) and real state and had resulted in drastic erosion on both level *viz.*, decline in number as well as acreage under landrace cultivation in Kerala. Goa had a rich diversity of native cultivars/ landraces *viz.*, *Korgut, Asgo* and *Shidde*, which are tolerant to salinity and cultivated in coastal saline soils (Manohara and Singh, 2013).

Wild Rice Status in WGR

Wild relatives possess desirable traits/genes, which are generally not available in cultivated genepool, are increasingly recognized as valuable resource for crop improvement. Species-wise account showed that maximum number of accessions were collected in *O. sativa* f. *spontanea* (19), followed by *O. meyeriana* var. *granulata* (11), *O. rufipogon* (10), *O. nivara* (4), *O. officinalis* (4), and *O. officinalis* subsp. *malampuzhaensis* (1) from this region. Among the states, highest number of accessions was collected from Kerala (26) while meagre collections were made from other states (Table 1). Variability was recorded for grain shape, size, colour and awn size in *O. sativa* f. *spontanea*.

Utilization of Landraces in Rice Breeding

Rice landraces valuable in the crop improvement programme played a vital role in achieveing **self**-sufficiency in the country. Literature analysis revealed that, out of 678 landraces, only a handful of landraces (43) have been identified/utilized for possessing breeding

Table 1. Wild rice collections in Western Ghats region of India

Species	Germplasm accessions collected from different states				Total accn.
	Karnataka (7)	Kerala (26)	Maharashtra (12)	Tamil Nadu (4)	
O. nivara	-	-	4	-	4
O. rufipogon	4	5	1	-	10
O. officinalis	2	2	-	-	4
O. sativa f. *spontanea*	1	11	7	-	19
Oryza meyeriana var. *granulata*	-	7	-	4	11
O. officinalis subsp. *malampuzhaensis*	-	1	-	-	1

traits of potential value. These traits include early and late maturity, aroma, high iron content, medicinal value, drought/cold/ salt tolerance and resistance to brown plant hopper (Table 2). Earlier Kumary (2016) reported that more than 36 rice landraces have been utilized for different traits, mostly suited to different ecological regions in Kerala state alone.

Gaps in Germplasm Collection and Conservation

Apart from 678 landraces collected/conserved from WGR, another 119 landraces documented/reported in various reports (Table 3) are yet to be assembled and conserved in the NGB. However, it is observed that considerable number of these (unassembled) landraces lie with the SAUs/NGOs/other stakeholders in this region who are almost reluctant to part them with ICAR-NBPGR. This indicates that priority needs to be given for their collection through fine grid survey coupled with grass-root level linkage with state department official and custodian/ conservation-oriented farmers. In general, the state of Kerala has been extensively explored for rice germplasm, though systematic collection of wild genepool needs attention. Besides focus is needed for wild rice (including *Porteresia coarctata*) collecting areas/tehsils representing deficit collection:

Kerala: Vaikom (Kottayam district); Karunagappalli (Kollam).

Karnataka: Madikeri, Somvarpet and Kundapura (Udupi).

Gujarat: Dharampur, Kaprada, Pardi and Umbergaon (Valsad); Bansda, Chikhli, Gandevi and Jalalpore (Navsari).

Table 2. Trait-specific rice landraces collected from Western Ghats region of India

S.No	Traits	Named rice landraces*	References
1.	Drought tolerance	Vaigunda[f]	Sathya 2013
		Sattari Saw[b], Shamari[b], Tranpandad[b] and Sathi[b]	Pathak *et al.,* 2011
		Chuvannamodan[c], Eravapandi[c], Kalladiyaryan[c], Kallele[c], Karuthapandi[c], Karavalu[c], Mundon[c]	Gopi and Manjula 2018
2.	Tall and late maturing (122days)	Damgo[a] and Babri[a]	Manjunath *et al.,* 2009
3.	Early maturing	Dhavi Patni[a] and Morod Kendal[a]	Manjunath *et al.,* 2009
4.	Medicinal uses (anti-dysenteric, diarrhoea and vomiting)	Njavara[c], Chennellu[c], Kunjinellu[c], Erumakkari[c], Karuthachembavu[c] and Kavunginpoothala[c]	Leena Kumary 2003
	(Treatment of cough)	Erumakkari[c] and Annoori[c]	Leena Kumary 2003
5.	Medium duration	Nermar[a], Kochri Patni[a] and Belo[a]	Manjunath *et al.,* 2009
6.	Cold tolerance	Chettuveliyan[c], Koduveliyan[c], Raajani[c], Malanellu[c]	Latha *et al.,* 2013
7.	Salt tolerance	Shidde[a]	Manohara and Singh 2013
		Kuthiru[c], Rajkayam[c] and Orkayama[c]	Vanaja *et al.,* 2010
		Pokkali[c]	Vanaja *et al.,* 2010; Latha *et al.,* 2013
8.	Aroma	Dhan Had[b], Ambamor[b]	Pathak *et al.,* 2011
9.	Deep water and salinity tolerance	Kuzhippulipokkali[c], Nedungodu pokkali[c], Odachan[c], Orpandy[c], Orkyma[c], Orumundakan (black kernel)	Latha *et al.,* 2013
10.	Resistance to brown plant hopper	Sigappu Kuruvikar[f]	Sathya 2013
11.	High iron content	Lal Kada[b]	Pathak *et al.,* 2011
12	Pest and diseases resistant	Adukkan[c], Chomala[c], Edavaka[c], Karindon[c], Odacha[c], Pokkali[c], Thondi[c], Thekkan[c], Viliyan[c]	Gopi and Manjula, 2018

a-Goa; b-Gujarat; c-Kerala; d-Karnataka; e-Maharashtra; f-Tamil Nadu

Table 3. Gaps in collection of rice landraces from different states of Western Ghats region of India

States	Rice Landraces	References
	Reported but yet to collect	
Gujarat (16)	Lal Kavchi, Hara, Dodi lal, Lal Kada, Sat paniu, Dodiu, Jiryu, Odibhat, Dhan had, Ambamor, Bhadravi, Kali tapki, Dolatpura, Chandrapura, Shamari, Tranpandad	Pathak *et al.,* 2011
Maharashtra (20)	Bhai bhat, Chimansal, Dangi, Dhundhunya, Jira bhat, Jhini, Kolpi, Kolam, Lal kudai, Malghudya, Masuri, Patanya, Agha Dhan, Ambimohar, Rajghudya, Sag bhat, Solam, Surati, Tornya, Tychun.	Marathe and Bhaskar, 2011
Goa (26)	Asgo, Dhave, Ek Kadi, Ghansal, Girga, Kalo Damgo, Kala Belo, Kalo Korgut, Kalo Novan, Karo Mungo, Khochro, Mudgo, Kolyo, Red Kochri, Kotimirsal, Muno, Kusago, Novan, Patni, Saalsi, Shidde, Taysu, Tamdi, Valay,Walayo, White Kochri.	Manohara and Singh, 2013; Bhonsle and Krishnan, 2016
Karnataka (21)	Adenkelthe, Ajippa, Allyande, Bilinellu, Gandhasale, Giddabatha, Gulvadisanna, Kalame, Kariadadi, Kavalakannu, Kayame, Kolakedora, Mascatti, Meesebattha, Medumsali, Mutalaga, Turumuri, Rasi, Gopal Dodiga, Dambersali, Bolasali.	Hanamaratti *et al.*, 2008; Prakash *et al.*, 2004
Kerala (22)	Malayudumban, Mavilan, Malakkaran, Mannuveliyan, Kalladiyaran, Jeerakachampav, Njavara (Red), Njavara (Unden), Cheriya Orpandy, Karunagapalli pokkali, Kulapandi, Kuzhippuli pokkali, Nedungodupokkali, Odachan, Oorpandy, Cherumundakan, Cheru virippu, Vettakkal, Kamanalichetti virippu, Malmoodan, Vella pokkali and Vettakkalchetti virippu	Vanaja *et al.,* 2010, Latha *et al.,* 2013, Leena Kumary, 2003
Tamil Nadu (14)	Arupatham, Poombalai, Kottarachenba, Kitchilichenba Ottadiyan, Kallundai, Kuruvai, Kumbaalai, Paal Kudavaalai, Sivappu Kudavaalai, Kalundai Samba, Suran Kuruvai, Sivappu Kuruvikkar, Suran Kuruvai.	Kasivenbaiyan, 2013; Ponambalam, 2015; Sathya, 2013; Sathya *et al.* 2011

Maharashtra: Ambegaon, Bhor, Indapur, Khed and Shirur (Pune); Dahanu, Talasari, Vada and Vasai-Virar (Palghar); Jaoli, Karad, Koregaon and Man (Satara).

Tamil Nadu: Agastheeswaram, Kalkulam and Vilavancode (Kanyakumari); Andipatti, Bodinayakanur, Periyakulam and Uthamapalayam (Theni); Rajapalayam and Srivilliputhur (Virudhunagar); Udumalaipettai and Avinashi (Tiruppur).

Conclusion

WGR is home to a number of rice landraces containing unique/trait-specific value and suitable for diverse agro-ecosystems that can help in sustaining nutritional/food security of the region. Rice landraces from Kerala are mostly collected while other state/areas representing deficit collection need to be explored on priority before they are lost forever due to ever-increasing developmental and anthropogenic activities in the region. Sustained research interest in incorporating salient traits of these landraces would strengthen the utilisation of precious germplasm conserved in *ex situ* repositories. In changing climate, their on-farm conservation and adaptation are also important.

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RESEARCH ARTICLE

Collecting Plant Genetic Resources from Gurez, An Underexplored Remote Valley of Jammu & Kashmir State of India

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For the first time, systematic exploration and germplasm collection trips were conducted across Gurez Valley, a remote locality near Line of Control with Pakistan in Bandipore district of Jammu and Kashmir during 2015 and 2017. Almost all the villages up to Chakvali (Tulail) were surveyed. A total of 68 accessions belonging to 28 species including 34 accessions of wild germplasm were collected from altitudinal variation of 2403-3491 meters above sea level. *Fagopyrum tataricum* subsp. *potanini* and *Crataegus pseudoheterophylla* were collected for the first time, besides good variability in wheat, maize and common bean. Other significant collections included common and tartary buckwheat, hull-less barley, field pea, black cumin, caraway, and wild germplasm of *Allium stracheyi*, *Elymus* spp., *Hippophae rhamnoides* subsp. *turkestanica* and *Malus baccata*. Once a common crop, proso millet was seen cultivated only by a lone aged farmer in the entire tract, thus becoming almost an extinct crop in that area. This paper highlights information on the germplasm collected/observed, cultivation practices, genetic erosion and future exploration potential.

Key Words: Exploration, Germplasm collection, Gurez valley, Plant genetic resources

Introduction

Gurez, known as 'Crown of Kashmir' and hailed as one of the nine virgin valleys of Asia, extending between 34°30′-34°41′ N latitude and 74°37′-74°46′ E longitude, is a picturesque, fertile cleft carved out of the high Himalayas at an average altitude of about 2400 meter above sea level by Kishanganga river in the Indian state of Jammu & Kashmir. It is located 123 km in the north-east direction from Srinagar and 86 km from Bandipore, the district headquarters of this valley. Gurez is surrounded on its north by Ladakh, south by Bandipore, southeast by Ganderbal and on the west by Kupwara with its peripheries touching Line of Control (LoC) that divide India and Pakistan (Fig. 1). It was a vital stopover on the famous ancient Silk Route connecting Kashmir to Kashgar, an oasis city in Xinjiang province of China. It was also a major path for migration as well as introduction of plant genetic resources between Europe and East Asia. Three main areas recognized in Gurez valley are: 1) Kanzalwan/ Bagtore area, a small steep semicircular region about 11 km in length 2) Dawar area, regarded as Gurez main is approximately 16 km in length comprised of several villages from Badwan to Chorwan including main town of Dawar and 3) Tulail area, a steep valley more than 110 km long extending from famous Habba Khatoon mountain in the east of Gurez main to Kaobal Gali alongside LoC. These areas are around 1-2 kms in width. Chakvali is the last village in Tulail area in the eastern side, after which the valley narrows down leading to mountain pass (Kaobal Gali) to glaciated Mushkoh Valley near Drass (Ladakh). Mighty Kishanganga river drains the entire area between Kaobal Gali in east and Kanzalwan in west and more than three dozen villages with a population somewhere between 30,000 to 35,000 are thus located alongside Kishenganga River (called Neelam in PoK), an important tributary of mighty Jhelum River with its origin in Kishansar Lake and merging into Jhelum River near Muzaffarabad in PoK. Gurez Valley is the homeland of the rare Dard tribe in India, which was a part of ancient civilization of Dardistan. Dawar, in fact was the old capital of Dardistan. The language of Dard tribe is Shin, also known as Sheena, Sina, Shinaki and Brokpa. Shina speaking populations are predominant in Gurez valley besides in neighbouring Drass, Da, Hanu, Beema, Darchik and Garkon areas of

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Ladakh. They practice subsistence farming and eke out a living from harsh mountain terrains.

While moving from Bandipore to Gurez, one has to cross tough Razdan Pass at about 3600m MSL that remains cut off from rest of the country for at least five months a year due to heavy snowfall. Harsh conditions together with physical barriers limit human settlements and intensive agricultural activities. The soils are sandy clay loam type, highly acidic (pH 5.45) with high organic carbon content (1.2%) and average NPK content are 250.8, 27.0 and 235.2 kg/ha, respectively. Out of an estimated 1100 ha area of land under cultivation, only half is irrigated. Potato occupies about 45% of the area; while other important crops are maize, wheat, common bean, fodder crops and vegetables (Badri *et al*., 2014).

While coniferous and broad leaved forests are present in Gurez and Tulail proper, vegetation is rather sparse and dotted mostly with moraines, boulders and slopes of varying steepness at higher elevations. Diverse topography, unique environment and varying habitats resulted in rich biodiversity with unique flora and fauna having good assemblage of rare medicinal plants, crop wild relatives, minor fruits and wild edible plants. Dad and Khan (2011) have reported that 26 plants under 21 genera and 14 families from alpine grasslands in Gurez valley are used as wild edibles by pastorals, nomads and other indigenous communities while Singh and Bedi (2017) described 42 wild edible species from this region. It is a home of endangered animals such as snow leopard, hangul deer, barking deer, musk deer, black bear, *markhor* and ibex.

This area has not been systematically explored for plant genetic resources, and only a meagre germplasm holding exists in the National Gene Bank (NGB) of ICAR-NBPGR, New Delhi, which was collected under National Agricultural Technology Project (1999-2004). Thus, extensive exploration trips were undertaken after a gap of more than a decade for collecting germplasm of different agri-horticultural crops from the region.

Materials and Methods

During the 2015 and 2017, expeditions were conducted across Gurez Valley covering the Gurez main and Tulail, and nearly all villages were surveyed. Prior to that information on region's flora, agriculture and results from previous collecting missions were gathered and analyzed with the specific aim of better planning of these explorations. Scientists of High Mountain Agricultural Research and Extension Station, Gurez, SKUAST (Kashmir) were also consulted in this regard. The main sources of germplasm samples of cultivated crops were farmer's fields or the threshing yards/farm stores in case the crop had already been harvested. In general, random sampling was followed for field collection and farm stored material whereas small samples were bulked in case of wild species. In a few cases samples were also collected from seed sellers, which made it possible to find out and collect old traditional material. The germplasm of wild species was collected from roadsides, on the sides of farmer's fields, grasslands and from rock crevices. At each collecting site a passport data sheet was filled in as per standard format (Moss and Guarino, 1995) using data from a hand-held GPS system that included latitude, longitude and altitude of the place of collection. In addition to the data recorded directly by the collecting team, further information was amassed through several interviews with local people. Each collection was assigned a unique collector number. The collected materials were deposited in the NGB. Important herbarium voucher specimens were deposited in the National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi.

Results and Discussion

All 68 germplasm samples belonging to 28 species were collected from 19 sites across Gurez and Tulail valleys at altitudes ranging from 2403-3491 meters above sea level (Table 1). This included 34 accessions of cultivated plants and 34 accessions of CWRs.

The agricultural activities start generally in the month of May as soon as the snow melts away. Due to very cold, harsh and long spell winter only *Kharif* crop system is followed. Potato, maize and common beans are cultivated everywhere both in Gurez and Tulail valleys, and their mixed cropping was commonly observed. Synthetic fertilizers are either not used or used at a very limited scale; therefore agricultural produce thus obtained is mostly organic. More than 0.1 million quintals of potatoes are produced annually from this area. We have observed a striking case of sustainable agriculture production system through mixed cropping of proso millet, maize, wheat, French bean, potato and other vegetables in some parts of Tulail (Fig. 2E). This area is treasure-trove for many crop wild relatives including minor fruits and vegetables. Besides, countless number of economically important species belonging to forages,

Table 1. Plant Genetic Resources collected from Gurez Valley of Jammu & Kashmir, India

S.No.	Species	Common name	Local name	No. of accessions collected	Remarks
Cereals					
1	*Triticum aestivum*	Wheat	Ghoom/ Kanak	07	Vary in seed size and color
2	*Zea mays*	Maize	Makai	06	
3	*Hordeum vulgare*	Barley	Yeao	01	
4	*Elymus dahuricus*	Dahurian wild-rye		03	
5	*Elymus nutans*			01	
6	*Elymus semicostatus*			04	Two distinct forms collected
7	*Elymus longearistatus*			01	
Pseudocereals					
8	*Fagopyrum esculentum*	Sweet buckwheat	Mure/Mori	01	
9	*Fagopyrum tataricum*	Bitter buckwheat	Barve/Chuti	01	
10	*Fagopyrum tataricum* subsp. *potanini*	Bitter buckwheat	Barve	01	Comes up spontaneously, not intentionally cultivated
11	*Amaranthus hypochondriacus*	Amaranth	Ganhar	01	
12	*Chenopodium album*	Chenopod		01	
Millets					
13	*Panicum miliaceum*	Proso millet	Woondu	01	
Grain legumes					
14	*Phaseolus vulgaris*	Frenchbean	Rajma	13	
15	*Pisum sativum* var. *arvense*	Pea	Kakun	02	Three types seen – pink striped, green-striped, blackish
Oil seeds					
16	*Brassica rapa* subsp. *oleifera*	Turnip rape	Tilagogol	02	Comes up as field weed
Vegetables					
17	*Allium stracheyi*	Jamboo	Jangli Pran	02	
Fruits					
18	*Malus baccata*	Wild apple	Chirkupalle	02	Fruit size and shape variable; >100 yrs old trees found; propagated through suckers apart from seeds
Minor fruits					
19	*Crataegus songarica*	Hawthorn	Shunt	01	Almost thorn less type
20	*Hippophae rhamnoides* subsp. *turkestanica*	Seabuckthorn	Ghurve (Pup)	02	Found in many places like Barnoie, Kaspath, Old Tulail, Neru, Zuagi
Forages legumes					
21	*Medicago falcata*	Lucerne		01	
22	*Medicago sativa*	Lucerne		01	
Spices & condiments					
23	*Bunium persicum*	Black cumin	Zeera/Hawui	05	
24	*Carum carvi*	Carum	Kral-e-Zeur	03	
Medicinal & aromatic plants					
25	*Aconitum violaceum* var. *robustum*	Violet Monkshood	Bishmool	01	
26	*Angelica glauca*	Smooth Angelica	Chora	01	
27	*Cichorium intybus*	Chicory	Kasni hund	01	
28	*Hyoscyamus niger*	Henbane	Bajarbang	01	
29	*Saussurea costus*	Kuth	Koth	01	

ornamentals, medicinal and aromatic plants also occur in this area.

Cereals, Millets and Pseudocereals

Maize is the main cereal crop; local landraces are short in stature, with small cobs having variation in grain size and color (yellow, orange or white) coupled with good taste. At Neru village, authors found a type of maize subjected to popping at ambient temperature (Fig. 2A). Maize with white kernels was informed to be tastier than rest of the types. Wheat is the second important cereal cultivated up to 3050 m MSL (in Chakvali),

Fig. 1. Map of Jammu & Kashmir state. Boundary of the study area in Bandipore district is marked in red color

however mostly in Tulail tehsil. Like maize, here also plants are shorter in stature with short spikes; both awned and awnless forms depicting variation in grain color and shape were collected. Threshing of harvested wheat was done by traditional method of trampling with bullocks and horses (the practice locally called as '*Khal*') and indigenous implements are still in use (Fig. 2D). Cultivation of barley is limited in this tract; hull-less type having seeds with reddish tinge is an interesting collection (Fig. 2B).

Authors were able to spot cultivation of proso millet only at one place (Sheikhpora, in Tulail). Plants of this easy-to-cook and tasty millet were only 30-40 cm tall, probably had cold tolerance trait. The aged farmer informed that his emotional bond with this traditional crop persuaded him to continue its cultivation, which was otherwise discontinued from cultivation in the entire Gurez and Tulail area, owing to low productivity and availability of better alternatives. Cultivation of another traditional crop buckwheat, according to the locals has also declined drastically. *Fagopyrum tataricum* subsp. *potanini*, a wild progenitor of tartary buckwheat having characteristic wavy seeds has been first time collected from the region from Izmarg, where it occurs as field weed (Fig 2F). In the nearby Bakhtoor village, red-husked grain amaranth was being cultivated at a small scale as medicinal plant (not as pseudocereal). Its roasted grains are given with honey to patients suffering from paralysis. Another pseudocereal of Himalayas, *Chenopodium album* occurs here only as field weed, and not cultivated for food purpose.

Germplasm of wild relatives of wheat and barley belonging to the genus *Elymus* (4 spp.) have been collected for the first time from this area. Foxtail millet progenitor *Setaria viridis* and grain amaranth relatives *Amaranthus hybridus* and *Amaranthus retroflexus* were seen common weeds in the surveyed areas. Besides, *Setaria pumila* and *Elymus caninus* were observed to a lesser extent.

Grain Legumes

Field peas and common beans are the two important grain legumes cultivated, with the latter being more common. Field peas are usually intercropped with maize; however we found it as a sole crop in large scale at Neru in Tulail. The variability collected in common beans especially is interesting and diverse, differing in grain size and color (Fig. 2G). Yellow grain types are comparatively more common in the region despite the fact that red grain types are preferred more by consumers. Scarlet runner bean (*Phaseolus coccineus*) is usually found cultivated in home gardens/backyards.

Vegetables and Oilseeds

Allium stracheyi with 20-25 cm long shoots having flat leaves and pale yellow inflorescences is locally called as

Fig. 2. Maize genotype subjected to popping at ambient temperature (A), interesting naked barley with reddish tinge (B), characteristic and picturesque fields near village Chakvali (Tulail) showing wheat and potato crops (C), indigenous traditional tools used in processing of threshed wheat (D), a small field in Sheikhpora (Tulail) showing multicrop farming (E), *Fagopyrum tataricum* subsp. *potanini* growing in a field in Izmarg (seeds in inset) (F), French bean variability collected (G) and impact of the Kishanganga hydro-electric power project dam–submerging prime agricultural land near Dawar (Gurez) (H).

'Jangli pran' and the locals collect it from wild and dry it for use in dishes in place of onion. Good populations of this species were found on both sides of Razdan Pass in rocky crevices. *Brassica rapa* subsp. *oleifera* with smaller leaves has been observed as a weed in crop fields. Both the red and normal skinned potatoes cultivated here are hardy in texture, superior in quality, and with long storage life without sprouting. In this regard, registering the produce under the tag of Geographic Indication and promoting domestic exchange and export of this high-value commodity would help enhancing the livelihoods of local people. Some high value household vegetables such as local turnip, radish (*muli*) and *Brassica oleracea* var. *sabellica* (haak; *kram*) are often protected from browsing by domestic animals through upright wooden planks. It is a common practice that storage of potatoes and some other vegetables are achieved through their deep burial in earthen pits at the beginning of winter. Such storage pits dug out in open land to store vegetables especially potatoes, cabbage, turnip etc. for winter season use are locally called as *deas*.

Fruits and Nuts

Variability for fruit size in *Hippophae rhamnoides* subsp. *turkestanica* Rousi has been collected from Tulail area. Locally this plant is called 'ghurve' while its ripe fruits are called 'pup'. According to the locals the fruits are only eaten by crows and occasionally by children, and there is no commercial utilization of fruit unlike in Leh areas. The fruits are also used to cure liver ailments. Temperate fruits such as apple, European pear, quince and sour cherry were found cultivated in village premises. Good variability in *Malus baccata* in terms of fruit size, leaf size and suckering habit was observed. Walnut abundantly grows wild in the forests especially in Gurez area, but nuts are very hard to crack with very low kernel recovery. However, elite walnut selections with thin shell and good kernel recovery were commonly found in backyards. This tract has bountiful wealth of minor fruits such as *Rubus saxatilis*, *Chenopodium foliosum*, *Viburnum foetens*, *Prunus cornuta*, *Prunus armeniacus*, *Fragaria nubicola*, *Corylus jacquemontii* (chamdai) and species of *Cotoneaster* and *Ribes*, indicating the need for future explorations for these species.

Spices and Condiments

Gurez has been famous for good production of kala zeera [*Bunium persicum* (Boiss.) B. Fedtsch]; a valuable seed spice and wild plant genetic resource having potential to support livelihood of thousands of local people. Its fruit size varies slightly from place to place. The fruits of this species and *Carum carvi* are collected from the wild by local people, sold and used as a spice. Hot decoction of their fruits is used to cure various digestive and abdominal ailments (Kapahi *et al*., 1993). Both these species have been over harvested which may be one of the reasons for their declining populations and production in the area.

Medicinal and Aromatic Plants

Representative samples of medicinal plants such as *Aconitum violaceum* var. *robustum*, *Angelica glauca*, *Cichorium intybus*, *Hyoscyamus niger* and *Saussurea costus* were collected. Other medicinal plants observed growing in the region include *Podophyllum hexandrum*, *Heracleum candicans*, *Origanum vulgare*, *Atropa acuminata*, *Achillea millefolium*, *Hypericum perforatum*, *Artemisia maritima*, *Dioscorea deltoidea* and *Lepidium apetalum*. *Lepidium apetalum* was found in Neru area and was earlier found by the authors cultivated locally in Zanskar (Ladakh) as "Amchi" medicine. State government forest nursery near Izmarg is involved in field conservation of several of these medicinal plants.

Other Crops

While one accession each of *Medicago falcata* and *Medicago sativa* have been collected from road side, well protected by concertina wire (razor wire) fences, other forage species – *Trifolium repens*, *Trifolium pretense*, *Lotus corniculatus*, *Medicago lupulina*, *Dactylis glomerata* and *Lolium* spp. were found growing at many places. Hops was observed as semi-wild throughout the surveyed areas. Other economic species found are *Salix* spp., *Trigonella emodii*, *Rosa macrophylla* and *Rosa webbiana*.

General Observations

The lifeline of Gurez and Tulail valleys is the motorable road passing through dangerous Razdan Pass, which remains blocked for nearly six months a year due to heavy snowfall, therefore the area remains physically isolated from rest of the country for half a year. Probably this isolation has protected and preserved the biodiversity and cultural identity of Gurez. Agricultural practices here are sustainable and eco-friendly, as they are still based on local cultivars, human labour, animal power and indigenous implements. Though, different kinds of cultivars are available here, they are not known by distinct

landrace names unlike other parts of the country. Genetic diversity that has been increasingly lost in traditional crops like proso millet and buckwheat in these areas is not due to the reason that older generations failed to pass on their knowledge or values to the younger generation but because of the reluctance of young generation to adapt to their wisdom to meet the food, nutritional and livelihood security.

Browsing by domestic animals is a serious threat to the survival of wild germplasm, particularly CWR. For this reason, we could find their good population amidst concertina wire fences prevalent in the entire area established for defense purpose, which are otherwise amenable to browsing. Besides, the valley is on the verge of being submerged by the dam of 330 MW Kishanganga hydro-electric power project. The main town of Dawar and nearby villages have been badly affected (Fig. 2H) and hundreds of acres of land has already been submerged. The impact on overall ecology and biodiversity is going to be massive. This necessitates an urgent need to further explore and rescue the potential germplasm before it is lost forever.

Conclusion

Maximum collections in French bean (13), followed by wheat (7), maize (6), *Bunium persicum* (5) and *Elymus semicostatus* (4) indicate that this area is rich in diversity of these crops. Rich species and genetic diversity in minor fruits, medicinal and aromatic plants, forages and wild ornamentals indicate the need for continued collecting missions. Unprecedented threat of submergence of prime agricultural land by the construction of dam for hydro-electric power project together with construction of more roads and browsing will continue to be major factors affecting genetic erosion and loss of local biodiversity. Reluctance of younger generation to carry forward the legacy of elders has contributed greatly towards loss of traditional crops. Community support initiatives are required to preserve them *in situ* (on farm), through the sharing of knowledge, publicity and cooperation with scientific researchers and governmental organizations.

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RESEARCH ARTICLE

Wheat (*Triticum aestivum* L.) Landrace Diversity in Traditional Production Landscapes of Uttarakhand Himalaya in North-Western India

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Wheat landraces are traditionally grown in rainfed farming landscapes of Uttarakhand hills. Except a few interspersed river valleys, where improved wheat cultivars are grown under assured irrigation, about 95% of the net sown area under rainfed farming mainly grows traditional wheat landraces. The present communication documents a total of 36 unique bread wheat (*Triticum aestivum* L.) landrace populations from diverse representative agro-ecologies of Uttarakhand hills. Information on their distinctive properties, informal community-based seed systems, private and public incentives of wheat landrace populations to farmer households and society, diversity loss from production landscapes over time and space, etc. were also documented from all niche habitats. Potential of making use of landrace diversity have been suggested as sources of resistance/tolerance to biotic and abiotic stresses, and more importantly the climate change resilience, as the extreme heat and drought has affected grain yields worldwide and threatened food security.

Key Words: Climate resilience, Traditional rainfed farming, Uttarakhand hill farming landscapes, Wheat landrace diversity

Introduction

Wheat (*Triticum aestivum* L.) is one of the first cereals known to have been domesticated and is the third most-produced cereal globally after maize and rice. The Fertile Crescent (the area known as the cradle of civilization surrounded by arid and semi-arid land in western Asia) was home to wild wheats and traditional varieties and other valuable crops of the modern world (Diamond, 2002). However, the migration process from the Fertile Crescent, as well as both natural and human selection, resulted in the development of local landraces. It is generally accepted that during the process of domestication and the spread of domesticated wheat, new adaptive traits suitable for new environments were selected (Charmet 2011; Peng *et al.,* 2011).

Wheat domestication was responsible for the increase in human population by enabling humans to produce food in large quantities, thereby contributing to the emergence of the human civilization (Zohary and Hopf, 2000). The domestication of wild emmer (*Triticum dicoccoides*), the progenitor of all cultivated wheats (Feldman and Kislev, 2007), was one of the key events during the emergence of agriculture in Southwest Asia, and was the prerequisites for the evolution of tetraploid durum and hexaploid bread wheat. However, the domestication of wild emmer in the Fertile Crescent and the subsequent breeding of domesticated durum and bread wheat drastically narrowed their genetic diversity (Dvorak *et al*., 1998). Upon domestication, it was estimated that initial diversity was reduced by 84% in durum wheat and by 69% in bread wheat. Historically, traditional farmers planted diverse assemblages of wheat genotypes (i.e. landraces) to lower the risk of failure and increase food security because they had limited capacity to control the spatially heterogeneous and temporally unpredictable environment (Jaradat 2006, 2013). This practice led to the development of landrace meta-populations of wheat and the emergence of farmers' seed systems through which they accessed and exchanged diverse genetic material. A meta-population structure, defined as a group of subpopulations interconnected by gene-flow and seed exchange among farmers, villages and eco-geographical regions, favours a dynamic evolution of diversity (Jaradat, 2013).

The material conserved either *ex situ* or *in situ* is a safeguard against genetic erosion and a source of resistance to biotic and abiotic stresses, improved quality and yield traits for future crop improvement. Although landraces of wheat are no longer grown in Europe and North America, they still continue to be important elsewhere (FAO, 2015).

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Throughout their history, farmers subjected wheat landraces to strong selection pressures; therefore, wheat landraces developed multi-locus structures as a result of selection, genetic drift, or fragmentation of their populations (Brown, 2000). These structures predominantly are retained through selection, isolation, lack of migration, and restrictions on outcrossing and genetic recombination. Little has been done to understand the genetic structure of wheat landraces and the inter-specific diversity available in the subsistence agro-ecosystems they still dominate in parts of the Old World (Altieri and Merrick, 1987).

The Green Revolution, which occurred throughout the 1940s to the 1960s, led to the development of high-yielding, disease-resistant wheat varieties with dwarfing genes; these were lodging resistant and highly responsive to inputs. The success of these varieties is probably the most important event in the history of modern agricultural research and enabled such wheat-importing countries as India and Pakistan to become exporters. Currently, modern high-yielding varieties grown in major wheat environments have an assembly of genes or gene combinations pyramided by breeders. However, increasing reliance on relatively few varieties in most breeding programmes has led to the loss of well adapted, genetic diversity. It is well documented that selection targeted at individual loci will reduce genetic diversity within and around the selected loci (Tanksley and McCouch, 1997). Selection in modern breeding programmes acts simultaneously upon many loci, controlling a variety of traits under selection, and such selection would greatly reduce diversity throughout the genome as has been predicted (Tanksley and McCouch, 1997). Decreases in genetic diversity are often recognized as genetic bottlenecks imposed on crop plants during domestication and in modern plant-breeding practices.

In traditional small-holder rainfed farming of Uttarakhand hills, wheat populations still consist of informal farmer-maintained populations often with high levels of morphological diversity. The reasons for their continued cultivation are, i) about 90% farming landscapes in hills are rainfed and only native landraces can only be grown under marginal management, and ii) farmers have several cultural and consumption preferences for these landraces. There has, however, been loss of landrace diversity mainly because of non-availability of seed of local landraces under poorly developed informal local-level seed exchange network. An investigation was, therefore, specifically designed with the objectives of documenting the wheat landrace diversity in production landscapes of Uttarakhand hills.

Materials and Methods

For documenting wheat landrace populations, all the thirteen districts of the Uttarakhand state were systematically surveyed during 2010-13. A participatory approach was adopted to document information on distinctive properties and diverse uses of native landrace populations. Unique wheat landraces from representative traditional farming landscapes were then collected (Fig. 1). The passport information of landrace

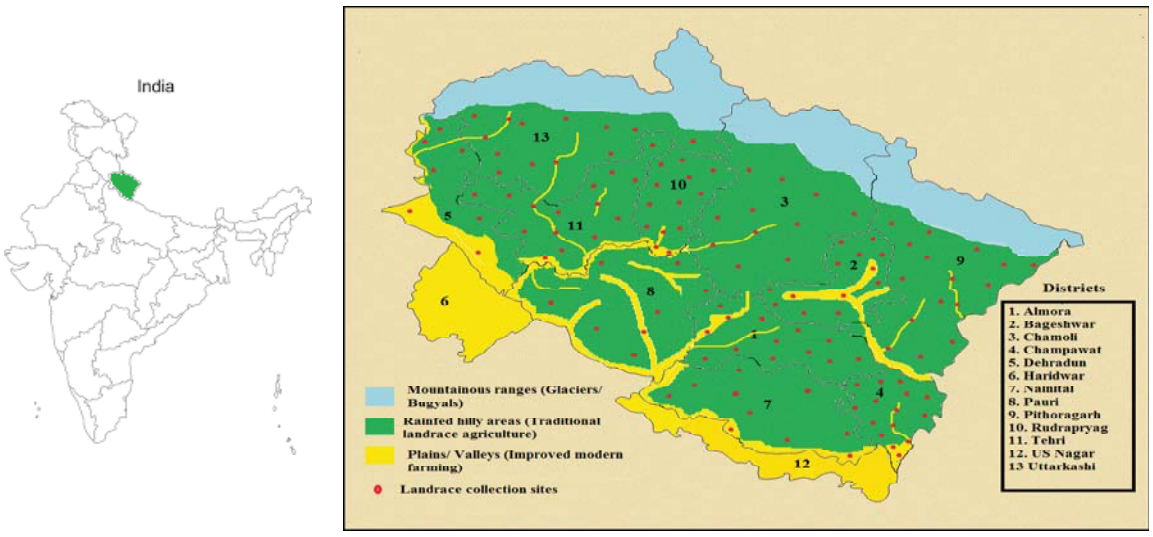

Fig. 1. Farming agro-ecologies and district-wise distribution of wheat landraces

Table 1. Passport information on wheat landrace diversity of Uttarakhand hills

S. No.	Accession Number	Landrace name	District	Altitude (masl)
1.	IC-266791	Gerua	Champawat	1710
2.	IC-266852	Dudh gehun	Pithoragarh	1430
3.	IC-266921	Mota gehun	Pithoragarh	1430
4.	IC-382664	Sona gehun	Rudraprayag	1340
5.	IC-383593	Lakha gehun	Chamoli	1800
6.	IC-398294	Jhunsi ninsa	Bageshwar	1350
7.	IC-398303	Chini	Bageshwar	2113
8.	IC-398305	Munnar	Bageshwar	2087
9.	IC-398307	Thull gehun	Bageshwar	2156
10.	IC-406724	Syat gehun	Champawat	1650
11.	IC-444226	Rajg gehun	Pithoragarh	2403
12.	IC-444232	Bhotia gehun	Pithoragarh	2685
13.	IC-564090	Mundari	Pauri	1511
14.	IC-564096	Bareek lal	Pauri	1362
15.	IC-564113	Lamba lal	Pauri	1316
16.	IC-564114	Safed mundia	Pauri	1316
17.	IC-564147	Lal chanosi	Pauri	598
18.	IC-573138	Syat mundia	Nainital	1456
19.	IC-573139	Rayat gehun	Nainital	1456
20.	IC-573152	Lamba Syat gehun	Nainital	1144
21.	IC-573165	Mundia	Nainital	1856
22.	IC-573167	Daulat khani	Nainital	1684
23.	IC-585633	Pahari	Bageshwar	1338
24.	IC-585635	Lal gehun	Bageshwar	1309
25.	IC-585641	Safed Jhunsi	Bageshwar	1294
26.	IC-585643	Dug gyun	Bageshwar	1350
27.	IC-585655	Dapaati	Bageshwar	1885
28.	IC-585659	Thang gehun	Bageshwar	2122
29.	IC-589276	Hasia	Uttarkashi	1320
30.	IC-589278	Gharia	Uttarkashi	1511
31.	IC-589288	Safed gehun	Uttarkashi	2037
32.	IC-589289	Lal mishri	Uttarkashi	1563
33.	IC-589296	Chhota lal gehun	Uttarkashi	1610
34.	IC-589300	Mishri	Uttarkashi	1045
35.	IC-595376	Jhusia	Bageshwar	1326
36.	IC-595395	Thanga	Almora	1870

diversity representing Uttarakhand hills is presented in Table 1.

Information on distinctive properties of wheat landraces; informal seed systems and landrace exchange at community level; incentives to farmers from traditional wheat landraces; diversity loss from production landscapes and factors responsible for their loss, etc. were also documented from all representative niche habitats. About 30 Focus Group Discussion (FGD) meetings were organized in hill farming agro-ecologies involving average 15-20 farmer participants, mostly elderly women farmers to document information on all above aspects.

The wheat landraces assembled were then characterized in on-station trials at the experimental farms of ICAR-NBPGR, Regional Station, Bhowali (Nainital), Uttarakhand for a set of 21 agro-morphological characters, 9 qualitative and 12 quantitative (Table 2). The range and pattern of variations (cluster and principal components analysis) were statistically analyzed using DARwin statistical software (Perrier and Jacquemoud-Collet, 2006).

Results

Distribution of Wheat Landraces

A total of 36 unique landrace populations were assembled. Distribution of landraces along different altitudinal gradients in Uttarakhand hills are presented in Table 3. Maximum 24 landraces were being cultivated between elevations 1500-2000 m followed by 20 landraces between 1000-1500 m; 4 landraces beyond 2000 m elevations, and lowest 2 landrace populations in lower elevation areas (<1000 m), with some overlaps. Unique landraces specifically grown in different elevations are also presented in Table 3. All the wheat landraces were invariably named with some landraces sounding alike but have different spellings (homophones).

Table 2. Descriptors for wheat landrace characterization and evaluation

Qualitative characters		
1.	Growth class	1-Winter; 2-Facultative; 3-Spring
2.	Early plant vigour	3-Poor; 5- Good; 7-Very good
3.	Plant growth habit	1-Erect; 2-Semi-spreading; 3-Spreading
4.	Lodging tendency	0- Nil; 3-Low; 5-Medium; 7-High
5.	Glume colour	1-White; 2-Red to brown; 3-Purple to black
6.	Glume pubescence	0-Nil; 3-Low; 5-Medium; 7-High
7.	Awn type	1-Awnless; 2-Awnleted; 3-Awned
8.	Awn colour	1-White; 2-Brown; 3-Black
9.	Grain colour	1-White; 2-Amber; 3-Brown; 4-Red; 5-Purple
Quantitative characters		
10.	Days to 80% spike emergence	
11.	Flag leaf length	
12.	Flag leaf width	
13.	Spike length	
14.	Number of spikelets/ spike	
15.	Number of effective tillers/plant	
16.	Number of grains/ spikelet	
17.	Plant height	
18.	Days to 80% maturity	
19.	Number of grains/spike	
20.	Grain yield/plant	
21.	100-seed weight	

Table 3. Distribution of wheat landraces along altitudinal gradients in Uttarakhand hills

Altitude	No. of landraces grown	Unique landraces
<1000 m	01	Chanosi (Lal chanosi)
1000-1500 m	17	Lal gehun, Bareek lal, Mishri, Syat gehun, Mota gehun, Safed mundia, Sona, Safed, Dudh, Hasia Jhunsi ninsa, Ryat gehun, Pahari, Dug gyun, Jhunsi, Lamba syat, Lamba lal
1500-2000 m	10	Chota lal gehun, Gerua, Mundari, Lakha, Thanga, Mundia, Daulatkhani, Safed gehun, Dapaati, Gharia
>2000 m	08	Lal mishri, Safed gehun, Bhotia, Munnar, Thull gehun, Thang gyun, Chini, Rajg gehun

Table 4. Frequency distribution of qualitative characters in different descriptor states

Descriptor	Descriptor state	Frequency (%)
Growth class:	1- Winter	8.3
	2- Facultative	63.8
	3- Spring	27.9
Plant growth habit	1- Erect	52.8
	2- Semi-spreading	44.4
	3- Spreading	2.8
Glume colour	1- White	91.6
	2- Red to brown	5.6
	3- Purple to black	2.8
Awn type	1- Awnless	30.6
	2- Awnleted	19.4
	3- Awned	50.0
Awn colour	1- White	50.0
	2- Brown	50.0
	3- Black	0
Grain colour	1- White	19.4
	2- Amber	61.2
	3- Brown	0
	4- Red	19.4
	5- Purple	0

Morphological Diversity of Wheat Landraces

Diversity for important qualitative characters is presented in Table 4. Substantial diversity was recorded for some of the qualitative characters viz. awn type, awn colour and grain colour. For growth class, most of the landraces were either facultative or spring types; either erect or semi-spreading in growth habit, and predominantly with white glume colour.

The range of variations for quantitative characters is presented in Table 5. Moderate variations were recorded for most of the quantitative characters studied, maximum variations recorded for traits grain yield /plant and no. of effective tillers/plant, whereas least variations were recorded for days to flowering and maturity.

The pattern of variations as revealed by cluster analysis classified the accessions in two major groups. Wheat landraces from high mountainous regions were, however, distinct and formed a separate cluster (Fig. 2). Large scale overlapping of landraces originating from different agro-ecologies in two clusters may be due to widespread informal seed exchange at community level. In principal components analysis (Fig. 3, Table 6), the first three PC axes explained a total of 96.97% variations. Individually, PC axes I explained 83.92%, PC axes II 9.02 % and PC axes III 4.30 % variations, respectively.

Important Wheat Landraces with their Distinctive Characteristics

Important wheat landraces and their distinctive properties are presented in Table 7. Better adaptation to various biotic/abiotic stresses, chapatti making quality and consumption characteristics have been the important features of traditional landraces rather than yield alone.

Private and Public Incentives of Wheat Landrace Diversity to Farmer Households and Society

Cultural and consumption preferences play a major role in decision making of farmer households. Market prices are a small fraction of the private incentive that farmer attach to maintaining wheat diversity. The surplus crop produce, if any, is sold locally in the community, sometime in barter system. With enhanced awareness about the nutritional importance of native landraces, in well-functioning markets, the native landraces can, however, be competitive, fetching a premium price.

Loss of Landrace Diversity and Factor Responsible for their Loss

Loss of landrace diversity from production landscapes and the factors responsible for diversity loss are presented in Table 8. Farmers recall cultivating a total of 52 landraces till 1990s. Over the years, 16 landraces were lost from production landscapes and presently only 36 landraces were recorded being grown in different farming ecologies of Uttarakhand hills. Widespread informal seed exchange at local level was recorded but none of the landraces were introduced in farming from outside the state boundaries.

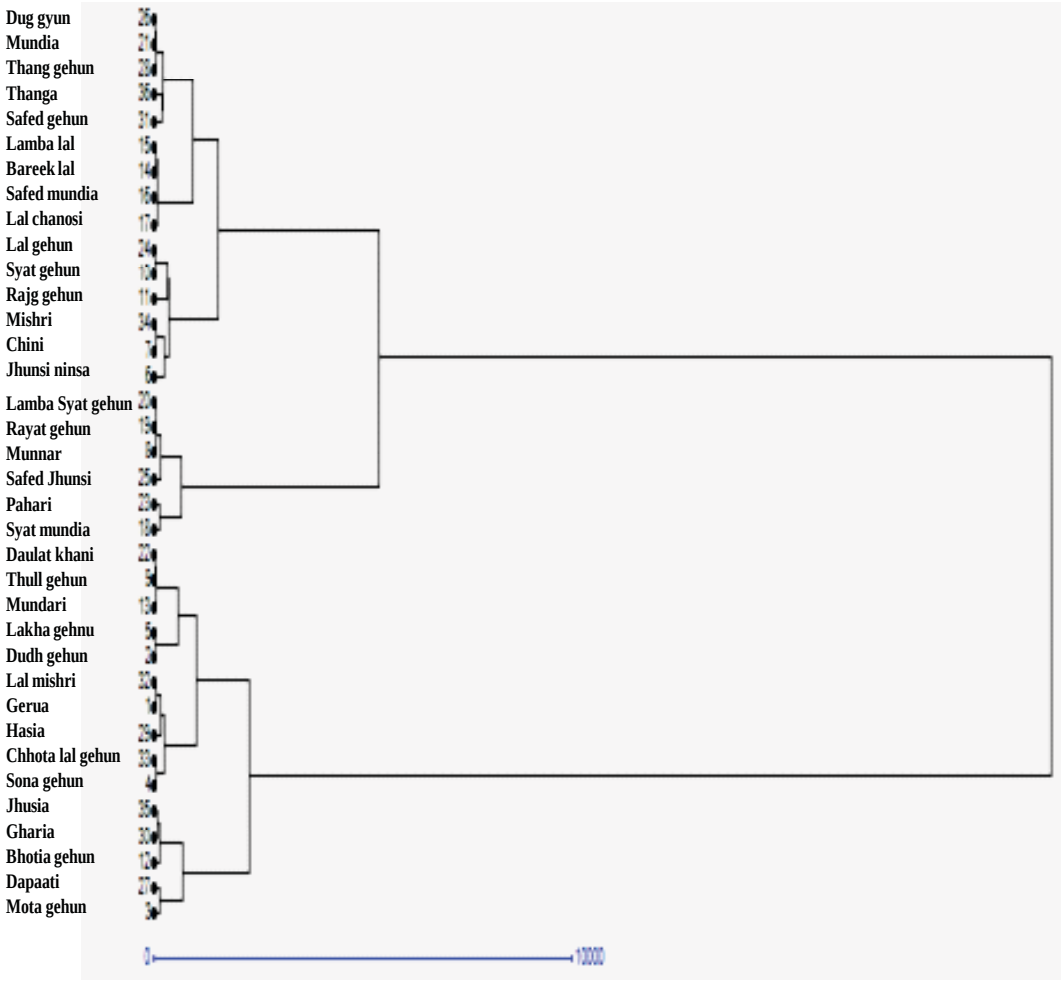

Fig. 2. Ward's minimum variance dendrogram of 36 wheat landrace accessions using quantitative characters

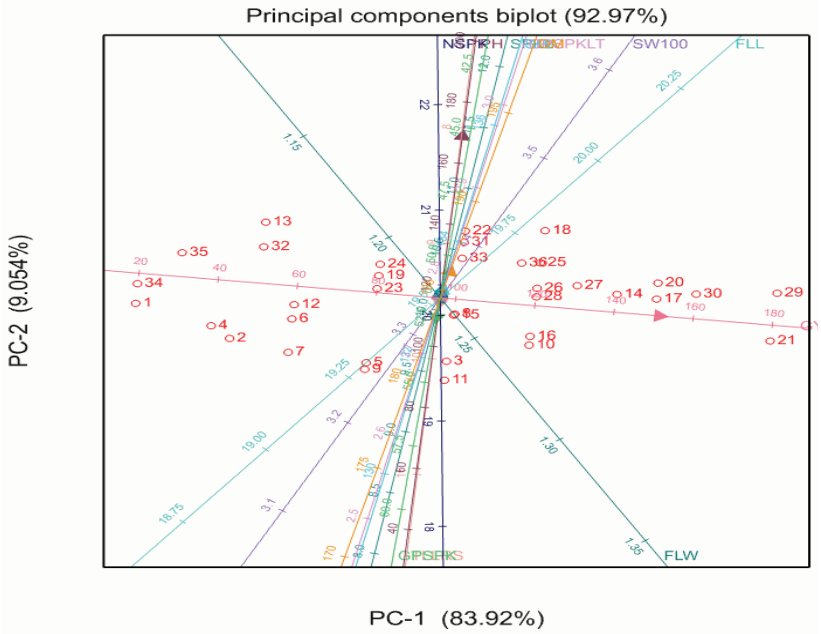

Fig. 3. Principal components biplot of 36 wheat landrace accessions using quantitative characters

Table 5. Range of variations for different quantitative characters

Characters	Min.	Max.	Mean	SD	CV (%)
Days to 80% spike emergence	119.0	149.0	133.0	6.6	5.0
Flag leaf length (cm)	17.0	26.2	19.5	2.9	14.9
Flag leaf width (cm)	1.0	1.6	1.2	0.2	13.5
Spike length (cm)	6.3	12.9	10.1	1.4	13.7
No. of spikletes/spike	17.2	24.8	20.2	1.9	9.5
No. of effective tillers/ plant	5.6	29.4	9.8	3.8	38.9
No. of grains/spikelet	2.4	3.4	2.8	0.2	8.3
Plant height (cm)	88.3	141.3	115.9	14.3	12.3
Days to 80% maturity	174.0	189.0	184.6	4.2	2.3
No. of grains per spike	31.6	71.8	51.7	8.9	17.1
Grain yield/plant (g)	20.0	180.0	96.1	42.1	43.8
100-seed weight (g)	2.7	3.9	3.3	0.4	10.7

Table 6. Principal components analysis of wheat landraces

PC axes	Variations explained	Cumulative variations	Characters with greater weightings
1	83.47	83.47	Grain yield per plant
2	9.02	92.49	Plant height, days to maturity
3	4.30	96.79	GPSPK, SPK

Replacement of local landraces by improved varieties was mainly recorded in river valleys (average 70-80%) than upland rainfed farming (2-3%).

The important factors responsible for landrace diversity loss include, i) non-availability of seed of native landraces, ii) changing climate particularly greater frequency and severity of droughts, iii) lack of manpower (family labour), iv) poor market infrastructure for local crops, and v) loss of ITK/LEK, in descending order of priority from farmers' perspective.

Discussion

On-farm Conservation of Wheat Landraces

It was found that traditional wheat landraces are still being cultivated and maintained on-farm in hill farming landscapes of Uttarakhand state. It provides the farming community enough opportunity to plant, select and continue cultivating the landrace populations for better climate resilience, and tolerance/resistance to other biotic and abiotic stresses. Most of the landrace populations are well adapted to specific agro-ecologies in traditional hill farming.

It is worth emphasizing that much of the wheat landrace germplasm available world over has been collected during the 1970-1990 and is being conserved across the world mostly in long-term national and international genebanks (Frison *et al*., 2011). However, a small portion of this diversity is being conserved and used on-farm where it continues to evolve (Brush and Meng, 1998). Both of these conservation methods have its merits and limitations. On-farm conservation strategy provides a natural laboratory for evolution to continue

Table 7. Important wheat landraces with their distinctive characteristics

Landrace name	Unique characteristics
Bhotia	Better adapted to mountainous high elevation areas, bird tolerance, late maturity
Chanosi	Better adapted to valleys up to 1500 masl, early maturity, better chapatti making quality and taste
Dapati	Better adapted to mid-hills, drought tolerance, better taste
Daulatkhani	Wider adaptation from 1000-2000 masl, medium tall, awned, better nutrition and excellent chapatti making quality, and delicious taste and aroma, bird tolerance
Dudh gehun	White seed colour, awned, suitable for valleys and mid hills up to 1500 masl, better yield
Lakha	Thick stemmed, medium tall, tolerance to hailstorms and snowfall
Lal mundia	Tall, red glume, awnletted, amber grain, adapted to mid- to higher elevation areas, better yield
Mundia	Tall, thick stem, awnletted, better quality
Thanga	Dwarf, thick stem, suitable for high altitude areas, red and bold grains, tolerance to hailstorm and snowfall, bird tolerance

Table 8. Loss of landrace diversity and factor responsible to their loss

Pattern of occurrence of landraces				Important factors responsible for diversity loss (*descending order of priority from farmers' perspective*)
Till 1990s	Loss of landraces	Landraces introduced into farming systems*	Presently grown	
52	16 (Lal Dandi, Rati, Thangi, Jausa, Jwapat, Lalnoi, Hara Pahari, Dogla, Kontha, Dhol Chudia, Muneri, Raje, Bhotta, Dabdi, Palthi, Naphal)	-Nil- Only improved cultivars got introduced in to farming Irrigated valleys VL738, Sonalika, VL 616, UP 1109, PBW 343 Rainfed areas VL 738, VL 832, VL 829, VL 616	36	Non-availability of seed of native landraces Changing climate: greater frequency and severity of droughts Lack of manpower (family labour) Poor market infrastructure Loss of ITK/LEK

* 70-80% replacement of traditional landraces by improved varieties in river valleys and 2-3% replacement in upland rainfed farming

and helps a gradual build-up of traits imparting adaptation to specific eco-geographical regions and those matching the requirements of traditional farming landscapes. The need for on-farm conservation of landraces is one of the most important aspects in plant genetic resources management worldwide (Le Boulch *et al*., 1994; Kebebew *et al*., 2001; Jaradat, 2013). Farmers continue to grow and maintain a wheat landrace if it meets their production and consumption needs. The total cost and benefit of landraces to farmer households are central to their on-farm conservation and continued utilization.

Farmers have private incentives to grow these traditional landraces. Farmers maintain crop landraces if these are valued either for cultural, social, economic, or even ecological reasons. Therefore, direct use values, particularly the quality traits that farmers regard as valuable for consumption are considered to be proxy indicators of private value of a landrace (Brush and Meng, 1998). However, the likelihood of wheat landraces to be conserved on-farm increases when the markets for their derived products are expanded through improved consumer access to information on recipes, nutritive and cultural values (Jaradat, 2013). Therefore, local knowledge of landrace diversity, when documented through interaction with farmers and linked to food traditions, local practices and social norms, is vital for on-farm conservation and would increase their competitive advantage if farmers have other alternative options (Bellon *et al*., 1997; Brush, 2004). For example, socio-cultural values and culinary attributes motivated farmers in central Ethiopia to conserve a durum wheat landrace on their farms; they appreciate its peculiar organoleptic qualities and multiple uses, including 14 dishes and two drinks, despite the availability of several improved durum wheat varieties in their locality (Kebebew *et al*., 2001). Moreover, hundreds of farmers who accessed the landrace through re-introduction program expressed their appreciation and future commitment to growing and conserving it on-farm. This example strongly indicated that farmers in a community collectively can sustain more crop and landrace diversity than individual farmers, thus meeting overall conservation needs and objectives (i.e., private and public values of a landrace). A renewed interest in and increased demand by farmers to grow this durum wheat landrace and the promotion of landrace-derived products generated income, created green jobs for local communities, and supported on-farm conservation of the landrace (Jaradat, 2013).

Along with economic benefits, on-farm conservation and utilization of such wheat landraces is also linked to peoples' cultural, social and ritual values. However, for individual farmers, private values of a landrace are the main motivating factors for growing landraces as a source of income and a means of survival. Therefore, *ex situ* conservation in a genebank may be the only practical option to conserve landraces having low private but high public value (Le Boulch *et al*., 1994).

Seed Systems and Exchange

The majority of the wheat landrace diversity maintained on-farm is managed by smallholder subsistence farmers of the Uttarakhand hills. Mainly the local community-level informal seed system (ISS) dominates and the formal seed system (FSS) plays a negligible role except in river valleys and the plain areas where improved farming is practiced under assured irrigation (Bisht *et al*., 2018). The seed systems in hill farming depend on free exchange of seeds among farmer households either through small gifts or barter exchange or to a limited extent trade. The system, therefore, needs protection from negative impacts of regulations designed to promote the FSS. Such negative impact may stem from IPR protection of FV, seed laws, biodiversity laws regulating access, etc. Further, the modern seed laws do not take into account important aspects of farmers' ISS. The FV in ISS are genetically heterogeneous as against the modern improved varieties under FSS that may be uniform and clearly distinct. The genetic heterogeneity of farmer landrace populations helps farmers' select and advance alleles of local adaptation.

Poorly developed seed systems have been a major constraint in deploying more landrace diversity in production systems (Bisht *et al.*, 2018). Improving farmers' capacities to select, produce, and manage quality seed of traditional landrace varieties will help strengthen the ISS of the community. The capacity building program should rely on farmers' IK and should involve the following, i) farmer participatory seed selection for desired adaptive variations in native/naturalized crops, ii) quality seed production, maintenance, and storage of seeds of elite crop landraces, iii) on-farm demonstrations on improved cultivation practices, and iv) community-based *in situ* maintenance of local improved seed varieties.

There is a strong need to establish a traditional seed system network in which the farmers' knowledge of their

traditional food system is acknowledged and reflected in the participatory nature of farming activities. Also there is a strong need that the capacity strengthening activities are built on the existing IK of the farming community.

Small-scale family farms worldwide traditionally save seed of heirloom or local varieties in order to sustain harvests and conserve well-adapted traditional crop varieties. Seed saving can contribute to lower supply costs, more diversified goods, improved human nutrition, and farm self sufficiency. On-farm seed saving by small farmers is essential in conserving global agricultural biodiversity (Witcombe *et al*., 1996), in general, and crop diversity, in particular. Recently, however, this effort has been undermined by corporate consolidation of seed markets and the contentious concerns about seed types, sources, and availability (Jaradat, 2013). Commercial and large-scale seed industries are constantly developing seeds that represent genetically uniform, high-yielding, and increasingly genetically modified crop varieties. These seed types are of little or no value to organic and low input farmers; they are usually designed for use in large-scale mechanized farming, and sometimes are packaged with chemical inputs. As modern industrialized farming extends over the global agricultural landscape, the seed industry has become both more technically specialized and increasingly controlled by large corporate firms. The new seed technologies may pose serious and complex economic risks to small farmers (Rijal, 2010); they can become dependent on expensive improved seed varieties and brands that are marketed along with complementary agrochemical packages. In addition, some commercial cultivars may not meet local dietary needs or market demand. Recreating and structuring local seed systems to simulate a source-sink meta-population model is a first step towards restoring the fragmented meta-population structures of wheat landraces. Through this model, stakeholders can (Almekinders *et al*., 1994; Zeven, 1999; Jaradat, 2013), i) identify the unit of analysis (e.g., the farmer as a decision maker and agent of conservation, the field or parcel representing a particular habitat, the landrace, or a seed lot), ii) incorporate variation among farmers in their practices, knowledge and gender, iii) quantify patterns of seed exchange among farmers and their impact on the biology parameters of landrace population, iv) identify the limiting factors that determine distribution and range of a landrace; and, v) define the minimum area needed to create a dynamic equilibrium between "colonization" and "extinction" of a landrace meta-population (Jaradat, 2013).

The goal of this type of participatory endeavour is empowering the farmers by supporting the formation of groups capable of assessing their own needs and addressing them either directly or through demands on publicly-funded research organizations. However, low income traditional farming households often have limited technical capability and facilities to produce and properly store seed lots, and thus can face risks in conserving and sustaining reliable and high-quality seed supplies for their planting needs.

Large scale local level seed exchange can be commonly seen in Uttarakhand hill farming. Traditional farmers periodically resort to replacing seed of their old varieties and landraces with seed from other farmers to combat what they consider as "seed degradation." This "inexplicable" seed replacement may have its origins in farmers' belief that homegrown seed degenerates after several generations of re-sowing under the same environmental and edaphic conditions and management practices (Zeven, 1999). Seed replacement and avoidance of traditional maintenance breeding by farmers could, however, be attributed to the existing, but mostly unsuspected, negative association between yield potential of the landrace and the competitive ability of individual plants within its genetically heterogeneous populations (Jaradat, 2013). As seed of many old varieties and landraces disappear across the world and sales of modern improved seed varieties increase exponentially, more low-income farmers may face difficult choices about the type and source of the seeds they utilize (Baniya *et al*., 2000).

Landraces and the Future of Wheat Diversity

It has been observed that 16 wheat landraces have been disappeared from production landscapes of Uttarakhand hills during past two to three decades, whereas not a single landrace was introduced in traditional farming. Under rainfed hill farming only, 2-3% net sown area is replaced by modern varieties, whereas in river valleys an average 70-80% cropped area have been replaced by improved varieties bred by formal sector institutions. In rainfed hill farming, farmers' are often forced to plant improved varieties when there is crop failure and farmers' are constrained for seed of local varieties available for planting in next season.

World over, durum and bread wheat landraces have been largely replaced, in their centres of diversity by monocultures of pure genotypes. This genetic erosion resulted in significant loss of valuable genetic diversity for quality traits and resistance or tolerance to biotic and abiotic stresses; whereas, the pure wheat genotypes do not have the wide adaptation and the diverse genetic background already present in landraces. Diversity of wheat landrace populations, when structured to build spatial and temporal heterogeneity into cropping systems will enhance resilience to abiotic and biotic stresses. Other resilience sources will include more robust genetic resistances and biochemical response mechanisms derived from landrace genotypes (Bonman *et al*., 2007).

Climate change is expected to differentially affect components of complex biological interactions in modern and traditional wheat production systems. Wheat yield and quality will be affected by climate change directly, and indirectly, through diseases (e.g., stem and leaf rusts) that themselves will change but remain important. These effects will be difficult to dissect and model as their mechanistic bases are generally not well-understood. The manner with which wheat landraces and their populations in and outside their centres of diversity might respond to climate change will determine their continued productivity, utility, and survival. Phenotypic plasticity, evolution, and gene flow, although each presents its own uncertainty, are possible avenues for surviving shifts in biotic and abiotic conditions caused by climate change. Whether there will be constraints on evolution in response to the abiotic and biotic stresses caused by climate change, modern wheat, but not landrace adaptation may not keep up enough to maintain fitness (i.e., seed production). Wheat plants will probably respond through shifts in morphology (e.g., tillering capacity, leaf area index, green leaf area duration), phenology (e.g., days to anthesis, days to maturity, duration of seed filling period), or development (e.g., rate of leaf emergence based on available growing degree days), which may help maintain fitness. However, phenotypic plasticity and gene flow (mainly through seed exchange) of landraces may not produce fully adapted phenotypes or the necessary genetic variation to combat climate change. Declining yields of landrace populations due to expected climate change would cause great concern to farming families and threatens their livelihoods. In their attempt to maintain yields, farmers would consider changing seed sources and discarding their adapted landrace populations (Zeven, 1999). This could result in the loss of certain landrace populations, entire landraces, or, in extreme cases, whole minor wheat species.

The development of new varieties from wheat landrace populations is a practical strategy to improve yield and yield stability, especially under stress and future climate change conditions. Further enhanced productivity and stability can be achieved through practicing continuous selection within landraces across the marginal production environments, to exploit the constantly released useful adaptive variation (Ehdaie and Waines, 1989). Non-breeding approaches to create demand for landrace products to promote on-farm dynamic conservation and sustainable utilization of wheat landraces include, i) raising public awareness regarding current and future value of landraces, ii) diversity fairs to allow for the exchange of landrace materials and associated indigenous knowledge, iii) visits among farmers in different localities to share seeds and experiences, iv) diversity contests to reward farmers who keep special varieties and or conserve the highest diversity, and v) recipe development and niche market creation for landrace products. Together, these activities are expected to complement each other and contribute positively towards sustaining on-farm conservation and landrace diversity for the foreseeable future.

Landraces, as an important genetic resource, have been included in international treaties and national decrees that protect and enhance their use in their local environments. However, legislation is needed to make it possible to market landraces as diversified genetic materials. National and international legislation was designed primarily to protect trade and return royalty income to expensively-funded plant breeding programs; as landraces become more attractive to use in local food production and sustainability, legislation changes are needed to facilitate this trend and to promote exportation and exchange of landrace diversity and encourage their use (Jaradat 1992, 2013; Joshi and Witcomb, 2003).

An unprecedented level of international wheat germplasm exchange has taken place during the past three to four decades resulting in a greater degree of genetic relatedness among successful cultivars globally. Despite considerable progress over the years, huge scope still exists for strengthening and making use of landrace diversity as sources of resistance/tolerance to biotic and abiotic stresses, and more importantly the climate change

resilience as extreme heat that have affected grain yields worldwide and threatened food security. Sources of specific adaptation related to drought and heat, as well as associated breeding of genetic traits, will contribute to maintaining grain yields in dry and warm years. Evaluation of wheat landraces stored in gene banks with highly beneficial untapped diversity and sources of stress adaptation, once characterized, should also be used for wheat improvement. Unified development of databases and promotion of data sharing among physiologists, pathologists, wheat quality scientists, national programmes, and breeders will greatly benefit wheat improvement for adaptation to climate change worldwide (Lopes *et al*., 2015).

Wheat Landraces as Functional Food

Beside being a major staple energy source and source of easily digestible quality protein, among health promoting phytochemicals in whole wheat grains, phenolic compounds have gained attention as they have strong antioxidant properties and can protect against many degenerative diseases (Leoncini *et al*., 2012). Profiling of grain phenolic extracts of modern and old common wheat varieties and evaluation of their potential antiproliferative or cytoprotective effect in different cell culture systems have indicated that increased intake of wheat grain derived products, particularly of old farmers' varieties, could represent an effective strategy to achieve both chemoprevention and protection against oxidative stress related diseases (Leoncini *et al*., 2012).

Further, nutrition profiling of farmer landrace diversity is essential as developing food composition database is considered vital for effective advocacy tools and critical for cross-sectoral policy and program development for food-based approach to community nutrition and health. Nap Hal, an Indian landrace of wheat, exhibiting unique characteristics suitable for biscuit making quality can be cited as an example here (Ram *et al*., 2007).

Conclusions

Despite loss of some wheat landraces, substantial diversity is still maintained in traditional production landscapes of Uttarakhand hills. Facilitating systematic documentation and registration of unique landraces are considered necessary to address Farmers' Rights. An integrated seed system, combining both community-level ISS and FSS, also needs to be developed to address the issue of quality seed production and trading of FV. The nutritional value of FV needs to be studied so that they can also be competitive in local markets and provide commercial opportunities of fetching a premium price. Adaptive response of FV to changing climate also needs to be duly documented in order to provide an evolutionary service to the society.

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RESEARCH ARTICLE

Yield Improvement of Tulaipanji Rice through Recombination Breeding and Selection

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Tulaipanji is a famous aromatic rice from West Bengal (GI tagged), cultivated only in the district of Uttar Dinajpur. Recombination breeding was attempted and crosses were made between Tulaipanji and three high yielding cultivars of rice namely, Ranjit, IR64 and Pusa Basmati 1460 to combine high yield with superior grain quality. One of the breeding lines of the cross (Tulaipanji × Ranjit), showed unique new trait which was red pericarp. Two most promising lines were selected from the cross (Tulaipanji × IR64) with enhanced yield and aroma. Grain length was 9.75-9.85 mm, width was 2.39-2.41 mm, 1000 seeds weight was 27.86-28.38 g, just with 27.09, 34.63 and 87.69 % improvement over Tulaipanji. Grain number per panicle was 186 in F5 lines but only 94 in Tulaipanji. Maturity time has been reduced to 135 days instead of 145-150 days in Tulaipanji. One F2 progeny line of a triparental cross (Tulaipanji × IR64 × PB1460) had enhanced yield potentiality and quality. Grain quality was judged using physicochemical parameters (ASV, sensory based aroma and GT).

Key Words: Pedigree selection, Pure lines, Rice landrace Tulaipanji, Yield increase

Introduction

Rice [*Oryza sativa* L.], the most important cereal crop, provide staple food for half of the World's population (> 3.3 billion). This staple food grain is the main energy resource providing 40-75% of the daily calorie intake to the world's poor people (Yu *et al*., 2002; Khush, 2005). Asia is considered as 'Rice Basket' because it produces 90% of the world's production (748 million tons, paddy rice, Mt). Total world production was 748 Mt from 163.1 million hectares with productivity of 4.6 tons/hectare (t/ha) in 2016 of which 676.5 million tons was produced by Asian countries. Global rice production must be doubled by 2050 (Ray *et al*., 2013; Arbelaez *et al*., 2015) to feed the more than 9 billion people (9BPQ). Narrow genetic base in released rice varieties has make the improvement in plateaus (Tanksley and McCouch, 1997; Tian *et al*., 2006). Genetic bottlenecks during domestication causes narrow genetic diversity (Tanksley and McCouch 1997) in the well adapted cultivars leading to yield stagnation. Breeder could manage the yield increase over released varieties through genetic gain by combining the yield related genes/QTLs from various genetic resources of rice germplasms either from cultivated local landraces (CLR) or from wild varieties. Germplasm diversity is the mainstay for crop improvement and genetic dissection of complex traits. Rice germplasm shows tremendous genetic diversity in both within the species and among the varietal groups (Godfray *et al*., 2010; Tester and Langridge 2010; Gill *et al*., 2011) and can be exploited to introgress these traits using knowledge of molecular breeding techniques such as marker assisted breeding (MAB) (Kilian and Graner, 2012; McCouch *et al*., 2012, 2013; Li and Zhang, 2013; Agarwal *et al*., 2016) or marker assisted selection (MAS). Efficient breeding designs are much needed to transfer the useful diversity to breeding lines. The MAGIC (Multi-parent Advanced Generation InterCross) breeding program has been designed to produce highly recombined populations with increased genotypic diversity leading to genetic enhancement (Bandillo et al 2013; Leung *et al*., 2015; Meng *et al*., 2017). Following Green Revolution, farmers stopped growing specific local fragrant rice varieties and replaced them with the new, fast growing, disease resistant, non-fragrant and high yielding varieties (Bhattacharjee *et al*., 2002; Itani *et al*., 2004) due to low yield of these fragrant varieties compared to HYVs. This led to tremendous reduction in the genetic diversity of fragrant rice. Many of the local fragrant landraces were out-competed and lost from the gene pool (Singh *et al*.,

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2000; Bhattacharjee *et al*., 2002; Garg *et al*., 2006). Nowadays there is a worldwide demand for fragrant rice due to progression of living standard and increasing income. Low yield in fragrant rice varieties is due in part to its susceptibility to diseases and insect pests (Lorieux *et al*., 1996; Sriboonchitta and Wiboonpongse, 2005; Toojinda *et al*., 2005) which is compounded by management practices (Yoshihashi *et al*., 2002; Itani *et al*., 2004). Fragrant rice exhibits higher aroma levels when grown in sub-optimal conditions.

Tulaipanji is a non-Basmati aromatic rice of West Bengal (GI tagged) and famous for its quality and fragrance but with low yield potential. Uttar Dinajpur district lies between latitude 25°11' N to 26°49' N and longitude 87°49' E to 90°00' E occupying an area of 3142 km². Total area under Tulaipanji rice cultivation in Uttar Dinajpur district was 6700 hectare during 2017-18 *kharif* crops and total production was 14,740 metric tons. Thus, the present project is designed to broaden the genetic base of the local rice landrace cultivar Tulaipanji of Uttar Dinajpur district by recombination breeding through hybridization with different genetic stock and to increase the yield potentiality through introgression of yield related gene/QTLs from different genetic resources of rice.

Materials and Methods

Plant Materials

Local rice landrace cultivar Tulaipanji of Uttar Dinajpur district was used as main parent for its improvement. It is a non-Basmati aromatic rice landrace of West Bengal (GI tagged, No 530, 2017, Govt. of India). It is characterized by medium grain quality with good aroma, drought avoidance, unresponsive to chemical fertilizer application and low yield (1.8 t/ha). Three varieties namely, Ranjit, IR64, Pusa Basmati-1460 were used as parents for genetic enhancement and yield improvement of Tulaipanji rice in this recombination breeding program.

Conventional Artificial Pollination for Hybridization

Hybridization was performed between cultivar Tulaipanji and Ranjit (2011), Tulaipanji and IR64 (2013) and Tulaipanji and PB-1460 (2016). Hybridization was done according to the standard protocols of artificial pollination in rice (Sleper and Poehlmer 2007; Sha 2013; Roy, 2017). Morpho-agronomic traits were recorded according to standard evaluation system of rice (SES, IRRI, 2002, www.irri.org) for evaluation of the rice lines. Alkali spreading value (ASV) (in a scale of 1 to 7) was measured according to the standard method (Little *et al*., 1958). A low ASV corresponds to a high gelatinization temperature (GT), conversely, a high ASV indicates a low GT. Sensory based aroma (in a scale of 0 to 3) was evaluated using standard procedure (Sood and Siddiq, 1978).

Statistics and Anova Analysis

Statistical significance of the field data were analyzed using Excel Stat data analysis software (MS office). Anova and t-test was performed at $p < 0.05$ (5% significance level).

Results and Discussion

Agromorphological and Physicochemical Data Analysis

Crosses were made between Tulaipanji × Ranjit (2011), Tulaipanji × IR64 (2012) (named as IRT64F1). One line IRT64F4 was again crossed with PB1460 in 2016 to increase the genetic base and F2 population seeds were harvested from the cross (IRT64F4 × PB1460) in 2017 *kharif* season. Agro-morphological studies were done based on DUS test protocol of rice for all the progeny lines (Table 1, Figures 2, 3 and 4). Kernel shape and size of different progeny lines were morphologically summarized (Figure 5). Nine morphological traits were considered for the present analysis–plant height, flag leaf length, flag leaf width, maturity days, awn length, panicle length, grain per panicle, 1000 seeds weight, grain length, grain width and grain length/width ratio (Table 1) and three physicochemical properties were considered for the evaluation of the progeny lines (Table 2, figures 6 and 7) to judge the grain quality.

Observed plant height was 135.1 cm, 135 cm, 135.2 cm in Tulaipanji, progeny F7 awn and progeny F7 awnless respectively. Short height was recorded in IR64, which was 100.9 cm and F5 progeny lines showed similar to mid-parent value, 125.3 to 125.4 cm.

F2 progeny lines of cross IRT64F4 × PB1460 also showed reduced plant height (125 cm) in compared to Tulaipanji parental line 135 cm. Plant height in subsequent F3 generation again decreased to 110 cm which is quite similar to PB1460 plant height of 105 cm. The plant height controlling gene *Sd1* had been introduced in IR8 through crossing from *Dee-Geo-*

Table 1. Summary of the statistical analysis of the Agro-morphological data in the parental and progeny lines.

	Tulaipanji	IR64	Progeny Aw F5	Progeny AL F5	PB1460	Progeny F2	Ranjit	Progeny Aw F7	Progeny AL F7
Plant height (cm)	*135.1±0.433	100.9±0.622	*125.3±1.042	*125.4±0.541	105±1.011	*125.4±0.702	103±0.843	135±0.930	135.2±0.827
Flag leaf length (cm)	*26±0.293	30.05±1.065	*29.03±0.523	*29.08±0.639	29.10±0.759	*35.09±0.917	27.02±0.435	30.08±0.507	30.04±0.559
Flag leaf width (mm)	9±0.137	15.07±0.280	15.02±0.192	15.03±0.186	14.04±0.165	13.51±0.229	17.02±0.143	9.02±0.075	10.02±0.144
Maturity days	*150.2±0.466	120±0.596	*135±0.516	*135±0.333	135±0.516	140.4±0.561	145±0.537	145±0.475	145±0.537
Awn length (mm)	30±0.542	00	23.07±0.271	00	31.06±0.516	12.08±0.381	00	18.01±0.380	00
Panicle length (cm)	*26±0.414	24±0.423	*30.01±0.314	*28.02±0.201	27±0.235	23±0.203	24.61±0.248	27.01±0.193	27±0.229
Grain/panicle	*94.1±0.525	130.1±0.433	*185±0.977	*186.1±1.159	120.4±0.819	*140.4±0.686	180.3±0.869	145.1±1.242	140.2±0.827
1000 seeds wt (g)	*15.12±0.053	25.02±0.203	*27.86±0.115	*28.38±0.155	24.60±0.240	*26.46±0.128	19.27±0.084	19.38±0.161	16.50±0.120
Grain length (mm)	*7.75±0.014	9.60±0.022	*9.75±0.017	*9.85±0.025	10.60±0.020	*10.55±0.045	7.84±0.028	8.47±0.021	8.87±0.018
Grain width (mm)	*1.79±0.007	2.40±0.009	*2.41±0.005	*2.39±0.004	1.94±0.011	*2.14±0.023	2.21±0.027	2.37±0.013	2.14±0.019
GL/GW ratio	4.32±0.013	4.00±0.021	4.04±0.026	4.12±0.036	5.45±0.021	4.92±0.015	3.54±0.021	3.57±0.013	4.14±0.036

Mean value of 10 plants± standard error. * Significant at p value < 0.05 level in t-Test in row wise.
[Progeny F5 (Tulaipanji × IR64), Progeny F2 (Tulaipanji × IR64 × PB1460), Progeny F7 (Tulaipanji × Ranjit), Aw- Awn, AL-Awnless].

Woo-Gen, a Taiwan variety. Due to short height and other genetic components, IR8 was high responsive to chemical fertilizer and water along with lodging resistant (Khush 1987; Mackill 2018; http://www.irri.org/ir8). The progeny lines of F5 and F3 were lodging resistant (Fig. 1) compared to the parental line Tulaipanji in the field. Genetic components of high tillering and increased grain number in these F3 and F5 progeny lines might have been inherited from parental line IR64. IR64 itself is a multiparental high yielding mega variety developed and released by IRRI in 1985 (Mackill and Khush, 2018). The F3 progeny lines had the characteristics of all the three parents namely Tulaipanji, IR64 and PB1460. Analysis of variance revealed that at least one of the three samples had significantly different means (Table 3).

Table 2. Summary of the physicochemical properties of the parental and progeny lines of different crosses.

Cultivars/progenies	Aroma	ASV	GT
Tulaipanji	3	4	3
IR64	0	1	7
F5AL (Tulaipanji × IR64)	3	4	3
F5AW (Tulaipanji × IR64)	3	3	5
F5Md (Tulaipanji × IR64)	1	3	5
F5Blk (Tulaipanji × IR64)	2	4	3
PB1460	1	7	1
Ranjit	0	1	7
F7AW (Tulaipanji × Ranjit)	2	3	5
F7AL (Tulaipanji × Ranjit)	0	2	7
F2 (IRT64F4 × PB1460)	2	4	3

[AVS: Alkali spreading value, GT: Gelatinization temperature]

Table 3. Summary of the ANOVA analysis for the morphological traits in parental and progeny lines.

a.	Anova of plant height (cm)		
	Source of Variation	*MS*	*P-value*
	Between Groups	2046.853	5.24E-58
	Within Groups	6.374	
b.	Anova of Flag leaf length (mm)		
	Source of Variation	*MS*	*P-value*
	Between Groups	63.90614	1.2E-12
	Within Groups	4.53148049	
c.	Anova for maturity days		
	Source of Variation	*MS*	*P-value*
	Between Groups	805.4778	2.054882
	Within Groups	2.592593	
d.	Anova for panicle length (cm)		
	Source of Variation	*MS*	*P-value*
	Between Groups	46.4987	1.25E-29
	Within Groups	0.842093	
e.	Anova for grain per panicle		
	Source of Variation	*MS*	*P-value*
	Between Groups	9958.128	3.58E-82
	Within Groups	7.655556	
f.	Anova for 1000 Grain weight (g)		
	Source of Variation	*MS*	*P-value*
	Between Groups	250.5303778	2.22E-79
	Within Groups	0.226058765	
g.	Anova for grain length (mm)		
	Source of Variation	*MS*	*P-value*
	Between Groups	11.55992	2.72E-88
	Within Groups	0.00626	

Table 4. Depicted the t-Test results showing significant variances between Tulaipanji and Progeny F5 Awn line (Tulaipanji × IR64).

a. t-test: Two-Sample assuming equal variances in plant height		
	137	125
Mean	134.889	125.333
Variance	1.611	12.25
P(F<=f) one-tail	0.0048	

b. t-Test: Two-Sample Assuming Equal Variances in Maturity days		
	150	*135*
Mean	150.222	135
Variance	2.4444	2.666
P(T<=t) two-tail	1.70731E-13	

c. t-Test: Two-Sample Assuming Equal Variances in panicle length		
	26	30.5
Mean	26.002	29.956
Variance	1.931	1.282
P(T<=t) two-tail	5.93035E-06	

d. t-Test: Two-Sample Assuming Equal Variances in grain per panicle		
	94	188
Mean	94.111	184.666
Variance	3.1111	9.5
P(T<=t) two-tail	6.00544E-22	

e. t-Test: Two sample assuming equal variances in grain length		
	7.73	9.75
Mean	7.752222222	9.75
Variance	0.002419444	0.0033
P(T<=t) two-tail	3.41858E-22	

Fig. 1. Experimental field trial in *Kharif* crop 2017, at Kaliyaganj, Dist. Uttar Dinajpur. Above: Transplanted in 30 cm × 20 cm based on DUS test protocol of parental and progeny lines F5 (Tulaipanji × IR64), and F7 (Tulaipanji × Ranjit). Clearly showing that F5 lines (Tulaipanji × IR64) was lodging resistance but Tulaipanji has been totally lodged in the field (bottom).

One of the progeny lines of the cross between Tulaipanji × Ranjit, developed a new unique trait, which is red pericarp formation from F4 generation. The trait red pericarp was totally absent in the parental lines (Tulaipanji and Ranjit) (Figure 5). Red pericarp is common in wild rice genotypes while cultivated genotypes mostly have white colour pericarp (Sweeney *et al*., 2007). This phenomenon of red pericarp coloration is associated with the domestication of rice crop (Izawa *et al*., 2009). Red pericarp has high nutritional value (Shirley, 1998; Furukawa *et al*., 2007).

Red pericarp colouration leads to accumulation of proanthocyanidin in grains of wild rice which helps in plant defense against pathogens or predators. Present observation might be consistent with the earlier findings (Brooks *et al*., 2008) that one wild type allele (*Rc*) changed to recessive null allele (*rc*) by deleting 14 bp in the exon seven of *Rc* allele of the parental line (Tulaipanji and Ranjit). There might be second mutation in the exon resulting in recovery of the reading frame of the wild type Rc allele leading to red pericarp development (Roy and Reddy, 2017).

Mainly four progeny lines were selected using pedigree selection method from the cross Tulaipanji × IR64 which was medium grained with awn, black husk coloured, long grained with awns and long grained without awns (Figures 2, 3 and 4). Field performance of two F5 progeny lines showed lodging resistance with strong and stout stem (Figure 1 lower panel). As the parental line Tulaipanji completely lodged in the field (Figure 1), lodging resistant gene must have been inherited from parental line IR64 in the progeny lines. Plant height in the progeny F5 line was similar to mid-parent value (125 cm) (Table 1), flag leaf character was as like as IR64. Maturity time reduced to 135 days instead of 145-150 days needed for Tulaipanji. The IR64 is early maturity high yielding variety takes 120 days. Panicle length has increased in progeny line 28-30 cm with high grain numbers (185-186) compared to Tulaipanji (94 grain/panicle) (Table 1). Grain length increased in F5 progeny lines (9.75 mm – 9.85 mm), whereas grain length was 7.75 mm in Tulaipanji. 1000

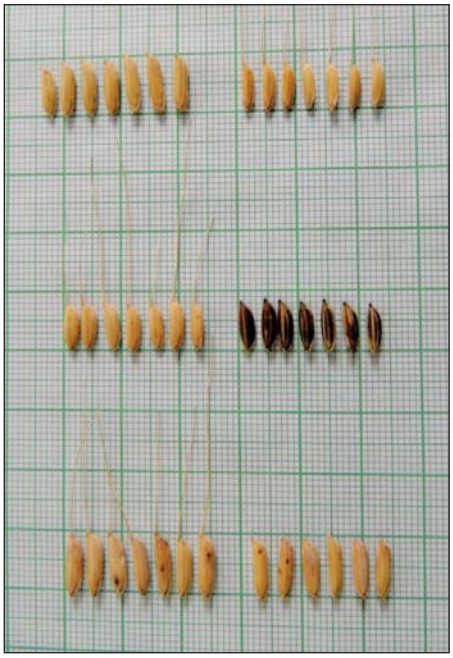

Fig. 2. Grain morphology of progeny lines in the cross Tulaipanji and IR64. First panel, IR64, Tulaipanji, second panel, F5 medium grain with awn, F5 black husk grain, third panel, F5 progeny Awn and F5 progeny Awnless

Fig. 3. Grain morphology of progeny lines. First panel, PB-1460, F5 Medium grain (Tulai × IR64), second panel, progeny F5 Awn (Tulaipanji × IR64), F5 awnless (Tulaipanji × IR64), third panel, Tulaipanji, progeny F7 AL, F7 AW, and Ranjit

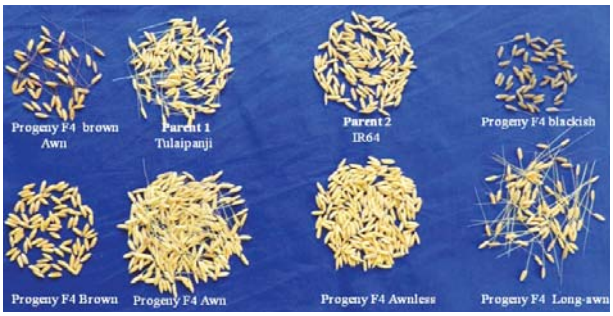

Fig. 4. Grain morphology of progeny lines of cross between Tulaipanji and IR-64, at F4 generations, *kharif* 2016

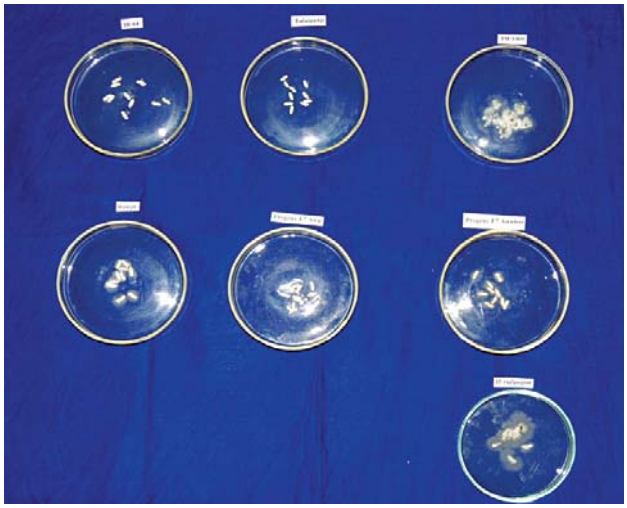

Fig. 6. Physicochemical properties of the progeny rice lines (Tulaipanji × Ranjit) at F7 stage was depicted for quality check. Showing the alkali spreading value, gelatinization temperature and sensory based aroma test

seeds weight was high in F5 lines (27.86 g–28.38 g) but only 15.12 g in Tulaipanji.

Aroma index was 3 in the progeny lines of the cross (Tulaipanji × IR64) in F5 stage with ASV values 3-4 and GT value 3 or 5. ASV showed distinct genetic variability among the parental and progeny lines (Figures 6 and 7). Cultivar IR64 showed low ASV (1), and high value of GT (7). ASV depends on the nature of the amylopectin molecules and is reported to be dependent on soluble starch synthase gene on chromosome 6. Both the traits (GT and ASV) are known to be governed by the enzymes of granule bound starch synthase I (GBSSI) encoded by the *Waxy* gene locus on short arm of chromosome 6 (Umemoto *et al*., 2002 and 2004).

In many breeding programs, the improvement of the quality of rice, especially its eating and cooking quality (ECQ), is an important objective as rice is mainly consumed in cooked form (Pang *et al*., 2016).

Fig. 5. Kernel shape and size of different progeny lines. Above: Tulaipanji, progeny F5 awnless (Tulaipanji × IR64), F5 awn (Tulaipanji × IR64), F5 medium grain with awn (Tulaipanji × IR64), F5 black husk (Tulaipanji × IR64), and IR64, and below: PB-1460, progeny F7 Awn (Tulaipanji × Ranjit), F7 awnless (Tulaipanji × Ranjit) with red pericarp, and Ranjit

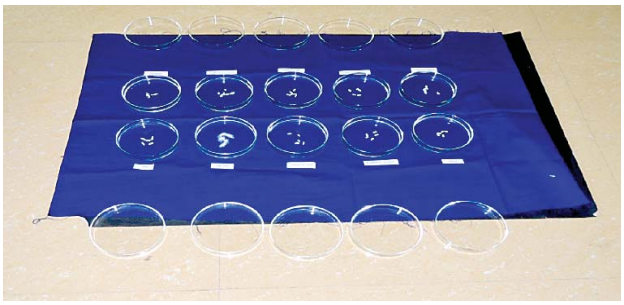

Fig. 7. Physicochemical properties of the progeny rice lines (Tulaipanji × IR64) at F5 stage was depicted for quality check. Showing the alkali spreading value, gelatinization temperature and sensory based aroma test

Rice grain consists primarily of starch (~90%) and is comprised of two components, amylose and amylopectin. It has many properties such as apparent amylose content (AAC), amylopectin structure, pasting viscosity, GT, gel consistency and texture. All the starch-related properties have various degrees of effect on the ECQ of cooked rice (Bao, 2012). A low or intermediate GT is desired for a high-quality rice variety (Juliano and Villareal, 1993). Some of the progeny lines had recorded low GT scores. The F5 awnless progeny line showed GT value 3 with ASV 4, and high aroma index 3. Progeny F2 lines (IRT64F4 × PB1460) had high grain quality with GT value 3, ASV 4 and aroma index 2.

Cross combining ability of Tulaipanji was maximum when crossed with IR64. Grain yield was doubled to 3.6 t/h in the progeny compared to the parental line Tulaipanji (1.8 t/h). In the same way other traits such as grain length, grain/panicle, short and stout stem related genes/QTLs introgressed appropriately into the genome of Tulaipanji and expressed the traits with maximum penetrance and expressivity. Thus yield increase doubled in the F5 progeny lines (Tulaipanji × IR64).

Recombination breeding was targeted to widen the gene pool of Tulaipanji rice by crossing ITR64F4 line with 3rd parental line PB-1460, to improve its grain quality. Progeny F2 lines showed grain length similar

to PB-1460 (Table 1, Figures 3, 4 and 5). F3 generation showed morphologically similar phenotype to parental line IR64. Grain quality was soft with aroma indicator value 3 (Figure 7). Plant height reduced to 110 cm, compared to F2 progeny lines, which was 125.4 cm (Table 1).

Conclusion

Intraspecific crosses were made for the improvement of local rice germplasm Tulaipanji. The RIL line (F7) of the cross between (Tulaipanji × Ranjit) has been registered under Breeders' Right act of Govt. of India and deposited to the NBPGR Gene Bank with IC no 626287 (Breeding line/NBUTRNF7-18). This F7 RIL line has unique trait of red pericarp development at the stage F4 and is stably inherited. Two promising breeding lines were identified from the cross, Tulaipanji × IR64. Line-1 is with awn and aroma but other line-2 is without awn but with aroma. Grain shape, size and weight were enhanced and showed transgressive segregation. The present study clearly showed better performing F5 recombinants (Tulaipanji × IR64) at the field level maintaining high grain quality and fragrance with improved yield (3.6 t/h), just double that of the Tulaipanji parental line (1.8 t/h). The F2 progeny line (IRT64F4 × PB1460) showed enhance grain quality based on physicochemical parameters. From this cross (IRT64F4 × PB-1460), two lines were selected. Both the lines performed better with respect to morphological and grain quality at F3 generation. Present investigation suggests that traditional rice varieties remain as a large reservoir of genetic diversity with potential to accelerate rice improvement if used properly in breeding program. Recombination breeding of local rice landraces, if improve their yield can retain them in farmers' fields in the long run.

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RESEARCH ARTICLE

Surveying Mango Diversity and its Custodian Farmers in the States of Bihar and Jharkhand, India

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In Bihar and Jharkhand, mango (*Mangifera indica* L.) is a very popular fruit grown extensively in the area with great economic importance for livelihood security of the orchardists. A survey was carried out in 35 districts of Bihar and 8 of Jharkhand based on a set of questionnaire and complemented by visits to the mango orchards in the region after the interaction with *DHOs* (office of District Horticulture Officers) and *KVKs* (Krishi Vigyan Kendras) of concerned districts about farmers growing more than 10 cultivars of mango in the locality. All surveyed farmers were men.

Through participatory rural appraisal (PRA) and interaction with mango growers, it was found that the Langra (vernacular name *Maldah* in the region) is the predominant cultivar of Bihar (likewise '*Jardalu*' in Bhagalpur Region) and '*Amrapali*' in Jharkhand. The unique local varieties which were conserved in the region are *Jalbanda* (large sized fruit with sweet at mature green stage), *Jalmarai* (uneven shape but very tasty with hard peel), *Bhastara* (syn. *Baramasi*, bearing twice in a year) *Sabja* (syn. Bombaiya, an early and sweet even at mature green stage), *Dalma* (syn. *Kalkatia Malda*, dark greened, large sized), Malda seedling (fruit weigh up to 750 g, superior in taste and sweetness compared to grafted one), *Bhont* (thin stoned, papaya shaped and mid maturing), *Sinduria* (earliest maturity), *Raja* (sweet and easily digestible), *Kaveri, Bahadura, Balajee*, *Kerwa*, *Tairia* (heavy fruit bearer with regularity), *Baelkhash* (leaves/fruits contains flavour of bael), *Chitranjan* (late maturity, taste like curd of buffalo milk), and '*Gaurjeet*, (good smelled and highly flavoured) of West Champaran which has an excellent market in the bordering area of Bihar, Uttar Pradesh and Nepal.

Key Words: Custodian farmers, Diversity, *in-situ* conservation, Mango

Introduction

Given that the native mango gene pool is the basic unit of conservation and the ultimate target of the current genetic resource collection, it is very important to correctly identify the varieties and capture maximum diversity of the species. The genetic materials are kept viable under field conditions as part of the *ex-situ* conservation activities by the mango orchardists. The diversity in mango comprises of native landraces, local selections, and elite cultivars. In Bihar and Jharkhand, mango (*Mangifera indica* L.) is a very popular fruit grown extensively with great economic importance for livelihood security of the orchardists. India has vast germplasm and varietal diversity with about 1100 named. No other country surpasses India in this respect, but only a few varieties are grown on a commercial scale. The mango genetic diversity and even the species diversity is threatened due to various human interventions. Concerted efforts are required to take corrective measures (Bhag Mal *et al*., 2011). Bihar and Jharkhand have enormous wealth of mango genotypes with respect to plant and fruit characteristics. The need has been felt to conserve the mango diversity at national and global levels. Due to shrinking land resources, smart strategies have to be developed for conservation of mango diversity. Different stages of conservation of mango diversity have been envisaged which include secret groves, forbidden orchards, cultivated orchards, field gene banks, diversity parks, homestead gardens and so on. In the centre of these conservation programmes, the *'custodian farmers'* who dedicate time and effort to conserve them [mangos] and make maximum use of diversity for their livelihood security. Such custodian farmers maintain, adopt and disseminate the agro-biodiversity over time and in space. Research and development links with these custodian farmers should be maintained and to conserve mango diversity over time.Furthermore, while geneticists and plant breeders are particularly interested in diversity at

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the molecular level, farmers are more concerned about visible morphological and agronomic variation, which helps them to identify cultivars that are productive and do well in their location specific environment (this refers to narrow adaptation given that farmers are unfamiliar with the characteristics of the many different cultivars of mango (Singh *et al*., 2015). While *ex-situ* conservation poses largely technical challenges, *in-situ* and *on-farm* conservation also need to consider several social parameters with regards to farming communities and the knowledge they hold. It is impossible to undertake *on-farm* conservation of 'nature' without considering people, their rights, their needs, their values and their relationships (Sthapit *et al*., 2016).

For the identification of custodian farmers and the mango diversity they maintain, a survey was carried out in some districts of Bihar and Jharkhand with the objective to see the gaps in improved practices they follow and to document the traditional knowledge they use to conserve and utilize mango diversity. An assessment of the diversity grown variants grown by the community may lead to identification of promising accessions/clones with regard to (better) quality and late or early maturity compared to locally acceptable varieties. The present paper highlights the need to group various cultivars based on mopho-physio-biochemical and molecular characterisation and screening for breeding purposes for improvement of commercial cultivars. It concludes that some of the superior germplasm can be directly release as variety for the region.

Material and Methods

An effort was made to collect information on indigenous diversity maintained by interested orchardists and to understand their motivating factors to conserve them (Department of Biotechnology, Govt. of India Sponsored '*National Database on Mango*' Project). The name of districts to be surveyed was given by the Nodal Officer, *National Database on Mango*' Project, ICAR-CISH, Lucknow. Concern districts were selected based on GIS Mapping of mango orchards. A survey was carried out in 35 districts of Bihar and 8 of Jharkhand based on a set of questionnaires (developed by ICAR-Central Institute for Subtropical Horticulture, Lucknow). This was complemented by exchanges with the DHOs and KVKs of concerned districts and by field visits to the mango orchards. Discussion with the farmers growing more than 10 cultivars in the locality were held (Table 1). We asked basic research questions to collect information about; a) Passport data and morphological characterization of genetic resources, b) Digitization of information regarding *on-farm* conservation, c) Characterization of farmers varieties, d) Data on

Table 1. List of custodian farmers conserving mango diversity

Name of the farmers	Location of orchard*	Longitude	Latitude	Altitude (± m)	Total No. of trees	No. of Mango varieties conserved
Sri Kaushal Motani	Gamharia Farm, Chauhatta, Mainatand, (West Champaran)	N27º14´58.0˝	E084º37´50.1˝	2	2000	17
Sri Pankaj Kumar Singh	Jalhan, Khajuria, (East Champaran)	N26º28´50.0˝	E084º43´21.6˝	3	250	26
Sri Shailesh Pandey	Dhamsar, Lahladpur via Jantabazar, (Saran)	N26º03´19.7˝	E084º37´40.8˝	2	150	16
Sri Abdul Rahim	Kumarbag, Sadar, Bettiah, (West Champaran)	NA	NA	-	360	28
Sri Anuj Kumar Rai	Malikaur, Pusa, (Samastipur)	N25º56´44.5˝	E085º38´19.5˝	2	150	21
Sri Vinod Kumar Rai	Jagdishpur, Pusa, (Samastipur)	N25º56´93.4˝	E085º39´25.1˝	34	300	36
Sri Vijay Kumar Sharma	Basuari, Pusa, (Samastipur)	E085º39´29˝	N 26º00´19˝	42	350	20
Sri Sanjay Sharma	Malinagar, Pusa, (Samastipur)	N26º00´28.5˝	E085º40´58.5˝	35	130	19
Sri Washi Akhtar	Dharmparsa, Manjha, (Gopalganj)	N26º21´30.6˝	E084º29´23.3˝	3	400	19
Sri Rajeev Nayan Tiwari	Dahibhata, Uchkagaon, (Gopalganj)	N26º28´42.7˝	E084º22´40.3˝	3	600	16
Sri Harsh Ranjan	Hasanpur Vajhi, Sakra, (Muzaffarpur)	N 26º00´5.16˝	E085º33´2.7˝	14	300	19
Sri Sudhir Kr. Pandey	Vishunpur Bakhari, Muraul, (Muzaffarpur)	NA	NA	-	100	16
Sri Amresh Kumar	Banwra Kothi, Sadar, (Katihar)	N25º36´30.9˝	E087º34´45.6˝	10	1500	17
Sri Kalidas Banerjee	Rautara, Kodha, (Katihar)	N25º39´37.5˝	E087º31´57.9˝	4	450	25
Sri Sameer Kumar Jha	Rampur Kamat, Hasanganj, (Katihar)	N25º37´50.2˝	E087º33´55.7˝	7	400	16
Sri Sanjeet Kumar	Chauhan Tola, Jalalgarh, (Purnea)	N25º56´57.0˝	E087º31´30.2˝	4	25	15
Sri Kumar Tarun		N25º56´54.4˝	E087º31´37.6˝	8	140	22
Sri Ashok Kr. Singh	Nagauali, Basantpur, (Siwan)	N26º09´41.6˝	E084º40´26.0˝	3	200	15

*District's name is delineated in brackets under column 2.

regional varieties, e) Updating information on TK, usage of mango fruits or any parts of mango trees and any new practices followed, f) Knowledge available with mango growers on nutritional and medicinal value of mango, g) The intensity of disease and pests and how fields are managed, and h) The number of germplasm in their field gene bank and what good practices of production and postharvest technologies are followed in their orchard. The selected villages of various districts were surveyed for assessment of *on-farm* mango diversity and motivating factors influencing their continued cultivation by the farmers. Farmers who cultivated multiple mango varieties were asked about the reasons for cultivating them concurrently without any economic profits unlike they would have obtained from an orchard of commercial varieties.

In the present paper, we made an inventory of the mango varieties cultivated with special importance given to local landraces and investigate the role of traditional ecological knowledge of the mango growers, concerning the management and conservation of the agro-biodiversity of Bihar and Jharkhand. During the survey, no any germplasm was collected, but information shared by mango growers was validated with answers to focussed questions given by neighbours/villagers of the vicinity.

Results and Discussion

The typology of motivational factors driving the custodian farmers to maintain agro-biodiversity, as suggested by Sthapit *et al.* (2013), includes personal (hobby, personal interest to collect); social value (heritage value and legacy/or respect for parents/forefathers, for exchange with relatives/friends); economic considerations (good income, risk management); cultural significance (traditions, customs, beliefs or because of its use in cultural or religious functions); natural virtues of a variety (disease or pest resistant or adapted to local climate and soil conditions, provision of eco-system services, regular bearer) and biological (taste, varietal preference) values.

A large array of cultivated and wild types of mango found in the surveyed areas and seedling races derived from mono-embryonic mango stones. They are the most important components of diversity available in India. Almost all commercial cultivars of mango have arisen as a result of seedling selection (Bhag Mal *et al*., 2011) and unique varieties conserved by custodian farmers in this investigation were mostly of seedling origin. Most of the mango diversity in India and the world is conserved *in-situ*, and amongst all diversity conserved, some stunning examples of local mango varieties are conserved by many mango growers in the region. Some unique mango diversity which was identified from the field gene banks includes *Mithua* (from *Patna), *Sewaiaya, Bhont, Jalbanda* (Saran), *Gaurjeet* (West Champaran), and *Baramasi* (Jamui) (Table 2).Others are listed in Table 3. These species possess important characteristics, such as disease resistance, desired fruit quality (which is lacking in the currently cultivated germplasms). [*District name given in parenthesis; name of unique varieties delineated in italic].

Table. 2. Enlisted varieties of mango *in-situ* conserved in various districts of Bihar

S.No.	Name of unique varieties	Conserved in the District
1.	*Jalbanda*	Saran
2.	*Jalmarai*	Purnea
3.	*Baramasi*	Samastipur
4.	*Lamba Bahadur*	Katihar
5.	*Hilsa Peti*	
6.	*Bhastara (syn. Baramasi)*	Siwan
7.	*Sabja (syn. Bombaiya)*	East Champaran and Gopalganj
8.	*Dalma (syn. Kalkatia Malda)*	
9.	*Malda seedling*	Samastipur
10.	*Bhont*	Saran
11.	*Suraypuri*	Purnea
12.	*Raja*	Gopalganj
13.	*Kaveri, Balajee*	
14.	*Esna*	Katihar
15.	*Baelkhash*	*Gopalganj*
16.	*Chitranjan*	Katihar and Purnea
17.	*Gaurjeet*	West Champaran
18.	*Kerwa*	Siwan
19.	*Tairia*	
20.	*Latkampu (Syn. Bahadura)*	*East Champaran and Gopalganj*
21.	*Hajipur Mithui'*	*Samastipur*
22.	*Madhukupia*	
23.	*Paharpur Sinduria*	
24.	*Rari mango*	
25.	*Kapuria*	
26.	*Hajipur Mithui*	
27.	*Ajgavi Sipia*	
28.	*Belwa*	
29.	*Chauaria*	Katihar
30.	*Navras*	
31.	*Jethua*	Purnea
32.	*Kala Pahad*	
33.	*Jing Jing*	

Table 3. Details of uniqueness of indigenous mango varieties conserved by custodian farmers of mango across Bihar and Jharkhand

S.No.	Name of unique varieties	Distinct attributes	District
1.	*Jalbanda*	Large sized fruit with sweet at mature green stage	Saran
2.	*Jalmarai*	Very tasty with hard peel hard peel, better shelf life Latest maturity (September) led to fruit fly attack Shape is not uniform i.e. distorted	Purnea
3.	*Baramasi*	Flowering thrice in a year; June –July crop is sour in taste and October crop is sweet	Samastipur
4.	*Lamba Bahadur*	Fruit is just like Fazli, shy bearer Large sized fruit (1-1.25 kg per fruit) Resistant to insect pest	Katihar
5.	*Hilsa Peti*	Heavy bearer, ideal sized fruit (4-5 in a kg)	
6.	*Bhastara (syn. Baramasi)*	Bearing twice in a year	Siwan
7.	*Sabja (syn. Bombaiya)*	An early and sweet even at mature green stage	East Champaran and
8.	*Dalma (syn. Kalkatia Malda)*	Dark greened, large sized	Gopalganj
9.	*Malda seedling*	Fruit weigh up to 750 g Superior in taste and sweetness than grafted one	Samastipur
10.	*Bhont*	Thin stoned, papaya shaped and mid maturing	Saran
11.	*Suraypuri*	Regular bearer, scented, bunch bearer Greenish while ripening with white pulp Small sized fruit with prominent beak, thin peel Sucking varieties, can be eaten as much as possible	Purnea
12.	*Raja*	Sweet and easily digestible	Gopalganj
13.	*Kaveri, Balajee*	Heavy bearer with regularity	
14.	*Esna*	Ripening in September (latest to ripen) Fibreless, and high yielder (4 quintal per tree) Bangladeshis are fond of pickle out of it	Katihar
15.	*Baelkhash*	Leaves/fruits contains flavour of bael	Gopalganj
16.	*Chitranjan*	Cross of Chauria × Bombai (presumed) Very sweet (taste like curd of buffalo milk) Tight skin with firm, yellow pulp Thin stone, High shelf life, Weight: 6-8 per kg Fibreless, light-yellow peel But milk sap is more and highly acidic Matures in mid-June and Fetch premium price Resistant to insect pests	Katihar and Purnea
17.	*Gaurjeet*	Good smelled and highly flavoured, has excellent market in the bordering area of Bihar, UP and Nepal	West Champaran
18.	*Kerwa*	Long and big sized fruit, (banana shape) A sucking variety matures in late August, Small seed with 3 inch in length, red shoulder with fibre.	Siwan
19.	*Tairia*	Heavily fruited, regular bearer, Even un-ripen fruit and peels are also sweet	
20.	*Latkampu (Syn. Bahadura)*	Big sized, matures in first week of July	*East Champaran*, *Gopalganj*
21.	*Hajipur Mithui'*	Thick peel, better shelf life	*Samastipur*
22.	*Madhukupia*	Pulp taste like honey	
23.	*Paharpur Sinduria*	Bears fruits in late July with firm pulp	
24.	*Rari mango*	Small but very juicy and sucking variety liked by many locals	
25.	*Kapuria*	Fibreless, firm pulp, red blush at shoulder Matures in Late June, high yielder (3 quintal per tree with 10 year old)	
26.	*Hajipur Mithui*	Big sized, yellow golden in colour, heavy bearer, Very less fruit drop	
27.	*Ajgavi Sipia*	Thin stoned, long fruited with thick shoulder	
28.	*Belwa*	Fibreless, pulp consistency like *malda* very sweet and ideal fruit sized, attractive red coloured Thick skin, makes suitable for long distance transport	

Contd.

S.No.	Name of unique varieties	Distinct attributes	District
29.	*Chauaria*	Early maturity and sweet even at un-ripened	Katihar
30.	*Navras*	Fibreless, with nine type of flavour, mid maturity	
31.	*Jethua*	Earliest to mature, long and small fruit Yellow pulp with scented aroma	Purnea
32.	*Kala Pahad*	Big sized fruit with thin peel Taste is better than Calcuttia malda	
33.	*Jing Jing*	Sucking varieties, small sized with yellow pulp	

Fig.1. 'Mallika' mango (Average fruit weight 720 g), conserved by Sri Anoj Kr. Rai, Malikaur, Samastipur

Fig. 2. Mango malformation in Jamui, and custodian Farmer of West Champaran, Bihar

Fig. 3. Custodian Farmer of Ranchi, Hazaribagh and Lohardaga district, Jharkhand

Fig. 4. Custodian Farmer of Gopalganj, Siwan and Katihar, Bihar

Fig. 5. Custodian Farmer of Samastipur, East Champaran districts, Bihar
[Note: All of the above farmers are conserving more than 10 varieties in their orchard, and standing near the tree of unique varieties they grow and conserve]

The farmers' responses to the survey questions underscore the importance of diversity as a mechanism for not only meeting the multiple needs of farmers, but also for increasing fruit availability for longer periods. While there was some overlap in the responses, farmers recognized that each variety reacts differently, season to season, depending on environmental conditions. Therefore, farmers seem aware that planting more varieties may assure yields which will be stabilized and maximized in due course of time in comparison to growing a single variety. Farmers mentioned several main motivational factors to maintain mango diversity: love for maintaining many varieties at the same time, interest in a maximum number of differently tasting fruits, regular source of income, recognised social status/prestige and availability of fruit, fuel and timber as a source of earning during emergency. Custodian farmers, apart from playing a critical role in conserving the rare varieties, act as local guides to disseminate the good practices. They also play as scions donors of local varieties to the community and share their traditional knowledge (Gajanana *et al*., 2015). One farmer of the Patna district (growing >11 cultivars of mango) practices grafting and has hobby of planting new trees. He has been distributing 20-25 plants every year to the neighbours, free of cost. He also shares meteorological information received as messages on his mobile and disseminates traditional knowledge and newer information related to marketing.

In the survey, we identified a maximum number of orchardists of *Darbhanga* (25) and *Samastipur* (16), *East Champaran* (15) and *Katihar* (15) district having more than 10 varieties in their orchard. Through the survey, we identified 22 orchardists who have more than 15 varieties in their orchard. Most of the mango growers of Jharkhand are conserving *on-farm* mango biodiversity using organic inputs, in Bihar there are fewer. Among 210 farmers of thirty four districts of Bihar and 8 districts of Jharkhand, the maximum number of varieties of mango is grown and maintained by Sri. Vinod Kumar Rai of *Jagdishpur*, Samastipur (36 in total) and Sri. Abdul Rahim of *Kumarbagh*, West Champaran (28 in total) (Table 1) and Sri Harendra Kumar Singh of Makhdumpur, Bihta, Patna. The later has been identified as torch bearer for farmers who needs information on e-marketing, weather forecast, skilled grafter/budder. This custodian farmer encourages farmers to grow *Jamun* and *Datepalm* as per land availability. Sri. Anoj Kumar Rai, Malikaur, Pusa, Samastipur are growing more than 25 types of fruit trees in their orchard including temperate and arid fruits, do self marketing and have the hobby of growing maximum number of varieties.

The major problems of orchards of Bihar found in the survey are young plant mortality, grazing of small plants by goat and blue bull, thefts of fruits, poor irrigating facility due to deep water table, drying of '*Sipia*' mango, dieback, fruit drop, burl disorder, monkeys (stealing fruit), termites, mealy bugs, stem borers, irregular bearing and lack of marketing of rare varieties. In Jharkhand, the main problems are black tip, hailstorm, mango malformation and fruit drop. The major problems affecting of mango orchards in West Champaran were fruit borers. Mango malformation was found to be severe in *Jamui* of Bihar and *Lohardaga* of Jharkhand and severe labour scarcity for various agricultural operations were mentioned in both the states.

Farmers reported that traditional varieties show superior performance in terms of pest resistance, flood resistance and have better adaptation to the variable production environment. Farmers in the study area have a deep knowledge about the characteristics of the traditional varieties and their performance under different

environmental stresses. Apart from *Sukul* mango (most suited for pickle making in Bihar), *Lal Malda*, *Dudhia Malda* are also used for pickle making in Patna. *Jarda* and *Bombai* are main sucking varieties, *Malda* is the main table variety and *Sukul* and *Fazli* are pickle varieties (see Table 3 for unique traits of mango varieties).

There is need of grouping of various cultivars based on mopho-physio-bio-chemical and molecular characterization and screening for breeding for improvement of commercial cultivars. Some of the superior germplasm can be directly release as variety for the region. The existing unique variety maintained by growers must be assessed for quality parameters to harness for breeding purposes and export demand. Singh's *et al*. (2015) study revealed that great variability exists among different mango seedling progenies and this can be exploited for the selection of elite genotypes in the future after evaluating their performance.

National policy support in the form of establishing a network of custodian farmers and upgrading of skill (e.g. grafting, management of genetic resources) and registration of farmers' varieties will go a long way to ensuring conservation of mango diversity on sustainable basis (Gajanana *et al*., 2015). The yield from traditional varieties is low but farmers still continue to cultivate them, even as they adopt newer varieties. The main reason is that compared to modem varieties the yield from traditional varieties is reliable and prevents the risk of yield failure (Harwood, 1979). The traditional varieties can serve as important source of genes for developing improved varieties. Swaminathan (1998) emphasized the urgent need to encourage and strengthen (mango) field gene bank such as describe here that already can be found at the village level for *in-situ* on-farm conservation.

Conclusion

One of the strategies of conserving diversity, *on-farm*, is identification of custodians and extending support to them. These farmers have maintained the diversity without any formal support. The farmers also choose varieties for conservation depending upon the type of motivation. Furthermore, while all custodians maintain diversity, a good number of them (50-60%) also promote and adapt the diversity. A concerted action is needed to locate the most useful variation in the entire genepool, to collect and evaluate it efficiently, and to exploit the most useful diversity both by direct use as well as through hybridization.

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RESEARCH ARTICLE

Citrus Diversity Fair: A Means of Locating Citrus Species Diversity and Selection of Superior Clones of Local Importance

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A citrus diversity fair was organized on 5th November 2011 by National Research Centre (NRC) on Litchi, Muzaffarpur in collaboration with Lt. Amit Singh Memorial Foundation, New Delhi at Mahmada, Bihar of Pusa Site of the UNEP/GEF Project to know the extent of citrus variability and selection of superior genotypes of citrus. Considerable diversity of citrus is observed in the study area due to conducive climate. A total of 109 farmers displayed 135 samples of nine *Citrus* species. Richest variability was displayed for pummelo (out of the 135 samples displayed, 127 belonged to pummelo). This fruit species showed rich natural variability due to its out-breeding habit and also the pummelo plants are raised traditionally through seeds in this area. Sixty-seven plants could be validated in the farmer's fields and only those samples were included in these studies. Based on morpho-physico-chemical traits, *viz*; fruit size, fruit shape, flesh colour, TSS (^{0}Brix), acidity percentage, number of seeds/fruit, rind thickness, juice percentage, taste, etc., 11 accessions, *viz;* 9, 62, 8, 17, 4, 6, 31, 39, 44, 51 and 52, were identified as superior genotypes, which could be multiplied and distributed to the farmers for quality fruit production of pummelo.

Key Words: Bio-diversity fair, *Citrus maxima* L., Clone, Genetic variability, Local seedling population, Pummelo

Introduction

Citrus is one of the most popular fruit crops and cultivated in around 140 countries. The genus has its centre of diversity in Northeast India, Malayan Archipelago, China, Japan and Australia (Swingle and Reece, 1967). In India, many *Citrus* species including mandarin (*Citrus reticulata*), sweet orange (*C. sinensis*), acid lime (*C. aurantifolia*) and lemon (*C. limon*) are grown commercially, whereas grapefruit (*C. paradisi*), pummelo (*C. maxima*), galgal (*C. pseudolimon*), citron (*C. medica*), etc. are grown in home gardens or mixed orchards for domestic consumption (Sharma *et al*., 2004). Most of these non-commercial types are grown as seedlings, and citrus being a cross-pollinated crop, considerable variability in the seedling population is observed. This genetic diversity is important from global as well as local point of view and is traditionally maintained in home gardens. The wealth of local citrus genetic diversity by and large remains non-collected.

Breeding of fruit crops is a lifetime work for any plant breeder because of the perennial nature. The variability in fruit trees, growing in home gardens and mixed orchards has been observed for a very long time for undertaking selection, exchange and breeding by fruit growers and villagers (Zeven, 1998). On farm conservation in collaboration with custodians of diversity is a cost-effective method. Genetic improvement in horticultural crops can be done through identification of elite materials (plus trees) available in the community followed by their characterization, evaluation and multiplicationfor community benefits (Sthapit *et al*., 2006; Sthapit *et al*., 2013; Sthapit *et al*., 2016). Diversity fair was initiated as a common tool for raising awareness among public on the importance of conserving diversity (Tapia and Rosa, 1993). The method is presently being used for identifying superior cultivars/accessions, promoting exchange of traditional knowledge and planting materials amongst farmers, identification of diversity rich areas and selection of elite materials (Sthapit *et al*., 2003; Gajanana

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et al., 2015). The present study with bio-diversity fair as a tool was undertaken with the objectives to raise citrus biodiversity awareness among rural communities, locate genetic diversity, assess extent of diversity, and identify elite materials for mother plant selection in order to introduce superior clones in the local production systems.

Citrus fruits and particularly pummelo are grown in almost every household of the study area in the eastern Bihar state of India and the fruits are mainly used for the holy festival "*Chhath Pooja*". Due to the poor quality of the seedling borne fruits, pummelo is not very much popular as a table fruit in the area under study. The identified clones from this diversity fair shall contribute in consolidating the genetic base of *Citrus* species which in turn might be helpful in improving the livelihood and nutritional security of the local people.

Materials and Methods

Selection of Site

The communities which were studied are based at Pusa (Samastipur), Bihar the site of study of the UNEP/ GEF project. The project aimed at conservation and sustainable use of cultivated diversity in the Samastipur district of Bihar in India. The climate of Pusa is humid and subtropical, with maximum and minimum average temperatures ranging from 31ºC to 19ºC respectively, and with an average annual rainfall of 1200 mm, distributed over 35–40 rainy days during the monsoon season. It is located at latitude of 25º46 N and longitude of 86º10 E with an altitude of 53m. Four project communities/ villages, form part of Pusa site namely *viz*; Mahmada, Jagdishpur, Dhobgama and Murliyachak. The Table 1 shows site characteristics data of these communities. Initially, the focus group discussion, four cell analysis and baseline survey were carried out to assess the citrus diversity in these project communities of Pusa site and it was observed that considerable amount (richness) and distribution (evenness) of citrus tree diversity is being maintained on-farm. Farmers are maintaining and using diverse traditional fruit tree diversity for their own welfare and benefit (Singh *et al*., 2016a). It is indicative of the cultural and religious importance of the citrus diversity and its subsequent conservation by the local peasant farmers.

Citrus Diversity Fair

A citrus diversity fair was organized at Mahmada (Pusa, Samastipur, Bihar), under the Project, on 5th November 2011. The methods of diversity fair were reviewed from the literature (Tapia and Rosa, 1993; Sthapit *et al*., 2003; Adhikari *et al*., 2012; May *et al*., 2014) and relevant checklists were developed for community consultations. Several discussions were held with different community groups regarding the objectives, venue and the time of the fair and based on the responses of the villagers, date and venue of the diversity fair was fixed and communicated to all the participating farming communities. The fair was organized in the premises of a local school to stimulate awareness among school children as an additional and fruitful outcome. An enthusiastic response was received from all the participating communities. A total of 109 farmers exhibited 135 samples of citrus diversity and 260 farmers visited the fair and perused the displayed diversity. The different species exhibited were sweet orange (*Citrus sinensis*), pummelo (*C. maxima*), acid lime (*C. aurantifolia*), lemon (*C. limon*), rough lemon (*C. jambhiri*), Rangpur lime (*C. limonia*), Cleopatra mandarin (*C. reshni*), galgal (*C. pseudolimon*) and sweet lime (*C. limettioides*).

Sample Collection

The fruit samples were collected in the fruit diversity fair. Based on visual observations and organoleptic

Table 1. Site characteristics and community richness of citrus diversity measured by four cell analysis (Source: Gajanana *et al*., 2014)

Characteristics	Mahmada	Jagdishpur	Dhobgama	Murliyachak
Total number of households	1124	500	744	200
Total fruits HHs	169	60	250	55
Community citrus richness	6	3	3	3
Common Citrus species	Acid lime$^{\delta}$	Acid lime$^{\delta}$	Acid lime$^{\delta}$	Acid lime$^{\delta}$
Rare Citrus species		Rough Lemon$^{\beta}$/Lemon$^{\Omega}$, Sweet lime*		Lemon$^{\Omega}$
Unique *Citrus* species	Pummelo**	Pummelo**	Pummelo**	Pummelo**

↑*Rare means few households and few trees; Unique means many households and few trees; Common means many households and many trees;* δ= *C. aurantifolia* L. (Acid lime; Kagzi nimbu); β =*C. jambhiri* (Rough lemon); Ω = *C. limon* (Lemon);*= *C. limettioides* (Sweet lime; Mitha nimbu) and ** *C. grandis/maxima* (Gagar/Bhogate)

taste by a group of experts, comprising of scientists, State Horticulture Officer and farmer's representatives, best fruit samples were identified. The genetic diversity collected through the diversity fairs was monitored at farmer's fields to validate the results of the fair and to characterize these landraces for physico-chemical characteristics. In the follow up programme, out of 127 exhibited samples of pummelo, 67 types of pummelo could be precisely located growing in the farmer's fields. After the confirmation of clones in the field, two fruits from each of these 67 samples were analysed for different physico-chemical characteristics *viz;* fruit colour, weight, length, breadth, presence or absence of oil glands, rind thickness, flesh colour, number of segments and seeds, TSS (ºBrix) and acidity.

Fruit Characteristics Study

The external characters of fruit *viz*; height and diameter were measured by Vernier callipers and fruit weight was measured by electronic digital balance. The qualities of fruit like peel, pulp and juice percentage were measured based on fruit weight. Titrable acidity (TA) was measured using the titration method (AOAC, 1989). The taste was judged by an organoleptic test (tasting by eight persons in the laboratory and giving the scores for edibility and acceptability). The TSS was measured with the help of hand-held digital refractometer (Singh, 2016). The juice percentage, TSS: acid ratio and fruit length: breadth ratio was calculated following standard procedures.

Selection of Elite Clones

Selection of superior clones was carried out based on the evaluation of fruit characters and the number of desirable characters such as fruit size, rind thickness, T.S.S., pulp colour, juice percentage and flavour. These characters are used as indicators for edible fruits and/ or for religious/ cultural utilization of the fruits. The preference of farmers is for sweet taste, red pulp and medium-sized fruits. The quality genotypes were adjudged by the number of desirable characteristics possessed by them.

Statistical Analysis

The experiment was conducted in Completely Randomized Design (CRD) with two replications. Data were subjected to one-way analysis of variance. *P* values ≤ 0.05 were considered as significant. All the seventeen physico-chemical characteristics were converted into bi- and multi-state code. Cluster analysis was performed using simple matching coefficient method using NTSYS ver. 2.10e software (Rohlf, 2000) based on unweighted pair group method with arithmetic average (UPGMA). Principal Components Analysis (PCA) of all clones was done by NCSS 2007 v 07.1.18 (Hintze, 2007).

Results

Maximum variability was represented in the case of pummelo at the citrus diversity fair, which was further validated by variability in the farmer's fields. Out of 127 pummelo samples collected during the diversity fair, only 67 were confirmed in the farmer's fields and one of the main reasons behind low on-field confirmation was that the farmers already harvested the fruits and marketed/ distributed for the festival of *Chhath Pooja*, the major reason for which the pummelo plants are maintained. A wide range of variability was observed amongst the pummelo plant samples for various characteristics observed. The fruit colour varied between 1-6 with 1 being the green and the 6 being the dark yellow. The fruit weight varied between 0.60 (Sample/clone no. 42) and 2.50 kg (Sample/clone no. 2). The range for fruit length was from 11.25cm to 23.30 cm in clone no. 8 and 12, respectively and the fruit width varied between 12.05 (in clone 39) and 23.90 cm (in clone 2). The flesh colour varied from white to dark red on a scale of 1 (white) to 6 (dark red). Rind thickness also exhibited variability and ranged from 0.80cm (in clone 62) and 3.75 cm (in clone 2). The number of segments/fruit varied between 11.50 (in clone 31) and 19.50 (in clone 16). The T.S.S. varied between 7.95 (in clone 14) and 12.85 ºBrix (in clone 39).

Seedlessness is an important character in context of edibility and consumer preference, however, no clone with seedless fruits could be found among the collected genotypes. The range for seeds/fruit varied between 17.50 (in clone 33) to 168.00 (in clone 16). The juice sacs could be classified in to either soft or hard categories. Acidity also exhibited wide variation amongst the selected clones with a minimum of 0.32% in clone no.46 and a maximum of 1.74% in clone no.14. From the ratio of fruit length and breadth, it is evident that the fruits were either elongated, round or flattened. Seed size and number were very small with a 100-seed weight of 23.14g (in clone 33) to bold with a 100-seed weight of 68.47 (in clone 21). Juice percentage also exhibited a wide range, 17.24 (in clone 4) to 45.86 (in clone 20). TSS: acid ratio varied between 5.44 (in clone 14) to 32.58 (in clone 46) (Table 2).

Table 2. Variability of the fruit characteristics in the collected (during diversity fair) seedling clones of pummelo

S. No.	Characteristics	Range (Clone No.)	Mean	SE (m)	SE (d)	CV (%)
1.	Fruit colour***	1.000 (7)-4.000 (67)	2.582	0.335	0.473	18.325
2.	Fruit weight (g)	0.632 (42)-2.497 (2)	1.350	0.127	0.179	13.260
3.	Fruit length (cm)	11.250 (8)-23.300 (12)	15.818	0.778	1.100	6.957
4.	Fruit width (cm)	12.050 (39)-23.900 (2)	16.468	0.851	1.203	7.306
5.	Flesh colour*	1.000 (14)-6.000 (66)	4.642	0.299	0.423	9.117
6.	Rind thickness (cm)	0.800 (62)-3.750 (2)	1.720	0.189	0.267	15.520
7.	Segments/ fruit	11.500 (31)-19.500 (16)	14.769	0.756	1.069	7.235
8.	TSS (ºBrix)	7.950 (14)-12.850 (39)	10.672	0.387	0.547	5.127
9.	No. of seeds/fruit	17.500 (33)-168.00 (16)	91.537	19.821	28.031	30.622
10.	Nature of juice sacs**	1.000 (1)-2.000 (66)	1.619	0.162	0.229	14.114
11.	Acidity (%)	0.320 (46)-1.736 (14)	0.596	0.056	0.080	13.399
12.	Fruit length: breadth	0.700 (65)-1.195 (12)	0.963	0.043	0.060	6.262
13.	100 seed wt. (g)	23.140 (33)-68.470 (21)	45.180	5.228	7.393	16.364
14.	Juice weight/fruit (g)	227.530 (3)-798.960 (16)	478.556	43.223	61.127	12.773
15.	Juice %	17.240 (4)-45.855 (20)	36.721	1.027	1.453	3.956
16.	TSS:Acid ratio	5.435 (14)-32.575 (46)	19.392	2.110	2.983	15.385
17.	Taste****	1.000 (14)- 4.000 (64)	2.433	0.323	0.457	18.789

* *Flesh colour*: 1 = white, 2 = light pink, 3 = pink, 4= light red, 5= red, 6 = dark red
***Nature of juice sacs*: 1= soft, 2= hard
*** *Fruit colour*: 1= Green, 2= Green Yellow, 3= yellow green, 4= yellow, 5= Dark yellow
*****Taste*: 1= Poor, 2= Good, 3= Very good, 4= Excellent

The organoleptic taste of the fruits also varied on a scale of 1-4 with 1 being the poor and the 4 being the excellent. Maximum coefficient of variation (30.62%) was recorded for number of seeds/fruit followed by taste (18.79%), fruit colour (18.33%) and 100-seed weight (16.36%), indicating a large amount of variability for these traits (Table 2). Other significantly variable traits were fruit weight, skin thickness, type of juice sacs, acidity and TSS: acid ratio on which selection can be exercised for the selection of superior clones. As far as the range for the quantitative and qualitative traits and the coefficient of variation are concerned, there exists a wide variability amongst the selected clones of pummelo and few of them can be selected for further testing in the replicated trials.

Cluster Analysis for Morpho-physico-chemical Traits

Based on the dendrogram (Fig. 1) generated based on morpho-physico-chemical data, all the 67 clones of pummelo were grouped into two major groups A and B at similarity value of 0.15. Major cluster A comprised 23.88% of studied clones and was further sub-divided into two sub-gruoups as A1 and A2 at 10.25% similarity value. Clone number 4 and 59 were found most distant the sub-groups A1 and A2, respectively. Sub-group A1 and A2 shared 37.50% and A2 62.50 % variability in clones, respectively. Major cluster B comprised most of the studied clones (76.11%). It is further grouped into two sub-groups as B1 and B2 at similarity value of 0.13. Sub-group B1 comprised 94.11% clones and divided into 8 minor groups *viz*., B1.1 to B1.8. Minor cluster B1.1 and B1.4 each comprised 12 clones. In minor cluster B1.1, clone number 5 and 61 exhibited 100% genetic similarity. Minor cluster B1.3 only comprised clone number 8 which was presented as an out-lier in the group (Table 3).

Principal Component Analysis (PCA) for Morpho-physico-chemical Traits

The result of the PCA showed that first eight components accounted for 99.99% of the total variability (Table 4). The fruit colour accounted for 93.38% while the fruit weight accounted for 5.65 % of the total variation. Thus, these traits should be given greater emphasis while making selections. PCA analysis successfully separated out different clusters of pummelo clones. The clone nos. 10, 16, 20, 23, 28 and 35 were scattered into first half of the coordinate whereas, clone nos. 3, 4, 33, 41, 44 and 64 were presented separately in second half axis of the coordinate (Fig. 2). The clone nos. 13 and 61 showed more relatedness (Fig. 1) and PCA results also revealed the same (Fig. 2). Moreover, clone no. 4 presented as an out group in cluster analysis was also confirmed to be a separate group by PCA analysis (Fig. 1).

Selection of Elite Clones

For the selection of the elite clones of pummelo, the clones were grouped in different groups for having desirable scores for the qualitative and quantitative traits (Table 5). The desirability of the quality was decided on the basis of participatory four cell analysis (Sthapit *et al*., 2006) and with farmer group discussion, 12 traits were identified as desirable for this grouping

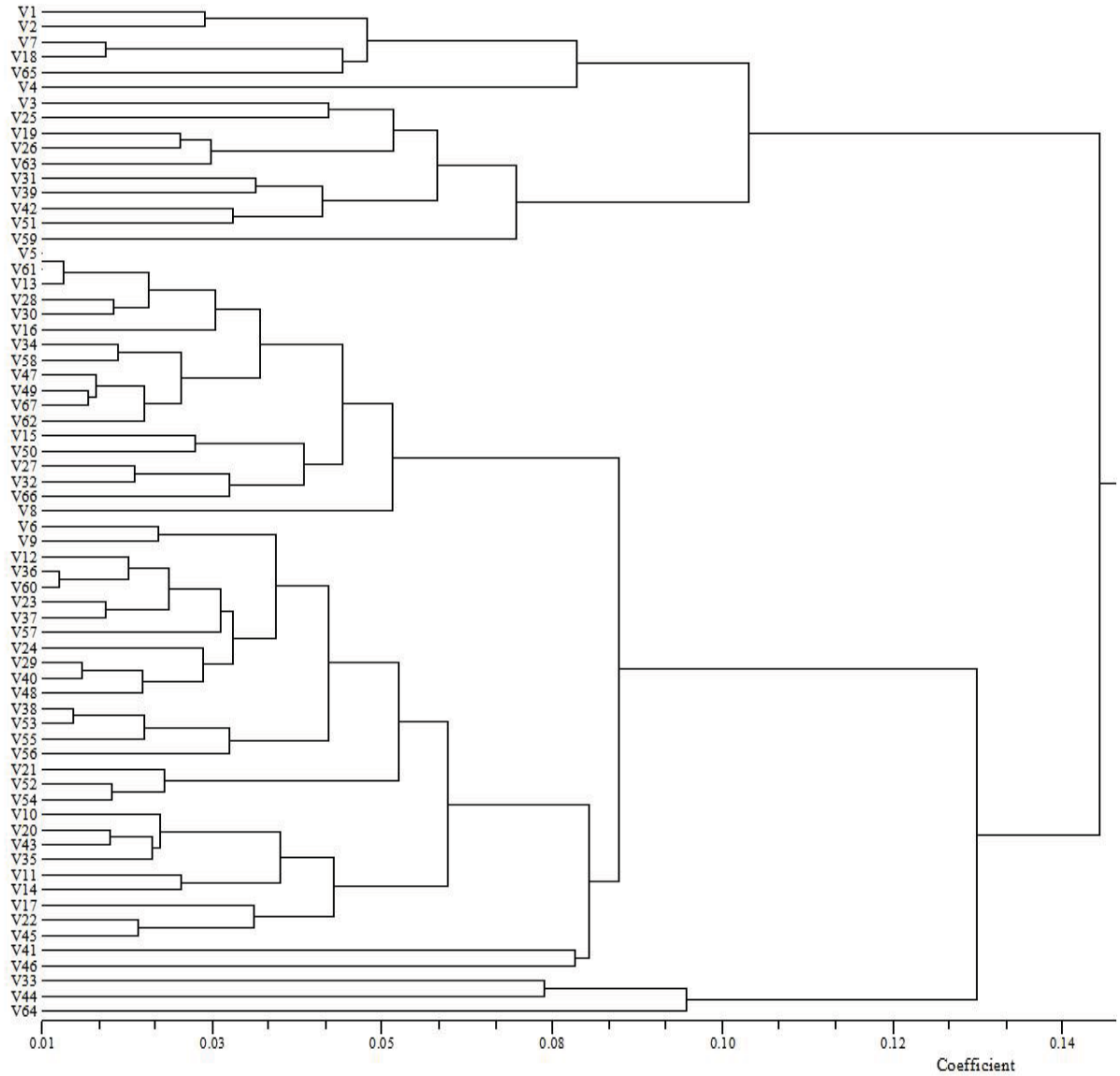

Fig. 1. Dendrogram of sixty-seven selected clones of pummelo based on morpho-physico-chemical traits using the UPGMA method

Table 3. Cluster details of 67 selected clones of pummelo using various morpho-physico-chemical parameters

Cluster Name and Percent clone	Sub-cluster	Total no of clones	Percent clones in sub-cluster	Clone number
A (23.88%)	A1	6	37.50	1, 2, 4, 7, 18, 65
	A2	10	62.50	3, 19, 25, 26, 31, 39, 42, 51, 59, 63
B (76.11%)	B1	48	94.11	
	B1.1	12	25.00	5, 13, 16, 28, 30, 34, 47, 49, 58, 61, 62, 67
	B1.2	5	10.41	15, 27, 32, 50, 66
	B1.3	1	2.08	8
	B1.4	12	25.00	6, 9, 12, 23, 24, 29, 36, 37, 40, 48, 57, 60
	B1.5	4	8.33	38.53, 55, 56
	B1.6	3	6.25	21, 52, 54
	B1.7	9	18.75	10, 11, 14, 17, 20, 22, 35, 43, 45
	B1.8	2	4.16	41, 46
	B2	3	5.88	33, 44, 64

Table 4. Principal Component Analysis among sixty-seven selected clones of pummelo showing the correlations of the first eight principle components (Eigen value >1) with the variables

Principal Component	Fruit Traits	Eigen-Value	%Variance	%Cumulative Variance
PC1	Fruit color	15256.31	93.38	93.38
PC2	Fruit weight (g)	923.33	5.65	99.04
PC3	Fruit length (cm)	83.71	0.51	99.55
PC4	Fruit width (cm)	42.70	0.26	99.81
PC5	Flesh color	23.10	0.14	99.95
PC6	Skin thickness(cm)	2.60	0.13	99.97
PC7	No of segments	1.49	0.02	99.98
PC8	TSS (%)	1.39	0.01	99.99

Table 5. Pummelo clones identified for different characteristics

Fruit character	Selected number of clones	Specific Clone selected
1. Fruit size (500-1000g)	14	3, 8, 17, 25, 26, 31, 39, 41, 42, 44, 46, 51, 59, 64
2. Flesh colour (Dark Red->5.00)	18	1, 4, 5, 6, 9, 16, 17, 22, 27, 28, 38, 43, 45, 50, 61, 62, 63, 66
3. T.S.S. (>11.50%)	11	2, 8, 9, 17, 28, 31, 34, 39, 51, 55, 64
4. Acidity (≤0.50 %)	20	1, 3, 4, 6, 8, 9, 10, 21, 22, 24, 33, 37, 46, 52, 54, 57, 59, 63, 65, 66
5. Number of seeds/fruit (<100)	42	11, 14, 22, 33, 44, 64, 3, 6, 8, 9, 10, 12, 17, 20, 24, 25, 29, 35, 36, 38, 39, 40, 41, 42, 43, 45, 46, 48, 49, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 62, 66, 67
6. Fruit length: breadth (0.96-1.05)	20	1, 4, 7, 9, 13, 19, 20, 21, 22, 25, 29, 38, 43, 45, 49, 54, 55, 56, 60, 62
7. Rind thickness (<1.00 cm)	8	9, 17, 29, 31, 39, 44, 51, 62
8. Fruit colour (>3.00)	16	6, 9, 26, 27, 28, 31, 33, 36, 48, 49, 52, 55, 59, 62, 65, 67
9. 100 Seed weight (< 40.00g)	18	1, 2, 3, 4, 8, 9, 11, 14, 16, 33, 39, 41, 42, 44, 48, 50, 62, 65
10. Juice % (>40.00%)	24	5, 6, 8, 9, 16, 17, 20, 21, 23, 27, 28, 29, 31, 40, 41, 42, 44, 46, 51, 52, 54, 61, 62, 66
11. TSS:Acid ratio (>20.00)	21	1, 4, 6, 8, 9, 10, 21, 22, 33, 37, 44, 46, 52, 53, 54, 57, 59, 62, 63, 65, 66
12. Taste (>3.00)	14	2, 4, 8, 9, 17, 18, 28, 31, 34, 39, 51, 52, 55, 64

were fruit size (500-1000g), flesh colour (Dark red > 5.00 score), T.S.S. (>11.50 ºBrix), acidity (<0.50%), no. of seeds/fruit (<100), fruit length : width (0.96-1.05), rind thickness (<1.00cm), Fruit colour (a score of >3.00), 100 seed weight (<40.00g), juice (>40.00%), TSS : acid (>20.00) and taste (a score of >3.00). Better genotypes of fruit trees can be selected by evaluating the fruit quality. Fruit weight, peel thickness, juice %, TA% and TSS are the major parameters to determine the quality of pummelo fruits. Therefore, elite genotypes of pummelo were selected on the basis of scoring of these fruit parameters.

Plant traits of these genotypes are almost similar, but the fruit physico-chemical characters exhibited variation. After this grouping, the clonal selection was made, and those clones were selected which were possessing more desirable fruit traits.

In this study, significant variation for qualitative and quantitative traits was found in pummelo accessions identified in the citrus diversity fair. On the basis of scoring of fruit characters, total 11 elite genotypes, *viz*; clone nos. 9, 62, 8, 17, 4, 6, 31, 39, 44, 51, and 52 were selected for conservation, breeding and variety development purpose (Table 6). Out of 12 characters considered very important for the evaluation of fruit quality, clone no. 9 (Fig. 3) was possessing eleven characters followed by clone numbers 62 and 8 (8 characters), 17 (7 characters) and clone numbers 4, 6, 31, 39, 44, 51, 52 (6 characters). Thus, it was concluded that diversity fair plays an important role for the identification and selection of elite genotypes of fruit crops for further conservation and utilization directly as superior clonal varieties or as breeding materials for the development of fruit crops.

Discussion

The diversity fairs are effective for documenting and collecting germplasm along with the associated knowledge pertaining to the use of fruits for edible and cultural purposes. They serve as useful tools of practical significance for assessment and collection of diversity of a geographic area or ethnic group. It is a visual method of assessment, and to locate diverse genetic materials, and custodians of diversity across locations (Sthapit *et al.,* 2012). A close interaction with farmers and communities

Table 6. Pummelo clones with six or more desirable fruit characteristics

S. No.	Clone No.	Farmer's name	Desirable fruit characteristics*
1	9	Mohammed Ishaque, Govindpur Chhapra	2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 (11)
2	62	Reet Lal Sahni, Mushahari	2, 5, 6, 7, 8, 9, 10, 11 (8)
3	8	Joginder Bhagat Shah, Govindpur Chhapra	1, 3, 4, 5, 9, 10, 11, 12 (8)
4	17	Ram Kumar Rai, Dhobgama	1, 2, 3, 5, 7, 10, 12 (7)
5	4	Sudhir Kumar, Mahmada	2, 4, 6, 9, 11, 12 (6)
6	6	Sabdi Devi, Mahmada	2, 4, 5, 8, 10, 11 (6)
7	31	Upender Pathak, Malinagar	1, 3, 7, 8, 10, 12 (6)
8	39	Roshan Kumar Thakur, Malinagar	1, 3, 5, 7, 9, 12 (6)
9	44	Kamal Rai, Mahmada	1, 5, 7, 9, 10, 11 (6)
10	51	Baleshwar Ram, Bhuskaul	1, 3, 5, 7, 10, 12 (6)
11	52	Krishna Shah, Gundi Bandra	4, 5, 8, 10, 11, 12 (6)

*1. *Fruit size* (500-1000g), 2. *Flesh colour* (Dark Red), 3. *Rind thickness* (<1.00 cm), 4. *T.S.S.* % (>11.50%), 5. *Acidity* (0.31-0.50%), 6. *Number of seeds/fruit* (<100 seeds/fruit), 7. 100 seed weight (<40g), 8. *Fruit length: breadth* (0.96-1.05), 9. *Fruit colour* (>3.00), 10. *Juice %* (>40.00), 11. *TSS: acid ratio* (>20.00), 12. *Taste* (>3.00)

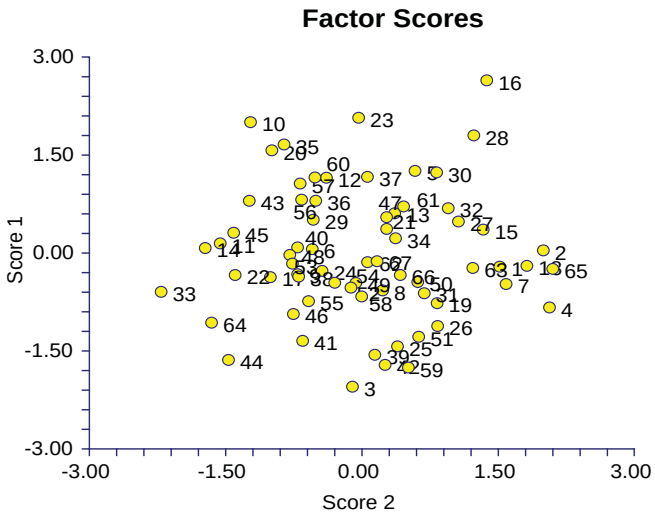

Fig. 2. A principal components analysis (PCA) scatter plot of 67 indigenous seedling clones of pummelo using seventeen morpho-physico-chemical parameters

also motivated them to participate in the germplasm conservation efforts (Mal *et al*., 2011).

The breeding of fruit trees is a long-term activity mainly because of the seedling juvenility. Most of the fruit crops are out-breeders and maintain heterozygosity. As pummelo is grown from seedlings in the study area, a lot of genetic variability can be expected that can be exploited for superior genotype selection. This variability can be explored by field surveys, focused group discussions with the farmers or through organization of diversity fairs as done in the present study. Nine *Citrus* species and varieties were displayed during the citrus diversity fair compared to five *Citrus* species in baseline survey indicate that diversity fairs encourage farmers and farming communities who display rare and unique species and diversities (Upadhyay *et al*., 2012). Selection of superior varieties is rewarding in pummelo owing to its genetic traits; the seeds of most citrus tend to reproduce the traits of the mother plant due to nucellar embryony, but pummelo seeds are monoembryonic and give rise to plants with entirely new horticultural traits. This produces a pool of variability.The results of this study revealed that fruit morphological and physico-chemical characterization may be key in in distinguishing cultivar groups within pummelo population also for selection of potentially better genotypes by the breeders as well as the farmers. Similar observations were made in the clonal selection of mango from the farmer's fields by Singh *et al*. (2016b). Cameron and Soost (1961) stated that pummelo species exhibits considerable variability due to sexual recombination and self-incompatibility. The present study confirmed these findings, re-emphasizing the importance of morphological characterization for improvement through selection and as a base for further studies involving biotechnological and biochemical tools as reported by Bozokalfa *et al*. (2009) and Martasari *et al*. (2012). It was emphasized that high degree of variability in pummelo is due to fruit traits. Further, use of fruit morphology is considerably effective for the recognition of cultivar (Susandarini *et al*., 2013).

Shrestha *et al*. (2012) reported that fruit traits, especially juice, TSS and TA were important parameters for the selection of elite genotypes of citrus trees, also confirmed by the present study. Elite genotypes of citrus fruits can be selected through the assessment of tree morphological traits and consumer's preference. It was reported earlier that farmers highly preferred

Fig. 3. Mature fruits of some of the identified elite seedling clones of pummelo collected during citrus diversity fair

the quality rather than size and yield of the fruits in pummelo (Paudyal and Haq, 2008) whereas consumers prefer the quality of acid lime as round, thin-skinned, yellow colour, juicy and medium size (Dhakal *et al*., 2003), indicating the selection and consumption are governed by farmers and consumers, respecitvely.

The monitoring of genetic diversity at community level helps to develop options for adding value to local crops. Knowing the extent and distribution of the genetic diversity of selected crops over space and time is one of the important outputs of this study. From this citrus diversity fair, it is expected that farmers and communities felt encouraged and appreciative of the efforts and interest to conserve citrus trees. Diversity fair followed by four cell analysis and *in situ* evaluation resulted in the identification of 11 superior clones of pummelo. These studies are in agreement of the previous studies in citrus where the Midsweet, Sunstar and Gardner varieties of sweet orange were selected as the naturally occurring seedling cultivars (Hearn, 1988). The citrus varieties presently grown are mainly the selections from bud-sport mutations and chance seedlings (Pena and Navarro, 1999).

Owing to the presence of natural variability, selection of superior varieties can be developed by this participatory method, which will encourage the cultivation and consumption of pummelo for improving the health and economic status of the farmers, maintaining these

plants. The most important is on-farm conservation for sustainable conservation and utilization of pummelo.

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RESEARCH ARTICLE

Validation of Functional Markers Associated with Genes for Fragrance in Rice (*Oryza sativa* L.)

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The presence of aroma determines the market price of rice and is associated with its local, cultural and national identity. The present study was carried out to validate five fragrance linked functional markers and to evaluate the fragrance locus based molecular diversity among the genotypes of rice. The experimental material consists of 24 genotypes of rice including both aromatic and non-aromatic indica and japonica types. None of the markers was found to differentiate all the fragrant genotypes from the non-fragrant ones with 100% efficacy. The markers could not differentiate fragrant genotypes like Mushk Budgi, Kamad, Kalanamak and Jeera Battis, from non-fragrant ones. Moreover, these fragrant genotypes were clustered with non-fragrant ones. This supports the existence of some other gene responsible for fragrance other than *badh2*, thereby indicating that aroma in rice is being governed by two or more genes. This also reveals the scope for development of more markers through fine mapping of large number of genotypes or through association mapping for differentiation of aromatic and non-aromatic rice.

Key Words: *Badh2*, 2AP, Fragrance, Functional markers, Rice

Introduction

Rice serves as the main staple food for half of the world population and two-third of Indians depend on rice for their survival. The quality considerations in this crop assume enhanced importance, especially in the countries which are self-sufficient in their production. As living conditions are steadily improving, human demand for high quality rice is continuously on increase. This demands in incorporation of preferred grain quality features as the most important objective next only to yield enhancement (IIRR, 2015). Among the various quality traits in rice, the presence of aroma determines its market price and is associated with local, cultural and national identity (Kovach *et al.,* 2009). Jasmine and basmati rices with distinct aroma are highly preferred by consumers throughout the globe.

Aroma is a highly complex trait and more than one hundred volatile aromatic metabolites are responsible for its expression. However, only a handful of these metabolites are considered to influence rice aroma significantly (Mathure *et al.,* 2014). Among these, 2-acetyl-1-pyrroline (2AP) is considered to be the principal component associated with a popcorn-like aroma in rice (Lorieux *et al.,* 1996). 2AP has a very low odour threshold and hence can influence the aroma phenotype and be detected by consumers at very low concentrations (Nadaf *et al.,* 2006). The compound is produced through a single recessive allele (*fgr*) at a locus on chromosome 8 (Lorieux *et al.,* 1996; Chen *et al.,* 2006), which corresponds to the gene that encodes betaine aldehyde dehydrogenase (*BADH2*). An 8-bp deletion in exon 7, introducing a premature stop codon upstream of key coding regions, makes this gene nonfunctional (*badh2*), and consequently the mutant *badh2* transcript leads to 2AP accumulation in aromatic rice (Hashemi *et al.,* 2013). Based on this locus, several PCR-based markers have been developed making its detection inexpensive, simple and rapid. However, most of the markers identified are located physically away from the gene and therefore may or may not be efficient in marker-assisted selection (MAS) for aroma. Although some functional markers have also been developed based on sequence variations within the *fgr* gene (Amarawathi *et al.,* 2008; Shi *et al.,* 2008; Sakthivel *et al.,* 2009), their evaluation in Indian aromatic germplasm has not been done so far. Moreover, these markers have been

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Table 1. Genotypes used in the present study.

S. No.	Genotypes	Origin	Fragrance	Remarks
1.	Jaya	Punjab	None	Released variety (Indica)
2.	NDR-359	Uttar Pradesh	None	Released variety (Indica)
3.	Sarjoo-52	Uttar Pradesh	None	Released variety (Indica)
4.	Basmati-370	Punjab	Strong	Traditional basmati (Indica)
5.	Taraori Basmati	Haryana	Strong	Traditional basmati (Indica)
6.	Type-3	Uttarakhand	Strong	Traditional basmati (Indica)
7.	Dehradun Basmati-1	Uttarakhand	Strong	Traditional basmati (Indica)
8.	Dehradun Basmati-2	Uttarakhand	Strong	Evolved basmati (Indica)
9.	Mushk Budgi	Jammu & Kashmir	Moderate	Landrace (Japonica)
10.	Kamad	Jammu & Kashmir	Moderate	Landrace (Japonica)
11.	Quadir Beigh	Jammu & Kashmir	None	Landrace (Japonica)
12.	Mehvan	Jammu & Kashmir	None	Landrace (Japonica)
13.	Begum	Jammu & Kashmir	None	Landrace (Japonica)
14.	Mazha	Jammu & Kashmir	None	Landrace (Japonica)
15.	Adam Chini	Uttar Pradesh	Strong	Landrace (Indica)
16.	Badshah Bhog	Assam	Strong	Landrace (Indica)
17.	Juhi Bengal	West Bengal	Strong	Landrace (Indica)
18.	Kalanamak	Uttar Pradesh	Strong	Landrace (Indica)
19.	Jeera Battis	Uttar Pradesh	Strong	Landrace (Indica)
20.	Tulsi Manjari	Bihar	Strong	Landrace (Indica)
21.	Hariram-48	Uttar Pradesh	Strong	Landrace (Indica)
22.	Dubraj	Madhya Pradesh	Strong	Landrace (Indica)
23.	Sonachur	Uttar Pradesh	Moderate	Landrace (Indica)
24.	Laung Choor	Uttar Pradesh	Moderate	Landrace (Indica)

developed for basmati and/or jasmine rice and their usefulness in short and medium-grained indigenous landraces have not been tested yet. The present study was carried out to validate some reported functional markers in a set of aromatic and non-aromatic rice genotypes. The level of fragrance locus based genetic diversity within this set of rice genotypes was also evaluated on the basis of these functional markers.

Materials and Methods

The study was conducted during 2015 at Central Laboratory Facility of the Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP). The site of study is situated at 25°18´N latitude and 83°03´E longitude at an elevation of 80.71 m above mean sea level. The experimental material consists of 24 genotypes of rice including aromatic, non-aromatic and temperate japonicas (Table 1). For molecular analysis, 5 reported (Rai *et al.,* 2015) fragrance related functional markers associated with linkage group 8 were used for the given set of genotypes (Table 2).

The young leaves were collected from 7-10 days old seedlings and immediately stored at -20°C till further processing. DNA extraction from these leaf samples were carried out following the CTAB extraction method (Doyle and Doyle, 1987) with few modifications. DNA quality was evaluated by electrophoresis in 0.8% agarose gel and quantification was accomplished using spectrophotometer. DNA amplification was carried out in 10 µl reaction mixtures containing 5 ng/10µl template DNA, 1×PCR buffer, 2.4 mM MgCl2, 0.12 mM dNTPs, 0.7 pM of each primer (forward and reverse) and 0.6 U of

Table 2. Allele size (bp) and polymorphism information content (PIC) of the functional markers used in the present study.

S. No.	Primer name	No. of alleles	Allele size (bp)	PIC
1.	ESP+IFAP+INSP+EAP	3	257/355/580	0.49
2.	CP04133	2	421/483	0.75
3.	nksbad2	2	82/90	0.75
4.	FMbadh2-E7	2	260/270	0.75
5.	BADEX7-5	2	95/108	0.75
6.	Total alleles	11	Average PIC	0.69

Taq DNA Polymerase. Polymerase chain reaction (PCR) was carried out in a thermal cycler (Eppendorf, USA) with the temperature cycle profile: Initial denaturation at 94°C for 4 min, 40 cycles each of 1 min denaturation at 94°C followed 30 sec annealing at 55°C to 65°C (depending on the primer used) and 1 min extension at 72°C, and finally 4 min at 72°C for the final extension. The amplified products were separated in 2.5 percent agarose gel prepared in 1×TAE (Tris-acetate-EDTA) buffer and stained with ethidium bromide. The gels were run in 1x TAE buffer at constant voltage of 65 V for 3 hours.

They were visualized and photographs taken using gel documentation instrument (BioRad). Clearly resolved and unambiguous bands for each primer were scored in the form of matrix as 1 (presence) and 0 (absence) for each genotype. The binary data matrix was then utilized to generate genetic similarity data among the genotypes.

The binary data matrix generated by functional markers was subjected to further analysis using NTSYS-pc version 2.11W (Rohlf, 1997). The SIMQUAL program was used to calculate the Jaccard's similarity coefficients. The similarity matrix was used as an input for generating the clusters. Unweighted Pair Group Method based on Arithmetic Average (UPGMA) clustering was done using SAHN module of NTSYSpc for dendrogram construction. Polymorphic information content (PIC) was estimated using the formula proposed by Nei (1973).

$$PIC_i = 1 - \Sigma P_{ij}^2$$

Where PIC*i* is the polymorphic information content of a marker *i*, P*ij* is the frequency of the j^{th} pattern for marker *i* and the summation extends over *n* patterns.

Results

The study was intended to validate five known functional markers and to evaluate the fragrance locus based molecular diversity among the genotypes of rice. All the five primers used were found to be polymorphic (Table 2) and yielded a total of 11 fragments (amplified products). The size of fragments varied from 82 bp (by marker nksbad2) to 580 bp (by allele specific primer ESP+IFAP+INSP+EAP). Maximum of three alleles were amplified by marker ESP+IFAP+INSP+EAP, while rest of the markers yielded two alleles each.

Allele specific amplification by marker ESP+IFAP+INSP+EAP generated three alleles of 257, 355 and 580 bp size. The largest fragment of 580 bp was amplified in all the genotypes. In addition, a second fragment of either 257 or 355 bp was amplified in the genotypes using this primer. In all the fragrant genotypes except, Mushk Budgi, Kamad, Kalanamak and Jeera Battis, a 355 bp fragment was amplified. The exceptional genotypes along with the non-fragrant ones amplified a 257 bp fragment, in addition to 580 bp fragment (Fig. 1). Marker CP04133 generated a 483 bp fragment in all the fragrant genotypes except Mushk Budgi, Kamad, Kalanamak and Jeera Battis. A 421 bp fragment was produced in these exceptional and in non-fragrant genotypes (Fig. 2). Marker nksbad2 generated an 82 bp fragment in all the fragrant genotypes except for Mushk Budgi, Kamad, Kalanamak and Jeera Battis. While a 90 bp fragment was produced in these exceptional genotypes and in non-fragrant ones. Marker FMbadh2-E7 generated a 260 bp fragment in all the fragrant genotypes with the exception of Mushk Budgi, Kamad, Kalanamak and Jeera Battis. While a 270 bp fragment was produced in these exceptional and in non-fragrant genotypes. Marker BADEX7-5 generated a 95 bp fragment in all the fragrant genotypes except for Mushk Budgi, Kamad, Kalanamak and Jeera Battis. These exceptional genotypes along with the non-fragrant lines produced a 103 bp fragment. Highest polymorphism information content (PIC) value of 0.75 was revealed by the primers CP04133, nksbad2, BADEX 7-5 and FM badh2-E7, while lowest PIC value of 0.49 was shown by the primer ESP+IFAP+INSP+EAP (Table 2).

The genetic similarity coefficient obtained in the present study ranged from 0.09 to 1.00 due to diversification in the genotypes at the fragrance locus. All the fragrant genotypes except Mushk Budgi, Kamad, Kalanamak and Jeera Battis, revealed the similarity coefficient of 1.00 among themselves. The non-fragrant genotypes along with Mushk Budgi, Kamad, Kalanamak and Jeera Battis, also revealed the similarity coefficient of 1.00 among themselves. The genetic similarity among the two groups (clusters) was found to be 0.09. A dendrogram based on Jaccard's similarity coefficients and constructed using UPGMA is shown in Fig. 3. In the dendrogram, 24 rice genotypes were grouped into two clusters. Clusters I and II consisted of 11 and 13 genotypes, respectively. Cluster I includes Jaya, NDR-359, Sarjoo-52, Mushk Budgi, Kamad, Quadir Beigh, Mehvan, Begum, Mazha, Kalanamak and Jeera Battis. On the other hand, cluster II includes Basmati-370,

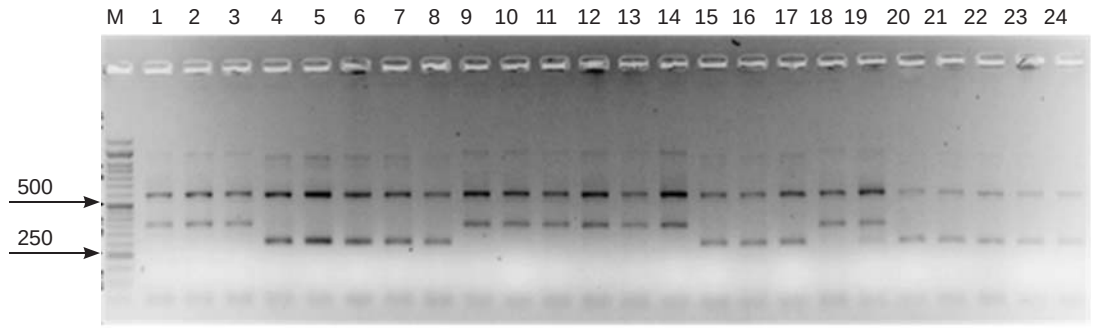

Fig. 1. Banding patterns generated by a functional marker ESP+IFAP+INSP+EAP. The lane number corresponds to the genotypes shown in Table 1.

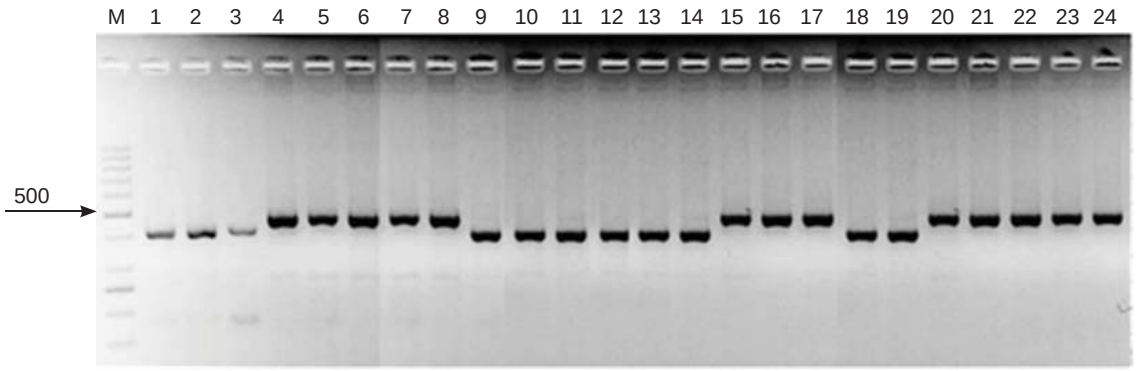

Fig. 2. Banding patterns generated by a functional marker CP04133. The lane number corresponds to the genotype shown in Table 1

Taraori Basmati, Type-3, Dehradun Basmati-1, Dehradun Basmati-2, Adam Chini, Badshah Bhog, Juhi Bengal, Tulsi Manjari, Hariram-48, Dubraj, Sonachur and Laung Choor.

Discussion

Identification of molecular markers related to grain and cooking quality features has been a matter of great interest since last several decades. The molecular markers serve several functions, including marker-assisted selection (Singh *et al.,* 2011), identification of regions affecting quantitative trait loci (Collard *et al.,* 2005) and estimation of genetic diversity (Myint *et al.,* 2012; Rai *et al.,* 2015). The practical application of MAS requires the development of tightly linked, cost effective and easy to use molecular markers. The present study illustrates the utility of molecular markers to identify the presence of *fgr* gene in rice and to establish genetic relationships among various fragrant and non-fragrant genotypes. In this study, five functional markers were evaluated for their efficacy to discriminate the fragrant and non-fragrant genotypes. Since the marker's importance is based on its proximity to a gene of interest, gene-derived functional markers are inherently more valuable than microsatellite or random sequence-based markers.

In the present study, none of the markers could differentiate all the fragrant genotypes from the non-fragrant ones with 100% efficacy. The markers could differentiate all the fragrant genotypes, except Mushk Budgi, Kamad, Kalanamak and Jeera Battis, from non-fragrant ones. Therefore, these markers can be used for identification, discrimination and MAS for aroma in traditional basmati, evolved basmati and local aromatic landraces, excluding Mushk Budgi, Kamad, Kalanamak and Jeera Battis. Mushk Budgi and Kamad are the japonica type fragrant genotypes and may have different gene for fragrance other than *badh2* locus. Rai *et al.* (2015) reported similar results while evaluating five functional markers in a set of 24 genotypes. Their studies revealed that none of the markers could differentiate fragrant and non-fragrant genotypes with 100% efficacy. This supports the hypothesis of a second gene for fragrance (Fitzgerald *et al.,* 2008) in some non-basmati aromatic genotypes (such as Kalanamak, Jeera Battis) and in aromatic japonicas (such as Mushk Budgi, Kamad).

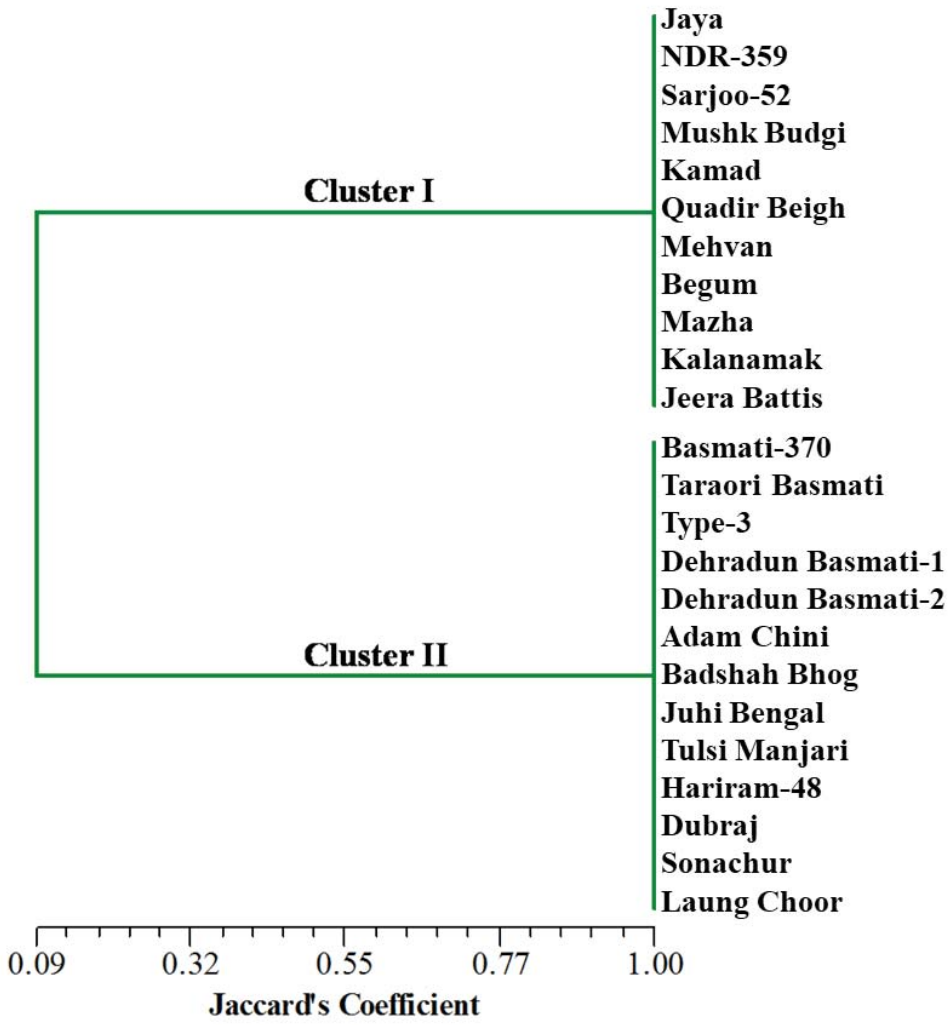

Fig. 3. UPGMA based dendrogram of 24 rice genotypes, generated by the data of five functional markers

The genetic diversity of Indian fragrant rice varieties is expected to be high due to its rich ecological diversity. In the present study, all the genotypes were grouped into two clusters corresponding to fragrant and non-fragrant clusters with few exceptions. All the non-fragrant genotypes along with Mushk Budgi, Kamad, Kalanamak and Jeera Battis were grouped into one cluster. The basmati types along with other short and medium grain fragrant genotypes were readily separated from the non-fragrant cluster. Among basmati type fragrant genotypes, all markers were monomorphic, indicating that they share a common gene for fragrance. The fragrant rices, Kalanamak and Jeera Battis, were separated distantly from all the medium-grained aromatic genotypes, most likely due to the presence of different gene for aroma. The locus based inter-cluster distance was very high and no difference was observed among genotypes of the same cluster. This may be due to the reason that the present study was based on a single locus and less number of markers were used for analysis.

The studies on diversity of *BADH2* gene in a large collection of accessions have revealed that an 8-bp deletion in the seventh exon is present in most of the aromatic accessions, but other less frequent mutations associated with fragrance have also been detected (Shi *et al.,* 2008; Kovach *et al.,* 2009; Myint *et al.,* 2012). Additionally, several aromatic accessions do not carry any mutation in their coding segments (Singh *et al.,* 2010; Myint *et al.,* 2012) and the reason for their fragrance is unknown. Fitzgerald *et al.* (2008) postulated that the production of 2AP is being driven by alleles of 2 different genes besides the different alleles of a

BADH2 gene. Thus, rice has indeed a second *BADH* enzyme, which acts in a similar way as that of *BADH2*, but is regulated differently. Furthermore, Mushk Budgi, Kamad, Kalanamak and Jeera Battis were clustered with non-fragrant genotypes, although they possess fragrance. This also indicates the existence of some other gene responsible for fragrance other than *badh2*. Annotation of the rice genome database between *aro4-1* QTL intervals indicate the presence of a gene for *BADH1*, which could be a likely candidate gene for aroma, due to its similar molecular function as that of *badh2* (Singh *et al.,* 2010). This further reinforces the speculation that the fragrance is being governed by two or more genes. This reveals the scope for development of more markers through fine mapping of large number of genotypes or through association mapping for differentiation of aromatic and non-aromatic rice.

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RESEARCH ARTICLE

Systematics Study on a Morphotype of *Allium tuberosum* Rottler ex Spreng. (Alliaceae) from Ladakh, India

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A morphotype of chinese chives (*Allium tuberosum* Rottler ex Spreng.) with pink mid-vein in white tepals on the abaxial surface growing in Leh, Ladakh (Jammu & Kashmir), India was studied on a comparative account with common type *A. tuberosum* (white tepals with green mid-vein) and a close wild relative, *A. ramosum* L. *Allium* subg. *Butomissa* (Salisb.) N. Friesen is discussed here with reference to taxa in India based on the study undertaken using observations from field, experimental, ecogeographical, herbarium and molecular data. A key is provided with some characters previously not included in the available diagnostic keys. Issues relating to use of terminology for plant characters are provided to the facilitate field identification.

Key Words: *Allium ramosum*, *A. tuberosum*, Collection, Ecogeographic study, Morphotype, Subgenus *Butomissa*, Taxonomic key

Introduction

Allium subg. *Butomissa* (Salisb.) N. Friesen is a small group characterized by taxa having elongated cylindrical-conic bulb, reticulate or fibrous brown outer tunic and membranous, thin, inner tunic, stout rhizome and simple chromosome morphology (Friesen *et al*., 2006; Li *et al*., 2010). The taxa are distributed in the Himalayas and eastern to central Asia upto bordering eastern Mediterranean region. On the basis of morphology, chromosome and serological data, this subgenus was suggested to have affinity with subg. *Anguinum* and subg. *Melanocrommyum* whereas molecular data have supported the mid-position between subg. *Rhizirideum* and subg. *Cyathophora* (Li *et al*., 2010).

Globally the subg. *Butomissa* is represented by two sections, *Butomissa* (Salisb.) Kamelin (*A. ramosum* L. and *A. tuberosum* Rottler ex Spreng.) and *Austromontana* (*A. oreoprasum* Schrenk and *A. gilgiticum* Wang & Tang) (Friesen *et al*., 2006; Pandey *et al*., 2017). Both the species of sect *Butomissa*– *A. ramosum* and *A. tuberosum* morphologically share characters and are debated for taxonomic distinctness (Blattner and Friesen, 2006). *A. tuberosum* is an important cultivated species from East Asia (Blattner and Friesen, 2006) while *A. ramosum*, is a less-known cultivated vegetable in north-eastern China (Choi and Oh, 2011).

North China is considered to be the centre of domestication and diversity for *A. tuberosum* (Oyuntsetseg *et al*., 2012); cytotypes of *A. tuberosum* are reported from Korea and north-eastern China (Friesen *et al*., 2006; Seregin and Korniak, 2013). It was introduced mainly by Chinese into other parts of the world and presently cultivated in the temperate and tropical regions (Hanelt *et al*., 1992).

In India, *A. tuberosum* has wider adaptability to diverse habitat in the area of occurrence; it is under sporadic cultivation in the Himalaya and the north-eastern region (Gohil, 1992; Negi and Pant, 1992; Pandey *et al*., 2008; Pandey *et al*., 2014). Occurrence as wild/semi-wild or as naturalized populations in India is doubtful (Gohil, 1992; Negi and Pant (1992); Sharma and Gohil, 2013; Pandey *et al*., 2014). The second author has observed wild and naturalized populations of this taxon in Bhavnagar area in Kinnaur district (Himachal Pradesh). It has been reported as wild in China and in western-southern coastal areas of Korea and Chinese

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border near North Korea (Yang *et al*., 1998; Xu and Kamelin, 2000; Blattner and Friesen, 2006; Choi and Oh, 2011).

The study undertaken on a morphotype of *A. tuberosum* collected from village Sumur of Nubra tehsil in Leh district (Jammu & Kashmir) having tepals with pink mid-vein on abaxial surface. It was compared with the type having green mid-vein on tepals, which is more common. Comparative study was also undertaken with *A. ramosum* and other taxa of this subg. occurring in India using selected material from field, experimental, herbarium and molecular evidences, and data from ecogeographical distribution to facilitate germplasm collection. Issues relating to usage of terminology for describing characters available in the existing literature were discussed. Also simplified identification key along with some more traits was provided for Indian taxa of subg. *Butomissa*.

Material and Methods

Study material of *A. tuberosum* (PMK 1707/ Leh-2) was used for field, experimental and herbarium studies. Plants were grown at two locations – field gene bank (FGB) at ICAR-NBPGR (ICAR- National Bureau of Plant Genetic Resources) Regional Station, Bhowali, Uttarakhand (29º20´ N, 79º30´ E, altitude 1600 m in cold humid, sub-temperate climate) and ICAR-NBPGR, New Delhi (altitude 250m). For comparison, selected accessions of *A. tuberosum* having white tepals with green mid-vein (IC321643, IC353524, IC383446, NEH, NG3189, VDK/AK/25; KCB/AP/605, KP/AP/701, VDV/KSN/51, Leh-1) were used. Live material of *A. ramosum* (EC328498/ PI-264799; coll. Russian Federation Collectors, White, George A, USDA-ARS) maintained at Bhowali and herbarium observations on *A. oreoprasum* collected from Leh, Ladak, J&K (MK134, 138; Khaltse, Hanupata) were used. The study was based on data from various resources including herbarium resources (a total of 32 specimens) of *A. tuberosum* and *A. ramosum* (41 specimens).

Data were recorded for vegetative (rhizome, bulb, leaf) and reproductive scape (perianth, stamen, pistil, fruit and seed) characters (measurements based on 10 samples). Micro-morphological characters of bulb, fibre and flower, and anatomy of leaf, scape and floral parts were observed in freshly harvested material using hand lens (10-40x magnification) and dissection microscope (Zeiss Stemi DV4). Floral morphology of taxa was done with freshly harvested material and data were recorded for separated floral parts. For anatomical observations, transverse sections of leaf and scape were studied under the stereomicroscope. Seed morphology for comparison between *A. tuberosum* and *A. ramosum* with respect to characters–shape, colour and testa texture was studied using dissection microscope (10x magnification)

Herbarium specimens located at the Botanical Survey of India (BSI-CAL, ASSAM and BSD), Forest Research Institute (DD), Dehradun, National Botanical Research Institute Herbarium (LWG), Lucknow and National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi and e-herbaria of K, P, E, were used. Eco-geographical data were gathered from areas of collection and availability of taxon (mainly based on data from herbarium notes– DD, CAL, NHCP; K, P, E, PE, and global databases such as GBIF, Kew Catalogue and distributional map drawn using software (DIVA GIS7.5). Vouchers (HS23159a, b) of the experimental material were deposited in National Herbarium of Cultivated Plants (NHCP), ICAR-NBPGR, New Delhi.

Sequence of the ITS (Internal Transcribed Spacer) region amplified from the five accessions of *A. tuberosum* i.e. from the Leh region (Leh-1 and Leh-2), the north eastern Himalayas (NEH), western Himalayas (NG3189) and the accession maintained at the field gene bank in Bhowali (IC353524) and *A. ramosum* (EC328498).

Molecular study of two morphotypes of *A. tuberosum* (one with pink mid-vein and four with green mid-vein on tepal) was undertaken with sequence analyses of the Internal Transcribed Spacer region amplified from five accessions of *A. tuberosum* and one of *A. ramosum* maintained at the field gene bank in Bhowali, ICAR-NBPGR. Phylogenetic and molecular evolutionary analyses were conducted using Mega version 6 (Tamura *et al*., 2013).

Result and Discussion

Field, Experimental and Herbarium Study

Morphological Study

Wild population of new morphotype was observed along the boulders in disturbed habitat in village Sumur [3,092m; Nubra, Leh district (Jammu & Kashmir)] by the second author during exploration in September 2014. Plants appeared to be self sown with thick keeled leaves, tough reticulate fibres on rhizome, flower with tepals having pink mid-line on abaxial surface and dark

Fig. 1. *Allium tuberosum* (top- left-right) a variant (with pink mid-vein on tepals and fibrous roots); *A. tuberosum* (second row) a normal type (with green mid-vein on tepals and fibrous roots); *A. ramosum* and roots (third row); inflorescence of *A. oreoprasum* (live, opened) (photo credit: PS Mehta, ICAR-NBPGR Bhowali)

pink anther lobes. Plants were taller (0.9-1.0 m vs 0.6 m) and robust when compared to populations studied by the authors in their previous work (Pandey *et al*., 2014) (Fig.1). On critical examination of the plant parts, new morphotype was identified as *A. tuberosum* (PMK 1707; IC612066). In floristic and herbarium records *A. tuberosum* has been described variously for flower characters – white and pink flower, tepal stripped with pink etc. (Baker, 1892; Murti, 2001; Das Gupta, 2006; CAL507916, 23/7/54, Stainton, Sykes and Williams 1982). In the same area of Ladakh region (Dha, Hanu) in Leh, the second author also observed plant populations of *A. tuberosum* with tepals having green mid-vein growing in rocky crevices.

Comparative Study

Allium tuberosum (PMK1707) was used for comparative study with *A. tuberosum* (green mid-line) and *A. ramosum* (Table 1).

Micromorphology

Comparison of seed micromorpholgical characters of *A. tuberosum* and *A. ramosum* using scanning electron microscopy also supported similarity in testa ornamentation as revealed by Oyuntsetseg *et al.* (2012). Seed micromorphology has been suggested as an important tool for taxonomic delineation of taxa in *Allium* (Ling *et al*., 2000; Ferhat *et al*., 2012). Friesen *et al.* (2006) reported seed testa ornamentation of sect. *Austromontana* (*A. oreoprasum*) to be differing in verrucose periclinal walls similar to that of the sect. *Butomissa* (*A. ramosum* and *A. tuberosum*). Seed morphological characterization revealed that seed shape and colour within subg. was more or less similar but minute differences were noted in the seed outline and testa ornamentation across subgenus. Comparative data for testa characters of *A. tuberosum* and *A. ramosum*, were captured under scanning electron microscope (Figure 2).

Ecogeographical Study

A. tuberosum with pink mid-vein on tepal showed variation in plant characters with respect to ecogeographical distribution, plant height, robustness of plant parts- stem, leaves, thicker fibre, colour of tepal as noted during field study. Plants of new morphotype were very tall (1.0m), robust with thicker fibre as compared to the green mid-vein type plant (0.5-0.75m); subterranean parts had more fibre in wild/semi-wild population as compared to the plants in disturbed habitats. Pandey *et al*. (2014) have studied the populations of *A. tuberosum* across

Table 1. Comparison of characters in *Allium tuberosum* (pink mid-vein and green mid-vein) and *A. ramosum*

Trait	*A. tuberosum* (pink mid-vein)	*A. tuberosum* (green mid-vein)	*A. ramosum*
Plant odour	Onion like	Onion like	Garlic like
Leaves	Linear, keeled, margin smooth	Linear, flat, margin smooth	Linear, keeled, margin smooth
Scape (cm)	50-70, two angled	25-60, two angled	25-60, terete, obscurely angled
Spathe	2-3 partite, persistent	2-3 partite, persistent	1-2 partite, persistent
Flower	Stellate	Stellate	Campanulate
Tepal colour	White with pink mid-vein abaxially	White with pale green mid-vein abaxially	White, tinged with pale red, pale red mid-vein
Tepal shape, size	Outer: oblong-lanceolate, 4-7×1.8-3mm Inner: ovate- elliptical, 4-7×2.1-3.5mm. shorter than outer, margin entire	Outer: oblong-lanceolate, 4-7×1.8-3mm Inner: ovate-elliptical, 4-6×2.1-3.5mm. shorter than outer, margin entire	outer oblong, slightly narrower than inner, 4.5-11×2-2.9 mm; inner: oblong-obovate (4.5-9×1.8-3.1mm
Tepal apex	Acute-acuminate	Acute- acuminate	Acuminate, reflexed
Umbel	Hemispheric-subglobose, laxy	Hemispheric-subglobose, laxy	Hemispheric-subglobose, sub-erect (not laxy)
Stamens	Six, subequal; stamens 4/5th the length of the tepals;	Six, subequal; stamens 4/5th the length of the tepals;	Six, shorter, half the length of the tepals
Anthers	Dark pink, inner ones slightly wider at base than outer at base	Green-yellow, inner ones slightly wider than outer at base	Mauvish, inner ones slightly wider than outer at base
Ovule (no.)/locule	Two	Two	Two-four
Capsules	Spreading	Spreading	Erect-suberect
Seed colour	Black	Black	Darkest brown
Seed shape, size	Irregularly rhomboidal-oval, rough; 3.8-4.1×2.8-3.1 mm	Irregularly rhomboidal-oval; rough; 3.2 × 2.5 mm	Oval, fringed margin smooth, shiny; 4.0-4.5 × 2.5-3.2 mm
Flowering period	August-September	August-September	June-August

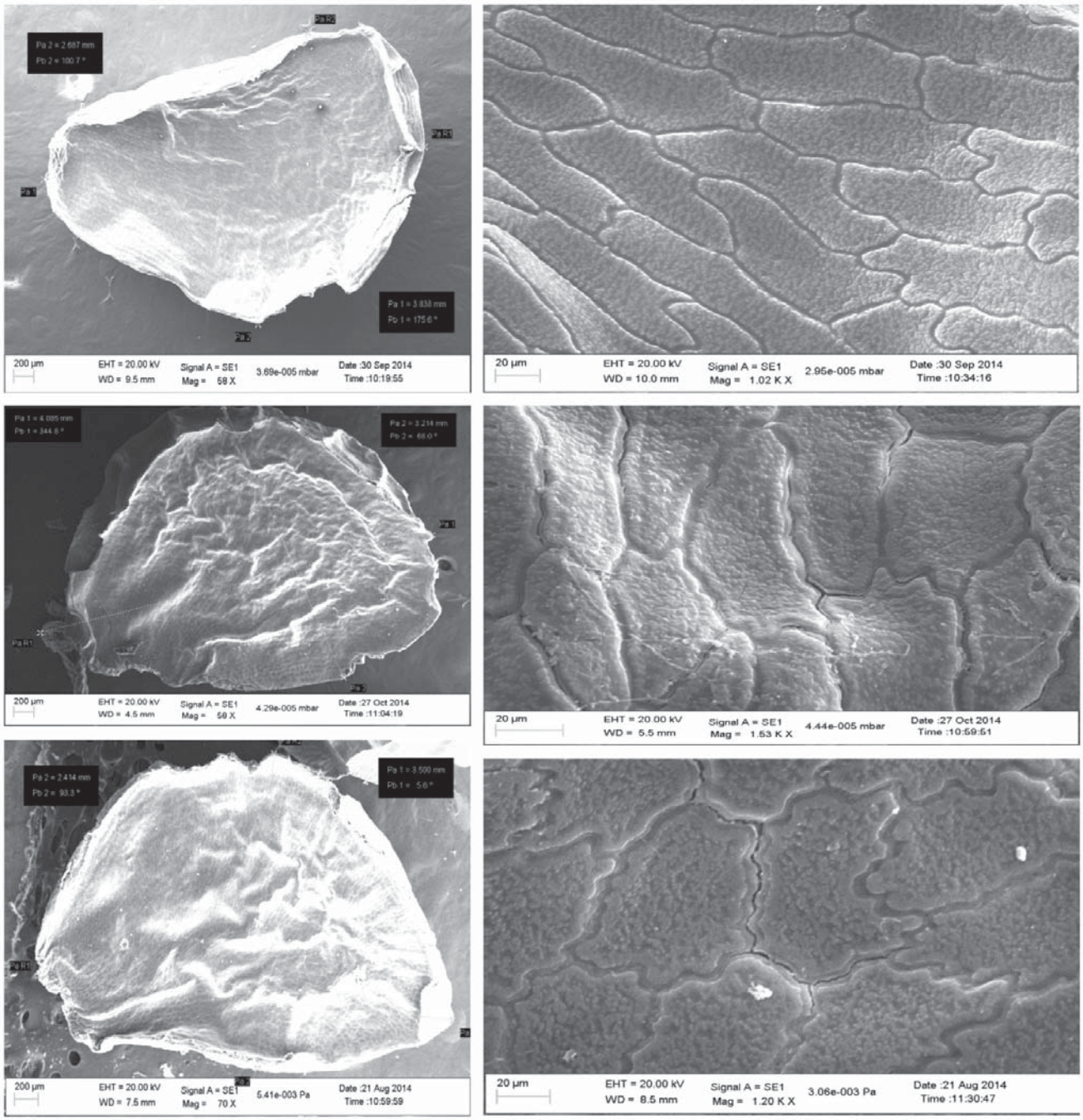

Fig. 2. Seed micro-morphology, general view and testa ornamentation: *A. tuberosum* (top row- pink mid-vein), *A. tuberosum* (middle row- green mid-vein); and *A. ramosum* (bottom row)

distribution range. In this study the morphotype with pink mid-vein on tepal was recorded as less-common type for India.

On the basis of available evidences and data in the present study the authors suggested that the pink-vein on tepal is very distinct from *A. ramosum* where the latter species does not occur in India though Murti (2001) opined its doubtful occurrence in the Indian Himalaya. Phytogeographically, *A. ramosum* occurs in steppes of Siberia, Mongolia and northern China, whereas *A. tuberosum* is native to South-western China (Oyuntsetseg *et al*., 2012). Sect. *Austromontana* is distributed in the mountainous region from eastern to central Asia upto bordering eastern Mediterranean region. *Allium*

oreoprasum Schrenk occurs in sunny slopes and stony river banks in Leh region, Ladakh Himalaya, J&K (1200-2700m). *A. gilgiticum* is rare endemic and reported only from its type locality in Gilgit, North Pakistan (Gohil, 1992).

Ecogeographical distribution map drawn using software (DIVAGIS7.5) showed that concentration of species diversity in Sect. *Austromontana* was more towards western parts of the Himalayas extending in higher altitudes of west Asia, whereas sect. *Butomissa* was distributed towards eastern part of Asia-northeastern China and Mongolia (Fig. 3). *Allium tuberosum* was wide spread from western to eastern parts, especially of North China to southern parts continued with its Indian boundaries. *A. ramosum* was confined to the northern part of eastern Asia. To our understanding, none of the available data indicated its occurrence in Indian region.

Molecular Studies

Molecular study using sequence analyses of ITS (Internal Transcribed Spacer) region revealed that two morphotypes of *A. tuberosum* were similar whereas they were very distinct from *A. ramosum* (Fig. 4). Zeder (2006) reported the distinction between *A. tuberosum* and *A. ramosum* based on data from RAPD and origin of the former species.

Phylogenetic and molecular evolutionary analysis conducted using Mega version 6 (Tamura *et al.,* 2013) showed that accessions of *A. tuberosum* (Leh-1 and Leh-2) were distinct from other accessions of *A. tuberosum* and *A. ramosum* (Fig. 4). The accession Leh-2 showed 95.4 per cent similarity to four accessions of *A. tuberosum* (Leh-1, IC353524, NG3189, NEH) used in the study and is distant from *A. ramosum* by 15.9 per cent based on the analysis of 285bp ITS region amplified from all these accessions. Leh-2 is pink- flowered *A. tuberosum* whereas Leh-1 was *A. tuberosum* (green mid-vein) collected from the same region.

Key to Subgenus *Butomissa*

Taxonomic identity of *A. tuberosum* and *A. ramosum* has always remained confusing due to gross morphological similarity of plant parts (Zeder, 2006; Sharma and Gohil, 2013). Previous studies based on marked differentiation of floral parts and life history in *A. tuberosum* and *A. ramosum* with regard to floral traits (stellate/campanulate flowers; narrow-ovate tepals with

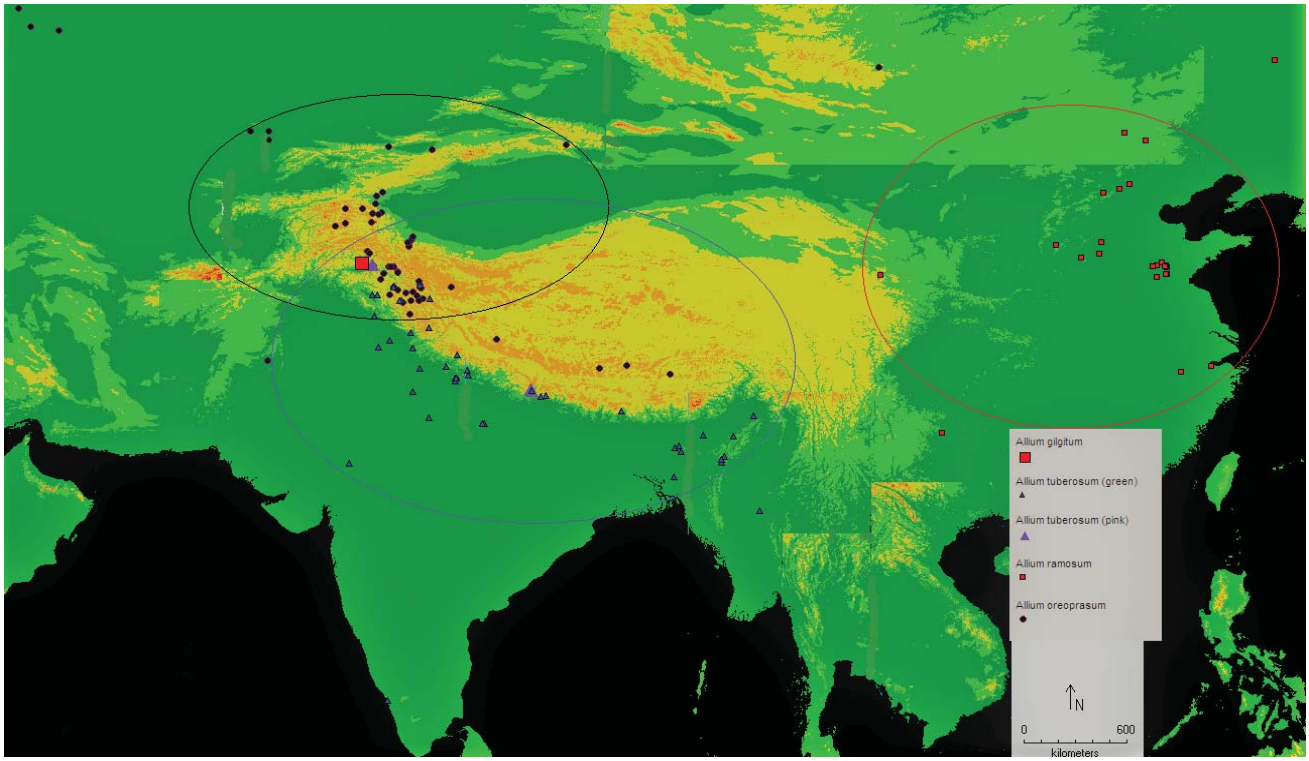

Fig. 3. Areas of occurrence of taxa in *Allium* subg. *Butomissa*: *Allium tuberosum* tepal with pink mid-vein and the common types with green mid-vein on tepal used in the study; other texa - *A. ramosum*, *A. oreoprasum* and *A. gilgiticum* (herbarium and other databases)

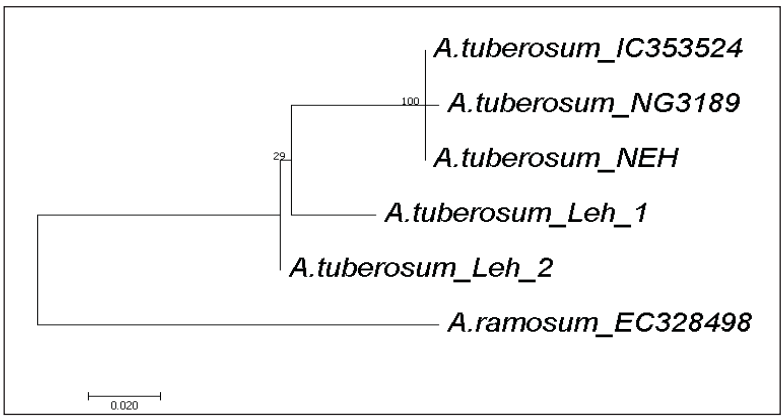

Fig. 4. Dendrogram based sequence analyses of the internal transcribed spacer region for two species of *A. tuberosum* and *A. ramosum*

green mid-vein/lanceolate-oblong tepals with reddish mid-vein; shorter tepals-5.6-6.9 mm/ 6-11 mm; stamens 4/5th the length of the tepals/stamens half the length of the tepals), ovaries with two vs two-four ovules/locule and phenology (August-October/June-August) advocated their status as separate species (Stearn, 1946; Hanelt, 1988; Sharma, 2005; Blattner and Friesen, 2006; Sharma and Gohil, 2013). *Allium odorum* L. is a synonym of *A. ramosum* L.

Among the most distinguishable features noted in this study for *A. ramosum* (comparison with *A. tuberosum*) were tepals margin wavy vs. entire, stamens length much shorter as compared to the tepal length and flower (campanulate), opening pattern-tepals never open wide as compared to that of widely opened tepals of *A. tuberosum* (widely open/stellate) (Fig. 1). The present study indicated that presence of pink mid-vein on tepal in *A. ramosum* is not a diagnostic trait as suggested by many workers (Stearn, 1946; Sharma, 2005; Sharma and Gohil, 2013). Some additional characters such as leaf anatomy, and orientation of tepals with respect to stamen, other tepal characters (tepal colour, margin and apex) have been suggested in field key for identification of taxa of the subg. *Butomissa*.

Field identification key for subg. *Butomissa* (Salisb.) Kamelin (modified from Friesen *et al*., 2006) is provided below:

Bulb cylindric, tunic coarsely reticulate-subreticulate; perianth white or pink

Leaf blades flat, not keeled; flowers wide open on maturity, stellate, inner tepals ovate- elliptical, outer tepals oblong-lanceolate, inner tepals shorter than outer, margin entire, white with pale green or pink mid-vein abaxially; ovules two per locule

---------- *A. tuberosum*

Leaf blades angled (keeled); flowers never open widely, not stellate, inner and outer tepals elliptical, inner tepals longer than outer, margin wavy, pinkish with reddish mid-vein abaxially, ovules two-four per locule

---------- *A. ramosum*

Bulb narrowly ovoid-cylindric, tunic reticulate or fibrous; perianth white-rosy purple

Bulbs ovoid-cylindric, tunic reticulate, leaves narrow, linear, 1-4mm wide, umbels few flowered, erect-suberect, tepals obovate-elliptic, acuminate apex with a reflexed point, pale pink-white with dark purple mid-line

---------- *A. oreoprasum*

Bulbs cylindric, tunic fibrous, leaves broad, obtuse,10-20mm wide, umbels many flowered, loosely arranged, tepals lanceolate, acute apex, rosy-purple with faded mid-line

---------- *A. gilgiticum*

Botany of Allium tuberosum

The plant has clustered cylindrical bulbs arising from horizontal rhizome; membrane reticulate-sub-reticulate and dull-yellow brown. Leaves – linear, shorter than scape, flat, solid, margin smooth; scape – slender, covered with leaf sheaths at base. Spathe–two-three partite, persistent. Umbel–hemispheric-subglobose, laxy, many flowered; flower–stellate, outer tepals oblong-lanceolate, inner tepals ovate-elliptical, shorter than outer, margin entire, white with pale green or pink mid-vein abaxially; filaments six, subequal with narrowly triangular base, as long as perianth segments, connate at base, adnate

to perianth segments, anther lobes yellow-dark pink; inner ones slightly wider at base than outer ones. Ovary–obconical-globose, minutely tuberculate, without concave nectaries at base. Capsules loose, spreading, seeds black, two per locule, about 1mm and irregularly rhomboidal.

Morphological Data–A Major Concern

The data recorded on plant characters during field, experimental, herbarium and ecogeographical studies needs special consideration for plant genetic resource and systematic study (Pandey *et al*., 2017; Negi *et al*., 2018). While studing the genus *Allium,* authors opined that the protologue description, data on available taxonomic literature and herbarium resources depicting characters are not clearly perceived. Data may vary with stage at which observations were recorded which may be misleading. The characters of *A. tuberosum*– tepal/flower colour, streaking white or pinkish white, flower red, white or pink, lilac, reddish-pink white with pink streak were recorded in the literature (Baker, 1892; Murthi, 2001; Dasgupta, 2006). Some new characters used from leaf anatomy, flower opening pattern, orientation of tepal and stamen, and tepal characters (tepal colour and mid-vein, margin, apex) have been included in field key for identification.

Leaf description for *A. ramosum* in protologue and other published literature has been given as hollow, fistulose which was not observed by the authors (Pandey *et al*., 2018). Authors believe that the term fistulose or hollow as attributed by Choi and Bu (2011) does not fit into the fistulose character of leaf in subg. *Cepa.* Anatomical study carried out using live material of *A. ramosum* revealed that the hollow leaf was an unstable character and varies with stage and habitat which may be linked to different soil conditions. We therefore prefer to use the term 'keeled' (ref. Baker 1892) instead of 'fistulose' used for *A. ramosum* (only observed when dissected). Further, many characters with respect to morphology vs. temporal variation have not always been interpreted as habitat-linked characters.

Such variations were noted by the authors in other species of *Allium* (*A. chinense* G. Don.; Pandey *et al*., 2016; 2018) growing under diverse ecological conditions. Criterion fixed by Kamelin who differentiated *A. tuberosum* and *A. ramosum* on the basis of fistulose leaves is therefore not agreeable to authors. Study on *A. gilgiticum* was undertaken only using the herbarium data (K000844282; K000844283). However, availability of insufficient material of *A. oreoprasum* and *A. gigiticum* made it difficult to comment on all the characters.

The following points need special attention for recording data: a) habit and ecogeography- plant height, tunic and fibre characters with variation in altitudinal, temporal and soil conditions; b) bulb- shape with respect to stage at which studied or prepared as herbarium specimen; c) tunic-character distinction between fibrous, coriaceous and reticulate; and d) flower colour at maturity level.

Conclusion

The above study clearly identified *A. tuberosum* in India with distinct tepal characters as compared to a common morphotype and classified it to be very distinct type from the related taxon *A. ramosum* based on morphology of fibre, leaf, flower and seed testa characters. The study has addressed issues on taxonomy of the subgenus with respect to: 1) need to support ecogeographic and herbarium data; 2) limitations on availability of material for indepth experimental study; and 3) correct usage of terminology for taxon description.

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SHORT COMMUNICATION

Agro-morphological and Physico-chemical Characterization of Indigenous Scented Lal Badshabhog Rice of West Bengal, India

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The agro-morphological and physico-chemical characterization of traditional aromatic Lal Badshabhog rice landrace was done at BCKV, Kalyani, Nadia, West Bengal, India during *kharif* season of 2012, 2013 and 2014. The variety had long-statured plants (scale 7, 140-150 cm height) and late maturity (scale 7, 130-138 days). The lemma and palea of matured grain was brownish-red in colour, while sterile lemma was red and the awnless grains were short in length (5.98 mm) with very low test weight (10.6 g). The white-coloured kernels belonged to short-bold group (length 3.80 mm and width 1.87 mm), which had low amylose content (18.1%), medium alkali value (score 3.3) and medium aroma (score 2.1).

Key Words: Agro-morphological traits, Aromatic rice, Grain quality

There is a long history for cultivation and use of small and medium-grained non-Basmati type scented rices in Bengal region of Eastern India. Among such 35-40 aromatic rice landraces, Lal Badshabhog is traditionally cultivated in *rahr* (red and laterite) areas of West Bengal for hundreds of years. The name of 'Lal Badshabhog' paddy has two parts, 'Lal' and 'Badshabhog'; where 'Lal' meaning 'red' in Bengali represented the brownish-red colour of grain (lemma and palea) and the word 'Badsha' meaning 'emperor' or 'king' in Hindi indicating the origin of nomenclature of the variety during *mughal* regime in undivided Bengal, and the word 'bhog' was used for the 'pulse-mixed rice' (*khichuri*) mainly offered to Hindu God or Goddess in Bengal.

With quick adoption of high-yielding rice varieties during last 4-5 decades, Lal Badshabhog like other landraces has been restricted to localized cultivation in a few villages of dry farming region with a reported reference from Chorpahari area of Purulia district of West Bengal (Deb, 2005). Farmers in native areas, cultivate Lal Badshabhog rice following traditional practices during *kharif* (wet) season mainly for their domestic uses. In the present-day agricultural system, agro-morphological and physico-chemical characterization needs to be done to ensure proper conservation-*cum*-cultivation of Lal Badshabhog rice in the state.

The seeds of Lal Badhsbhog landrace were collected from Model Organic Farm of Bidhan Chandra Krishi Viswavidyalaya (BCKV) and 25 days old seedlings @ single / hill were transplanted in an open puddled field with five replications at RKVY Project on 'Bengal Aromatic Rice' Centre, 'C' Block Farm (22º59´N, 88º27´E and 9.75 m above mean sea level) of BCKV, Kalyani, Nadia, West Bengal, India during *kharif* season of 2012, 2013 and 2014. Each experimental unit consisted of 6-metre row length comprising 30 rows with row to row distance of 30 cm and plant to plant distance of 20 cm. The morphological and related characteristics of Lal Badshabhog rice were recorded following 'DUS Test Guidelines for Rice' of PPV&FRA, Government of India (PPV&FRA, 2007). Grain quality parameters like size and shape of grain and kernel, amylose content, alkali spreading value and aroma were determined at Aromatic Rice Laboratory, Department of Agronomy, BCKV, Mohanpur, Nadia, West Bengal, India.

Lal Badshabhog rice was usually adaptable to rainfed medium land in *rahr* region of West Bengal, whose characteristics are described in Table 1.

Plant: Lal Badhabhog rice belonged to long-duration type with late heading (scale 7, 105 days) and late maturity (scale 7, 134 days) (Fig. 1).

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Table 1. Plant characteristics of Lal Badshabhog rice following DUS guidelines

Sl. No.	Characteristics	Scale	Remarks measured values etc.
1	Coleoptile: colour	1	White
2	Basal leaf sheath colour	1	Green
3	Leaf : Intensity of green colour	5	Medium
4	Leaf : anthocyanin colouration	1	Absent
5*	Leaf : distribution of anthocyanin colouration		
6	Leaf sheath : anthocyanin colouratin	1	Absent
7	Leaf sheath: intensity of anthocyanin colouration		
8	Leaf: pubescence of blade surface	5	Medium
9	Leaf : Auricles	9	Present
10	Leaf : anthocyanin colorations of auricles	1	Colourless
11	Leaf : collar	9	Present
12	Leaf : anthocyanin colouration of collar	1	Absent
13	Leaf : ligule	9	Present
14	Leaf: shape of ligules	3	Split
15	Leaf: colour of ligule	1	Green
16	Leaf : length of blade	7	Long (70.1 cm)
17	Leaf : width of blade	3	Narrow (10.6 mm)
18*	Culm : attitude (for floating rice only)		
19	Culm : attitude	3	Semi-erect
20	Time of heading (50% of plants with panicles)	7	Late (105 days)
21	Flag leaf attitude of blade (early observation)	3	Semi-erect
22	Spikelet : density of pubescence of lemma	3	Weak
23	Male sterility	1	Absent
24	Lemma: anthocyanin colouration of keel	1	Absent
25	Lemma: anthocyanin of area below apex	1	Absent
26	Lemma: anthocyanin colouration of apex	1	Absent
27	Spikelet : colour of stigma	1	White
28	Stem: thickness	5	Medium (0.57 cm)
29	Stem: length (excluding panicle)	7	Long (143.5 cm)
30	Stem: anthocyanin coloration of nodes	1	Absent
31	Stem : intensity of anthocyanin colouration of nodes		
32	Stem : anthocyanin colouration of internodes	1	Absent
33	Panicle: length of main axis	5	Medium (25.6 cm)
34	Flag leaf: attitude of blade (late observation)	3	Semi-erect
35	Panicle: curvature of main axis	3	Semi-straight
36	Panicle: number per plant	3	Few (10.67)
37	Spikelet: colour of tip of lemma	4	Red
38	Lemma & Palea : Colour	6	Brown (Tawny)
39	Panicle: awns	1	Absent
40*	Panicle: colour of awns (late observation)		
41*	Panicle: length of largest awn		
42*	Panicle: distribution of awns		
43	Panicle : presence of secondary branching	9	Present
44	Panicle : secondary branches	2	Strong
45	Panicle : attitude of branches	3	Erect to Semi-erect
46	Panicle: exertion	7	Well exerted
47	Time of Maturity	5	Medium (134 days)
48	Leaf : senescence	5	Medium
49	Sterile lemma: colour	3	Red
50	Grains: weight of 1000 fully developed grains	1	Very low (10.6 g)
51	Grain : length	1	Very short (5.98 mm)
52	Grain : width	2	Narrow (2.23 mm)
53	Grain : phenol reaction of lemma		

Sl. No.	Characteristics	Scale	Remarks measured values etc.
54	Decorticated grain: length	1	Very short (3.80 mm)
55	Decorticated grain: width	1	Very narrow (1.87 mm)
56	Decorticated grain shape	2	Short bold
57	Decorticated grain: colour	1	White
58	Endosperm: presence of amylose	9	Present
59	Endosperm: content of amylose	3	Low (18.1%)
60*	Varieties with endosperm of amylose absent only-polished grain : exertion of white core		
61	Gelatinization temperature through alkali spreading value	3	Medium (score 3.3)
62	Decorticated grain : aroma	9	Present (score 2.1)

* Not applicable

Fig. 1. Lal Badhabhog paddy at maturity stage

Fig. 2. Ligule and auricle of Lal Badshabhog

Fig. 3. Panicle of Lal Badshabhog

Fig. 4. Change of grain colour of Lal Badshabhog rice

Stem: It had long statured plant with average stem length of 143.5 cm excluding panicle. The thickness of stem was medium (scale 5) with mean diameter of 0.57 cm. There was no anthocyanin colouration on nodes and internodes. The attitude of the culm could be categorised as semi-erect (scale 3) at booting stage.

Leaf: The variety produced long, narrow and green leaves. The colour of basal leaf sheath was green (scale 1), while the intensity of green colour of the leaf was medium (scale 5) with no anthocyanin colouration on leaf sheath. The average length and width of leaf blade were noted as 70.1 mm and 10.6 mm, respectively. The split-type ligule (scale 3) and sickle-shaped auricle at leaf base were found in the plant (Fig. 2). The attitude of the flag leaf was semi-erect (scale 3) at both early and late observation.

Inflorescence: The length of panicle of Lal Badshabhog rice was categorized as medium (scale 5, 25.6 cm) with the curvature of the main axis as semi-erect (scale 3) (Fig. 3). The plant produced few (scale 3, mean 10.67) well-exerted panicles in the field. The colour of lemma and palea was green at anthesis, which turned to brownish-red at ripening stage (Fig. 4). The variation in colour of grain between Badshabhog (golden-yellow) and Lal Badshabhog (brownish-red) was reported by Roy (2015), which could be considered as an important parameter to differentiate these two scented rice varieties.

Flower: The variety produced bi-sexual flowers including six yellow coloured anthers, and an ovary with white coloured feathery stigma.

Grain: The grains of Lal Badshabhog rice were short in size (mean length 5.98 mm and width 2.23 mm) and awnless. The weight of 1000 fully-developed grains was very low (10.6 g). The colour of lemma and palea was brownish-red (scale 6) (Fig. 5), while that of sterile lemma was red (scale 3).

The kernels were short-bold in shape (length 3.80 mm and width 1.87 mm) and white in colour (Fig. 5), which had low amylose content (18.1%), medium alkali spreading value (score 3.3) and medium aroma (score 2.1).

Fig. 5. Grains and kernels of Lal Badshabhog

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SHORT COMMUNICATION

Assessment of Genetic Variability and Diversity for Quantitative Characters in Naked Barley (*Hordeum vulgare* (L.) var. nudum Hk. f.)

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Forty genotypes of hulless barley were studied to understand the extent of genetic variability and diversity based on 7 quantitative characters. A wide range of variation was observed for seed yield per plot followed by plant height, tillers per meter and 1000-grain weight. High heritability coupled with high genetic advance as percent of mean was registered for seed yield per plot and tillers per meter in genotypes indicating the predominance of additive gene action for these traits. Based on D^2 statistics, 40 genotypes were grouped into 7 clusters in which cluster IV consisted of only single genotype (Geetanjali) while other six clusters involved multi-genotypes. The maximum inter-cluster distance was observed between cluster IV and VII (120.82) followed by cluster IV and V (107.43). Geetanjali of cluster IV exhibited highest seed yield per plot and tillers per meter along with early days to 50% heading. The genotypes involved in cluster IV and VII may be utilized in hybridization programme for improving the characters like early maturity, tillers/meter, short plant height and seed yield/plot.

Key Words: Diversity, Hulless barley, Quantitative characters, Variability

Hulless barley (*Hordeum vulgare* (L.) var. nudum Hk. f.) an important cereal crop is widely distributed all over the world, although it is highly preferred in East Asian countries such as China, Korea and Japan and chiefly high in Tibet and Northern parts of Nepal, India and Pakistan. In India, it is mainly grown in the high altitude areas of Himalaya and is utilized as food crop in the tribal areas of hills and plains. Hulless barley is utilized not only as grain crop, bio-fuel and livestock feed but also used as raw material for malt products such as beer. In recent years, importance of hulless barley is increasing as human food due to presence of water soluble plant fibers essential in human diets to reduce the serum cholesterol (Shimizu *et al*. 2008). In this perspective, hulless barley may be helpful in reducing the sugars of diabetic patients and also to lower the serum cholesterol of heart patients (Pins and Kaur, 2006). Thus, hulless barley is a potential crop and its genetic improvement is needed for high yield, wide adaptation, good quality and resistance to biotic and abiotic stresses.

Assessment of genetic variability and diversity is important to detect the source of genes for a particular character within the available germplasm. Hence, knowledge of nature and magnitude of genetic variability present in the germplasm and extent of heritability of economic characters is of greater help in identifying the parents with novelty and diversity for planning a suitable breeding strategy. Therefore, the present study was undertaken to understand the nature and magnitude of genetic variability and diversity in hulless barley genotypes collected from different geographic origins.

The present study was carried out on 40 hulless barley genotypes from mid-term storage facility at ICAR-IIWBR, Karnal. The experiment was conducted in a randomized block design with three replications; each plot had three rows of 2.5 meters long and 30 cm apart, under timely sown irrigated conditions at Seed and Research Unit, IIWBR, Hisar during 2014-15. The recommended package of practices was followed for raising the good crop stand. The data were recorded on 5 randomly selected plants for 7 quantitative characters viz., days to 50% heading, days to maturity, plant height (cm), tillers/meter, spike length (cm), 1000-grain weight (g) and seed yield/plot (g). The mean values of replicated data were subjected for analysis of variance as per standard statistical procedure. The genotypic

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and phenotypic variance, genotypic and phenotypic coefficients of variation and heritability were estimated as per the standard formulae (Singh and Chaudhary, 1985). Genetic advance was estimated by the method suggested by Johnson *et al*. (1955).The genetic diversity was analyzed by the non-hierarchical Euclidean cluster analysis for seed yield and its components using statistical software available at computer centre, IIWBR, Karnal, for clustering of genotypes into different groups and also to indicate the extent of diversity available in set of genotypes studied. Ward's minimum variance clustering method was used to classify genotypes in discrete clusters (Sneath and Sokal, 1973).

The study on genetic variability revealed that a wide range of variation was observed for seed yield/plot followed by plant height, tillers/meter and 1000-grain weight indicating a wide scope for improving these characters through selection. These findings are in agreement with the results of Zeng (2015). In general, magnitude of phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters, indicating the significant role of environmental interaction for the expression of all the characters studied. Seed yield/plot exhibited high difference between PCV and GCV in comparison to other characters indicating more environmental influence on this character. The range of PCV was registered from 2.92 to 35.44 whereas GCV ranged from 2.05 to 30.82. The high degree of phenotypic and genotypic coefficients of variation was observed for seed yield/plot and tillers/meter. Present findings are in confirmation with Eshghi *et al*. (2012).

Heritability and genetic advance are important genetic parameters in selection programme. In the present study, broad sense heritability (h^2) estimates ranged from 49.40% for days to maturity to 75.7 % for seed yield/plot (Table 1). The high values of heritability were recorded for seed yield/plot. Similar findings were observed by Derbew *et al*. (2013**).** However, moderate heritability was observed for characters like tillers/meter, days to 50% heading, spike length, 1000-grain weight and plant height. These results are in agreement with Shtaya *et al.* (2015). High heritability coupled with high genetic advance as percent of mean was registered for seed yield/plot and tillers/meter in genotypes indicating the predominance of additive gene action for these traits, hence direct selection may be highly effective in barley improvement. Similar findings were reported by Yadav *et al.* (2015).

Forty genotypes of hulless barley comprising indigenous and exotic germplasm lines were grouped into 7 clusters in which cluster IV consisted of only single genotype while other six clusters involved multi-genotypes. Maximum number of genotypes (10) were observed in cluster VI followed by cluster V (8). However, Clusters II, I, VII and III encompass (7), (6), (5) and (3) genotypes, respectively. The composition of genotypes in each cluster is depicted in Figure 1. Geetanjali (Indigenous) was more divergent from other genotypes as it represents a separate cluster.

The inter-cluster distances were greater than intra-cluster, indicating wide genetic diversity among the genotypes of different clusters than those of same cluster. The maximum inter-cluster distance was revealed between cluster IV and VII (120.82) followed by cluster IV and V (107.43). On the other hand, minimum distance was noticed between cluster I and II (27.90), suggesting close relationship between these clusters would not play a critical role in improvement of barley. The greater distance between clusters showed wider genetic diversity among genotypes. The highly diverse genotype would create a broad spectrum of variability in the subsequent generations which enables further selection and improvement. The maximum intra cluster

Table 1. Analysis of variance and estimates of genetic parameters for seven characters in 40 hulless barley genotypes

Traits	Mean square (Genotype)	Mean ± S.E	Range of variation	Coefficient of variation		Heritability (in broad sense %)	Genetic advance (% of mean)
				GCV	PCV		
Days to 50% heading	22.95**	94.06 ± 1.42	86.50-99.50	3.27	3.91	70.10	5.64
Days to maturity	21.26**	129.25 ± 1.89	121.00-134.00	2.05	2.92	49.40	2.97
Plant height (cm)	323.73**	79.83 ± 7.17	50.28-97.55	13.16	18.29	51.70	19.50
Tillers/meter	308.89**	65.03 ± 4.8	41.00-86.50	17.60	20.51	73.70	31.12
Spike length (cm)	1.13**	7.33 ± 0.34	5.70-9.33	9.15	11.23	66.30	15.34
1000-grain weight (g)	38.64**	40.29 ± 2.37	29.06-50.14	9.19	12.39	55.00	14.05
Grain yield/plot (g)	27652.39**	353.99 ± 43.75	129.00-606.00	30.82	35.44	75.70	55.25

*, ** Significant at 5% and 1% level of significant, respectively

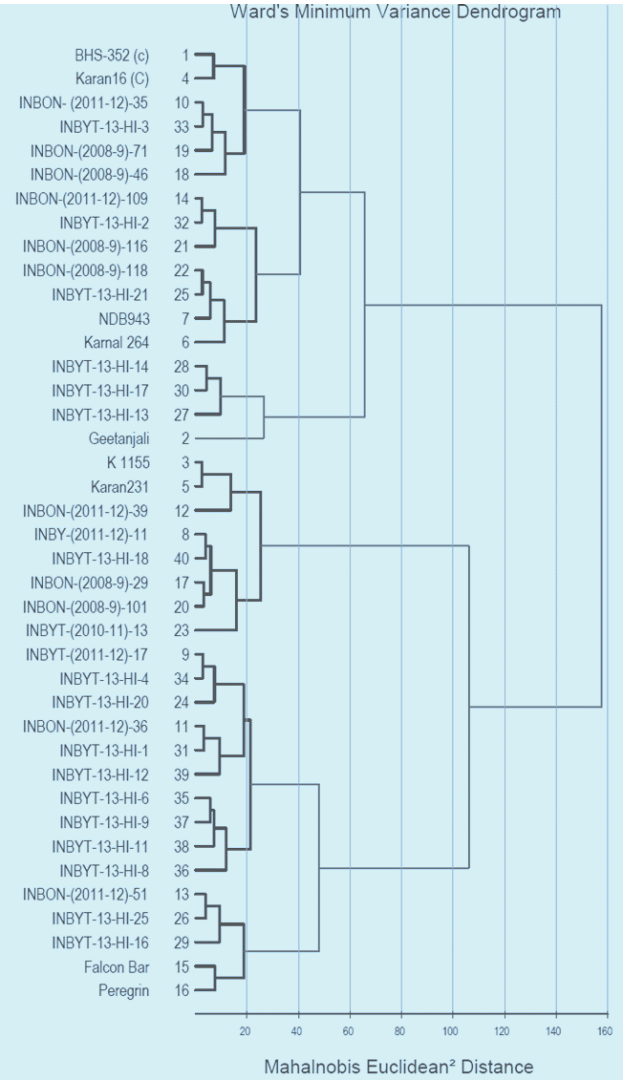

Fig. 1. Clustering of hulless barley genotypes (Wards' dendrogram)

distance was observed for cluster V (20.17) followed by cluster VII (19.86) and cluster VI (19.39). It is suggested that genotypes within the cluster with high degree of diversity would produce more desirable breeding material for attaining maximum genetic advance.

Cluster I revealed the highest mean values for spike length (8.08cm) with maximum 1000-grain weight (45.04g). However, cluster II exhibited the highest mean value (90.81cm) for plant height and better seed yield/plot (475.36g). Cluster IV consisted of highest mean values for tillers/meter (85) and seed yield/plot (563.00g) accompanied with early days to 50% heading (86). Cluster VII had short plant height (76.56cm). The use of genotypes from clusters IV and VII in hybridization for improving the yield and its contributing characters appears to be gainful. In addition, incorporation of diverse parents in hybridization is likely to produce heterotic hybrids and desirable transgressive segregants in further generations.

Cluster IV exhibited highest seed yield/plot and tillers/meter accompanied with early days to 50% heading whereas cluster VII had the genotypes exhibiting short plant height. The exotic genotypes involved in cluster VII such as INBON-(2011-12)-51, INBYT-(2013)-HI-25, INBYT-(2013)-HI-16, Falcon Bar and Peregrin and indigenous genotype (Geetanjali) in cluster IV may be used as a parent in hybridization programme for improving the characters like early maturity, plant height, tillers/meter and seed yield/plot.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXVIIth meeting held on October 23th, 2017 at the ICAR-National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 64 germplasm lines out of 87 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. TNAU 60S (IC0622805; INGR17028), a TGMS Line of Rice (*Oryza sativa)*

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The use of male sterility is a prerequisite for commercial exploitation of heterosis since rice is a self-pollinating crop. Following the landmark finding of rice genotypes reversibly turn male fertile to male sterile and *vice versa* with changes in environmental factors, such as temperature and/or day length during critical phases of plant growth, the concept of two-line breeding emerged as an alternative to the three-line approach (Yuan, 1997) in China. The main advantages of two-line heterosis breeding include the ability to use a wide range of genotypes as male parents, absence of negative effects associated with sterility-inducing cytoplasm and no need for maintainer lines. Higher temperature (> 30^{o}C) results in sterility while lower temperature (<23^{o}C) results in fertility. These characteristic features of TGMS ease out the hybrid seed production and subsequently it was demonstrated that the TGMS was more effective in increasing grain yield and seed production efficiency (Yuan, 1990). The prevailing wide range of temperature differences in Tamil Nadu favour both hybrid seed production and the maintenance of TGMS in different locations (Siddiq and Ali, 1999). Hence, this study was started and the new TGMS line TNAU 60S was identified as spontaneous mutant from the rice variety PMK 3 with desirable floral characteristics and stable sterility.This TGMS line has the duration of 125 days with semi dwarf plant type. The panicle exertion percentage is 76.9% with wide angle of glume opening which makes the line with higher out crossing potential highly amenable for commercial exploitation. The grain quality of the TGMS line is highly preferable. TNAU 60 S has been used in hybridization and many heterotic hybrids were developed. TNAU 60 S is found promising for the characters stable pollen sterility, panicle exsertion, angle of glume opening and it can be successfully utilized for the development of two line hybrids for hybrid rice breeding.

Seed production potential in the TGMS lines during fertility reversion phase can be enhanced by growing them under medium hill regions of Gudalur (1500m MSL) in Nilgiris district (Aarasakesary *et al.,* 2015). At Gudalur, the temperature range during the month of July and August was less than 20ºC. The appropriate sowing date of TGMS lines was fixed during June-July in such a way that the critical stages of panicle development would be exposed to the required temperature.The individual lines were maintained under isolation and genetically pure seeds were produced at Gudalur. The TGMS line TNAU 60S was evaluated at different locations for their stability in sterility and it was proved that under high temperature (Coimbatore) it expressed 100% sterility and at low temperature it produced more than 90% seed set at Gudalur (Manonmani *et al*., 2016). This line with wider pollen sterility period under plains can be very well exploited for developing two line rice hybrids during the period of December to April. The same lines can be easily seed multiplied at Gudalur during July to November. Thus TGMS system has great potential for revolutionizing hybrid rice production through

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simple, less expensive and more efficient seed production technology.

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2. CSR 53 (Bulk 18) (IC0619320; INGR17029), a Rice (*Oryza sativa*) Germplasm with Tolerance to Salinity Stresses up to ECe 10.0dS/m

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Soil salinity negatively affects agricultural production worldwide. Globally, more than 800 million hectares of land globally 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 (both saline and alkaline) and 2.96 million ha affected by saline soils. Genetic improvement of salt tolerance in rice appears to be economically feasible and a promising strategy for maintaining stable rice production globally. The line CSR 53 (Bulk 18) was developed for saline areas where ECe is up to 10.0 dS/m from the cross CSR23/CSR27 through bulk breeding method at the Division of Crop Improvement, Central Soil Salinity Research Institute, Karnal, Haryana.

Morpho-agronomic characteristics: This is a medium duration, semi dwarf culture, with green foliage, erect flag leaf, compact panicle, medium slender grains and complete panicle exertion. During 2012, CSR 53 (Bulk 18) showed superiority yield advantage of 16.4%, 17.86%, 73.68, 50.02, 198.66% and 17.44% over CSR 44 (Qualifying line 1), NDRK 50032 (Qualifying line 2), RP Bio 4919-363-5 (Qualifying line 3), CSR 36 (National check), Local Check, Jaya (Yield check) and CSR 23, respectively under high salinity condition in Karnal district of Haryana. During 2013, CSR 53 (Bulk 18) showed superiority yield advantage of 27.94 %, 25.63%, 29.24 % and 133.17% over CSR 36 (National check), Local check, CSR 23 (National check) and Jaya(Yield check), respectively across salt affected locations of Karnal, Rohtak and Panipat in Haryana and Gangavathi in Karnataka. During 2014, CSR 53 (Bulk 18) showed superiority yield advantage of 14.39%, 13.36%, 13.88% and 104.92% CSR 36 (National check), Local check, CSR 23 (National check) and Jaya (Yield check), respectively across salt affected locations of Karnal and Panipat in Haryana.

The line CSR 53 (Bulk 18)was found superior in yield over CSR 36 (National check), Local check, Jaya (Yield check) and CSR 23 (National check) by 37.76%, 32.03% 145.58% and 19.86%, respectively across the three years (2012, 2013 and 2014) in salt affected locations of Haryana (Karnal, Rohtak and Panipat) and Karnakata (Gangavathi).

Associated characters and cultivation practices: CSR 53 (Bulk 18) is saline tolerant high yielding, medium slender grained variety and moderately resistant/tolerant to major insect pests and diseases such as stem borer, leaf folder, case worm, blue beetle, WBPH, leaf blast and brown spot. It is also less responsive to higher doses of nitrogen. The yield reduction and yield gain respectively at lower and higher doses of fertilizers are less in Bulk 18 indicating its high nutrient use efficiency. It has

high milling recovery (79.9%) and head rice recovery (66.2%), medium slender grains, good cooking quality with medium alkali spreading value (4.7), intermediate amylose content (24.0%) and medium gel consistency (30.7mm).

The performance of CSR 53 (Bulk 18) was consistently high under salinity for three successive years in Haryana and Karnataka. It showed yield superiority over national check (CSR 36), local check (CSR 23) and yield check (Jaya). This Germplasm could be used in future breeding programmes aiming at development of high yielding salt tolerant rice varieties for saline soils.

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3. HSRBW-2 (IC0623528; INGR17030), a Wheat (*Triticum aestivum* L.) Germplasm with High Tolerance to Head Scab

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Head scab of wheat caused by *Fusarium* species is a destructive disease of humid and semi humid wheat growing areas of the world and is generally characterized by bleaching of the wheat spike, shrivelled kernels and accumulation of mycotoxins, which may cause various ailments in humans and animals. In India, this diseasewas reported from Arunachal Pradesh, Wellington and Tamil Nadu (Chaudhary *et al.,* 1991). The yield losses up to 21.6% were recorded in wheat variety PBW 222 in Punjab (Kaur *et al.,* 2000). Under the new trade policies, wheat quality will be of paramount importance as this disease may hinder exports. Keeping this in view, breeding program was designed to introgress head scab resistance from resistant parent Sumai#3 to high yielding, but susceptible genotypes HD 2967, PBW 502 and DPW 621-50 following the back cross pedigree method.

Genotype HSRBW-2 was developed from the cross Sumai #3/HD2967 following a back cross pedigree breeding approach to introgress resistance. Selections were practised in the segregating generations for spring growth habit as Sumai#3 is of facultative winter habit, since in India only spring types are grown and preferred by the farmers.

Morpho-agronomic characteristics: The head scab donor parent Sumai #3 and susceptible parental line HD 2967 along with derived lines were evaluated consecutively for three years under artificial conditions. The genotype HSRBW-2 showing high level of resistance to the head scab over three years was identified (Table 1) as depicted from the average spikelet infection score of 3 over three years of evaluation under artificial conditions.

Table 1. Evaluation of genotypes for head scab resistance under artificial conditions in polyhouse at ICAR- IIWBR, Karnal.

Genotype	Pedigree	% Average spikelet infection			Highest Score	Average score
		2013-14	2014-15	2015-16		
Donor Parent	Sumai#3	3	2	4	4	3
Recipient Parent	HD 2967	66	68	65	68	66
HSRBW-2	Sumai#3/*2HD 2967	3	2	2	3	3

Table 2. Mean performance of HSRBW-2 and parents for agronomic characteristics during 2015-16

Genotypes	Days to heading	Days to maturity	Plant height	Thousand grains weight
HSRBW-2	83	129	92	38
Sumai#3	92	143	105	35
HD 2967	80	129	92	39

Associated characters and cultivation practices: HSRBW-2 takes about 83 days to flowering and in total 129 days from seed to seed (Table 2). This genotype is having a height of 92 cm and thousand grains weight of about 38 g. The high level of head scab resistance in HSRBW-2 plus spring background makes it a potential donor for use in hybridization programmes targeted to improving head scab resistance in future wheat genotypes.

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4. HSRDW-2 (IC0623529; INGR17031), a Durum Wheat (*Triticum durum* L.) Genotype Highly Tolerant to Head Scab

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Fusarium head blight is a destructive disease in all the wheat growing areas of the world where the climate is humid and semi humid. Typical symptoms of head blight are bleaching of the wheat spike, shrivelled kernels and accumulation of mycotoxins which may cause adverse effects on health. This disease is of economic importance, as it may affect exports since *Fusarium* spp. are known to produce mycotoxins in grains under the WTO regulation regime (Saharan *et al.,* 2007). During 2005, due to continuous rain in March in Punjab, head scab appeared in a severe form on durum variety PDW 274 in Gurdaspur area (Bagga and Saharan, 2005) and is becoming a problem in NEPZ and NWPZ as none of the released bread or durum wheat variety is resistant to head scab. A modified backcross pedigree approach was used to introgress head scab resistance from donor parent Sumai#3 to susceptible but high yielding genotype PDW 291. Selections were practised in the segregating generations and fixed genotypes from this cross were evaluated for head scab resistance under artificial conditions. This genotype, in the tetraploid background, may be used for transferring head scab tolerance in durum improvement.

Morpho-agronomic characteristics: The durum wheat genotype HSRDW-2 showing high level of resistance to the head scab over three years was identified under artificial screening for the disease. HSRDW-2 showed high level of resistance as depicted from the average spikelet infection score of 3 over three years of evaluation under artificial conditions (Table 1). The infection score in this genotype is equivalent to that of donor Sumai#3.

Table 1. Evaluation of genotypes for head scab resistance under artificial polyhouse conditions at Karnal.

Genotype	Pedigree	% Average spikelet infection			Highest spikelet infection Score	Average spikelet infection
		2013-14	2014-15	2015-16		
Donor Parent	Sumai#3	3	2	4	4	3
Recipient Parent	PDW 291	72	79	75	79	75
HSRDW-2	Sumai#3/*2PDW 291	2	3	3	3	3

Table2. Mean performance of proposed stocks and checks for Agronomic characteristics during 2015-16.

Traits	Entry	Donor parent	Recipient parent
	HSRDW - 2	Sumai # 3	PDW 291
Days to heading	88	92	87
Days to maturity	134	143	137
Plant height (cm)	85	105	86
1000-grains weight (g)	43	35	42

Associated characters and cultivation practices: HSRDW-2 flowers in about 88 days and takes about 134 days from seed to seed (Table 2). This genotype is having a height of 85cm and thousand grains weight of about 43g. The high level of head scab resistance in HSRDW-2 in a spring background makes it a potential donor for use in hybridization programmes targeted to improving head scab resistance in future durum wheat genotypes.

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5. HI 8751 (IC0623451; INGR17032), a Wheat (*Triticum turgidum* ssp. *durum*) Germplasm with Resistance to Stem Leaf and Stripe Rusts, Karnal Bunt and Flag Smut

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Diseases like stem, leaf and stripe rusts, flag smut and Karnal bunt cause severe yield losses in durum wheat production. Karnal bunt is a major problem as far as wheat exports are concerned. In view of their continued evolution, broadening of genetic base for host resistance is necessary in order to minimize the losses caused by these pathogens.

HI 8751 (HD 4685/HI 8634),durum wheat genotype was identified to be resistant to stem, leaf and stripe rusts, Karnal bunt and flag smut in multi-location testing *viz*., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2012 to 2016 (Table 1). It showed high levels of adult-plant resistance to most prevalent and virulent

Table 1. Field responses of HI 8751 to stem, leaf and stripe rusts of wheat

Year of testing	Trials	Stem rust		Leaf rust				Stripe rust	
		South		South		North		North	
		HS	ACI	HS	ACI	HS	ACI	HS	ACI
2012-13	NIVT 5B	20MR	3.0	5MR	0.4	30S	9.3	20MS	3.6
2013-14	AVT I	20S	4.1	20MR	2.3	10MR	1.6	20S	5.3
2014-15	EPPSN	20S	10.6	20MR	2.6	5S	1.2	5MS	1.8
2015-16	MDSN	10MS	2.8	5S	1.3	0	0.0	20MS	4.8

(HS-Highest score, ACI–Average Co-efficient of Infection)
Source: AICW&BIP – Crop Protection Reports (2012-16)

Table 2. Adult-plant responses in Advance Varietal Trial I of HI 8751 to specific pathotypes of stem leaf and stripe rusts of wheat (2013-14).

Stem rust pathotypes				Leaf rust pathotypes			Stripe rust pathotypes	
40A		117-6		77-5		104-2	46S119	78S84
Indore	Pune	Indore	Pune	Delhi	Ludhiana	Delhi	Ludhiana	Ludhiana
5MR	10MR	10S	10MR	TR	0	5R	20MS	40MS

Table 3. Seedling responses of HI 8751 to individual pathotypes of stem, leaf and stripe rusts (2013-14).

Stem rust pathotypes													
11	11A	24A	34-1	40A	40-1	40-3	117-1	117-2	117-3	117-5	117-6	184	295
R	R	MS	R	R	R	R	S	R	R	R	MS	MX	R

Leaf rust pathotypes																							
11	12	12-2	12-3	12-5	12-7	12-9	77	77-1	77-2	77-5	77-7	77-8	77-9	77-10	77A-1	104-2	104-3	104-4	104B	106	107-1	162-1	162-3	162A
R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	R	R	R	R	R

Stripe rust pathotypes												
78S84	46S119	K	T	P	31	38A	L	14A	I	A	20A	N	13
MR	R	MS	R	MX	S	R	MS	S	R	R	R	R	R

Table 4. Disease scores of Flag smut and Karnal bunt

Year of testing	Trial	Flag smut (%)		Karnal bunt (%)							
		HS	Avg	Jammu	Hissar	Delhi	Dhaulakuan	Ludhiana	Karnal	HS	Avg
2012-13	NIVT 5B	-	-	-	-	-	0.0	3.5	-	**3.5**	**1.7**
2013-14	AVT I	**0.0**	**0.0**	4.2	0.0	13.0	0.5	0.5	0.0	**13.0**	**3.0**
2015-16	MDSN	**0.0**	**0.0**	-	-	-	-	-	-	**1.0**	-

pathotypes like 77-5 and 104-2 of leaf rust, 40A and 117-6 of stem rust, and 46S119 and 78S84 of stripe rust in isolated nurseries (Table 2). It showed seedling resistance to the leaf rust pathotypes and to most of the stem and stripe rusts pathotypes tested (Table 3). It also showed resistance to other diseases like flag smut and Karnal bunt (Table 4). Hence, it can be used as potential resistance donor to breed varieties against these multiple pathogens as it is often difficult to find multiple disease resistance in a single genotype.

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6. QBP 12-11 (IC0624127; INGR17033), a Wheat (*Triticum aestivum*) Germplasm with Low Hardness Index (Soft Endosperm)

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The milling and baking industry of India is rapidly expanding and is valued at ~Rs 69 billion. Biscuits occupy an important place in the bakery industry of India. In fact, India is the third largest producer of biscuits next to USA and China. However, the flour used in India for local production of biscuits is generally an "all purpose flour' and not specific to the production of a particular end-product. Thus, such a flour is not entirely suitable for biscuit making and as a result, chemicals/ improvers are required to be added to the flour during baking. Exporting nations such as Australia, Canada, USA etc. have lessened their dependence on the use of such chemicals and have made genetic improvement in the quality of their flour. Biscuits in these countries are made from flour that is derived from wheat grains that are soft in texture. Texture of the grain (endosperm) is determined by the hardness index it produces on crushing. Lower the grain hardness index (GHI), softer the grain. However, in India all commercially used varieties are hard grained. Therefore, genetic improvement to produce soft grained wheat suited for biscuit quality is a priority for wheat quality breeders. So far, one genetic stock namely QLD 28 having soft grain (GHI=27) has been registered with NBPGR. ICAR-IARI have developed a new strain QBP12-11(Wbll1*2/Kkts*2/3/T. dicocconPI272533/Ae.squarrosa (458)//Cmh81a.1261/ Vee#10-7) with much higher grain softness than QLD 28. This line is a selection of a CIMMYT entry and was evaluated in the Quality Component Screening Nursery (QCSN) conducted by IIWBR and its cooperators at 12 locations for three consecutive years (2012-13, 2013-14 and 2014-15) by IIWBR cooperators all over India. QBP 12-11 recorded lowest GHI (17.7) among bread wheat genotypes in all the three years. Since molecular markers for grain softness are available, QBP 12-11 stock can be used as a donor for marker based transfer of grain softness in new elite materials to develop soft grained genotypes suitable for biscuit quality breeding.

7. HI KK 10 (NP4 + *Lr*13) (IC0624491; INGR17034), a Wheat (*Triticum aestivum*) Germplasm Carrying *Lr*13 as Locally Adapted Differential for Indian Pathotypes of Wheat Leaf Rust (*Puccina triticina*)

and

8. HI KK 11 (NP4 + *Lr*18) (IC0624492; INGR17035), a Wheat (*Triticum aestivum*) Germplasm Carrying *Lr*18 as Locally Adapted Differential for Indian Pathotypes of Wheat Leaf Rust (*Puccina triticina*)

and

9. HI KK 12 (NP4 + *Lr*19) (IC0624493; INGR17036), a Wheat (*Triticum aestivum*) Germplasm Carrying *Lr*19 as Locally Adapted Differential for Indian Pathotypes of Wheat Leaf Rust (*Puccina triticina*)

and

10. HI KK 13 (NP4 + *Lr*26) (IC0624494; INGR17037), a Wheat (*Triticum aestivum*) Germplasm Carrying *Lr*26 as Locally Adapted Differential for Indian Pathotypes of Wheat Leaf Rust (*Puccina triticina*)

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Leaf rust caused by *Puccinia triticina* Eriks. (*Pt*) is most common among three rust diseases of wheat (*Triticum aestivum* L.). Leaf rust differentials being used in India consist of sets 0, A and B (Nayar *et al*., 2001). Majority of the leaf rust differentials in set 'A' and most varieties in set 'B' are winter types, which require a long photoperiod for flowering. Hence, maintenance of these differentials is difficult, particularly in the plains of India due to their long duration and often there is either seed set failure or production of shriveled grain. Hence, need was felt for developing near-isogenic *Lr* lines in the background of a locally adapted variety. NP 4 was selected as a background parent which is not known to carry any *Lr* gene or suppressor factor (Kaushal *et al.*, 1982) for leaf rust resistance, and being early maturing, slow rusting, lodging-tolerant, non-shattering, heat and drought tolerant, and bold seeded variety. Hence, a backcross programme was initiated in 1997-98 for transferring the *Lr* genes in NP4 background.

NP4 lines carrying *Lr1, Lr2a, Lr2c, Lr3a, Lr9, Lr10, Lr15, Lr17a* and *Lr20* genes singly have already been registered with ICAR-NBPGR. They are: HI KK1 (NP4+*Lr1*, INGR 16024), HI KK2 (NP4+*Lr2a*, INGR 16025), HI KK3 (NP4+*Lr2c*, INGR16026), HI KK4 (NP4+*Lr3a*, INGR 16027), HI KK5 (NP4+*Lr9*,INGR16028), HI KK6 (NP4+*Lr10*,INGR16029), HI KK7 (NP4+*Lr15*, INGR 16030), HI KK8 (NP4+*Lr17a*, INGR16031), and HI KK9 (NP4+*Lr20*, INGR 16032).

Thatcher backcross lines carrying the target *Lr* genes *viz*., *Lr13, Lr18, Lr19* and *Lr26* were used as donors. A total of six backcrosses were done in succession followed by selection and testing which was completed in 2015-16. Intense selection was made during each generation for NP 4 plant type (awnless spikes and pubescent glumes) coupled with resistance phenotype of the target gene. The latter was identified in the field through syringe inoculation after 30-35 days of sowing with aqueous suspension of the uredospores of an avirulent pathotype. Leaf rust pathotype (pt) 12-2 (1R5) was used for selecting resistant plants carrying singly the gene(s) *Lr26*; pt 12-5 (29R45) for *Lr13* and *Lr19*; and pt 108-1 (57R27) for *Lr18.*

The lines developed were seedling tested with several avirulent pathotypes for confirming homozygosity for target *Lr* gene (DR. Knott, Pers. comm.). Close

Table 1. Comparison of seedling infection types (at 16-20^0 C) to selected avirulent leaf rust pathotypes of the newly developed near-isogenic lines (HI KK 10-13) with the corresponding donor *Lr* lines (RL Nos.) and the recurrent parent NP 4

Wheat genotypes	Seedling infection type[1]	Avirulent leaf rust pathotypes used for testing
HI KK 10 (NP4+*Lr13*)	0;	11, 12, 16-1, 63, 106
RL 4031 (Tc+*Lr13*)	0;	
NP 4	33+	
HI KK 11 (NP4+*Lr18*)	0;2$^+$	12, 12-4, 77A-1, 106, 162A
RL 6009 (Tc+*Lr18*)	0;2$^+$	
NP 4	33$^+$	
HI KK 12 (NP4+*Lr19*)	;1	10,12-1,16-1,104-2,106,107
RL 6040 (Tc+*Lr19*)	;1	
NP 4	3$^+$	
HI KK 13 (NP4+*Lr26*)	0;	10, 11, 12-4, 12-8, 16-1, 17, 63, 77, 77A-1, 106, 108, 162A
RL 6078 (Tc+*Lr26*)	0;	
NP 4	3$^+$	

[1]As described by Roelfs *et al.* (1992)

similarity between seedling infection types of the newly developed backcross lines and the corresponding donor lines confirmed successful transfer of the target *Lr* genes in NP 4 background (Table 1).

Homozygous resistant lines carrying singly four genes *viz*., *Lr13, Lr18, Lr19* and *Lr26* have been developed. These near-isogenic lines having early maturity and other desired agronomic traits of NP4 are easy to maintain under Indian conditions, and hence, should be widely useful for virulence analysis and genetic studies.

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11. HI 8765 (IC0624495; INGR17038), a Wheat (*Triticum turgidum*) Germplasm with Resistance to Stem, Leaf and Stripe Rusts, Karnal Bunt & Flag Smut. High Yield Potential

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HI 8765 (HI 8504/CPAN 6206//HI 8627), durum wheat genotype was identified to be resistant to stem, leaf and stripe rusts, Karnal bunt and flag smut in multi-location testing *viz*., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2013 to 2017 (Table 1). It showed high levels of adult-plant resistance to most prevalent and virulent pathotypes like 77-5 and 104-2 of leaf rust, 40A and 117-6 of stem rust, and 46S119 and 78S84 of stripe rust in isolated nurseries (Table-2). It showed seedling resistance to most of the prevalent and virulent pathotypes of stem and leaf rusts like race 40-group of stem rust and races 77-group and 12-group of leaf rust. Even though, it showed seedling susceptibility to stripe rust pathotypes, it has shown high levels of field resistance (Adult plant resistance) (Table 3). It also showed resistance to other diseases like flag smut and Karnal bunt (Table 4). HI 8765 showed significant superiority in grain yield of 38.1% in NIVT and on par in AVT-I in comparison to zonal check variety AKDW 2997-16 in Peninsular Zone (Table 5).As the availability of multiple disease resistant high yielding genotypes is rare, HI 8765 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 8765 to stem, leaf and stripe rusts of wheat

Year of testing	Trial	Stem rust		Leaf rust				Stripe rust	
		South		South		North		North	
		HS	ACI	HS	ACI	HS	ACI	HS	ACI
2013-14	NIVT 5B	10MS	2.9	10S	4.9	10S	2.2	10MS	2.0
2014-15	AVT I	40MR	3.1	5S	1.9	5MS	0.5	40S	4.9
2015-16	EPPSN	10MR	1.0	20S	6.0	10MR	0.7	0	0
2016-17	MDSN	20MS	8.3	20MR	2.1	TR	0.1	10S-20MS	5.5

(HS-Highest Score, ACI-Average Coefficient of Infection); Source : AICW&BIP Crop Protection Reports (2013-17)

Table 2. Adult-plant responses in Advance Varietal Trial I of HI 8765 to specific pathotypes of stem, leaf and stripe rusts of wheat (2014-15)

Stem rust pathotypes						Leaf rust pathotypes					Stripe rust pathotypes			
40A			117-6		77-5			104-2			46S119	78S84		
Indore	Pune	Power kheda	Indore	Pune	Delhi	Ludhiana	Power kheda	Delhi	Ludhiana	Ludhiana	Delhi	Ludhiana	Delhi	
20RMR	20MR	TR	5S	30MS	20R	0	0	10R	0	10S	TR	0	40S	

Table 3. Seedling responses of HI 8765 to individual pathotypes of stem, leaf and stripe rusts (2014-15)

Stem rust pathotypes																		
11	11A	15-1	21	21A-2	24A	34-1	40A	40-2	40-3	122	117-1	117-3	117-4	117-5	117-6	184	184-1	295
R	R	R	R	R	MS	R	R	R	R	R	MR	MR	R	R	MS	S	R	MS

Leaf rust pathotypes																												
11	12	12-2	12-3	12-5	12-7	12-9	16-1	77	77-1	77-2	77-5	77-7	77-8	77-9	77-10	77-12	77A-1	104-2	104-3	104-4	104B	106	107-1	108-1	162-1	162-3	162A
R	R	R	R	R	R	R	MS	R	R	R	R	R	R	R	R	R	R	S	R	S	R	R	R	R	MS	R	R

Stripe rust pathotypes															
78S84	46S119	K	T	P	38A	L	14A	I	A	20A	N				
S	S	S	MS	S	R	MS	R	S	R	R	R				

Table 4. Disease scores of Flag smut and Karnal bunt

Year of testing	Trial	Flag smut (%)						Karnal bunt (%)								
		Ludhiana	Hissar	Durgapura	Karnal	HS	Avg	Jammu	Hissar	Delhi	Dhaula-kuan	Ludhiana	Karnal	Pant nagar	HS	Avg
2013-14	NIVT 5B	-	-	-	-	-	-	-	-	-	0.0	1.0	-		1.0	0.5
2014-15	AVT I	0	0	0	1.2	**1.2**	**0.4**	8.4	0.0	13.2	1.6	0.0	0.0	0.6	**13.2**	**3.4**
2016-17	MDSN	-	-	-	-	**10.0**	**3.3**	-	-	-	-	-	-		0.0	0.0

Table 5. Grain yield (q/ha) of HI 8765, compared to zonal check variety AKDW 2997-16

Year of testing	Trial	No. of locations	HI 8765	AKDW 2997-16	CD
2013-14	NIVT 5B	2	21.4 (38.1)	15.5	2.8
2014-15	AVT I	4	17.0 (NS)	18.2	2.1

Note: Value in parenthesis is percentage increase over check variety, NS : Non-significant

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12. LBPY 11-2 (IC0624496; INGR17039), an Early Maturing Wheat (*Triticum aestivum*) Germplasm with Bold Seed for Warmer Areas of India

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Wheat is an important staple food crop grown over range of environments and grain yield is adversely affected in hot dry environments in Central and Peninsular India. It is reported that heat stress adversely affects grain yield, biomass, maturity duration and grain size in wheat (Balla *et al*., 2014). Genotypes having high thousand grain weight (TGW) are considered better for improving yield as it has a strong positive correlation with grain size. Accordingly, LBPY 11-2 was developed (cross NL297/BL2022) and identified as an early maturing bold seeded genotype possessing bold grains.

Morpho-agronomic characteristics: LBPY 11-2 had high 1000-grain weight (49.3g) over three years (2012-15) in Yield Component Screening Nursery (YCSN) and also possessed more grains/spike and tillers/meter and thus was promoted from YCSN to National Genetic Stock Nursery (NGSN). Further its performance across locations (Dharwad, Niphad, Akola and Pune) in peninsular zone and central zone (Indore, Bilaspur, Vijapur, Junagadh, Jabalpur, Powarkheda, Sagar, Kota and Bhavnagar) under NGSN (2015-16), established 10 days advantage in flowering and maturity duration as compared to the best check Sonalika.

Associated characters and cultivation practices: The mean performance of the LBPY 11-2 under NGSN across zones revealed its superiority for combination of traits like; early flowering, early maturity, medium plant height, high tillers/meter, spike length and 1000-grain kernel weight, established its usefulness as potential donor for earliness and high grain weight (50g) across warmer regions of India.

Table 1. Performance of LBPY 11-2 in central and peninsular zone for different traits.

Trait	Central Zone		Peninsular Zone	
	Entry	Check	Entry	Check
	LBPY 11-2	Sonalika	LBPY 11-2	Sonalika
Days to maturity	**105**	110	**100**	110
1000 grain weight (g)	**50**	42	**50**	37

Table 2. Overall performance of LBPY 11-2 for agronomic & quality traits in NGSN during 2015-16.

Trait	Genotype	Checks	
	LBPY 11-2	Sonalika	HD 2967
Days to heading	73	75	84
Days to maturity	119	121	124
1000 grain wt. (g)	46	40	37
Spike length (cm)	12	9	11
Protein content	11.7	10.7	10.7
Grain iron concentration (ppm)	39.2	36.4	34.7
Grain zinc concentration (ppm)	40.8	37.2	33.6

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13. FLW31 (IC0624500; INGR17040), a Wheat (*Triticum aestivum*) Germplasm with Resistance to Black and Brown and Rusts Ug99 Pathotypes. Carries *Sr*24/ Lr24 and Unutilized *Sr*43 in Good Agronomic Background

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Rusts are important diseases of wheat (*Triticum aestivum* L.) throughout the world. The preferred way of controlling these pathogens is through the use of resistant varieties. There are several genes that can express resistance to these diseases. However, changes in pathogen virulence can render them less useful for use in breeding new varieites (Bhardwaj et al., 2016). The emergence of the Ug99 group of stem rust races (TTKSK, TTKSF, TTKST, TTTSK) which have defeated *Sr31* and many other stem rust resistance genes has reaffirmed the need to deploy diverse and effective resistance sources to safeguard wheat production (Pretorius *et al.*, 2000). Keeping in view the need to deploy diverse resistance gene against brown and black (including Ug99) rusts, the genotype FLW31 was developed through pedigree method from cross between HI1500(*Lr24/Sr24*) and exotic line KS10-2 C83.4(*Sr43*) backed by marker assisted selection. FLW31 having two gene based resistance would be useful in diversifying resistance for brown and black rusts in all wheat growing zones of India.

Seedling and adult plant resistance response against most virulent and prevalent pathotypes under controlled conditions showed that F LW31 is resistant to black and brown rusts (Table 1). FLW31 carries *Sr43* and *Lr24/Sr24* genes for resistance to wheat rusts. *Sr43* also confers resistance to Ug99 virulences of stem rust (Singh *et al*., 2015).

Plants of FLW31 have moderate waxiness on leaf sheaths and peduncles. It has average plant height of 105cm and matures in about 155 days under Shimla Conditions. Its grains are reddish-amber coloured, semi hard and thousand-grain weight of 41.6g.

Table 1. Seedling response of FLW31 for brown and black rust pathotypes under artificial controlled conditions

Pathotypes	Black rust						Brown rust			
	34-1	40A	40-1	40-3	117-1	117-6	12-5	77-2	77-5	104-2
Reaction	0;	0;	0;	;	;	;	0;	;1	;1	;1

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14. FLW32 (IC0624501; INGR17041), a Wheat (*Triticum aestivum*) Germplasm with Resistance to Black Rust Including Ug99 Pathotypes; It Carries Unexploited *Sr*26 in the Background of Raj3765

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Wheat black or stem rust (*Puccinia graminis* f. sp. *tritici*), is highly variable and devastating pathogen. It evolves quickly to evolve new pathotypes/races, rendering resistant wheat varieties susceptible and pose a serious threat to wheat production in different parts of the world (Bhardwaj *et al.,* 2016). The new pathotype, designated as TTKSK and its variants, popularly known as Ug99, have the ability to overcome the resistance conferred by a

majority of the stem rust resistance genes, including *Sr31* (Prasad *et al*., 2016). Keeping in view the need to deploy diverse resistance gene against FLW32 was developed from cross Raj3765/Eagle (*Sr26+Sr9g*). *Sr26* is known to confer long time black rust resistance in Australia. *Sr26* being in winter wheat background cannot be used directly in wheat breeding programme in India. *Sr26* has not been used in Indian wheat breeding programme. Therefore, *Sr26* was transferred into spring wheat variety Raj3765 using marker assisted backcross breeding and pedigree selection. FLW32 would be useful to wheat breeders in diversification of black rust resistance in Central and Peninsular zones of India.

FLW32 showed high resistance (0; to; 1) to black rust when evaluated against most virulent and predominant pathotypes under controlled condition (Table 1). It also showed resistance against Ug99 pathotypes of black rust when tested in Kenya in 2013.The adult plant reaction (APR) of FLW 32 to black rust showed resistant response. Two backcrosses followed by pedigree selection for resistance and yield attributes were undertaken to develop this stock. FLW32 provides complete resistance against stem rust pathotypes and adult plant resistance against brown rust also. Presence of *Sr26* in FLW32 has been confirmed through molecular marker. It also carries rust resistance genes *Lr10, Lr13, Sr2,* and *Sr9g*. Plants of FLW32 showed moderate waxiness on leaf sheaths, peduncles and glumes. FLW32 has an average plant height of 99 cm and takes 152 days to mature under Shimla conditions. The grains are amber coloured, semi hard with thousand-grain weight of 42.1g.

Table 1. Seedling response of FLW32 for brown rust pathotypes under artificial controlled conditions

Pathotypes	Black rust pathotypes							
	11	21-1	34-1	40A	40-1	40-3	117-1	117-6
Reaction	0;	0;	0;	0;	0;			;

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15. FLW33 (IC0624649; INGR17042), a Wheat (*Triticum aestivum*) Germplasm with Resistance to Black and Brown Rusts of Wheat; Resistant to Ug99 pathotypes; Carries *Sr*32, *Sr*24/*Lr*24 in Good Agronomic Background

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Rusts are economically the devastating diseases of wheat as they pose major threat to wheat production in most of the wheat growing areas of the world (Khan *et al*., 2017). Deployment of rust resistant wheat cultivars has been the most economical and environmentally friendly strategy to control rust diseases. However, changes in pathogen virulence can render them susceptible and not useful for breeding after some time (Bhardwaj *et al*., 2016). The emergence of the Ug99 group of stem rust races (TTKSK, TTKSF, TTKST, TTTSK) which has defeated *Sr31* and many other stem rust resistance genes has reaffirmed the need to deploy diverse and effective resistance sources to safeguard wheat production world over (Pretorius *et al*., 2000). Keeping in view the need to deploy diverse resistance gene against brown and black (including Ug99) rusts, the genotype FLW33 was developed from the cross HI1500/C77.19 (*Sr32*). Ug99 resistant C77.19 carrying *Sr32* is a winter wheat germplasm and cannot be used directly in Indian wheat breeding programme. FLW33 having unutilized Ug99 resistance gene Sr32, will add to the genetic diversity in wheat breeding programme for black rust prone areas of Peninsular and Southern Hill Zones of India.

FLW33 was found to be completely resistant to black and brown rusts when tested against most virulent pathotypes (Table 1). Black rust resistance is based on two resistance genes (*Sr24* and *Sr32*) each conferring complete resistance to field population of stem rust in India. It was also found resistant to Ug99 pathotypes of black rust when tested in Kenya in 2013. Presence of *Sr24/*

Lr24 and *Sr32* in FLW33 has been confirmed through robust molecular markers. FLW33 shows waxiness on leaf sheaths, flag leaves, peduncles and glumes. Average plant height is 93 cm and maturity duration is 145 days under Shimla conditions. Its grains are semi hard and reddish-amber having thousand-grain weight of 41.4g.

Table 1. Seedling response of FLW33 for brown and black rust pathotypes under artificial controlled conditions

Pathotypes	Black rust pathotypes						Brown rust pathotypes				
	11	34-1	40A	40-1	117-1	117-6	12-5	77-2	77-5	77-9	104-2
Reaction	0;	0;	0;	0;	;	;	0;	;1	;1	;1	;1

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16. DWRB173 (IC0624123; INGR17043), an Extra Early Heading Hooded Barley (*Hordeum vulgare*) Germplasm

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DWRB173 is early heading hooded barley genotype and highly desirable sources in breeding programmes, especially for rainfed areas and to alter the awns for better feeding ability for animals. The genotype DWRB173 is hooded barley, which was selected from ICARDA material (YAGAN/CAPUCHONA 20) for extra earliness and evaluated during *rabi*, 2014-15 to 2016-17 at karnal and during *rabi*, 2015-16 at Hisar (Table 1). The genotype showed spike emergence in nearly 53-55 days (Anonymous, 2017; Kumar *et al*., 2016) and details are given below-

Table 1. Heading (days) data of DWRB173 and checks

Location	Year	Genotype	Checks		
		DWRB173	DWRB92	DWRB101	BH902
Karnal	2014-15	54	89	90	88
Karnal	2015-16	55	85	87	89
Karnal	2016-17	54	89	88	91
Hisar	2015-16	53	84	85	87
	Mean	54	87	87	89
% advantage		-	38	38	39

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17. DWRB175 (IC0624124; INGR17044), an Extra Dwarf Barley (*Hordeum vulgare*) Germplasm

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Barley is very important coarse cereal for feed, food and malt purposes but heavily prone to lodging and resultantly facing higher yield losses. The genotype DWRB175 is two-row barley genotype, selected from segregating exotic ICARDA material (NACKTA/HJA A33//FNC1) for short plant height (Anonymous, 2017). After selection the genotype DWRB175 was further purified and observed with extra dwarf plant height during *rabi*, 2014-15, 2015-16 and 2016-17 and found promising with mean plant height of 60.8 cm (Table 1). The genotype DWRB175 will be highly useful genetic resource for barley breeders for shortening plant height and to check the lodging up to a greater extent. The details are given below-

Table 1. Plant height (cm) of DWRB175 and checks

Location	Year	Plant height (cm)		
		DWRB175 (Hulless)	BH902 (Check)	NDB 943 (Hulless Check)
Karnal	2014-15	61.5	96.0	105.0
Karnal	2015-16	60.0	94.0	104.0
Karnal	2016-17	60.5	94.0	102.0
Hisar	2015-16	61.0	95.0	104.0
	Mean	60.8	94.8	103.8
% advantage		-	35.9	41.4

References

Anonymous (2017). Annual report 2016-17, ICAR-IIWBR, *Eds*: L Kumar, K Venkatesh, HM Mamrutha, R Sendhil, V Gupta, Rinki, A Jha and GP Singh. ICAR-IIWBR, Karnal, India. P. 152.

18. DWRB176 (IC0624125; INGR17045), a Barley (*Hordeum vulgare*) Germplasm with Long Spikes with More Number of Grains and Resistance to Stripe Rust

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The genotype DWRB176 is highly desirable genetic resource for long two-row spikes, high number of grains with high 1000 grain weight of 55g (48-62 g). The genotype was developed by pedigree method at ICAR-IIWBR, Karnal. The genotype DWRB176 (BK1509-DWRB62/DWRB73) is unique for two rowed long spikes (12.5-13 cm) and possess more number of grains per spike (34-36) in comparison to the malt barley checks viz. DWRUB52 (8.5-9.5 cm and 24-26 grains), RD2849 (8.5-9.5 cm and 24-26 grains), DWRB101 (8-9 cm and 22-24 grains) and DWRB123 (8.5-10.0 cm and 24-26 grains), respectively (Table 1, Anonymous, 2017a).

In addition, DWRB176 is also desirable for stripe rust (*Puccinia striiformis* f. sp. *hordei*) resistance and was confirmed under artificial epiphytotics in coordinated multi-location initial barley disease screening nursery (IBDSN-2015-16) and in Elite barley disease screening nursery (EBDSN-2016-17) (Anonymous, 2016; Anonymous, 2017b). In seedling resistance test (SRT) DWRB176 also showed resistant reactions for the barley stripe rust races viz. 24, Q, G, 57 and MS reactions for the race M.

Table 1. Spike length of DWRB176 and checks

Year	Location	DWRB176 (BK1509)	Checks			
			DWRUB 52	DWRB 101	DWRB 123	RD 2849
2014-15	Karnal	13.2	9.0	8.7	10.0	8.5
2015-16	Karnal	12.7	8.5	9.0	9.0	9.5
2015-16	Hisar	12.8	8.9	8.3	8.4	9.0
2016-17	Karnal	13.1	9.5	9.5	10.2	10.0
	Mean	13.0	9.0	8.9	9.4	9.3

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19. DWRB180 (IC0624126; INGR17046), a Barley (*Hordeum vulgar*e) Germplasm with Resistance to Spot Blotch

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Spot blotch (*Bipolaris sorokiniana*) is a devastating disease in barley and nearly all the cultivars released are highly susceptible for spot blotch in India. The in-built resistance is always desirable over chemical control to save environment from hazardous effects of the fungicides and *vis-à-vis* to enhance profitability of small and marginal farmers. DWRB180 is six-row barley genotype, which showed resistance reactions for spot blotch under coordinated evaluation (*artificial inoculation*) in initial barley disease screening nursery (IBDSN) during 2016-17 (Table 1).

The genotype DWRB180 was selected from exotic material (P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/PETUNIA1/6/M111) for morphological characters coupled with spot blotch resistance and evaluated at Karnal during *rabi*, 2014-15 to 2015-16. During *rabi*, 2016-17, the genotype was evaluated in IBDSN at the centres namely, Pantnagar, Varanasi, Kanpur and Faizabad and showed resistance for spot blotch (Anonymous, 2017).

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Table 1. Multi-location screening for spot blotch (artificial inoculations) of DWRB180 and checks

Year	Location	DWRB180 (BK1626)	Checks			Infector
			BH902 (NWPZ)	HUB113 (NEPZ)	BH959 (CZ)	
(2016-17)	Pantnagar	25	67	78	99	68
	Varanasi	24	68	89	89	89
	Kanpur	24	36	36	79	89
	Faizabad	24	57	57	79	78

20. GJG 0814 (IC0623452; INGR17047), a Chickpea (*Cicer arietinum*) Germplasm with Fusarium Wilt Resistance

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Introduction

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). As per survey conducted by Kumar and Bourai (2012), the yield loss was up to 72.16 per cent due to this disease. This genotype was found to be resistant in wilt sick plot at ICRISAT, Kanpur, Rahuri and Junagadh during different years (2009-10, 2012-13, 2013-14, 2015-16) of testing.

The line GJG 0814 (IC0623452; INGR17047), 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 (JG 315 × GCP 9605) × JG 315.

Morpho-agronomic characteristics of GJG 0814

Entry	Year	Yield (Kg/ ha)	Maturity days	100 seed wt. (g)
GJG 0814	2010-11	1831 (8)	103 (7)	22.2 (8)
	2011-12	2007 (9)	112 (8)	19.1 (9)
	2012-13	2263 (9)	107 (8)	20.3 (9)
Mean		2033.7	107.3	20.5

(Source: AICRP report)

Associated characters and cultivation practices

Resistant to *Fusarium* wilt disease	Semi spreading growth habit
Medium maturity (107 days)	Single flower per peduncle
Average Yield (2034 Kg/ha)	Brown seed colour
Medium seed size (20.53 g/100 seeds)	Angular seed shape

Seed rate: 60 Kg/ha; Spacing: 45×10 cm; Fertilizer dose: 20:40:00 N:P:K

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21. DRMR MJA 35 (IC0622804; INGR17048), an Indian Mustard (*Brassica juncea*) Moricandia system based CMS line with Resistance to White Rust Disease

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White rust caused by *Albugo candida* (Pers. ex Lev.) Kuntze is one of the most devastating diseases of Crucifers and causes severe losses in Indian mustard (*Brassica juncea*). Symptoms of the disease may appear at vegetative stage itself and sustain even at flowering stage. Maximum damage is caused by stag head formation due to malformation of flowering buds directly causing the yield losses. Indian germplasm of *B. juncea* generally has been reported to have susceptibility against existing pathogen. Resistance to white rust has been shown to be governed by a single dominant gene. Development of hybrids has been a long sought goal

to enhance the yield potential in *B. juncea*. Dominance of resistance over susceptibility will result in resistant phenotype of F1 hybrid even if one of the two parents carries resistant gene. Considering these facts, efforts were initiated to introgress white rust resistant gene(s) from exotic germplasm (ZEM 2) expressing resistance. Crosses between donor (ZEM 2) and susceptible parent HB 9916 were attempted during 2002-03. Resulting F_1 was backcrossed with recurrent parent HB 9916 till BC_3 was obtained. Subsequent two generations were advanced following pedigree method. Finally one resistant line with good agronomic base was selected and named as MJB 35. This selected resistant line was crossed with existing *moricandia* based cytoplasmic male sterile line MJA 5 as pollen parent. Accordingly, MJB 35 was converted to cytoplasmic male sterile line having resistance against white rust following backcross method. Consequent upon five backcrosses with MJB 35, cytoplasmic male sterile line DRMR MJA 35 was developed and inducted to AICRP-RM uniform disease nursery trial. The resultant white rust resistant CMS line DRMR MJA 35 was evaluated for disease reaction at five locations during 2012-13 and at six locations during 2013-14 along with resistant and susceptible checks; EC 399299 and Rohini, respectively. Observations on leaves were recorded at 75 days and 100 days and for staghead formation at flowering stage.

DRMR MJA 35 expressed resistance reaction at Hisar and Morena centres during both years. On the basis of mean performance for disease severity of total eight environments in two years, proposed strain DRMR MJA 35 (disease severity 8.1%) was at par with resistant check EC 399299 (7.0%) at 75 days stage and at 100 days stage. DRMR MJA 35 (disease severity 5.4%) showed better performance than resistant check EC 399299 (9.2%). Similarly, the performance of DRMR MJA 35 (0.3%) was better than resistant check (4.4%) for stag head formation at flowering stage. On the basis of above mentioned results, it is concluded that proposed strain DRMR MJA 35 has expressed resistant reaction against white rust. Two independent loci *viz*. AcB1-A4.1 & AcB1-A5.1, governing resistance to *Albugo candida* causing white rust in Indian mustard tagged in two east European lines, Heera and Donskaja, respectively by Panjabi-Massand *et al.* (2010) were validated in DRMR MJA 35. DRMR MJA 35 is the first *moricandia* based white rust resistant cytoplasmic male sterile line of Indian mustard The proposed line shall be useful in developing white rust resistant hybrid cultivar in Indian mustard.

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22. RG-2661 (IC0374272; INGR17049), a Castor (*Ricinus communis*) Germplasm with Resistance to Leafhopper (*Empoasca flavescens*)

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Leafhopper, *Empoasca flavescens* Fabr. (Hemiptera: Cicadellidae) is one of the major crop damaging insect pests in castor (*Ricinus communis* L.). It could cause yield loss to the extent of 22-89% (Lakshminarayana and Duraimurugan, 2014). Host-plant resistance is the most reliable, economical and eco-friendly measure to control leafhopper. Availability of resistant source is the prerequisite to breed resistant cultivars. In order to identify leafhopper resistant sources, several castor germplasm selections were screened against leafhopper across locations in multi-years under heavy insect pressure by taking up late August sowing using infester row method.

Morpho-agronomic characteristics: RG-2661 (IC0374272) has been developed from a semi-wild castor population (Semi-wild-2) collected from Maharashtra through progeny selection followed by pedigree breeding and inbreeding for 12 generations. It is a medium duration (57-67 days to flowering and 123-141 days to maturity), tall plant (104-134 cm) type with very big leaves and thick stem having 18-19 stem nodes; and possessing triple bloom nature.

Associated Characters and Cultivation Practices: RG-2661 was found to be stably resistant to leafhopper (0-1 hopper burn score on 0-4 scale) across locations over years when screened under heavy insect pressure for six years at Hyderabad and for four years at Palem and Yethapur locations while the susceptible checks, DPC-9 and DCH-177 had 4 hopper burn score on 0-4 scale. RG-2661 is identified as a valuable donor for leafhopper resistance to utilize in resistant breeding programmes. It can also serve as base material for developing mapping populations for tagging the gene (s) responsible for leafhopper resistance.

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23. NRCPB rapa 8 (IC374272) (IC0623820; INGR17050), a Yellow Sarson (*Brassica rapa*) Germplasm with Potential as a Parent for Resynthesis of *B.juncea*

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The resynthesis of *B. juncea* is a very cumbersome process involving *in vitro* ovary and embryo culture (Srivastava *et al*., 2004; Bansal*et al.,* 2009; Chatterjee *et al*., 2016) and special technical expertise and laboratory facilities (*in vivo* and *in vitro*), which may not be available with plant breeders. Although low frequency of hybrid seed recovery has been reported in interspecific crosses between *B. rapa* and *B. nigra*, the results are not consistent and depends on genotype combination, environmental conditions and so on (Prakash 1973).

NRCPB *rapa* 8 enables efficient resynthesis of *B. juncea* by bypassing the *in vitro* embryo rescue procedures.NRCPB *rapa* 8 when pollinated with different *B. nigra* genotypes, consistently yields high frequency (about 16 to 42.67 %) of hybrid seeds (amphihaploid). Therefore, it greatly simplifies resynthesis of *B. juncea* and increases the efficiency of hybrid recovery with all accessions of *B. nigra*. Further, this trait can be transferred to other *B. rapa* genotypes to extend the scope of resynthesis with other *B. rapa* accessions. Use of this accession would thus help in creating novel genetic variability in *B. juncea*, that could further be utilized in breeding improved varieties and hybrids.

The material was purified by selecting and intermating plants showing similar agronomic and morphological features from a yellow sarson seed sample which was collected from local market in Kolkata in 1996. Subsequently, uniform, homozygous line was developed by selfing a selected plant. This line is named as NRCPB *rapa* 8.

Morpho-agronomic characteristics and cultural practices: Important agronomic features of NRCPB *rapa* 8 are presented in Table 1. It is a self-compatible, yellow sarson genotype possessing tetralocular silique. It is comparable to other yellow sarson genotypes for reaction to major biotic and abiotic stresses and can be cultivated following standard agronomic practices recommended for other mustard varieties.

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Table 1. Morpho-agronomic characteristics of NRCPB *rapa* 8

Trait	Locule in silique	Days to flowering	Days to flower termination	Days to maturity	Plant height (cm)	No. of siliques on main raceme	No. of primary branches	No. of secondary branches	No. of seeds per silique	1000 seed weight (g)	Oil content (%)	Seed colour
Mean	4	48	70	128	133.9	35.12	16.94	29.78	36.33	3.56	39	Yellow

24. CS 15000-1-2-2-2-1 (IC0624502; INGR17051), an Indian mustard (*Brassica juncea*) Germplasm with High Tolerance to Salinity (ECe 12 dS/m) and Alkalinity (pH 9.4)

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Globally, 932.2 million hectare area is affected with salinity and sodicity stresses (Metternicht and Zinck, 2003), out of which, an area of nearly 6.73 million hectare is affected by these stresses in India (Singh *et al.*, 2014). Indian mustard [*Brassica juncea* (L.) Czern and Coss] is an important oil-seed crop in the world and is grown in more than 50 countries across the globe, which often experiences saline stress as it is grown extensively in the arid and semi-arid regions of the world. Salinity stresses contribute to yield losses and this low economic yield is related to the crop's susceptibility. There is a greater need to improve crop plants for salinity tolerance. Hence, it becomes necessary to develop salt tolerant genotypes in Indian mustard. One of the approaches is the characterization of the available germplasm for identification of tolerant genotypes that provides an initial germplasm base for breeding salt-tolerant crops. Consistent breeding efforts at ICAR-Central Soil Salinity Research Institute (ICAR-CSSRI), Karnal resulted in the development of an improved salt tolerant genotype CS15000-1-2-2-2-1 by crossing two salt tolerant genotypes CS 54 and CS 610-10-1-5 (CS 52: a highly salt tolerant variety; CS 610-10-1-5: a high yielding (Seed and oil) salt tolerant genotype, both developed at ICAR-Central Soil Salinity Research Institute, Karnal). Pedigree method was followed for selection and evaluation of germplasm in salt affected soils for high seed yield and tolerance to soil salinity conditions.

Morpho-agronomic characteristics: On the basis of three year (2013-14 to 2015-16) trials conducted for saline/alkaline conditions in AICRP on Rapeseed and Mustard CS15000-1-2-2-2-1 seed yield of 1840 kg/ha which was 17% and 19% higher than yields of two checks i.e. CS 54 (1566 kg/ha) and Kranti (1552 kg/ha), respectively. It also provided 13% to 16% higher oil yield (721 kg/ha) than Kranti (637 kg/ha) and CS 54 (620 kg/ha). This strain matures, on an average, in 134 days and takes 60 days to flower. The strain attains the height of approximately 171cm and produces high number of primary branches (6), secondary branches (8), main shoot length (70) and 1000 seed weight (5g) (Table 1).

Associated characters and cultivated practices: CS15000-1-2-2-2-1 also showed resistance to Alternaria blight under natural conditions compared to check Rohini, YSB-9 and RTM-314 and also AB severity in pods. Further, CS15000-1-2-2-2-1 also showed much lesser incidence of WR, PM, DM, Stag head and SR compared to check Rohini, EC399301, EC399299 and PHR-2. Under artificial conditions also, similar performance was recorded. Against mustard aphid, data of 26 trails showed lesser average aphid infestation index compared to checks Varuna and at par with CS 54, Kranti and Rohini. CS15000-1-2-2-2-1 responded favorably to the additional doses of fertilizer (NPK). Further 100% RDF was found suitable for this genotype. Looking to its seed and oil yields and disease resistance under high salt stress condition CS 15000-1-2-2-2-1 is being proposed for registration as a national genetic stock/ donor for the development of salt tolerant mustard genotypes to affected soils and water conditions (saline and alkaline) of *Rabi* season in the states of Haryana, Punjab and Uttar Pradesh.

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Table 1. Multi-location performance on important traits like yield and yield components [Locations: Salinity [Agra (ECiw 12 dS/m) Karnal (ECe 10.7 dS/m), Hisar (ECe 10.6 dS/m)]; Alkalinity: Karnal (pH 9.3) and Lucknow (pH 9.4)]

Parameters	Year of testing	Proposed genotype	Check 1	Check 2
		CS15000-1-2-2-2-1	CS 54 (NC)	Kranti (NC)
Mean Seed Yield (Kg/ha)	2012-13	2173	1861	1818
	2013-14	1732	1550	1502
	2014-15	1616	1288	1337
	Mean	1840	1566	1552
Per cent increase (+) or decrease (-) over checks	2012-13		+17	+20
	2013-14		+12	+15
	2014-15		+25	+21
	Mean		+17	+19
Mean Oil Yield (Kg/ha)	2012-13	844	723	706
	2013-14	677	639	683
	2014-15	641	498	523
	Mean	721	620	637
Per cent increase (+) or decrease (-) over checks	2012-13		+17	+20
	2013-14		+6	-1
	2014-15		+29	+23
	Mean		+16	+13
Plant height (cm)	2012-13	169.3	179.4	185.2
	2013-14	160.5	167.2	167.4
	2014-15	183.9	187.5	185.9
	Mean	171.2	178.0	179.5
Main shoot length (cm)	2012-13	71.1	57.2	69.1
	2013-14	64.8	62.4	58.1
	2014-15	74.5	76.3	74.8
	Mean	70.1	65.3	67.3
1000 Seed weight (g)	2012-13	4.8	4.9	4.4
	2013-14	5.2	5.0	4.2
	2014-15	5.1	4.9	4.2
	Mean	5.0	4.9	4.3

[Source – AICRP on R&M Annual Report 2013-14 (Page PB 80, Table 2.3.30a) and 2014-15 (Page PB 75, Table 2.3.33) and 2015-16 (Table 2.3.38a and 2.3.38b, PB 76).

25. Him Stevia (CSIR-IHBT-ST-01) (IC0624505; INGR17052), a Stevia (*Stevia rebaudiana*) Germplasm with Reb-A/Stevioside ratio=1.25; Rebaudioside-A content (%)=7.34; Stevioside content (%)=5.87

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Stevia rebaudiana, a perennial herb of the Asteraceae family, has been recognized worldwide for its excellent sweetening property. Leaves of stevia produce diterpene glycosides (stevioside and rebaudiosides), which are non-nutritive, non-toxic, high-potency sweeteners, 300 times sweeter than sucrose (Tanaka 1982) and substitutes for sugar (Rajasekaran *et al*., 2007). Rebaudioside-A is of particular interest among the glycosides produced in the leaves of stevia because of the most desirable flavour profile (DuBois 2000), while, stevioside is responsible for after taste bitterness. CSIR-IHBT, Palampur has developed a new clonal genotype of *S. rebaudiana* with higher content of rebaudioside-A and reduced content of stevioside for utilization of this source of natural sweeteners.

Morpho-agronomic characteristics: Chemical characterization of stevia genotype 'HIM STEVIA'

(CSIR-IHBT-ST-01) has a desirable glycoside profile, Rebaudioside-A (7.34%), Stevioside (5.87%) and Total glycoside content of 14.49% at Palampur conditions. Him Stevia has been selected based on higher proportion of Rebaudioside-A than stevioside (ratio of Rebaudioside-A to stevioside is ≥1), thereby making a desirable improvement in sweetness profile of the plant.

Associated characters and cultivation practices: The selection has a potential of yielding 3.68 t/ha of dry leaf yield during the second year of production and performed consistently and is vigorous in growth as evaluated in field trials over a period of two years at Palampur location and has excellent nursery performance with respect to rooting and early establishment. It has compact stature and dark green leaves.

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26. CSIR-IHBT-ST-02 (IC0624506; INGR17053), a Stevia (*Stevia rebaudiana*) Germplasm with Delayed flowering by 120 days. Prolonged Vegetative Phase with More number of harvests per year

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Stevia rebaudiana has been recognized worldwide for its excellent sweetening property. Leaves of stevia produce nine diterpene glycosides which are non-toxic, high-potency sweeteners. Stevia is a short-day plant that flowers from January to March in the southern hemisphere and from September to December in the northern hemisphere (Valio and Rocha 1977; Zaidan *et al*., 1980). Mutagenesis is a potential tool to broaden variability and to isolate desirable economic traits in a shorter period compared to conventional breeding procedures. CSIR-IHBT, Palampur has developed a new clonal mutant genotype of *S. rebaudiana* with delayed flowering trait through gamma irradiation which prolong the vegetative phase of the stevia crop.

Morpho-agronomic characteristics: A clonal solid mutant genotype CSIR-IHBT-ST-02 for delayed flowering (prolonged vegetative phase) was identified in stevia population treated with 5kR gamma irradiation at CSIR-IHBT, Palampur. The mutant CSIR-IHBT-ST-02 forms flower buds during the 1st week of January instead of 1st week of September as in case of control (at least 120 days delayed flowering as compared to controlCanada-2-3-1) at Palampur location. The mutant trait is observed to be stable over the years (Fig. 1).

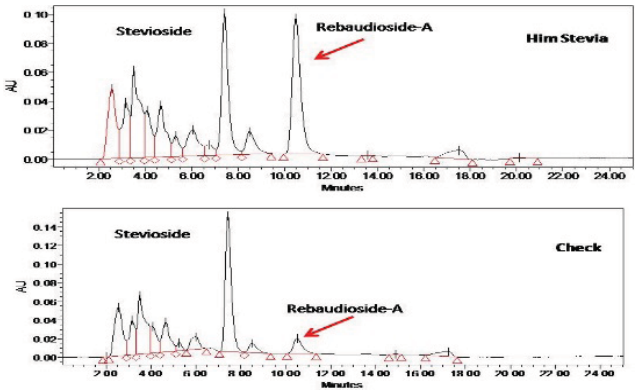

Fig. 1. Representative HPLC chromatogram of leaf samples of genotype 'Him Stevia' (CSIR-IHBT-ST-01) in comparison to check

The glycoside profile of the mutant genotype is given in Table 1.

Associated characters and cultivation practices: This delayed flowering trait in the mutant genotype CSIR-IHBT-ST-02 can prolong vegetative phase of the stevia crop which in turn increase number of harvests resulting in higher foliage yield which is the economic part of the plant.

Table 1. Flower bud initiation and Steviol glycoside profile of Mutant CSIR-IHBT-ST-02 at Palampur location

	Mutant CSIR-IHBT-ST-02			Check (Canada-2-3-1)		
Year	Flower bud initiation	Stevioside (%)	Rebaudioside-A (%)	Flower bud initiation	Stevioside (%)	Rebaudioside-A (%)
2009-10	2nd January	5.30	0.01	1st Sept	5.80	1.30
2010-11	5th January	7.40	0.10	6th Sept	6.70	1.80
2011-12	5th January	7.70	0.80	2nd Sept	6.70	2.00
2012-13	7th January	3.50	0.01	5th Sept	7.00	2.10
2013-14	6th January	8.60	0.10	5th Sept	6.60	2.40
Mean	5th January	6.50	0.20	4th Sept	6.56	1.92

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27. PG-IIIM-101 (IC0624503; INGR17054), a Rose-scented Geranium (*Pelargonium graveolens*) Germplasm with Higher Fresh Foliage, High Oil Content (0.14-0.18%), High Rhodinal Content (66-75%)

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Pelargonium graveolens L'Hér. (Rose-scented geranium; Family-Geraniaceae) is a high value aromatic crop which is cultivated for its essential oil obtained from distillation of above ground freshly harvested shoot/leaf biomass (Ravindra *et al*., 2004). The oil finds extensive use in aromatherapy, flavour and fragrance industry besides being used for the production of a commercial aroma chemical- rhodinol (a mixture of citronellol, geraniol and linalool) which has a wider use in fine grade perfumes (Rajeswara Rao *et al*., 1996, 2002). Rose-scented geranium is a sexually sterile crop due to genome complexity (2n=7x=77) (Lis-Balchin, 2003). Reproductive failure restricts its genetic improvement through conventional breeding methods. In absence of sexuality, we resorted to biotechnological interventions through tissue culture. We employed 'Bourbon' cultivar (Saxena *et al*., 2000; Ravindra *et al*., 2004) as a parental genetic stock for its improvement. Young leaf tissues of 'Bourbon' were used to induce callus formation and subsequently using appropriate plant growth regulators and cultural conditions, totipotentiality of dividing cells was used to regenerate complete plants. Since callus represents mass of proliferating cells which lose control over their growth and as a consequence genetic anomalies creep into the dividing cells. The whole process resulted in the development of deviant *in vitro* phenotypes which were successfully transferred under the field conditions for evaluation of different growth parameters, essential oil content and quality (GC-MS profiling). Among 176 somaclonal regenerants, the variety designated as PG-IIIM-101 was selected on the basis of higher oil content and quality essential oil profile. It was further evaluated at four muilti-locational sites for its stability and quality profile for two growing seasons. The study was conducted at CSIR-Indian Institute of Integrative Medicine, Jammu, India (32°44′ N longitude, 74°55′ E latitude, 304 m asl).

Morpho-agronomic characteristics: Rose-scented geranium is a multi-branched crop that grows 1-1.5 m in height and has a spread of about 1m. Its foliage is fragrant with broad lobed leaves. The lobes are dentate, pubescent with acute apices. The texture of leaves is shiny with cuticular wax.The variety developed (PG-IIIM-101) was evaluated at four locations namely Jammu (32.44° N, 74.55° E, 304 m asl), Pulwama, Kashmir (33.87° N, 74.89° E, 1650 m asl), Bhaderwah

(32.98° N, 75.71° E, 3110 m asl) and Rajouri (33.37° N, 74.31° E, 940 m asl) (J & K state) over two years. The comparative data of yields at different locations is provided in Table 1.

Associated characters and cultivated practices: The variety developed (PG-IIIM-101) is superior to parental genetic stock 'Bourbon' in terms of oil content (0.14-0.18%), essential oil profile (citronellol: 36.9-42.5%, linalool: 14.4-16.7%, geraniol: 15.6-19.9%, geranyl formate: 5.6-7.8%, γ-eudesmol: 1.3-1.9%) and fresh herb yield (1170-1430 g/plant). It shows wider range of adaptability as it can be grown as a short duration winter crop under sub-tropical Jammu conditions (November-April) and as a summer crop under temperate conditions of Kashmir and Bhaderwah (April-September). During cultivation experiments and muilti-locational trials, there was no incidence of any disease or insect-pest infestation. It grows in well drained, light to medium textured sandy loam soils having pH 5.0–8.5. It is cultivated vegetatively through terminal cuttings of 10-15cm long. A light irrigation at the time of planting is necessary for the establishment of cuttings. The crop is planted with inter-row spacing of 60 cm and intra row spacing of 70 cm. Decomposed farm yard manure (FYM) at the rate of 7-8 tonnes/ha is recommended before planting the crop. During growing season 2-3 irrigations are required. The crop matures in 160-170 days and the optimum stage of harvest in relation to essential oil quality and quantity is coincident with flowering stage. Fresh biomass is steam distilled for 2-3 hours using 1-2 kg/cm^2 steam pressure. The oil is stored in air tight aluminium or amber-coloured glass containers, capped tightly and kept in cool and dark place.

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Table 1. Comparative multilocational evaluation of yield and yield components of Rose-scented geranium (PG-IIIM-101) in comaprison to parental genetic stock*

Location/ Coordinates	Plant height (cm)	Plant spread (cm)	No. of branches/ plant	Herbage yield/ plant (g)	Oil content (%)	Herbage yield/ ha (Tonne)	Oil yield/ha (kg)
CSIR-IIIM (Jammu) 32. 44° N, 74. 55' E, 304 m asl	120-150 x̄ 135.70; SD ±18.38	95-105 x̄ 100.30; SD 6.36	31-39 x̄ 36.60; SD ±2.83	1170-1430 x̄ 1320.57; SD ±77.66	0.14-0.18 x̄ 0.15; SD ±0.015	35-36 (31-32)	40-42 (28-30)
	*105-125 x̄ 118.18; SD ±11.31	87-100 x̄ 98.80; SD 4.94	24-33 x̄ 28.09; SD ±5.65	1120-1280 x̄ 1183.18; SD ±48.08	0.10-0.12 x̄ 0.11; SD ±0.009		
Pulwama (Kashmir) 33.87° N, 74.89° E, 1650 m asl	107-142 x̄ 126.50; SD ±14.85	92-100 x̄ 96.40; SD 4.24	32-36 x̄ 33.80; SD ±0.70	1130-1340 x̄ 1234.00; SD ±74.44	0.14-0.16 x̄ 0.15; SD ±0.009	33-34 (31-32)	39-40 (32-33)
	98-118 x̄ 108.00; SD 9.19	89-104 x̄ 94.70; SD 4.23	31-35 x̄ 33.10; SD ±0.69	1110-1220 x̄ 1158.20; SD ±378.96	0.10-0.12 x̄ 0.11; SD ±0.007		
Bhaderwah 32.98° N, 75.71° E, 3110 m asl	93-122 x̄ 108.60; SD 14.85	80-98 x̄ 94.00; SD 9.19	31-35 x̄ 33.40; SD ±1.41	1045-1260 x̄ 11769.50; SD ±80.84	0.13-0.18 x̄ 0.15; SD ±0.017	31-32 (28-29)	38-39 (25-26)
	85-112 x̄ 109.00; SD 12.72	76-93 x̄ 84.00; SD 4.24	26-32 x̄ 28.60; SD ±2.12	980-1120 x̄ 1049.30; SD ±40.69	0.10-0.12 x̄ 0.11; SD ±0.008		
**BGSBU Campus (Rajouri) 33.37° N, 74.31° E, 940 m asl	63-78 x̄ 71.20; SD 8.48	72-83 x̄ 79.30; SD 5.65	18-25 x̄ 22.10; SD ±4.24	690-810 x̄ 748.00; SD ±41.85	0.08-0.10 x̄ 0.09; SD ±0.008	20-21 (17-18)	14-15 (11-12)
	60-72 x̄ 67.20; SD 3.53	65-76 x̄ 69.80; SD 6.36	18-23 x̄ 19.71; SD ±0.71	540-780 x̄ 649.00; SD ±74.94	0.07-0.09 x̄ 0.08; SD ±0.007		

*Data shown for parental genetic stock 'Bourbon' as control.
**BGSBU Campus, Rajouri is not recommended for commercial cutivation of Rose-scented geranium (PG-IIIM-101) due to its poor performance.

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28. DPO-9 (IC0623443; INGR17055), an Extended Bract Mutant of Isabgol (*Plantago ovata*)

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Isabgol is a wonderful bulking fiber for constipation besides it is used for treatment of diarrhea, constipation, and hemorrhoids. India is the sole exporter of this crop in the world market and earns considerable foreign exchange every year. It is also an excellent source of dietary fiber and has hypocholaesterolemic activity and is widely accepted as food additive in several processed materials like cookies, ice-cream, bread, and others (Trautwein *et al.,* 2000). It is being cultivated in arid and semi-arid regions of Gujarat, Rajasthan and parts of Madhya Pradesh as rainfed *rabi* crop (November to March) with supplementary irrigations and harvested at 110-120 days after sowing. Being an introduced crop from Mediterranean region, the genetic variability available in this crop is low and collection from foreign countries is becoming very difficult due to strict IPR regime. Hence, the additional variability has to be obtained either through mutation or by inter-varietal/inter-specific crosses. Even to develop the DUS guidelines, the number of descriptors available is very low. It is always desirable to have morphological characters that are easily identifiable before the flower opening/anthesis. Such markers will not only help in identifying the true to type plant and its maintenance, it also useful as development of high yielding varieties with distinct morphological characters. In this direction DMAPR has developed DOP 9, an isabgol mutant with a distinct morphological maker, extended bract.

Single plant with extended bract was identified and isolated in M_2 generation of DES treated Isabgol cultivar GI-2. It was self pollinated and advanced to next generation. In M_3 generation, it was bred true. It was advanced for few more generations and its extended bract marker trait was confirmed in the M_4 to M_7 generations. The distinct characters of DPO 14 in comparison with its parent GI-2 is presented in the Table 1.

DOP 9 mutant will be useful in many ways: i) it can be used as marker character for DUS guidelines, ii) as it is a qualitative trait, it can be used to study the inheritance pattern of extended bract, and iii) it can also used to develop high yielding varieties with this important marker that can be identified during pre-flowering stage to produce genetically pure seeds.

Table 1. Morphological description of Isabgol mutant DPO 9 as compared to its parent GI-2 (As per DUS guidelines of Isabgol)

Characteristics	DPO 9	GI-2 (Parent)
Leaf: Colour	Green	Green
Leaf: Pubescence	Medium	Medium
Leaf : Breadth (cm)	Medium (1.00 to 1.40)	Medium (1.00 to 1.40)
Plant: Growth habit	Drooping (Caespitose)	Drooping (Caespitose)
Plant: Height (cm)	Medium(35-50)	Medium(35-50)
Plant: Number of branches	Medium (5-15)	Medium (5-15)
Spike: Arrangements	Compact	Compact
Spike : Peduncle	Unbranched	Unbranched
Anther: Appearance	Normal	Normal
Peduncle: Axis	Partially filled	Partially filled
Spike: Flower arrangement	Compressed	Compressed
Spike: Length (cm)	Medium (3-7)	Medium (3-7)
Spike: Number	Medium (50-100)	Medium (50-100)
Spike: Number of seed bearing spikes	Medium (50-100)	Medium (50-100)
1000 seed weight (g)	Medium (1.6-1.8 g)	Medium (1.6-1.8 g)
Flower: Bract	Extended	Normal

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29. DWS-37 (IC0623444; INGR17056), an Ashwagandha (*Withania somnifera*) Germplasm with Revolute Rolled Leaves

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Ashwagandha is an erect, evergreen, perennial shrub belongs to the family *Solanaceace*. Ashwagandha native to Indian sub-continent is also known as 'Indian ashwagandha' and the roots are compared with Chinese ginseng (*Panax ginseng*) roots for their restorative properties. Breeding efforts in India has led to development of high yielding varieties viz., JA20, JA134, JA100 from Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RSVKVV), Mandsaur, Madhya Pradesh, India, AWS-1 from Anand Agricultural University (AAU), Anand, Gujarat and Rakshita and Poshita from the CISR-Central Institute for Medicinal and Aromatic Plants (CIMAP), Lucknow, India. Pure lines form an important genetic resource for improvement of yield and quality. All the varieties are havening normal leaves, where no rolling of leaf lamina has been observed. For the first time, DWS-37, a pure line selection with revolute leaf rolling (leaf lamina rolled downwards or towards the abaxial surface) was identified at the Directorate of Medicinal and Aromatic Plants Research, Anand, Gujarat (Table 1). A single plant selection with revolute leaf rolling phenotype as against the normal (no rolling) was selected during 2007 from open pollinated natural population of ashwagandha variety, JA 134 and was advanced through plant-to-row progeny by repeated selfing every year and a pure line (DWS 37) with revolute (rolled downwards or towards the abaxial surface) leaves was obtained. DWS 37 is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics of leaf rolling in Ashwagandha. Further, this trait can be used as DUS character for identification of elite germplasm lines and cultivars. As the trait can be easily identified during the vegetative stage, it helps in early generation selection of some of important quantitive traits.

Table 1. Morphological description of ashwagandha DWS-37 a revolute leaf rolling genetic stock

Characteristics	JA 134 (Parent)	DWS-37
Plant height	Medium (60-80 cm)	Tall (90 cm)
Stem types	Erect	Semi-Errect
Number of branches from base	A few	A few
Branch position	Acrocaulous	Acrocaulous
Branch arrangement	Less diverge	medium
Leaf orientation (Transverse posture)	Geniculate	Straight
Leaf orientation (longituditional)	Conduplicate	Straight
Leaf colour (Young leaves)	Green	Light green
Lamina length (cm)	Medium	Medium
Lamina width (cm)	Narrow	Medium
Leaf shape	Elliptic	Elliptic
Leaf base	Attenuate	Oblique
Leaf margin	Undulate; medium wavy	Undulate; medium wavy
Leaf apex	Obtuse	Acute
Leaf rolling	Normal (no rolling)	Revolte (leaf lamina rolled downwards or towards the abaxial surface)
Lamina abaxial surface	Less hairy	Less hairy
Lamina adaxial surface	Less hairy	Less hairy
Petiole	Less hairy	Glaborous
Midrib surface	Less hairy	Less hairy
Stem internodes length	Short	Short
Stem surface	Less hairy	Medium hairy
Flower: pedicel length	Short	Short
Flower: corolla colour	Pale yellow	Pale yellow
Berry colour	Yellow	Yellow
No. of berries/plant	Medium	Medium
No. primary roots	Medium (4-6)	More (more than 7)
Root length (cm)	15-25	15-20
Withanolide-A content	Low (0.390 mg g^{-1} dry weight)	Low (0.259 mg g^{-1} dry weight)

Table 4. Quality profile of roots of DWS-37 and JA-134 during 2014-15

Acc.	Replications	Withaferin-A (ug/mg)	12-deoxy-withastramano-lide (ug/mg)	Withanolide-A (ug/mg)
DWS-37	R1	1.847	0.240	0.260
	R2	1.685	0.234	0.258
	R3	1.668	0.230	0.260
	Mean	1.733	0.235	0.259
	Stdev.	0.099	0.005	0.001
JA-134	R1	0.057	0.206	0.394
	R2	0.070	0.205	0.388
	R3	0.075	0.207	0.389
	Mean	0.067	0.206	0.390
	Stdev.	0.009	0.001	0.004

30. DWS-127 (IC0623445; INGR17057), an Ashwagandha (*Withania somnifera*) Germplasm with Yellow Young Leaves

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Ashwagandha (*Withania somnifera* (L.) Dunal) (*Solanaceae*) is an important medicinal plant widely used as an antioxidant, adaptogen, aphrodisiac, anti-inflammatory agent and recently proved to combat against ulcers, arthritis, venom toxins and cancer like diseases. Four varieties *viz.*, JA 20, JA 134 RAV 100 and AWS-1) have been released and being cultivated by farmers. All varieties are having normal green colour leaves. For the first time, a selection with yellow young leaves (DWS-127) was identified at the Directorate of Medicinal and Aromatic Plants Research, Anand, Gujarat. DWS-127 bears yellow young leaves as against normal green leaves. DWS-127 bears yellow young leaves turn to normal green leaves up on leaf maturity (Table 1). A single plant selection with yellow colour young leaves as against the normal green leaves was selected from open pollinated natural population of ashwagandha variety, JA 134 during 2007 and was advanced through plant-to-row progeny by repeated selfing every year and a pure line (DWS 127) with yellow young leaves was obtained. DWS-127 is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics of leaf color in Ashwagandha. Further, this trait can be used as DUS character for identification of elite germplasm lines and cultivars. DWS-127 may be useful to study epigenetics of chlorophyll biosynthesis in plants.

Table 1. Morphological description of ashwagandha DWS-127 a yellow young leaf pure line observed during 2014-15 at ICAR-DMAPR, Anand

Characteristics	JA 134 (Parent)	DWS-127
Plant height	Medium (60-80 cm)	Medium (60cm)
Stem types	Erect	Erect
Number of branches from base	A few	A few
Branch position	Acrocaulous	Acrocaulous
Branch arrangement	Less diverge	Less diverge
Leaf orientation (Transverse posture)	Geniculate	Geniculate
Leaf orientation	Conduplicate	Conduplicate
Leaf color (Young leaves)	Green	Yellow
Leaf color (Mature leaves)	Green	Green
Lamina length (cm)	Medium	Medium
Lamina width (cm)	Narrow	Narrow
Leaf shape	Elliptic	Elliptic
Leaf base	Attenuate	Attenuate
Leaf margin	Undulate; medium wavy	Undulate; medium wavy
Leaf apex	Obtuse	Obtuse
Lamina abaxial surface	Less hairy	Less hairy
Lamina adaxial surface	Less hairy	Less hairy
Petiole length	Less hairy	Less hairy
Midrib surface	Less hairy	Less hairy
Stem internodes length	Short	Short
Stem surface	Less hairy	Less hairy
Flower: pedicel length	Short	Short
Flower: corolla colour	Pale yellow	Pale yellow
Berry colour	Yellow	Yellow
No. of berries/plant	Medium	Medium

31. IIHR Musa Hybrid (Cal4X M.r) (IC0395101; INGR17058), a Banana (*Musa spp.*) Inter-specific Hybrid with Intermediate Characters, Flowers (Inflorescence) Bright & Semi Erect. Intermediate Height with Broad Leaves (can be used for leaf production)

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Bananas have evolved in nature by inter-specific hybridization (Simmonds 1962) and mutations combined with development of parthenocarpy and seedless nature. Hence they are difficult to breed, but continuous efforts by the breeders has helped in identifying the desirable hybrids in countries like Honduras, France, Nigeria, Uganda, Brazil etc. It is important to develop intermediate diploid hybrids with desirable characters which can help in further breeding. We at IIHR are involved in developing mapping populations which can help in functional genomics studies under NPTC. *Musa acuminata* ssp. *burmannica* (Calcutta-4) of section Eumusa, is a breeders favorite wild species which is resistance to black leaf streak and sigatoka leaf spot, several races of Fusarium wilt and partially resistant to *Radopholus similis* and other nematodes. Morphologically this subspecies has waxless foliage, light brown markings on the pseudostem and compact pendulous bunch with purple bracts (Promusa website). It is known to be male and female fertile. *Musa rubra* of section Rhodochlamys (Cheesman, 1947) is a dwarf plant highly sensitive to availability of water and humidity normally found in North Eastern Hilly regions of India which produces erect bunch with attractive orange bracts the fruits are very small full of seeds. It is generally referred as ornamental banana. Both species have basic chromosome number of n=11. A cross was made between Calcutta-4 (female parent) and *M.rubra* (pollen parent).

Morpho-agronomic characteristics: The proposed hybrid will be useful as a genetic stock in the breeding programs as a source of dwarf genes as it is showing intermediate chracteristics. It can be grown in all banana growing areas.

Associated characteristics and cultivation practices: Interestingly the hybrids are dwarf, have green broad foliage like the female parent Calcutta-4 and bright orange semi erect inflorescence like resembling *Musa rubra*. Hybrids can be used for leaf purpose as well as ornamental purpose. The hybrid nature was confirmed by molecular analysis.

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Table 1. Morphological characters among parent and hybrid of IIHR *Musa* hybrid (*Musa acuminata* ssp. *burmannica* (Calcutta-4) X *M.rubra*)

F_1/parents	Plant height(M)	Girth (Cm)	No. suckers	No. Leaves	Leaf Length (Cm)	Leaf Breadth (Cm)	Bunch Length (Cm)	Bunch type	No. Hands	No. Fingers
P1-Calcutta4 (Female)	1.43	11.0	5	3	144.0	56 .0	18.4	Horizontal (Deep Purple)	4 .0	54
P2-*M. r.* (Male)	0.44	2.0	1	4	66.0	20.0	7.0	Erect (Bright Orange)	2.0	15
F1 Hybrid	1.14	7.42	5.5	5.25	98.8	30.2	12.63	Semi- erect (Orange)	4.25	48.58

32. IIHR2-47 (IC0623437; INGR17059), a Chrysanthemum (*Dendranthema grandifloruim*) Germplasm with Flower Colour: 77.B, Purple Group, Fan 2. Stellate Ray Florets (Cylindrical shape)

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Chrysanthemum is one of the most important flowering plant commercially grown for cut flowers, garden display, floral arrangements and pot culture. It belongs to the family Asteraceae. The selection IIHR2-47 is derived from cv. Pink Cloud through half-sib selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13° 58' N Latitude, 78°E Longitude and at an altitude of 890 meter above mean sea level), India. IIHR2-47 is unique for flower colour (77.B, Purple group, Fan 2) and Stellate ray florets (cylindrical shape).

Morpho-agronomic characteristics: Plants are tall (51.75 cm), semi-spreading (48.27 cm) and takes 82.56 days for flower bud appearance. It produces average 17.03 branches and 78.77 flowers per plant. Its flower diameter is 4.77 cm and flowering duration 31.87 days. It has vase life of 5.97 days (Table 1).

Table 1. Morpho-agronomic description of chrysanthemum half-sib selection IIHR2-47

Trait Description	Pooled data of three years
Plant height (cm)	51.75
Number of branches per plant	17.03
Plant spread (cm)	48.27
Days taken to first bud appearance	82.56
Number of flowers per plant	78.77
Diameter of flower head (cm)	4.77
Average weight of single spray (g)	35.98
Duration of flowering (day)	31.87
Vase life (day)	5.97
Flower colour (R.H.S. colour chart)	77.B, Purple group, Fan 2
Type of flower	Stellate (cylindrical ray florets)

Associated characters and cultivation practices: Chrysanthemum is commercially propagated through terminal cuttings and suckers. It grows well in sandy loam soil rich in organic matter and nutrients with pH of 6.5 to 7.2. Healthy uniform rooted cuttings are planted at spacing of 30 cm x 30 cm during March-April under Bangalore condition. Pinching of terminal growing portion is practiced after 30 to 40 days of transplanting. In general, recommended dose of fertilizer is 8-10 tones of farmyard manure, 50 kg N, 160 kg P_2O_5 and 80 kg K_2O per hectare as basal dose (Janakiram and Rao, 2004). The crop is to be irrigated once or twice in a week depending upon the soil and weather conditions. The major insect pests of chrysanthemum are caterpillar, mealy bug, leaf miner and thrips.

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33. IIHR5-23 (IC0623438; INGR17060), a Chrysanthemum (*Dendranthema grandifloruim*) Germplasm with Flower Colour: 162.D, Gray Yellow Group, Fan 4. Stellate Ray Florets (Cylindrical shape)

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Chrysanthemum is one of the most important flowering plant commercially grown for cut flowers, garden display, floral arrangements and pot culture. It belongs to the family Asteraceae. The selection IIHR5-23 is derived from cv. Red Stone through half-sib selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13°58′ N Latitude, 78° E Longitude and at an altitude of 890 meter above

mean sea level), India. IIHR 5-23 is unique for flower colour (162.D, Gray yellow group, Fan 4) and Stellate ray florets (Cylindrical shape)

Morpho-agronomic characteristics: Plants are medium (41.02 cm), erect (20.33 cm) and takes 48.00days for flower bud appearance. It produces average 12.78 branches and 80.39 flowers per plant. Its flower diameter is 4.02 cm and flowering duration 22.29 days. It has vase life of 4.92 days (Table 1).

Associated characters and cultivation practices: Chrysanthemum is commercially propagated through terminal cuttings and suckers. It grows well in sandy loam soil rich in organic matter and nutrients with pH of 6.5 to 7.2. Healthy uniform rooted cuttings are planted at spacing of 30 cm x 30 cm during March-April under Bangalore condition. Pinching of terminal growing portion is practiced after 30 to 40 days of transplanting. In general, recommended dose of fertilizer is 8-10 tones of farmyard manure, 50 kg N, 160 kg P_2O_5 and 80 kg K_2O per hectare as basal dose. The crop is to be irrigated once or twice in a week depending upon the soil and weather conditions. The major insect pests of chrysanthemum are caterpillar, mealy bug, leaf miner and thrips.

Table 1. Morpho-agronomic description of chrysanthemum half-sib selection IIHR5-23

Trait Description	Pooled data of three years
Plant height (cm)	41.02
Number of branches per plant	12.78
Plant spread (cm)	20.33
Days taken to first bud appearance	48.00
Number of flowers per plant	80.39
Diameter of flower head (cm)	4.02
Average weight of single spray (g)	28.42
Duration of flowering (day)	22.29
Vase life (day)	4.92
Flower colour (R.H.S. colour chart)	162.D, Grayed-yellow group, Fan 4
Type of flower	Stellate (cylindrical ray florets)

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34. VMT 5-1 (IC0623450; INGR17061), a Meiotic Tetraploid (MT) Potato (*Solanum tuberosum*) with 2× Genome from Semi-Cultivated Species *S. verrucosum* and other 2× from Cultivated Potato cv. K. Lalima. Highly Resistant to Late Blight. Performs Well Under Short & Long Day Conditions

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Pre-breeding strategy was employed at Central Potato Research Institute, Shimla for transferring late blight resistance from diploid, resistant, wild/ semi-cultivated *Solanum spp.* into cultivated potato cultivars through production of meiotic tetraploids (MTs) by unilateral sexual polyploidization (USP) scheme. The MTs (VMT-series) were developed following hybridization between resistant diploid Verrucosum Derived Selections (VDS clones) and susceptible tetraploid commercial cultivars. The MTs were screened for field resistance to late blight by detached leaf method following challenge inoculation with complex races of *P. infestans* in the lab and under natural field conditions at Kufri and Modipuram (Kaushik *et al*., 2008). Based on agronomic performance and late blight resistance, promising MTs including VMT 5-1 were used as parental lines in the late blight breeding programme. VMT 5-1 is one diverse tetraploid parent with fertile pollens and is being exploited in the hybridization. VMT 5-1 is one of the parents in three F_1C_3 clones viz., SM/11-77, SM/11-79 and SM/11-109 possessing high late blight resistance.

Before multi-location trials, VMT 5-1 was evaluated for 4 years at Kufri for total tuber yield and late blight resistance. The hybrid consistently out-yielded all the controls for total and marketable tuber yields at 100 days crop duration. The hybrid possesses consistently high level of resistance against late blight over the years.

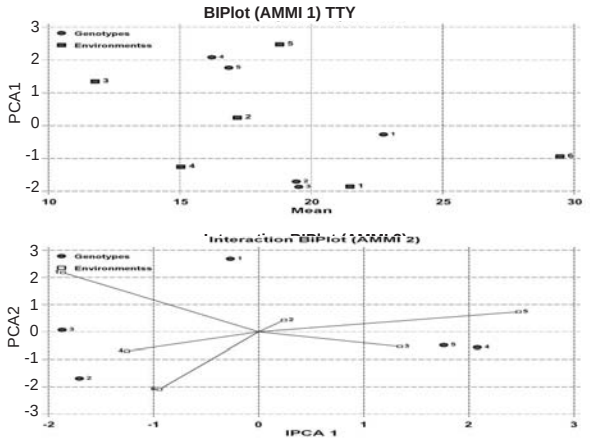

Fig. 1. Bi-plot (AMMI) for total tuber yield. Genotypes: 1:SM/00-42, 2:SM/00-120, 3: VMT 5-1 and controls viz., 4: K. Himalini, 5: K. Jyoti. Environments: 1:Hassan 2:Kufri 3: Ooty 4: Ooty (HSN) 5: Ranichauri 6: Srinagar.

Hybrid, VMT 5-1 had the 2nd highest stability and mean total tuber yield among evaluated genotypes in multi-location trials under AICRP (P) (Fig. 1). Besides, all the 3 late blight resistant hybrids, including VMT 5-1 had either higher or at par resistance to the best controls at Kufri, Ooty (ARS, Hassan), Pune, Ranichauri and Srinagar (AICRP-Potato Annual Report, 2015-16).

Till date, CPRI has developed and deployed 53 commercial cultivars suitable for growing under different eco-geographical locations. None of the present potato variety released by CPRI Shimla possesses widely diverse genes from *S. verrucossum*, therefore VMT 5-1 can serve as a boon in future breeding programmes for ensuring diversity and late blight resistance.

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35. Crd-6 (IC0623449; INGR17062), a Meiotic tetraploid, Somatic Male Fertile Hybrid potato (*Solanum tuberosum* (+) *S. cardiophyllum*) Carrying Resistance to Late Blight Introgressed from Wild Species *S. cardiophyllum*

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Solanum cardiophyllum Lindl. (PI 341233) (2n = 2x = 24, 1EBN) is a diploid wild potato species highly resistant to late blight, the most serious disease of potato. However, it poses a problem of sexual incompatibility with common potato. So to circumvent this problem, in this study, we developed interspecific potato somatic hybrids between cultivated *S. tuberosum* dihaploid C-13 and wild species *S. cardiophyllum* via protoplast fusion. Out of 26 regenerants, only 4 were confirmed as true somatic hybrids containing both parental genomes based on molecular markers and phenotypes. Somatic hybrids were identified by RAPD, ISSR, SSR, AFLP and cytoplasm (chloroplast and mitochondrial genomes) type molecular markers. Intermediate phenotypes of somatic hybrids were confirmed by leaf, flower and tuber traits. Late blight resistance of the hybrids was assessed by challenge inoculation of *P. infestans* under controlled conditions. Somatic hybrids were found tetraploid by FC analysis, exhibited high pollen stainability by acetocarmine staining and formed berries and viable seeds after crossing with a common potato variety. Somatic hybrids possessed diverse cytoplasm types (W/α, W/γ and T/β) as assessed by chloroplast and mitochondrial genome-specific markers. Further, cluster analysis generated based on the Jaccard's coefficient of molecular profiles generated by all above markers showed genetic distinctness in somatic hybrids and parents. Taken together, these interspecific somatic hybrids with diverse cytoplasm background have potential to employ in potato breeding programmes to widen the cultivated gene pool through conventional and molecular methods.

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36. MS/6-1947 (IC0623447; INGR17063), a Drought Tolerant Advanced Potato Hybrid (*Solanum tuberosum*) with Good Keeping Quality and High Tuber Yield

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Potato is a drought sensitive crop and the detrimental effects of water stress on potato tuber yield and other related traits are well known. Water deficit is responsible for decreased number of leaves, plant water potentials, leaf area, plant height, ground coverage and tuber number which ultimately culminate in to tuber yield reduction. Identification of drought tolerant genotypes for yield maintenance and breeding purposes is need of hour to increase drought tolerance of the potato crop, saving irrigation water and ensuring yield and food security in changing scenario of global climate and growing demand of water.

Morpho-agronomic characters: In initial investigation during winter crop season (2007-2008), segregating population of cross MS/82-638 x JX 576 were evaluated under reduced irrigation regimes (only three irrigations as against 5-6 irrigation during 90 days crop duration) and promising clones MS/6-1947 was identified for its better yielding ability under reduced water regime. The clone MS/6-1947 successfully passed through initial evaluation clonal generations. Subsequently in three advanced generation yield trials during 2009-2011 at Modipuram, the MS/6-1947 produced significantly higher total tuber yield than the best control Kufri Pukhraj by margin of 15% at 80 days (2009-10). The germplasm with 39 t/ha tuber yield showed yield advantage of 33%, 11% and 18% over controls Kufri Bahar (29 t/ha), Kufri Pukhraj (35 t/ha) and Kufri Sadabahar (33 t/ha) respectively at 75 days. At 90 days, the germplasm with 52 t/ha tuber yield exhibited yield advantage of 49%, 13% and 21 over controls Kufri Bahar (35 t/ha), Kufri Pukhraj (46 t/ha) and Kufri Sadabahar (43 t/ha) respectively.

Under drought tolerance trials (2010-2013) at Modipuram, MS/6-1947 outperformed under normal irrigation, mild deficit irrigation and severe drought conditions as compared to the best control Kufri Pukhraj as yield reduction was comparatively lower in MS/6-1947 under mild deficit and severe drought conditions. In this trial, MS/6-1947 produced significantly high marketable (29.7 t/ha, 19% higher) and total tuber (32.1 t/ha, 21% higher) yield than the best control Kufri Pukhraj (24.9 and 26.6 t/ha) under severe drought conditions. MS/6-1947 yielded 25% higher marketable and 22% higher total tuber yield under severe drought conditions in comparison to Kufri Bahar, the popular variety of the region having comparable tuber dry matter. The germplasm also possessed high drought tolerance index ie 1.02 and 0.79 under mild and severe drought respectively as compared to Kufri Pukhraj (0.85 and 0.58) and Kufri Bahar (0.79 and 0.51).

In drought tolerance trials (2012-2015) at Jodhpur, MS/6-1947 outperformed under normal irrigation and mild water deficit than best control Kufri Pukhraj as yield reduction was comparatively lower in MS/6-1947 under mild water deficit. In this trial, MS/6-1947 produced

significantly high marketable (27.8 t/ha, 13% higher) and total tuber (29.4 t/ha, 4% higher) yield than the best control Kufri Pukhraj (24.6 and 28.3 t/ha) under mild water deficit. The MS/6-1947 yielded 73% higher marketable and 62% higher total tuber yield under mild water deficit in comparison to Kufri Surya, the heat tolerant variety. The germplasm also possessed high drought tolerance index (1.08) under mild drought as compared to control Kufri Pukhraj (1.00) and Kufri Surya (0.41) at Jodhpur.

Under early planting conditions (2010), MS/6-1947 with total tuber yield (18 t/ha) out yielded the controls like Kufri Pukhraj (14.72 t/ha) and heat tolerant variety Kufri Surya (12.85 t/ha).by margin of 23% and 41% respectively.

Associated characters and cultivation practices: The germplasm possessed good keeping quality and moderate level of late blight resistance. MS/6-1947 produces 9 to 10 medium sized attractive light white cream ovoid tubers with shallow eyes and cream flesh colour. Its tubers are easy to cook (15-20 minutes) and cooked/boiled potatoes are free from discolouration. It possesses pleasant flavour and mealy texture. The above results indicates that the germplasm MS/6-1947 can be good choice for integration in cereal based cropping sequences, for its exploitation as early/short duration crop and for attaining sustainable productivity in areas where water is limiting factor for raising the successful potato crop. This elite genetic stock can be well used in breeding progarmmes aiming high productivity under abiotic stress conditions.

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Annual Report (2011-12) Central Potato Research Institute, Shimla, P33-34.

37. MS/8-1565 (IC0623448; INGR17064), a Purple Skin Coloured Advanced Potato Hybrid (*Solanum tuberosum*) with Very Good Keeping Quality and High Tuber Yield

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In India, mostly white/yellow skin or flesh coloured potatoes are preferred, however red skinned potatoes are liked in eastern part of India and Jammu & Kashmir. Coloured potato originates from the accumulation of pigments, i.e. carotenoids and anthocyanins (antioxidants). Coloured potatoes are liked by people to add colour and taste/interest to their meal.

Morpho-agronomic characters: The concerted breeding efforts at Central Potato Research Institute, led to development and identification of purple skin coloured germplasm MS/6-1565 from the segregating population of MS/89-1095 x CP3290 during 2007-08 rabi crop season. The germplasm successfully passed through initial clonal generations and based on consistence performance in advanced stage replicated trials, MS/8-1565 has been introduced in AICRP for multi-location testing. The germplasm is suitable for specialty sector and produced higher tuber yield (36.80 t/ha) than Kufri Arun (31.42 t/ha), Kufri Lalima (30.71 t/ha), Kufri Sindhuri (26.14 t/ha), Kufri Bahar (31.79 t/ha) at 75 days). Its yield advantage was 17%, 20%, 41% and 16% over Kufri Arun, Kufri Lalima, Kufri Sindhuri and Kufri Bahar, respectively. At 90 days, MS/8-1565 produced higher tuber yield (42.81 t/ha) than Kufri Lalima (39.64 t/ha), K Sindhuri (36.32 t/ha), Kufri Bahar (38.10 t/ha). Its advantage was of 8%, 18% and 12% than Kufri Lalima, Kufri Sindhuri and Kufri Bahar, respectively.

Associated characters and cultivation practices: It is medium maturing and produces attractive unique purple coloured ovoid tubers with shallow eyes and yellow flesh colour. MS/8-1565 possesses moderate 18-19% tuber dry matter, very good keeping quality

and moderate resistance to late blight than Kufri Bahar at Modipuram. It has mealy texture, very good flavor & taste and free from discolouration after cooking. The germplasm is suitable for specialty sector due to its unique purple attractive purple ovoid shallow eyed tuber which leads to less peeling losses than Kufri Lalima and Kufri Sindhuri. The tubers of MS/8-1565, seldom exhibits external/internal defects and are not susceptible to skin damage at harvest. The new germplasm MS/8-1565 with unique purple skin colour will add to new colour in meal and develop increased interest of consumers for potatoes thereby expanding the promotion of potatoes. This elite genetic stock can be well used in breeding progarmmes for developing varieties with variable colour combinations having high nutritional values.

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Annual Report (2014-15) Central Potato Research Institute, Shimla, P 28.

38. MP/6-39 (IC0623446; INGR17065), an Advanced Potato Hybrid (*Solanum tuberosum*) for Processing with Excellent Keeping Quality and High Tuber Yield

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In India, out of total potato production, about 68% are utilized for table purpose, 7.5% for processing; 8.5% for seed and remaining 16% produce goes waste due to pre and post-harvest handling. Potato is a perishable commodity and its harvest time (Feb/March) in subtropical plains coincides with steep rise in temperature. Therefore, the potato has either to be consumed within a short period or is required to be shifted to the cold stores. Diversification of potato consumption was widely discussed as a tool for avoiding situation of potato over-production. High yielding varieties with multipurpose uses as table and processing purpose with ability to withstand under country store or ambient conditions for 60-75 days can be another tool to minimize the post-harvest losses. Breeding efforts in this direction led to identification of advanced stage hybrid MP/6-39 with high yield, excellent organoleptic, processing and keeping quality attributes. The hybrid derived from cross Kufri Himsona × Kufri Pukhraj during 2006 possesses moderate-high tuber dry matter with low reducing sugars and acceptable chip/fry colour.

Morpho-agronomic characters: Based on the mean performance in five states (Uttar Pradesh, Punjab, Gujarat, West Bengal and Madhya Pradesh), the hybrid MP/6-39 produced 28% higher processing grade (37 t/ha) and 22% total tuber yield (43 t/ha) than the best control Kufri Chipsona-3 (29 and 35 t/ha) at 90 days after planting. It produced 38% higher processing grade (37 t/ha) and 34% total tuber yield (43 t/ha) than the French fry control variety Kufri Frysona (27 and 32 t/ha) at 90 days after planting. The hybrid possessed 18-20% tuber dry matter content and its fry colour was in acceptable range (2.8) as compared to Kufri Chipsona-3 (2.7) and Kufri Frysona (2.5).

Associated characters and cultivation practices: The hybrid produces attractive white cream, ovoid tubers with shallow eyes and cream flesh. The hybrid possesses moderate resistance (AUDPC 290) to late blight as compared to most susceptible variety Kufri Bahar (AUDPC 750) during 2013-2015 at Modipuram. It has waxy texture, pleasant flavour and excellent organoleptic taste on boiling. Results on storage behaviour over three year (2014-16) revealed that advanced hybrid MP/6-39 have long dormancy period as it did not sprout even after 75 days of storage and also have minimum total weight loss (9.6%) as compared with Kufri Chipsona 3 (17%) and Kufri Frysona (11%). The produce of MP/6-39 can be exported to long distances owing to its long dormancy period and excellent keeping quality. The superior organoleptic and processing attributes of MP/6-39 makes the hybrid multi-purpose for use as table purpose in cooler regions and for chips/French fries in warmer region of the country. The multi-purpose advanced potato hybrid MP/6-39 can be helpful in expanding the potato

production and its utilization in country.

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39. RP 5449-RIL-320 (IC0619226; INGR17066), a Novel Dual Donor Rice (*Oryza sativa*) with Resistance at Vegetative and Reproductive Stages to Brown Plant Hoppers (BPH) and White Backed Plant Hoppers (WBPH)

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At ICAR-Indian Institute of Rice Research, Hyderabad, a recombinant inbred line (F_9) *viz.*, RP 5449-RIL-320 was identified as a dual donor against planthoppers namely Brown planthopper (*Nilaparvata lugens* Stal) (BPH) and whitebacked planthopper (*Sogatella furcifera*) (WBPH), the most dreaded pests of rice. It possessed stable resistance during reproductive and vegetative stages. It was developed by crossing TN1 and Sinnasivappu, the susceptible and resistant parents to planthoppers respectively using single seed descent method of pedigree selection. A set of 250 RILs (F_9)were subjected to field screening at APRRI, Maruteru, the hot spot centre against planthoppers for 3 successive years 2012, 2013 and 2014. Simultaneously screened for 2 years (2013 and 14) in glass house for confirmation. In the first year (2012), a set of 30 RILs showed resistance when crop was affected by hopper-burn during flowering stage. RP 5449-RIL-320 could withstand high insect population of 495-600 WBPH and 35-40 BPH insects/hill during *kharif*, 2012; and 470-790 BPH and 10-15 WBPH insects/ hill during *rabi*, 2012 with a damage score (DS) of 3. (IIRR Annual report, 2012-13). In 2nd year (2013) during hopper-burn high infestation of 350-515 BPH and 80-130 WBPH insects/hill existed for a period of > 10 days during kharif, 2013 while 500-600 BPH and 5-10 WBPH insects/hill for about 20 days during *rabi* 2013. RP 5449-RIL-320showed consistent resistant reaction for both insects (DS: 4.5) (DRR newsletter, 2015). In third year (2014) also RP5449-RIL-320 recorded resistance (DS: 3) under hopper-burn in the presence of 390 to 450 BPH and 25 to 33 WBPH insects/hill during 2014, kharif and 500 to 600 BPH + 30 to 40 WBPH insects/ hill during 2014, *rabi*. The remaining RILs showed moderate resistance to susceptibe reaction.

For confirmation, the same set of 30 resistant RILs were screened in glass house in 2013 and 2014, *Kharif* and *Rabi* during early seedling stage. Separate screening experiments were conducted for BPH and WBPH reaction.

In glass house RP 5449-RIL-320 showed resistant reaction to both BPH (DS: 2.8 to 4) and WBPH (DS: 3 to 3.2) during 2013; BPH (DS: 3-3.5) and WBPH (DS: 3-3.6) during 2014. The resistant checks, Ptb 33 and MO1 for BPH and WBPH recorded mean damage scores of 3 and 2.9 respectively. It is a late duration culture (145 days) with intermediate plant height (118 cm), non lodging bearing short bold grains. It recorded good quality traits such as high head rice recovery (50%), intermediate desirable amylose content (24 %) and alkali spreading value (7).

Since RP5449-RIL-320 showed reproducible resistance to planthoppers over three years (2012, 2013 and 2014) in the field and 2 years (2013 and 14) in glasshouse, it could be utilized as a promising donor in the generation of resistant rice varieties against planthoppers.

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40. IET 24784 (RP 5866-Agami) (IC0619227; INGR17067), a Rice (*Oryza sativa*) Germplasm Rich in Zinc Micronutrient and Tolerant to Coastal Salinity

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Consumption of polished rice leads to micronutrient malnutrition due to Zinc deficiency. It inhibits growth, development and restricts normal functioning of immune system. Genetic enrichment of rice with Zinc is the most promising method compared to diverse diets, food fortification and supplementation approaches. IET 24784 (RP 5866-Agami), a selection from Agami possesses coastal saline tolerance (EC: 7 to 8) and enhanced Zn content (25.49µg/g).

Agami, a locally improved salt tolerant japonica cultivar of Egypt was introduced to ICAR-IIRR, Hyderabad through INGER nursery *viz*., 32nd International Rice Soil Stress Tolerant Nursery-Module 2, 2010. Within the population of Agami certain phenotypically superior plants possessing intermediate plant height (120 cm) and medium maturity (130 days) were selected and evaluated separately in progeny rows. The seed of one of the superior progenies was bulked and designated as RP 5866-Agami. It was found coastal saline tolerant (EC: 7 to 8; pH: 7.2 to 7.65) upon screening at Agricultural Research Station, Machilipatnam, a coastal saline centre of ANGRAU, AP during 2011, 2012 and 2013. It recorded 1.4 to 3.2 t/ha yield which is on par with coastal saline yield check, Indra (1.6 to 3.3 t/ha) during 2011 to 2013.

Incidentally RP 5866 -Agami was found to have high grain Zn content (>20 µg/g) and therefore tested in IVT- Biofortification trial during *Kharif*, 2014 bearing IET number 24784. It was evaluated along with 44 entries including 2 yield checks (IR64 and Samba Mahsuri) as well as 2 micronutrient checks (Chittimutyalu and Kalanamak) across the country in 17 locations spread over 12 states. Zinc content in polished rice was estimated by X-ray Fluorescence Spectrophotometer (XRF) at ICAR-IIRR, Hyderabad. IET 24784 displayed a mean grain yield of 2.8t/ha and high Zn content of 25.49µg/g in polished rice (10%) and 30.6 µg/g in brown rice and which is greater than that of micro nutrient checks, Kalanamak (18.29 µg/g) and chittimutyalu (21.49 µg/g) (ICAR-IIRR, Progress report, vol 1. 2014).

It displayed good cooking and eating quality parameters *ie.,* desirable amylose content (22.9 %), intermediate alkali spreading value (4) and soft gel consistency (63 mm); good physical quality traits like high head rice recovery (69.6%) and high milling outturn (71. 5%) (Padmavathi *et al.,* 2015). It possessed multiple resistance to three diseases namely blast (SI: 2.3), sheath rot (SI: 4.4) and RTD (SI: 5).

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41. CSR 47 (CSR 2K 232) (IC0639318; INGR17068), a Rice (*Oryza sativa*) Germplasm with Tolerance to Alkalinity Stresses up to pH 9.9

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Globally, more than 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 47 (CSR 2K 232) is a alkaline tolerant high yielding has been developed using Jaya and CSR 13 as parent through pedigree breeding method at the Division of Crop Improvement, Central Soil Salinity Research Institute, Karnal, Haryana. The line CSR 47 (IET 20328) was developed for alkaline areas where pH is up to 9.9. Of the two parents, CSR 13 is tolerant to alkalinity (pH ~9.9) and another parent Jaya has high yield potential. Hence, this culture combines the high yield from Jaya and tolerance from CSR 13 for alkalinity.

Morpho-agronomic characteristics: It possessed long bold grains and 95 days flowering duration. This is a semi dwarf culture, with green foliage, erect flag leaf, compact panicle and complete panicle exertion. This line has been evaluated through All India Coordinated Rice Improvement Programme (AICRP - Rice) IIRR, Hyderabad for three years (2011, 2012 and 2013) across five alkaline locations (pH up to 9.9) in Haryana (DRR 2012; DRR 2013; DRR 2014). Based on the data recorded during kharif 2011, 2012 & 2013, across the alkaline stress locations of Haryana. The line CSR 47 (IET 20328) was found superior in yield over the checks CSR 36 and Local check by 20 % and 20 %, respectively across the three years (2011, 2012 and 2013) in 5 salt affected locations of Haryana (Annual report, 2014-15).

Associated characters and cultivation practices: Based on screening in NSN1 and NSN2, IET 20328 showed moderately resistant/tolerant to major insect pests and diseases such as stem borer, leaf folder, case worm, blue beetle, leaf blast and brown spot. Quality parameters studied at IIRR, Hyderabad showed that IET 20328 has high head rice recovery (63.9 %), desirable alkali spreading value (5.0) and intermediate amylase content (23.7 %). CSR 47 (CSR 2K 232) is salt tolerant high yielding, long bold grained variety. The above values are indicative of excellent cooking quality of IET 20328.

The performance of CSR 47 (IET 20328) was consistently high under alkalinity for three successive years in Haryana. It showed yield superiority over national alkaline check and local check. Therefore, CSR 47 (IET 20328) was promising in the states of Haryana under alkalinity. This Germplasm can be used as a genetic stock for future breeding programmes aiming at development of high yielding salt tolerant rice varieties for alkaline soils.

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42. Salkathi (PB-289) AC-351181 (CSR 2K 232) (IC0256801; INGR17069), a Rice (*Oryza sativa*) Germplasm Resistant to Brown Plant Hopper

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The purified landrace 'Salkathi' showed resistance to brown plant hopper (BPH) consistently for last several years in All India Coordinated Rice Improvement Programme trials. Phenotyping of RILs against the BPH population at ICAR-NRRI, Cuttack, Odisha showed continuous skewed variation, suggesting the involvement of quantitative loci for resistance to BPH in Salkathi. Since no separate biotype was confirmed location-wise in India, this landrace was tested against different populations in different locations as mentioned in the Progress reports of the AICRIP.

Morpho-agronomic characteristics: The data on multilocation test were generated for four years through AICRIP, ICAR-IIRR, Hyderabad in which the said entry was showing promising results against BPH. In addition, it was also identified as a potential donor for having multiple resistance to several insect pests of rice.

Associated characteristics and cultivation practices: Salkathi was recommended for promotion to yield trial or for utilization in breeding programme for biotic stress like BPH resistance and also for resistance to multiple insect pests of rice. It was also recommended by the Institute Research Council (IRC) and Research Advisory Council (RAC) for registration as well as utilization in breeding programme. Basing on the recommendations, this donor has been utilized in making different cross combinations in breeding programmes of the ICAR-IRRI collaborative programmes and other rice research stations across the country. The breeding lines thus evolved were also showing highly resistant reaction against BPH.

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43. FLW18 (IC0621835; INGR17070), a Wheat (*Triticum aestivum)* Germplasm with Resistance to Brown Rust carrying Yr39+ in the background of PBW343

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Rusts are economically the most damaging diseases of wheat as they pose major threat to wheat production in most of the wheat growing areas of the world. The most effective and environmentally sound strategy to manage these diseases is through the deployment of resistant cultivars (Bhardwaj *et al*., 2016). Wheat cultivars become susceptible to new pathotypes of brown rust periodically (Prasad *et al*., 2017). At Regional Station ICAR-IIWBR, Shimla, FLW18 was developed from the cross PBW343/ *Lr39* (KS92WGRC15). Germplasm accession KS92WGRC15, donor of *Lr39* is in agronomically poor background as the line is derived from *Aegilops tauschii*. Therefore, the genetic stock FLW18 was developed in good agronomic background. FLW18 carrying *Lr39* and *Yr9*/*Lr26*/*Sr31*, which have been validated through molecular markers, provides resistance to all the brown and black rusts pathotypes reported in India.

FLW18 was found immune (0;) at seedling stage to all the pathotypes of brown rust under controlled and optimum conditions (Table1). The adult plant reaction (APR) of FLW 18 to brown and black rusts also showed resistant response. FLW18 has waxiness on leaf sheath, peduncle and glumes. It has average plant height of 89cm and matures in 122 days under Karnal conditions.

Its seeds are amber coloured with soft texture and has thousand-grain weight of 38.0 g.

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Table 1. Seedling response (2013-2016) of FLW18 to most virulent pathotypes of brown and black rusts

	Brown rust pathotypes								Black rust pathotypes			
Pathotype	12-5	77A	77-2	77-5	77-7	77-8	77-10	104-2	34-1	40A	40-1	117-6
Score	0;	0;	0;	0;	0;	0;	0;	0;	0;	2-	2-	2-

44. NRCSFR 09-3(IC0621475; INGR17071), a Sorghum (*Sorghum bicolor*) Germplasm with Improved Shoot Fly Resistance over the Elite Parent, 296B. Better level of Resistance to Grain Moulds compared to 296B. Derivative to Biparental Mating involving Two Shoot Fly Resistant Sources

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Sorghum shoot fly, *Atherigona soccata* Rondani is one of the major pests that destabilizes the performance of sorghum cultivars and ultimately reduces sorghum production in many parts of the world. It causes damage to the late sown crop in *kharif* and early sown crop in *rabi*. The seriousness of the shoot fly problem in sorghum, combined with the high costs and toxicity hazards of using chemical control, renders it necessary to develop new varieties or hybrids that possess resistance to this pest. In order to incorporate resistance into sorghum parental lines, intensive breeding efforts were initiated at IIMR, by crossing the elite parental lines with shoot fly resistant germplasm.

A series of crosses were made during 2003-2006 by using the elite parental lines and the shoot fly resistant sources from germplam such as IS 18551, IS 2312, IS 2122 and RSE 03. The F_2 population was sown by mid July, so that the plants are exposed to sufficient shoot fly pressure. From F_3 onwards, selections were made in the shoot fly nursery where high pest population is build up. The seed of the resistant F_6 progenies was multiplied and the genotypes were tested in multilocation under AICSIP.

NRCSFR 09-3 Is A Derivative Of The Biparental Mating Involving F_2s Of Two Crosses. The Parents Involved Are One Elite Parent 296B And Two Shoot Fly Resistant Sources From Germplasm, I.E. IS 2122 And IS 18551. It Has Much Better Level Of Shoot Fly Tolerance Compared To 296B, And Agronomically Better Compared To Both The Shoot Fly Resistant Sources. NRCSFR 09-3 Is Of Medium Height With Tan Background And Has Shoot Fly Resistance On Par With The Resistant Parent. For The Traits Contributing For Shoot Fly Resistance Such As Glossiness And Number Of Eggs Per Plant, NRCSFR 09-3 Was Found To Perform On Par With The Resistant Check, IS 18551 In AICSIP Trials. In The Pest And Disease Nursery Of AICSIP, NRCSFR 09-3 Has Recorded Better Level Of Resistance To Grain Moulds, An Important Disease During Kharif. Hence NRCSFR 09-3 Can Be Used As An Improved Source Of Resistance In The Shoot Fly Resistance Breeding Program.

Table 1. Performance of NRCSFR09-3 for shoot fly resistance in AICSIP trials over three years (10 environments)

Genotype	Pedigree	Shoot fly deadheart % at 28 DAE			
		2009	2010	2011	Av.
NRCSFR 09-3	{(296 B × IS 2122) × (296B × IS 18551)}	47.4	38.7	39.3	41.8
296 B		62.8	60.8	–	61.8
IS 18551		41.1	31.6	28.5	33.7
DJ 6514		82.6	79.2	80.8	80.9
CD 5%		11.0	8.9	14.5	
CV (%)		12.1	12.1	19.4	

NRCSFR 09-3 was evaluated in pest and disease nursery of AICSIP for three years during 2013 to 2015 and was found to perform well for shoot fly resistance traits, seedling glossiness and shoot fly eggs per plant (Table 2). In all the years, it showed less shoot fly deadheart percentage compared to the elite parent, 296B. In the pathology PDRN trials for two years, 2014 and 2015, it was found to have better level of tolerance to grain molds compared to its elite parent, 296B (Table 3).

Table 2. Performance of NRCSFR 09-3 for the traits associated with shoot fly resistance in the Pest and disease nursery (PDRN) of AICSIP during 2013-2015 (9 environments)

Genotype	Seedling glossiness (1-5 scale)				Shoot fly eggs/ 5 plants				Shoot fly DH% at 28 DAE			
	2013	2014	2015	Av	2013	2014	2015	Av	2013	2014	2015	Av.
NRCSFR 09-3	3.2	3.25	3.22	3.22	2.3	4.78	8.5	5.19	47.2	36.9	46.5	43.5
296 B	4.3	3.75	4.39	4.15	3.3	3.22	12.3	6.27	72.7	70.5	85.9	76.4
IS 18551	3.0	2.67	3.17	2.95	3.0	3.33	5.17	3.83	40.0	32.2	42.0	38.1
Swarna (sus check)	4.3	4.5	3.89	4.23	4.0	9.33	14.0	9.11	79.7	83.1	89.0	83.9
CD 5%	1.27	1.0	0.82	-	1.4	2.58	7.5	-	7.5	14	15.8	-
CV (%)	19.9	20.7	13.9	-	26	32.7	40.9	-	8.1	16	15.1	-

Table 3. Performance of NRCSFR 09-3 in the Pest and disease nursery (PDRN) of AICSIP Pathology during 2014-2015 (Four environments)

Genotype	Grain mold score-PGS*			Grain mold score-TGS**		
	2014	2015	Av	2014	2015	Av
NRCSFR 09-3	3.7	4.0	3.85	4.5	3.5	4.0
296 B	5.3	5.7	5.5	5.7	5.8	5.75
CD 5%	2.6	1.6	-	2.3	1.5	-
CV (%)	35.8	19.2	-	29.4	18.0	-

*PGS- Panicle grain mould score; **TGS-Threshed grain mould score

This line can be used as resistant source in the shoot fly resistance breeding program aiming at development of parental lines and genotypes with shoot fly resistance along with agronomic acceptability.

45. Sdf (Super dwarf) Mutant (IC0621946; INGR17072), a Extremely Dwarf Mutant of Jute (*Corchorus olitorius*) with around 1/10th Plant Height of Wild Type

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and

46. Llpf (Low Lignin Phloem Fibre) Mutant (IC0621948; INGR17073) of Jute (*Corchorus olitorius*) with Low Lignin Content of Fiber (6.7%) at 120 Days after Sowing. Unique Morphology having Undulated Stem, Petiole and Main Leaf Vein

SB Choudhary, HK Sharma, A Anil Kumar, J Mitra, PG Karmakar, J Souframanien[2] and Sanjay Jambhulkar

and

47. Pfr 59 (pre-mature flowering resistant 59) (IC0621949; INGR17074), a Jute (*Corchorus olitorius*) Germplasm with Absolute Absence of Pre-mature Flowering when Sown in First Week of February

SB Choudhary, HK Sharma, A Anil Kumar, Dileep Kumar, J Mitra, PG Karmakar, J Souframanien[2] and Sanjay Jambhulkar

and

48. WCIN 009 (IC0621650; INGR17075), a Jute (*Corchorus olitorius*) Germplasm with High Iron content in leaves (173.75 mg/kg fresh weight)

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Tossa jute cultivars starts flowering even after 40 days of sowing without completing vegetative growth, if sown in February or March months. The phenomenon called pre-mature flowering and adversely affect both fibre yield and quality. A mutant germplasm (*pfr* 59) of *tossa* jute (*Corchorus olitorius* L.) found free from pre-mature flowering even after sowing in the 1st week of February during 2012-2015. In contrast, the best available check and parent of the mutant recorded significantly high pre-mature flowering (34.56%) over the years under identical conditions. It is noteworthy that the mutant recorded normal flowering after 140 days of sowing and produces viable seeds. Therefore, the mutant is pre mature flowering resistant. Further a low lignin phloem fiber mutant (*llpf*) of the species found morphologically distinct with undulated stem and petiole. Fibre of the mutant is low lignin containing (6.7%) compare to all *tossa* jute cultivars and genetic resources (13-18%). The attribute is important for realizing commercial potential of jute based diversified industrial products. In addition, an extremely dwarf mutant (*sdf*) of *tossa* jute (*Corchorus olitorius* L.) having only 1/10th plant height of the wild type (JRO 204). It can serve as one of the parent for developing plant height specific mapping population. A wild accession of *Corchorus aestuans* L. Bearing IC no. WCIN 009 found useful source of dietary nutrition particularly leaf iron and β-Carotene. It can utilize either directly by consuming young tender leaves as vegetable or indirectly as a high leaf iron source to bio-fortify iron content in jute leaves.

49. IC01572 (IC-001572; INGR17076), a Blackgram (*Vigna mungo*) Germplasm with Resistance to Mung Bean Yellow Mosaic Virus

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Low productivity of grain legumes is due to several biotic stresses especially yellow mosaic disease causing yellowing or chlorosis of leaves followed by necrosis, shortening of internodes and severe stunting of plants with no yield or few flowers and deformed pods with small, immature and shriveled seeds, Major problem for resistance breeding programme in blackgram is the lack of suitable resistant germplasm/genotype and also the unavailability of robust and efficient screening methods that make use of both field and artificial techniques. No specific large scale systematic screening has been conducted in India to identify resistant sources against yellow mosaic viruses by combining field screening, vector inoculation and agroinoculation. Therefore, 344 germplasm accessions originally collected from different geographic regions of India and conserved in the National Gene Bank at National Bureau of Plant Genetic Resources, India, were evaluated or their response against YMD. Based on disease incidence and severity of the symptoms under field conditions with natural disease pressure the response was different among the accessions during three cropping seasons (*Kharif* 2010, 2011, 2012). Field experiments were conducted at NBPGR experimental farm, New Delhi (geographical coordinates $28^{o}64^{/}$N, $77^{o/}$ E).Two popular blackgram cultivars namely Barabank Local (highly susceptible 0 and T-9 (high yielder) were used as checks. Germplasm accessions indicating resistance response during three consecutive years under natural disease pressure were further subjected to screening through artificial inoculation using viruliferous whiteflies. Those germplasm accessions which showed resistance response after whitefly inoculation were further tested for validation of the resistance through agro inoculation with the infectious cloned DNA-A and DNA-B components of a New Delhi isolate of MYMV. A germplasm (IC001572) collection from Delhi. India, was identified as highly resistant against MYMV. Yield attributing traits of selected accessions were also recorded along with susceptible (Barabanki local) and agronomic checks (T-9) and on his basis IC001572 germplasm also exhibited desirable agronomic attributes viz. short height (32.0cm), early maturity (75 days), medium to high grain yield (13.6 gm / plant) with medium seed size (100 seed weight 3.1 gm). The above mentioned germplasm accession can be used in YMD resistant breeding programme or can be released directly for cultivation after verifying its adaptation to various regions and accepting quality traits.

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50. DRMR-2019 (IC0598622; INGR17077), An Indian Mustard (*Brassica juncea*) Germplasm with White Rust Resistance

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and

51. DRMR-2035 (IC0598623; INGR17078), An Indian Mustard (*Brassica juncea*) Germplasm with White Rust Resistance

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Indian mustard (*Brassica juncea* L.) is an important oilseed crop contributes nearly 80 percent of the total rapeseed-mustard production in India experiences severe biotic and abiotic stresses. Among biotic stresses, white rust disease causes drastic yield losses, depending upon its severity. Therefore, the development of WR resistant genotypes is highly desirable to minimize the economic losses. Keeping this in view, two genotypes DRMR 2019 (EC399288/ BEC107) and DRMR 2035 (PHR1/ BEC107) were developed through systematic breeding at ICAR-DRMR, Bharatpur (India). These were selected through rigorous screening for WR during 2010-11 to 2016-17 at Bharatpur, Wellington (Hot Spot for WR) and different locations under AICRP-RM (NDN/ UND trials, 2015-16 & 2016-17) along with resistant (BIOYSR, PHR-2) and susceptible (Rohini, Varuna) checks (DRMR Annual Report, 2011-17; AICRP-RM Reports, 2016 & 2017). DRMR 2019 and DRMR 2035 exhibited stable resistance at different locations and identified as resistant sources for WR. The WR resistance of the genotypes has also been validated at molecular level using genotype non-specific molecular markers At541560 and At2g36360 reported (Panjabi *et al*., 2010) closely linked with WR resistance loci AcB1-A4.1 and AcB1-A5.1. DRMR 2019 revealed distinguishing bands of size 430bp and 750bp with both the markers, respectively while DRMR 2035 revealed loci AcB1-A4.1 of size 430bp confirming their resistance. These genotypes had superiority over resistant checks for 1000-SW and seed yield. Additionally, DRMR 2035 exhibited tolerance to Sclerotinia rot which is highly devastating disease emerging in India (DRMR Annual Report, 2015-16). Thus these genotypes could be highly useful in breeding programmes for development of high yielding white rust resistant varieties.

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52. DCA-121 (IC0610825; INGR17079), a Senna (*Cassia angustifolia*) Germplasm with Small Size Pod

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Senna (*Cassia angustifolia* Vahl.) is a medicinal plant used as purgative, laxative, expectorant, wound dresser, antidysentric, and carminative. The medicinal properties are attributed to production of sennosides (anthraquinone glycosides). Senna is cultivated commercially in India in arid parts of Rajasthan, Gujarat and Tamil Nadu. Leaves and pods are economic parts used in the treatment various Indian systems of medicine. India exports large quantity of senna leaves and pods in the world market and earns approximately Rs. 50 crores revenue every year. Germplasm constitute the basic raw materials required for the improvement of senna. Even though this crop is important and being cultivated for many centuries in India, the number of varieties released are less (Sona, KKM-01 and AFLT-2). Increasing demand of senna leaves and pods in the national and international market calls for the developing high yielding varieties with desired marker traits. For the first time, a selection

Table 1. Agro-morphological description of DCA-121 of Senna

Characteristics	DCA-121	ALFT-02
Morphological traits		
Plant habit	Erect	Erect
Leaf color	Dark green	Green
Leaf Apex shape	Acute	Acute
Leaf Apex habit	Straight	Straight
Leaf type	Normal	Normal
Flower bud size	Intermediate	Intermediate
Pod shape	Normal	Normal
Pod size	small	medium
Pod Pubescence	moderate	moderate
Stem pigmentation	Middle	Mostly basal
Seed shape	Narrowly obovate	Obovate
Agronomic traits		
Days to first phase of flowering (days)	108	100
Days to second phase of flowering (days)	194	181
Days to maturity (days)	234	234
Plant height (cm)	100	130
Number of primary branches (cm)	10	13
Number of racemes on main branch	7	9
Number of pods/raceme	15	9
Pod size (L × B cm)	Small (3 × 1 cm)	Medium (5 × 2 cm)
Test weight (g)	2.6	2.9
Trichome density (Adaxial)	27.7	25.3
Trichome density (Abaxial)	97.6	96.4
Sennoside content (%)	1.44	2.08
Elemental profile leaves		
Potassium (%)	0.406 (±0.003)	0.405 (±0.01)
Sodium (%)	0.067 (±0.008)	0.058 (±0.006)
Calcium (%)	0.894 (±0.012)	0.865 (±0.009)
Magnesium (%)	0.382 (±0.003)	0.362 (±0.004)
Zinc (ppm)	12.97 (±0.83)	9.26 (±1.7)
Copper (ppm)	2.52 (±0.35)	2.80 (±0.43)
Iron (ppm)	187.7 (±1.85)	159.3 (±6.2)
Manganese (ppm)	61.43 (±1.27)	36.24 (±2.06)

with small pod size (DCA-121) was identified at the ICAR-Directorate of medicinal and aromatic plants Research, Anand, Gujarat. DCA-121 was having a pod length of 3 cm and breath of 1 cm which was 50% smaller pod size than cultivar ALFT-2 which is having a pod size of length 5 cm and breath 2 cm (Table 1). The genotype DCA-121 produced smaller pods also at MPKV, Rahuri during 2015-16 indicating the stability of the character. The smaller pod size selection (DCA-121) could be an important source for natural alleles for pod size variation in senna which may be used to develop high pod yielding cultivars. The selection is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics of pod size variation in senna. Further, this trait can be used as DUS character for identification of elite germplasm lines and cultivars.

53. DCA-124 (IC0610826; INGR17080), a Senna (*Cassia angustifolia*) Germplasm with Broad Leaves, Broad Pod Shape

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Table 1. Agro-morphological description of DCA-124, a broad pod and leaf germplasm

Characteristics	DCA-124	ALFT-02
Morphological traits		
Plant habit	Semi spreading	Erect
Leaf color	green	Green
Leaf Apex shape	Acute	Acute
Leaf Apex habit	Straight	Straight
Leaf type	Broad	Normal
Flower bud size	Intermediate	Intermediate
Pod Shape	Broad	Normal
Pod size	Medium	Medium
Pod Pubescence	Moderate	Moderate
Stem pigmentation	Mostly basal	Mostly basal
Seed shape	Obovate	Obovate
Agronomic traits		
Days to first flowering (days)	100	100
Days to second flowering (days)	179	181
Days to maturity (days)	219	234
Plant height (cm)	112	130
Number of primary braches (cm)	10	13
Number of racemes/main branch	10	9
Number of pods/raceme	11.9	9
Pod size	Medium	Medium
Test weight (g)	3.4	2.9
Trichome density (Adaxial)	33.00	25.3
Trichome density (Abaxial)	105.0	96.4
Sennoside content (%)	1.66	2.08
Elemental profile leaves		
Potassium (%)	0.443 (±0.01)	0.405 (±0.01)
Sodium (%)	0.072 (±0.003)	0.058 (±0.006)
Calcium (%)	0.892 (±0.005)	0.865 (±0.009)
Magnesium (%)	0.389 (±0.003)	0.362 (±0.004)
Zinc (ppm)	17.67 (±0.31)	9.26 (±1.7)
Copper (ppm)	2.94 (±0.16)	2.80 (±0.43)
Iron (ppm)	174.4 (±0.31)	159.3 (±6.2)
Manganese (ppm)	40.67 (±0.86)	36.24 (±2.06)

Senna (*Cassia angustifolia* Vahl. is synonymous with *Senna alexandria* Mill.), popular as "Tirunelveli senna" is used worldwide as natural laxative. The drug senna is mentioned in various texts of indigenous systems of medicine (Ayurveda, Siddha Unani and homoeopathy) in India, pharmacopeias of United States, United Kingdom, Germany and other counties. Tirunelveli is a place in south India where senna was introduced in India for the first time in the mid-eighteenth century and it is extensively cultivated, processed and exported to various countries under the brand name "Tirunelveli senna" hence the name. The drug senna is widely used as a purgative, laxative, expectorant, wound dresser, antidysentric, and carminative. The drug senna is also used as a cathartic, febrifuge, in treatment of splenetic enlargements, anemia, typhoid, cholera, biliousness, jaundice, gout, rheumatism and tumours. Even though the species brought to cultivation for many centuries, systematic efforts on germplasm management and development of high yielding varieties are getting important only in recent years. For developing high yielding varieties, the size of leaves besides the number of leaves is an important trait to get maximum economic yield. Interestingly, a germplasm, DCA-124 with a broad leaves and broad pod shape has been collected from Bikaner, Rajasthan during 2012 and characterized at ICAR-DMAPR, Anand, Gujarat during 2013-14 and at MPKV, Rahuri during 2015-16 (Table 1 and Figure 1-2). The accessions DCA-124 produced broad leaves and pods over locations and seasons indicating its stability. The broad pod shape collection DCA-124 could be an important novel source for natural alleles for broad pod shape and broad leaf variation in senna which may be used to develop high pod yielding cultivars. The selection is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics of pod shape variation as well as broad leaf in senna. Further, this trait can be used as DUS character for identification of elite germplasm lines and cultivars.

54. Bharamputra–1(IC0610826; INGR17081), an Aromatic ginger (*Kaempferia galanga*) Germplasm with High rhizome yield (10 tones/ha) and Dry Rhizome Recovery. High Essential Oil.

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Kaempferia galanga, known as Chandramula in Hindi is a rhizomatous herb that belongs to the zingiberaceae family is cultivated mainly for its aroma and other medicinal importance. It is widely cultivated in India in the states of Tamilnadu, Kerela, Karnataka and West Bengal (Raina *et al*., 2015, Lal *et al.,* 2017).It is a potent aromatic medicinal plant suitable for cultivation in shady areas. Its growth, yield and quality are dependent on planting time and type of seed material. The use of this active secondary chemical compounds in the medicinal as well as perfumery holds a great promise in ancient as well as modern era. The rhizomes also have good nutritive value and are quite rich in protein and carbohydrate but low in fat.

In the view of the needs and great prospect of cultivation of this crop successfully in various region of India, it is necessary to evolve high rhizome yielding genotypes for respective locations (Lal *et al*., 2017). Due to the limited improved genotypes for high rhizome yield, its cultivation is not popular among farmers. The current price of the rhizome is more than Rs 400/- per kg. Therefore, there is a need to develop superior genotypes of *K. galanga* for high rhizome yield. Thirty-five germplasm of *K. galanga* were planted and propagated vegetatively in randomized complete block design keeping a check in respect of rhizome yield. A high rhizome yielding unique germplasm was identified yield named as Bharamputra-1.

The germplasm was planted in four different locations in Northeast India. The data showed that this new genotype contains more rhizome yielding capacity recorded at harvest was found to be 10 tons/hectare. The dry recovery was 32% of fresh rhizome yield and superior to the check variety. This elite variety maintained

its superiority over the other varieties in terms of rhizome yield and named as Bharamputra-1. Plants of this variety were propagated through vegetative means using the rhizome. The plants are stable for commercial cultivation.

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55. IC0597686 (DOPR G 22; Palm no.45) (IC0597686; INGR17082), a Oil Palm (*Elaeis oleifera*) Germplasm with Slow Vertical Stem Growth (Low Annual Height Increment of 15 Cm per Year). Early Fruit Maturity (4.5 months) with Long and Slender Bunch Stalk. High Fruit Set of 53.4% than other Oleiferas (28.0% to 46.0%)

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American oil palm (*Elaeis oleifera* (HBK) Cortes) is endemic to tropical countries of South and Central America. A feature of the palm that distinguishes it from the widely cultivated oil palm (*Elaeis guineensis* Jacq.) is its dwarf and often procumbent trunk which facilitates easy harvesting of bunches. Reducing height has always been interest to oil palm industry because of high cost of harvesting tall palms which accounts up to 18% of the total production cost. (Murugsan and Sunilkumar, 2014).Developing dwarf planting material so as to overcome the difficulties of harvesting tall palms is one of the main objectives in the ICAR-IIOPR's oil palm breeding programme. There are four sources of wild oil palm available in India. Out of four sources three are available at ICAR-IIOPR Research Centre Palode and another source is located at Cithara estate of Oil Palm India Limited (OPIL), Kerala. One accession of Surinam origin (which was introduced along with commercial planting material and pedigree information is recorded in the germplasm register) planted during 1988 at Field Gene Bank of IIOPR Research Centre, Palode, Kerala was taken as experimental material (Murugesan *et al*., 2008; Anonymous 2010). Surinam is considered as one of the centres of diversity of *oleifera* which are found scattered throughout the forest, open pasture along banks of streams. According to Corley and Tinker (2003), *oleifera* stand in Surinam declined considerably and emphasized preservation of collected *oleifera* gene pool. Generally, *oleifera* shows poor fruit set with a range of 28 to 46% and present Surinam *oleifera* recorded 53.36% with 9.25% oil to bunch (Murugesan *et al*., 2011a; Murugesan *et al*., 2011b). The proposed genetic stock has precocity in bunch ripening (4.5 months, normal bunch takes 5.5-6.0 months) which is considered as desirable trait (Murugesan and Shareef 2014). In fruit and seed development study conducted in the proposed stock, fruit has been developing steadily in size and weight from anthesis (0.27 g) to (8.62 g) 135 days after anthesis (DAA). The kernel was liquid at 48 DAA and started solidification at 65 DAA onwards. The embryo matured at 78 DAA and shell became hard and lignified during 113 to 126 DAA. Surinam *oleifera* fruit bunches requires about 4.5 months (135 DAA) for fruit ripening and harvestable maturity (Murugesan *et al*., 2011) whereas other accessions of oleifera population took 186 days for fruit maturity, ripening and other

physiological maturity (Murugesan *et al*, 2011).

Morpho-agronomic characteristics: The identified *oleifera* palm has short height (4.1m), reduced trunk increment (15cm), short leaflet length (97.3cm), breadth (6.2cm) and short intermodal length (6.2cm). This palm recorded 12.5 kg of bunch weight with average bunch yield of 75Kg FFB/Palm/year. This palm had 9.25% mesocarp oil to bunch and 3.1% kernel oil to bunch. It has recorded 54 % fruit to bunch and 76 % mesocarp to fruit. It has very less height increment of 15cm with frond production of 24 numbers per year. Other distinct characteristics of proposed genetic stock are early disintegration of bunch spathes, long slender bunch stalk of both male and female inflorescences (Murugesan and Sunil kumar, 2014). Colour of the petiole of selected palm is dark green colour similar to leaflet. The proposed genetic stock is considered as valuable resource because of less common fruit type which is deep orange to red at maturity and developed from green colour immature fruit turning olive green and pale yellow (Murugesan *et al*, 2009).

Utilization of genetic stock: Currently interspecific hybrids and progenies developed from the genetic stocks are being evaluated in the field trial to develop compact varieties. The selected *oleifera* accession has been backcrossed with high yielding *E.guineensis* to produce interspecific hybrids to retain unique characteristics in the planting material to be developed using promising palms of *E. guineensis.*

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57. IC0597687 [EC382627; DOPR G53 (61)] (IC0597687; INGR17083), a Oil Palm (*Elaeis guineensis*) Germplasm withVirescens Fruit Colour. Dura Fruit Forms

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Fruit colour is an important trait in terms of bunch harvesting at right stage of maturity and, to obtain maximum oil extraction rate in oil palm. A change in color is associated with fruit ripeness in oil palm. For this reason, this trait is one of the indicators usually used by field workers to help identify ripe bunches during harvest. However, sometimes this indicator is not adequate for bunches of *nigrescens* fruits (black color in normal type), because the color change when ripe is often subdued and the workers frequently cut bunches with sub-optimal degrees of ripeness and lower oil contents. The oil palms produce either *nigrescens* or

virescens fruit types. *Nigrescens* fruits are usually deep violet to black at the apex and yellow at the base when unripe, with minimal change in colour of the apex upon ripening. For *nigrescens* palms, harvesters rely on the presence of detached fruits on the ground to determine that bunches are ripe. Although the *virescens* trait is dominant, the number of *virescens* palms found in natural populations is small. *Virescens* palms were used in ancient ceremonial rites explaining their occurrence among wild-type *nigrescens* palms, trees matching the description of *virescens* palms were reportedly used in tribal sacrificial ceremonies in West Africa (Zeven, 1967). *Virescens* palms are recorded by Singh (2014) which were from either the Ghana or Nigeria collections. However, majority of them were reported as heterozygous.

Morpho-agronomic characteristics: The proposed genetic stock was developed from open pollinated fruit samples of palm collected from Tanzania Accession No DOPR G53 (61)) which were planted during 1998 at DOPR Research Centre, Palode and identified through evaluation and intensity of fruit colour is prominent bright indicating reflecting degradation of chlorophyll and accumulation of carotenoids predominantly (Pillai *et al*. (2000)). The Tanzanian accessions (TS-10) were collected from grove consisting all *virescens* bearing palms located at a place called Ujiji in Tanzania with thin shell of dura fruit form (Pillai, 1995). The majority of the TS-10 progeny populations were exhibited *virescens* fruit forms (Anonymous 2009-10). Phenotypic screens of these collections as per IBPGR (1989) descriptors revealed a significant diversity for the valuable agronomical characteristics. The reported germplasm with *virescens* and *dura* fruit characteristics was selected based on the phenotypic data described by Corley *et al*. (1971), such as: (1). Bunch number, weight and production; (2) fresh fruit bunch and oil content; (3) vegetative characters; (4) fruit shell thickness; (5) fruit colour etc., and bunch analysis as per Blaak *et al*. (1963). All the vegetative characters were measured during June month of every year and average of four years was reported. Bunch production and number of bunches were recorded quarterly, bunch analysis was done for three bunches during peak season and average of four years were reported for all the measured parameters.

Associated characters and cultivation practices: Since, virescence character is governed by dominant gene 'Vr' it would be advantageous to develop planting materials with *virescens* fruits so as to have harvesting of ripe bunches with higher oil contents. A *virescens* fruit type has also non fruit shedding traits and has long shelf life. The proposed *virescens dura* genetic stock of DOPR G53 (61) was crossed with DOPR G54 (E65) of *virscenspisifera* for the production of hybrid *tenera* population which were later planted in the farmers field in Andhra Pradesh. The results revealed that almost all the progeny population (99%) exhibited *virsecenstenera* fruit form. The phenotypic evaluation was also resembled with its progenitors.

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57. IC0597688 (DOPRG-44-E 33) (61) (IC0597688; INGR17084), an Oil palm (*Elaeis guineensis*) Germplasm with Long Bunch Stalk (53 cm)

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Oil palm growers are demanding for agronomic traits, such as low growth rate and broad ecological adaptations, for which restricted genetic variability has been found on *E. guineensis* germplasm (Simmonds, 1993). In oil palm, male and female flowers occur separately on the same palm. Each inflorescence consists of a stout peduncle of 30-45 cm length with spikelets arranged spirally around it which varies both with age and position in the rachis. The fruits are very compact due to the arrangement of spikeletís and bunches are housed in leaf axils. This creates problem while harvesting bunches in matured palms. The female inflorescence at anthesis is in the axils of the 17th leaf from the center spear and by the time the bunch is ripe, it is subtended by about the 30th leaf. The bunch leans out from it subtending leaf on to a leaf in a lower whorl, so it is not the leaf subtending the bunch that support. In oil palm bunches appears very compact due to the arrangement of spikeletes and fruits and they are housed in leaf axils leading to harvest problem especially in matured palms. Character of obvious importance for easy harvest in oil palm is bunch stalk (peduncle). Bunch stalk is housed inside the leaf axils. Bunches possessing long stalk facilitates access for effortless harvest and pollination. Extremely low values have been observed for percentage of long bunch stalk (peduncle) for material collected in Brazil (Miranda Santos *et al*., 1984). Ooi *et al*. (1981) emphasized these characteristics, pointing out that in some cases this was as low as 6.0 cm.

Morpho-agronomic characteristics: To broaden the oil palm genetic base, Pillai *et al*. (2000) collected different exotic genetic resources during 1995. Thirty one accessions of such resources were planted during 1998 in the field gene bank at ICAR-Indian Institute of Oil Palm Research (Formerly known as Directorate of Oil Palm Research), Research Centre, Palode. Asapart ofcrop improvement programme, characterization andyield evaluation wasundertaken asperIBPGR (1989) descriptor withnecessary additional characteristics. The proposed genetic stock (GB palm no.33) has long bunch stalk (53 cm) and possess high sex ratio (DOPR annual report 2009-10). This character (Fig. 1) has been introgressed into new oil palm breeding lines.

Associated characteristics and cultivated practices: The advantage of long bunch stalk is ease of harvesting without the requirement of pruning the frond below the bunch. Another advantage of long bunch stalk is its protruding structure that allows the convenience of weevil pollinators to pollinate the entire inflorescence to produce well pollinated fresh fruit bunch. Oil palm hybrid with lower height and short fronds and compact crown results in higher economical life span; hence space efficient and 148 palms can be planted per hectare; high number of fresh fruit bunch with average weight helps to buffer against the environmental stress for consistent fresh fruit bunch production and oil extraction rate. Other advantages include smaller palm size, small and lighter fronds thus easier for harvesting (http://www.aarsb.com.my/the-advancement-of-oil-palm-breeding). Murugesan and Gopakumar (2010) had reported maximum mean length of 18.13cm in Guinea Bissau population at Athirapilli field gene location of Kerala, India. Rajanaidu (1984) reported variation in preponderance of female inflorescence in African germplasm and bunch characteristics in the germplasm planted in Malaysia.

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58. IC0597689 (EC382636; DOPRG-54-E65)(IC0597689; INGR17085), an Oil Palm (*Elaeis guineensis*) Germplasm with Sterile Pisifera Palm. Virescens Fruit

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The narrowness of gene pool is considered as a major obstacle to increase the productivity as the oil palm planting materials are presently derived from an extremely narrow genetic base (Corley RHV and PBH Tinker, 2003).Oil palm is propagated commercially through hybrid seeds and the cultivated species *Elaeis guineensis* Jacq. the African oil palm has three distinct fruit forms, which are distinguished by shell thickness *viz*: 1) *dura* (thick shell of 2-8 mm), 2) *tenera* (hybrid between *dura* × *pisifera* cross with thin shell of 0.5 to 4 mm) and 3) *pisifera* (shell-less and female sterile). The *pisifera* palms are classified either as fertile (producing mature ripe bunches with high fruit set) or semi fertile (with partial fruit set) or sterile forms (no fruit set). The sterile *pisiferas* are preferred in hybrid seed production and used as male parent in *Dura*× *Pisifera* hybridization programme for the production of cultivated *tenera*. Preliminary investigations on *pisifera* palms characterization and allied components were studied by Pillai and Nampoothiri (1981). Characterization of *pisifera* palms were also undertaken in a *tenera* inter se matted progeny population as a part of breeding for hybrid seed production by Murugesan *et al*. (2008) using Thodupuzha materials which were extensively used in the Indian breeding programme. However, there is a necessity to introgress new and distant *pisifera* sources into the ongoing programme and identify potential *pisiferas* for the pollination of many *dura* mother palms over a long period. The benefit to be obtained from *pisifera* progeny testing will depend on the amount of genetic variation within *pisifera* population.

Morpho-agronomic characteristics: To broaden the oil palm genetic base, Pillai *et al*. (2000) collected different exotic genetic resources during 1995 under FAO sponsored programme. Thirty one accessions of such resources were planted during 1998 in the field gene bank at ICAR-Indian Institute of Oil Palm Research (Formerly known as Directorate of Oil Palm Research), Research centre Palode. Phenotypic screenings of these collections are done as per IBPGR (1989) descriptors (whichever characters available for *pisifera* fruit form) revealed a significant diversity for the valuable agronomical characteristics. The reported germplasm with *virescens* and sterile fruit characteristics was selected based on the phenotypic data described by Corley *et al*. (1971), such as: (1). bunch numbers, weight and production; (2) fresh fruit bunch and oil content; (3) vegetative characters; (4) fruit shell thickness; (5) fruit colour and bunch analysis as per Blaak *et al*. (1963). All the vegetative characters were measured during June month of every year and average of four years was reported. Bunch production and number of bunches were recorded quarterly, bunch analysis was done for three bunches during peak season and average of four years were reported for all the measured parameters.

Associated characters and cultivation practices: The fruit form analysis in the open pollinated progeny population of exotic oil palm block revealed that out of 87 individual palms of 37 accessions, three *pisifera*, one *tenera* and 83 *dura* palms were recorded. The identified three *pisifera* palms were further evaluated by

Murugesan and Goutam Mandal (2010) for vegetative and bunch characteristics and the results revealed that two *pisiferas* (DOPRG-53-E-75 and DOPRG-54-E-65) showed aborted bunches throughout the evaluation period where as other one *pisifera* (DOPRG-53-E-66) showed fertile character which recorded normal bunch and fruit development with 25% fruit to bunch ratio. Few fruit set occurred two times in IC0597689 due to spraying of 2,4,5-TP (2,4,5- Trichlorophenoxy propionic acid) revealed the presence of *virescens* fruit colour and presence of shell less kernel. Close examination of these fruits revealed that the stylar ends of the fruits were either dark green or orange in colour and their pedicellar ends were creamy white or yellow and weight ranged from 1g to 5g. Oil analysis revealed that orange colour fruits recorded 89 % of oil/fruit, whereas green coloured and white fruits recorded no oil. The reported sterile *pisifera* with *virescens* (IC0597689) in terms of vegetative characteristics showed no significant differences with other two checks (DOPRG-53-E-66 and DOPRG-53-E-75) (Anonymous, 2009). The frequency of *virescens* in the natural population in Nigeria was unexpectedly low even though gene controlling this particular character is dominant. This type is relatively uncommon which was noticed only in *dura* and *tenera* forms of fruits. *Virescens pisifera* are very rare which are called 'Gracilinux'– *virescens pisifera* as reported by Chevalier during 1910. It would be advantageous to produce planting materials with *virescens* fruits for easy identification of ripe bunches. The reported *pisifera* palm DOPRG-54-E65 (IC0597689) with *virescens* fruit and sterile characteristics is considered as valuable genetic resource with practical utility as it could be used as male parent along with *virescens dura* parent available with ICAR-IIOPR for the production of *virescens tenera*. DOPRG-54-E65 could be considered as ideal *pisifera* and the general as well as specific combining ability is being tested with advanced *dura* mother palms for hybrid seed production and supply to farmers.

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59. IC0597690 (DOPR G23-48) (IC0597690; INGR17086), a Dwarf Oil Palm (*E. guineensis* × *E. oleifera*) Germplasm with 12 cm Annual Height Increment. High Fruit Set (69.09%)

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The genus *Elaeis* consists of two species namely, *Elaeis oleifera* HBK and *Elaeis guineensis* Jacq. The former one is called American oil palm which is a wild relative of cultivated type. Wild oil palm has low oil yield but it has several desirable characteristics, *viz.* slow vertical growth, disease resistance and best oil quality. A palm oil with a greater proportion of unsaturated fatty acids attracts new market opportunities for oil palm planters (Montoya *et al.* 2013). American oil palm is native to Central America and northern South America, is an important source of genetic variability for oil palm breeding. To sustain high yields, *E. oleifera* × *E. guineensis* (O×G) hybrids are backcrossed with *E. guineensis* and the progenies resulting from this breeding strategy present variability.

Morpho-agronomic characteristics: The interspecific hybrid combinations evolved from the pure stand of *E. oleifera* of exotic germplasm accession planted at the field gene bank established during 1994 under the tropical climate of Kerala, South India (8° 45'N and 77° 59' E and 210 m above sea level) were utilized to develop promising palms of O × G hybrids. *E. oleifera* has a marked tendency towards the production of parthenocarpic fruits. This character is fully dominant in the hybrid. Because of this the percentage fruit per bunch in the hybrids tends to become higher than *E. guineensis* partly offsetting the lower percentage oil to mesocarp. Hybrid progenies of *E. guineensis* × *E. oleifera* were planted during 1998 in forest laterite soil at Research Centre of ICAR-Indian Institute of Oil Palm Research. A transfer of genes from the species *Elaeis oleifera* to the oil palm species (*Elaeis guineensis*) was made using backcrosses, with an objective of obtaining a cultivar with high fruit and oil production per unit of area with slow rate of growth. A progeny population from one combination namely (progenitor 16 *Elaeis oleifera (1992planting)* × 18 *Elaeis guineensis (1992)* observed with unique characteristics *viz*., high fruit set and unique fruit colour (deep red skin and yellow mesocarp) apart from compact slow height increment.

Associated characters and cultivation practices: According to Escobar and Alvarado, (2004), the original compact palm (OCP) was discovered in observation plots planted in Coto, Costa Rica, which were planted with open-pollinated seeds from an *E. oleifera* × *E. guineensis* inter-specific hybrid (O × G) with outstanding characteristics of slow growth and short leaves, identified in 1966 in Quepos, Costa Rica, but unfortunately their bunches were reported to be poor in fruit set, whereas proposed genetic Stock DOPRG 23 (IC 0597690) has compact characteristics and high fruit set (DOPR Annual Report 2009-10, DOPR Vision, 2030, DARE/ICAR Annual Report, 2010-11). The progenies generated from the proposed genetic stock also recorded compact characteristics; high fruit set and exhibited stabilised characteristics similar to that of cultivated type of oil palm (DOPR News, 2012).

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60. IC0597691 (DOPR G21-221)(IC0597691; INGR17087), an Oil Palm (*Elaeis guineensis*) Germplasm with Slow Vertical Stem Growth (low annual height increment of 25 cm per year). Compact Palm with Tenera (thin shell thickness of 1.56 mm) Fruit Form

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The Oil palm (*Elaeis guineensis* Jacq.) is a commercial crop demanding large tracts of land for its exploitation. High yielding compact palms with slow stem elongation and short leaves become good alternative for prolonging commercial exploitation (Escobar and Alvarado, 2004). Advantage of reduced height increment is only seen after many years, when height starts to have an effect on harvesting cost. Reducing height has always been interest to oil palm industry because of the high cost of harvesting tall palms (Bakoume and Louise, 2007). However, selection for yield will tend to favour taller palms and Corley and Lee (1992) reported that selected Deli *dura* were 15-22% taller at the same age than unselected material. Dumortier (2000) found a significant positive correlation between progeny means for yield and height. According to Corley and Tinker (2003), finding special small and productive palms with potential commercial value is not an easy task and only a few examples of such palms have been documented worldwide. Nampoothiri (1998) emphasized the usefulness of compact characters in breeding for dwarfness for sustainable development of oil palm in India. Several exotic germplasm collections were made from different oil palm growing countries to India (Pillai, 1994).

The Nigerian *tenera* population with the progenitor of 26.3999 D × 25.380P were introduced to India through National Bureau of Plant Genetic Resources (NBPGR) vide code number E 130756 during 1979 which were field planted at Research Centre of ICAR-IIOPR at Palode during 1981. One *tenera* palm from Nigerian introduction showed dumpy characteristics (Pillai, 1994; Nampoothiri, 1998) as they recorded low vertical growth compared to similar aged and simultaneously planted crosses/progenies. Dwarf *tenera* was subjected to characterization and yield evaluation as per IBPGR (1989) descriptor with necessary additional characteristics. Bunch Analysis was done as per standard procedures. Five Fresh Fruit Bunches (FFB) from each palm were utilized for bunch analysis.

Morpho-agronomic characteristics: The results of evaluation in terms of morpho-agronomic characters revealed that the proposed dwarf *tenera* recorded an average yield of 118 kg/palm/year with 9.1 bunch numbers and 24 cm height increment (Murugesan *et al*., 2008). Rajanaidu and Jalani (1994) reported short height increment of 15-25 cm within dwarf populations from Nigerian collections at Palm Oil Research Institute of Malaysia (PORIM). The present proposed genetic stock has short rachis length (4.85 m), inter nodal leaflet distance (2.5 to 3 cm), leaflet length (85.33 cm), petiole width (8 cm), petiole depth (2.92 cm), leaflet breadth (4 cm), frond base length (75 cm), frond base width (10 cm), frond base scar measured at two feet from the ground level (5 cm) and other vegetative characteristics when compared to commercial *tenera* of same age planted adjacent to this palm. Adon *et al*. (2001) observaed high heritability for oil palm height increment. Other notable compact characters of the proposed *tenera* were stunted fronds with reduced leaflet length, compact crown, dumpy canopy structure and reduced inter nodal leaflets (Murugesan *et al*., 2009; Murugesan and Sunil Kumar, 2014).

Associated characters and cultivation practices: Considering over all dumpy nature, the proposed palm of genetic stock DOPR G1 (221) has been incorporated into breeding programme of ICAR-Indian Institute of Oil Palm Research (IIOPR) and this palm has been subjected to selfing and *inter se* crossing and progenies were established at ICAR-IIOPR, Pedavegi, Andhra Pradesh. Out of the 58 palms evaluated, 23 recorded height increment of < 40 cm, four palms recorded < 30 cm and one palm recorded 25 cm annual height increment

with Bunch Index of 0.43 as against the standard value of 0.30 for normal *tenera* (*dura* × *pisifera*) material (Anonymous, 2012; Anonymous, 2013). Four individual palms which were screened from the progeny trial were selfed/ *inter se* mated for the establishment of seed garden and seed production for dwarf palms.

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61. IIHRG 6 (IC0621473; INGR17088), a Gladiolus (*Gladiolus hybridus*) Germplasm with Unique Floret Colour [Purple (78.A) middle, Red–Purple (72.A) Margin with Green-Yellow (1.D) blotch], Open-faced Floret and Double Rows of Floret Placement

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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 6 is derived from the cross Poonam x Gold Medal 412 followed by selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13° 58' N Latitude, 78°E Longitude and at an altitude of 890 meter above mean sea level), India. The hybrid selection IIHRG 6 is unique for its floret colour [Purple (78.A) middle. Red–Purple (72.A) margin with Green-Yellow (1.D) blotch], open-faced floret and floret placement is in double rows.

Morpho-agronomic characteristics: The plants are tall (121.85 cm) and on an average produces florets in 65.03 days. Its average spike length is 104.55 cm and

rachis length (45.80 cm) which bears 13.01 florets per spike. On an average, it also produces 1.82 number of marketable spikes per corm, 2.22 number of corms and 27.24 number of cormels per mother corm.

Associated characters and cultivation practices: Gladiolus is commercially propagated through corms and cormels. It grows well in sandy loam soil rich in organic matter and nutrients with pH of 6.5 to 7. The corms of 4 to 5 cm diameter should be planted at a spacing of 30 cm × 20 cm at about 5 cm depth of the soil. Before planting, brown scales on the corms are removed and the corms have to be treated with carbendazim (0.2%) and captan (0.2%) for 15 to 20 minutes for protection against *Fusarium* wilt. In general, recommended dose of fertilizer is 25 tones of farmyard manure, 200 kg N, 200 kg P_2O_5 and 200 kg K_2O per hectare as basal dose (Rao *et al.,* 2010). Earthing up to a height of 10-15 cm at three and six leaf stage is required. In and around Bangalore planting during the June, October and November months found to be the best considering the quality of the spike. The major insect pests of gladiolus are thrips, caterpillar and mites. In India, it is grown in Uttar Pradesh, Maharashtra, Sikkim, Delhi, Punjab, Karnataka, West Bengal, Jammu and Kashmir, Himachal Pradesh, Haryana, Assam, Nagaland and Rajasthan.

Table 1. Morpho-agronomic description of Gladiolus hybrid selection IIHRG 6

Trait Description	Pooled data of three years
Days to spike emergence	54.09
Days to flower	65.03
Plant height (cm)	121.85
Spike length (cm)	104.55
Rachis length (cm)	45.80
Floret size (cm)	9.61
No. of florets per spike	13.01
Florets remain open at a time (No.)	6.38
Total spikes per corm (No.)	2.00
Marketable spikes per corm (No.)	1.82
Flowering duration (Days)	8.18
Vase life (Days)	7.67
Spike weight (g)	48.33
Corm per corm (No.)	2.22
Cormel per corm (No.)	27.24
Size of corm (cm)	5.99
Size of cormel (cm)	1.08
Weight of corm (g)	60.33
Weight of comel (g)	0.56

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62. IIHRG 12 (IC0621474; INGR17089), a Gladiolus (*Gladiolus hybridus*) Germplasm with Unique Floret Colour [Purple Violet (82.A) having Purple (77.A) Margin, Green White (157.C) Line on Lower Lip] and Early Flowering (61.54 Days)

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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 12 is derived from the cross Junior prom × Poonum followed by selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13º58' N Latitude, 78ºE Longitude and at an altitude of 890 meter above mean sea level), India. The hybrid selection IIHRG 12 is unique for its floret colour [Purple Violet (82.A) having Purple (77.A) margin. Green White (157.C) line on lower lip] and early flowering.

Morpho-agronomic characteristics: The plants are tall (131.00 cm) and on an average produces florets in 61.54 days. Its average spike length is 107.66 cm and rachis length (51.87 cm) which bears 14.88 florets per spike. On an average, it also produces 1.59 number of marketable spikes per corm, 1.82 number of corms and 52.56 number of cormels per mother corm.

Associated characters and cultivation practices: Gladiolus is commercially propagated through corms and cormels. It grows well in sandy loam soil rich in organic matter and nutrients with pH of 6.5 to 7. The corms of 4 to 5 cm diameter should be planted at a spacing of 30 cm x 20 cm at about 5 cm depth of the soil. Before planting, brown scales on the corms are removed and the corms have to be treated with carbendazim (0.2%) and captan (0.2%) for 15 to 20 minutes for protection against *Fusarium* wilt. In general, recommended dose of fertilizer is 25 tones of farmyard manure, 200 kg N, 200 kg P_2O_5 and 200 kg K_2O per hectare as basal dose (Rao *et al.,* 2010). Earthing up to a height of 10-15 cm at three and six leaf stage is required. In and around Bangalore planting during the June, October and November months found to be the best considering the quality of the spike. The major insect pests of gladiolus are thrips, caterpillar and mites. In India, it is grown in Uttar Pradesh, Maharashtra, Sikkim, Delhi, Punjab, Karnataka, West Bengal, Jammu and Kashmir, Himachal Pradesh, Haryana, Assam, Nagaland and Rajasthan.

Table 1. Morpho-agronomic description of Gladiolus hybrid Selection IIHRG 12

Trait Description	Pooled data of three years
Days to spike emergence	51.54
Days to flower	61.54
Plant height (cm)	131.00
Spike length (cm)	107.66
Rachis length (cm)	51.87
Floret size (cm)	9.62
No. of florets per spike	14.88
Florets remain open at a time (No.)	5.59
Total spikes per corm (No.)	1.85
Marketable spikes per corm (No.)	1.59
Flowering duration (Days)	9.63
Vase life (Days)	8.00
Spike weight (g)	58.33
Corm per corm (No.)	1.82
Cormel per corm (No.)	52.56
Size of corm (cm)	5.16
Size of cormel (cm)	1.12
Weight of corm (g)	55.22
Weight of comel (g)	0.69
Floret Type	Open-faced
Floret texture	Medium
Floret structure	Wavy
Floret placement	Good

References

Rao T M, Meenakshi Srinivas and P B Gaddagimath (2010) Wealth of Ornamental Crops–Varieties developed at IIHR. *Technical Bulletin*. Director, ICAR-IIHR, Bangalore. p. 63.

63. IIHR 3-34 (IC06214771; INGR17090), a Gerbera (*Gerbera jamesonii*) Germplasm with Unique Flower Head Colour (68D, Red Purple Group) and Double Type Flower Head

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Gerbera (*Gerbera jamesonii* Bolus ex. Hooker F.), family Asteraceae, is one of the important cut-flowers grown for domestic and export markets. Gerbera is grown under 820 ha with productivity of 17,500 t/ha, amounting to the fourth most important cut-flower in India. The gerbera hybrid IIHR 3-34 is novel genetic stock for its flower head colour (68D, Red Purple Group) and double type flower head. It was developed through half-sib method of breeding where superior line IIHR-3 was crossed with pollen mixed from different varieties. The F_1 hybrids seeds obtained from this cross were germinated *in vitro* on suitable media. A large number of plants were obtained through tissue culture to initially evaluate for novel traits and flower quality. This hybrid was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13^{o}58' N Latitude, 78^{o}E Longitude and at an altitude of 890 meter above mean sea level), India.

Morpho-agronomic characteristics: The hybrid IIHR3-34 recorded flower diameter (10.85 cm), flower stalk length (61.06 cm), flower stalk diameter (6.42 mm), number of flowers/month (3.23), vase life (7.30 days) and flower head colour as per RHS colour chart (68D, Red Purple Group) (Table 1).

Associated characters and cultivation practices: The hybrid IIHR 3-34 is novel for its flower head colour as per RHS Colour Chart (68D, Red Purple Group) and

Table 1. Evaluation of gerbera hybrid IIHR 3-34 for flower quality traits under polyhouse

Hybrid/ genotype	Flower diameter (cm)	Flower stalk length (cm)	Flower stalk diameter (mm)	No. of flowers/ month	Vase life (days)	Thrips (% flowers damage)	Whitefly (Nos. on 3rd leaf)	Mites damage (Nos./leaf)	RHS Colour Chart
IIHR 3-34	10.85	61.06	6.42	3.23	7.30	17.75	7.15	5.35	68D, Red Purple Group
IIHR-3 (parent)	11.41	49.75	6.74	2.83	7.05	17.05	7.30	5.67	52A, Red Group
Elite (check)	10.91	60.38	6.62	2.96	7.47	18.85	7.40	5.27	24A, Orange Group
SEm±	0.18	1.85	0.04	0.12	-	-	-	-	-
CD at 5%	0.55	5.55	0.16	0.36	NS	NS	NS	NS	-

double type flower head. It recorded % flowers damage by thrips (17.75), number of whitefly on 3rd leaf (7.15), number of mites damage/leaf (5.35). However, data on damage from thrips, white fly and mites was on par with the parent and the check variety. Gerbera is commercially gerbera is grown in polyhouse or shade house. Day temperature of 22°-25°C and night temperature of 12-16°C is ideal for growth and flower production. It grows well on raised beds of loamy soil, rich in organic matter with soil pH of 5.5-6.5 and EC less than 1 dS/ cm^2. The beds are drenched with commercial formalin to minimize infestation of soil-borne pathogens. On average water requirement may be 500 to700 ml/plant/ day (4.5-6.0 litres/day/m^2). During first three months of planting apply 10:15:20g 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, better growth and increased flower production. Application of micronutrients *viz.,* boron, calcium, magnesium and copper @ 0.15% once in a month is desirable for obtaining good quality flowers (Aswath *et al,* 2015).

References

Aswath C, Rajiv Kumar, TM Rao, MV Dhananjaya, V Sridhar, S Sriram and Sudha Mysore (2015) Polyhouse cultivation of gerbera. *Extension Folder No. 91*. Director, ICAR-IIHR, Bangalore.

64. IIHR 8-45 (IC0621472; INGR17091), a Gerbera (*Gerbera jamesonii*) Germplasm with Unique Flower Head Colour (50A, Red group) and Double Type Flower Head

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Gerbera (*Gerbera jamesonii* Bolus ex. Hooker F.), family Asteraceae, is one of the important cut-flowers grown for domestic and export markets. Gerbera is grown under 820 ha with productivity of 17,500 t/ha, amounting to the fourth most important cut-flower in India. The gerbera hybrid IIHR 8-45 is novel genetic stock for its flower head colour (50A Red Group) and double type flower head. It was developed through half-sib method of breeding where superior line IIHR-1 was crossed with pollen mixed from different varieties. The F_1 hybrids seeds obtained from this cross were germinated *in vitro* on suitable media. A large number of plants were obtained through tissue culture to initially evaluate for novel traits and flower quality. This hybrid was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13° 58′ N Latitude, 78°E Longitude and at an altitude of 890 meter above mean sea level), India.

Morpho-agronomic characteristics: The hybrid IIHR8-45 recorded flower diameter (10.43 cm), flower stalk length (61.11 cm), flower stalk diameter (5.63mm), number of flowers/month (2.89), vase life (7.15 days) and flower head colour as per RHS Colour Chart (50A Red Group) (Table 1).

Associated characters and cultivation practices: The hybrid IIHR 8-45 is novel for its flower head colour as per RHS Colour Chart (50A Red Group) and double type flower head. It recorded % flowers damage by thrips (17.89), number of whitefly on 3rd leaf (7.31), number of mites damage/leaf (5.15). However, data on damage from thrips, white fly and mites was on par with the parent and the check variety. Gerbera is commercially gerbera is grown in polyhouse or shade house. Day temperature of 22°-25°C and night temperature of 12-16°C is ideal for growth and flower production. It grows well on raised beds of loamy soil, rich in organic matter with soil pH of 5.5-6.5 and EC less than 1 dS/cm^2. The beds should be drenched with commercial formalin to minimize infestation of soil-borne pathogens. On average water requirement may be 500 to 700 ml/plant/day (4.5-6.0 litres/day/m^2). During first three months of planting apply 10:15:20g 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, better growth and increased flower production. Application of micronutrients *viz.,* boron, calcium, magnesium and copper @ 0.15% once in a month is desirable for obtaining good quality flowers (Aswath *et al.,* 2015).

References

Aswath C, Rajiv Kumar, T M Rao, M V Dhananjaya, V Sridhar, S Sriram and Sudha Mysore (2015) Polyhouse cultivation of gerbera. *Extension Folder No.* 91. Director, ICAR-IIHR, Bangalore.

Table 1. Evaluation of gerbera hybrid IIHR8-45 for flower quality traits under polyhouse

Hybrid/ genotype	Flower diameter (cm)	Flower stalk length (cm)	Flower stalk diameter (mm)	No. of flowers/ month	Vase life (days)	Thrips (% flowers damaged)	Whitefly (Nos./3rd leaf)	Mites (Nos./leaf)	RHS Colour Chart
IIHR 8-45	10.43	61.11	5.63	2.89	7.15	17.89	7.31	5.15	50A Red Group
IIHR1 (parent)	10.25	51.98	4.69	2.49	7.00	17.62	7.42	5.35	30A, Orange Red
Elite (check)	10.91	61.38	6.63	2.96	7.25	18.85	7.41	5.25	24A, Orange Group
SEm±	-	0.93	0.06	0.14	-	-	-	-	-
CD at 5%	NS	2.79	0.18	0.39	NS	NS	NS	NS	-

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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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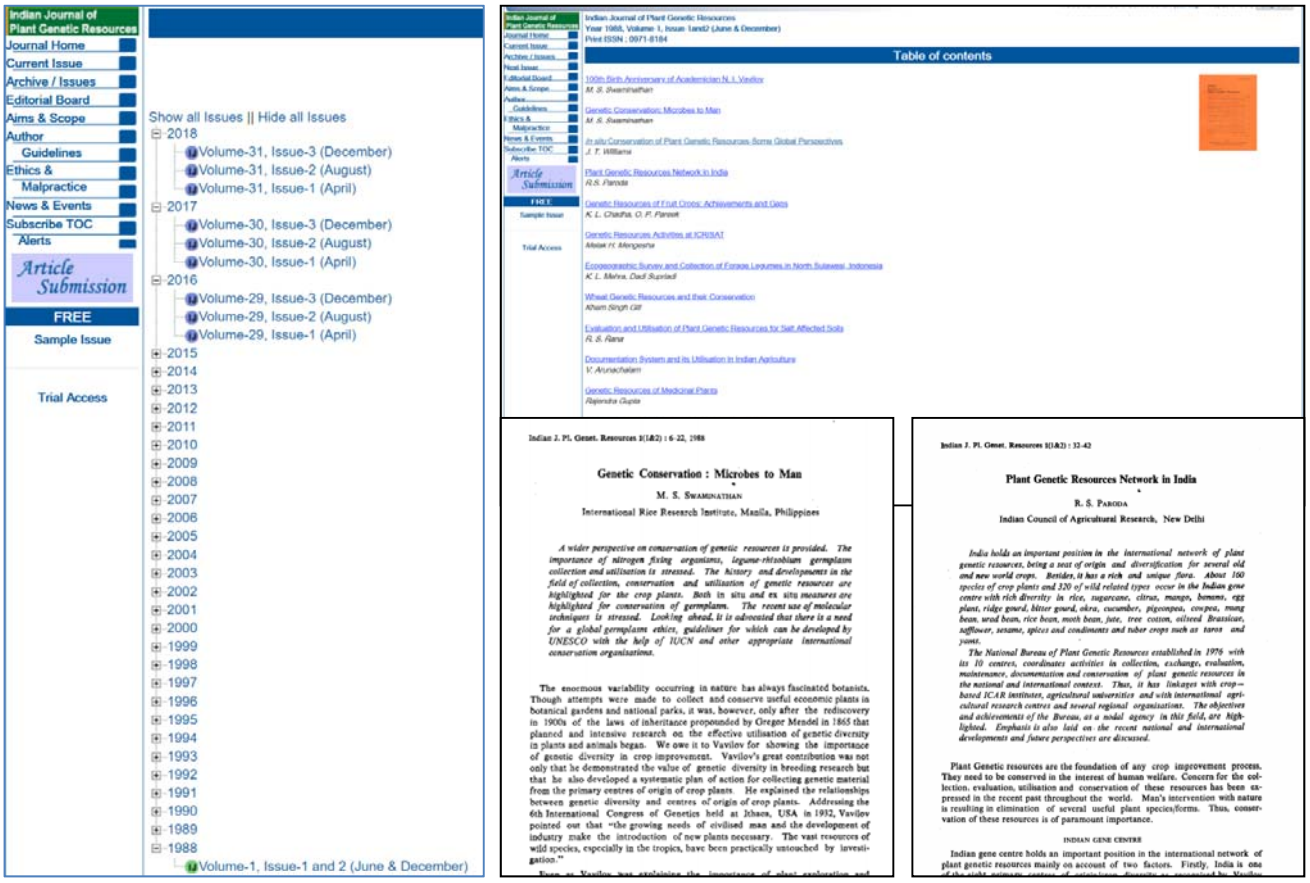

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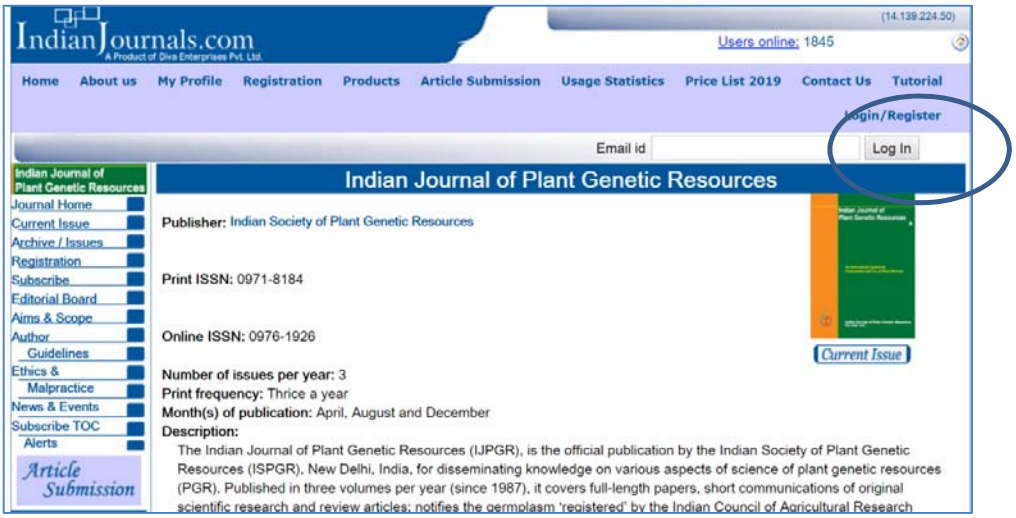

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