Vol. 37 No. 3 2024

Print ISSN: 0971-8184
Online ISSN: 0976-1926

Indian Journal of Plant Genetic Resources

An International Journal for Conservation and Use of Plant Diversity

Indian Society of Plant Genetic Resources
New Delhi, India

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(Registration No. S/18336)

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ISSN: 0971-8184
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INDIAN SOCIETY OF PLANT GENETIC RESOURCES
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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.01

Indian Journal of Plant Genetic Resources

REVIEW ARTICLE

Current Status and Potential of Temperate Fruit Crops for Livelihood and Nutritional Security in India

MK Verma*, OC Sharma, JI Mir, WH Raja and Sajad Un Nabi

Abstract

The horticultural sector in India has emerged as a formidable force in global production, with the nation claiming the position of the second-largest producer worldwide. In the fiscal year 2022-23, India's horticultural output reached an estimated 351.92 million tons, showcasing a notable increase of approximately 4.74 million tons (1.37%) compared to the preceding year. Fruit crops, a significant component of this sector globally, span an extensive area of approximately 68.05 million hectares, yielding a staggering 867.77 million metric tons annually, averaging 12.75 tons per hectare. India's contribution to this domain is notable, with fruit production totaling around 107.51 million metric tons, cultivated across 7.06 million hectares, boasting an average productivity of 15.22 tons per hectare. The Indian Himalayan region stands out as a promising landscape for the cultivation of temperate horticultural crops, including fruits, vegetables, ornamental plants, and medicinal and aromatic species. Encompassing latitudes 26°20′ to 35°40′ N and longitudes 74°50′ to 95°40′ E, this region spans from the foothills in the south (Siwalik's) to the Tibetan plateau in the north (trans-Himalaya), comprising approximately 95 districts of the country. Despite its fragile terrain, characterized by snow-clad peaks and dense forests, the Indian Himalayas contribute significantly, covering 16.2% of India's total geographical area. Temperate fruit cultivation thrives predominantly in Jammu & Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, and Arunachal Pradesh, capitalizing on the region's climatic advantages. Notably, a diverse range of temperate fruits such as apple, pear, peach, plum, apricot, cherry, almond, and walnut flourish in this region. With its relative climatic advantages and conducive environmental conditions, the Indian Himalayan region continues to serve as a vital hub for the production of temperate fruits, underscoring its significance in India's horticultural landscape.

Keywords: Current status, India, Livelihood, Nutritional security, Temperate fruit crops.

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Received: 19/06/2024 **Revised:** 17/08/2024

Accepted: 30/08/2024

How to cite this article: Verma MK, OC Sharma, JI Mir, WH Raja and SU Nabi (2024) Current Status and Potential of Temperate Fruit Crops for Livelihood and Nutritional Security in India. *Indian J. Plant Genet. Resour.* 37(3): 387-403. **DOI:** 10.61949/0976-1926.2024.v37i03.01

Introduction

The Indian Himalayan region emerges as a promising landscape for the cultivation of temperate horticultural crops, encompassing a diverse array of fruits, vegetables, ornamental plants, and medicinal and aromatic species. Spanning latitudes 26°20′ to 35°40′ N and longitudes 74°50′ to 95°40′ E, this region extends from the foothills in the south (*Siwalik's*) to the Tibetan plateau in the north (trans-Himalaya), encompassing approximately 95 districts of the country. Despite its fragile terrain, characterized by snow-clad peaks and dense forests, the Indian Himalayas significantly contribute, covering 16.2% of India's total geographical area. Temperate fruit cultivation thrives predominantly in Jammu & Kashmir, Himachal Pradesh, Uttarakhand, Sikkim, and Arunachal Pradesh, capitalizing on the region's climatic advantages (Ahmad *et al*., 2021; Mitra and Roy, 2013). Notably, a diverse range of temperate fruits such as apple, pear, peach, plum, apricot, cherry, almond, and walnut flourish in this region. With its relative climatic advantages and conducive environmental conditions, the Indian Himalayan region continues to serve as a vital hub for the production of temperate fruits, underscoring its significance in India's horticultural landscape (Verma *et al.,* 2010; 2013; 2023). India's production of temperate

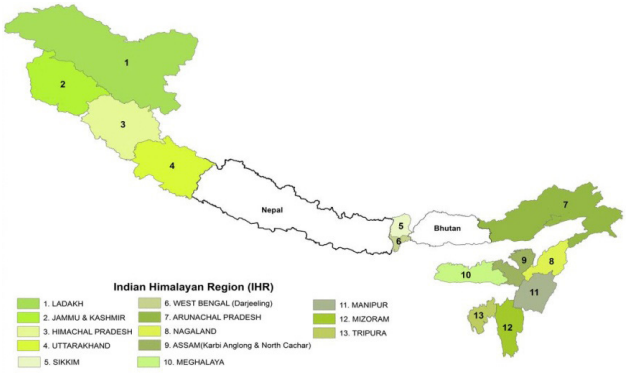


Figure 1: Temperate fruit-growing states in the Indian Himalayan region

fruits is substantial, with the Himalayan region being a significant contributor. Temperate fruit cultivation is a major source of income for farmers in the Himalayan states, particularly in remote and mountainous regions (Figure 1). These crops contribute significantly to the rural economy by generating employment opportunities, supporting agro-based industries, and enhancing household incomes. The export of certain temperate fruits, such as apples, contributes to foreign exchange earnings and trade balance. The productivity of temperate fruit crops varies across regions and depends on factors such as altitude, soil type, and orchard management practices. While some areas achieve high yields per hectare, there is still room for improvement through the adoption of modern cultivation techniques.

Current Area and Production Scenario of the Temperate Fruit Industry in India

The horticultural sector in India has emerged as a formidable force in global production, positioning the nation as the second-largest producer worldwide. In the year 2022-23, India's horticultural output soared to an estimated 351.92 million tons, marking a noteworthy increase of approximately 4.74 million tons (1.37%) compared to the preceding year. Fruit crops, a pivotal component of this sector on a global scale, occupy an expansive area of approximately 68.05 million hectares, yielding a staggering 867.77 million metric tons annually, averaging 12.75 tons per hectare. India's substantial contribution to this domain is evidenced by its fruit production, totaling around 107.51 million metric tons, cultivated across 7.06 million hectares, boasting an impressive average productivity of 15.22 tons per hectare. There are several dozens of temperate fruit crops from pome, stone, nuts, berries and other groups (Table 1). However, only 25 to 30 fruits/nuts are commercially grown around the world for fresh fruits as well as processed products (Retamales, 2011; Verma *et al.,* 2013).

Almond, apple, apricot, kiwi fruit, peach, pear, pecan, plum and walnuts are commercially cultivated in the states of Jammu & Kashmir, Himachal Pradesh, Uttarakhand and

Table 1: List of temperate fruit crops grown and suitable for commercial cultivation.

Group	*Fruit crops*
Pome fruits	Apple, pear, quince
Stone fruits	Peach, nectarine, plum, prune, plumcot, apricot, sweet cherry, sour cherry
Nuts	Almond, walnut, hazelnut, chestnut, pecan nut, pistachio nut, pine nut
Other fruits	Kiwi fruit, persimmon, fig, grape, strawberry, mulberry, fig, seabuckthorn, olive
Berries	Blackberries, raspberries, loganberry, blueberries, huckleberries, cranberries, currants, gooseberries,

Arunachal Pradesh (Mandal *et al*., 2021). In addition, a small area is increasing under low chills temperate fruits like apples, pears, peaches and plums in Punjab, Sikkim, Chhattisgarh, Nagaland, Tamil Nadu, Haryana, Madhya Pradesh, Mizoram, Manipur, West Bengal, Kerala, Maharashtra and Telangana (Table 2). As per the reports published by the Ministry of Agriculture and Farmers Welfare (PIB, 2022), the total temperate fruit production is 3417.91 thousand metric tons from an area of 520.92 thousand hectares. The average productivity is 6.56 t/ha and ranges from 1.20 t/ha (West Bengal) to 21.09 t/ha (Punjab). The maximum productivity among the different states was recorded in Punjab (21.09 t/ha) followed by Haryana (14.27 t/ha), Tamil Nadu (14.27 t/ha), Madhya Pradesh (11.54 t/ha), Manipur (10.45 t/ha), J&K (8.28 t/ha), Nagaland (6.99 t/ha), Himachal Pradesh (4.51 t/ha), Chhattisgarh (4.05 t/ha). The low productivity levels are mainly from high chilling areas (J&K, HP, UK and Arunachal Pradesh) as compared to low chill areas located in Punjab, Haryana and Tamil Nadu (Tables 2 & 3).

Among the temperate fruit crops, the maximum average productivity was recorded in apple (8.20 t/ha) followed by pear (7.05 t/ha), and peach (6.33 t/ha). However, the minimum productivity levels are generally recorded in nut crops, *viz.,* pecan nut (0.54 t/ha), almond (1.72 t/ha) and walnut (2.79 t/ha) (Table 3). The commodity-based largest producers' states are almond J&K for almond, apple and walnut; Arunachal Pradesh for kiwi fruit; Punjab for pear and peach; Himachal Pradesh for pecan nut and Uttarakhand for plums. The data regarding apricots is not available from the above source; however, Ladakh is the largest apricot-producing area in the country (Table 4). The maximum area is covered by apple (60.33%) followed by walnut (19.87%), pear (8.42%), plum (4.58%), peach (3.68%), almond (1.97%) and pecan nut (0.17%). Similarly in production, the largest volume is made up of apple (75.60%) followed by pear (9.04%), walnut (8.45%), peach (3.55%), plum (2.53%), almond (0.35%) and pecan nut (0.01%) (Table 3). The state-wise detailed data regarding area, production and productivity under different crops are given in Table 4. The range of productivity is varied widely among various crops

Table 2: Area, production and productivity of temperate fruits in India during 2021-22 (PIB, 2022)

	Major temperate fruit crops grown	*Area ('000 ha)*	*Production ('000 MT)*	*Productivity (t/ha)*
Jammu & Kashmir	Almond, apple, apricot, kiwifruit, peach, pear, plum and walnut	275.70	2281.81	8.28
Himachal Pradesh	Almond, apple, apricot, kiwi fruit, peach, pear, pecan, plum and walnut	145.64	657.08	4.51
Uttarakhand	Almond, apple, apricot, kiwi fruit, peach, pear, plum and walnut	74.35	245.12	3.30
Arunachal Pradesh	Apple, kiwi fruit, peach, pear, plum and walnut	9.12	15.13	1.66
Punjab	Peach, pear and plum	7.47	157.53	21.09
Sikkim	Kiwi fruit, peach, pear	2.21	6.64	3.00
Chhattisgarh	Pear	2.12	8.58	4.05
Nagaland	Apple, kiwi fruit, peach, pear, plum	1.44	10.07	6.99
Tamil Nadu	Peach, pear, plum	1.11	15.84	14.27
Haryana	Peach, pear, plum	0.68	11.17	16.43
Madhya Pradesh	Pear, plum	0.41	4.73	11.54
Mizoram	Kiwi fruit	0.30	1.03	3.43
Manipur	Kiwi fruit	0.29	3.03	10.45
West Bengal	Kiwi fruit	0.05	0.06	1.20
Kerala	Almond, peach	0.02	0.05	2.50
Maharashtra	Plum	0.01	0.03	3.00
Telangana	Apple	-	0.01	-
Total		520.92	3417.91	6.56

Table 3: Crop-wise area, production and productivity of major temperate fruit crops in India during 2021-22 (PIB, 2022)

Crops	*Area ('000 ha)*	*%share in total area*	*Production ('000 MT)*	*%share in total production*	*Productivity (t/ha)*
Almond	10.27	1.97	12.04	0.35	1.72
Apple	314.25	60.33	2584.01	75.60	8.2
Kiwi fruit	5.09	0.98	15.84	0.46	3.11
Peach	19.16	3.68	121.21	3.55	6.33
Pear	43.85	8.42	309.01	9.04	7.05
Pecan nut	0.91	0.17	0.49	0.01	0.54
Plum	23.86	4.58	86.4	2.53	3.62
Walnut	103.5	19.87	288.79	8.45	2.79
Total	520.89	100.00	3417.79	100.00	

(Table 5). In addition, information is given on share under area and production with productivity levels for respective crops under different states in Table 6.

The above data are clear indicative that the yield level is very low among all the temperate fruit crops in entire temperate regions of the country. However, the low-chilling temperate fruit crops, mainly pear, peach and plum, are doing well in the sub-tropical areas of Punjab, Haryana and Tamil Nadu. Therefore, there is an urgent need to increase the productivity levels in the temperate regions of the country. In addition, area expansion under sub-tropical areas is profitable to harness the potential of temperate fruit crops utilizing low chill varieties.

Import-Export Scenario of the Temperate Fruit Crops in India

Production, marketing and trade are an integral part of the fruit crop industry (Atteri, 2003). As per the reports published by FAO (2022), India is importing 31 commodities related to temperate fruit and nut crops as fresh fruits as well as value-added products to the tune of 855,534.07 thousand metric tons and spending 1,999,360 thousand USD. However, exporting the small quantity (56,266.38 thousand metric tons) of temperate fruits including value added products and earning foreign exchange of 33,584 thousand USD (Table 7). That resulted in the huge negative balance of trade (BoT) to the tune of 1,965,776 USD during year 2022.

Table 4: Temperate fruit growing states in India (2021-22)

Crop	Area, production and productivity in major states
Almond	Jammu and Kashmir (5,460 ha; 9,810 MT; 1.80 t/ha), H.P. (4,800 ha; 2,220 MT; 0.46 t/ha), Kerala (10 ha)
Apple	Jammu and Kashmir (168,570 ha; 1,898,590 MT, 11.26 t/ha), HP (1,150,20 ha; 611,900 MT, 5.32 t/ha), Uttarakhand (25,980 ha; 64,880 MT; 2.50 t/ha), Arunachal Pradesh (4,440 ha; 6,830 MT; 1.54 t/ha), Nagaland (240 ha; 1,780 MT; 7.41 t/ha), Kerala (10 MT); Tamil Nadu (10 MT), Telangana (10 MT).
Kiwi fruit	Arunachal Pradesh (3,560 ha, 7,110 MT; 2.00 t/ha), Manipur (290 ha; 3,030 MT; 10.45 t/ha), Sikkim (410 ha; 2,170 MT; 5.29 t/ha), Nagaland (300 ha; 1,690 MT; 5.63 t/ha), Mizoram (300 ha; 1,030 MT; 3.43 t/ha), Himachal Pradesh (200 ha; 720 MT; 3.70 t/ha), Jammu and Kashmir (300 MT), West Bengal (50 ha; 60 MT; 1.20 t/ha).
Peach	Punjab (2,620 ha; 46,980 MT; 17.93 t/ha), Uttarakhand (8,280 ha, 52,860 MT; 6.38 t/ha), Tamil Nadu (660 ha; 9,910 MT; 15.01 t/ha), Jammu and Kashmir (2,500 ha; 7,600 MT; 3.02 t/ha), Himachal Pradesh (4,900 ha; 5,800 MT, 1.18 t/ha), Haryana (330 ha; 5,380 MT; 16.80 t/ha), Nagaland (260 ha; 1,770 MT; 6.81 t/ha), Tamil Nadu (70 ha; 400 MT; 5.71 t/ha), Sikkim (140 ha; 330 MT; 2.56 t/ha), Arunachal Pradesh (50 ha; 70 MT; 1.40 t/ha), Kerala (10 ha; 30 MT; 3.00 t/ha).
Pear	Punjab (4,340 ha; 101,570 MT; 23.40 t/ha), Jammu and Kashmir (14,160 ha; 81,530 MT; 12.26 t/ha), Uttarakhand (13,250 ha, 73,780 MT; 5.57 t/ha), Himachal Pradesh (6,650 ha; 19,520 MT, 2.94 t/ha), Chhattisgarh (2,120 ha; 8,580 MT; 4.05 t/ha), Haryana (270 ha; 4,540 MT; 16.81 t/ha), Sikkim (1,660 ha; 4,140 MT; 2.49 t/ha), Madhya Pradesh (250 ha; 2,820 MT; 11.28 t/ha), Nagaland (200 ha; 2,060 MT; 10.30 t/ha), Arunachal Pradesh (290 ha; 560 MT; 1.93 t/ha), Kerala (10 MT).
Pecan nut	Himachal Pradesh (910 ha; 490 MT; 0.54 t/ha)
Plum	Uttarakhand (9,080 ha, 34,840 MT; 3.84 t/ha), Jammu and Kashmir (4,280 ha; 16,820 MT; 3.93 t/ha),Himachal Pradesh (8,900 ha; 14,160 MT; 1.59 t/ha), Punjab (510 ha; 8,980 MT; 17.61 t/ha), Tamil Nadu (380 ha; 5,520 MT; 14.53 t/ha), Nagaland (440 ha; 2,770 MT; 6.30 t/ha), Madhya Pradesh (160 ha; 1,910 MT; 11.94 t/ha), Haryana (80 ha; 1,250 MT; 15.63 t/ha), Arunachal Pradesh (40 ha; 140 MT; 3.50 t/ha), Maharashtra (10 ha; 30 MT; 3.00 t/ha).
Walnut	Jammu and Kashmir (80,730 ha; 267,160 MT; 3.31 t/ha), Uttarakhand (17,760 ha, 18,760 MT; 1.07 t/ha), Himachal Pradesh (4,260 ha; 2,270 MT, 0.53 t/ha), Arunachal Pradesh (740 ha; 420 MT; 0.57 t/ha).

Table 5: Productivity scenario of the different fruit crops in India

Crop	*Range (t/ha)*	*Average (t/ha)*	*Maximum (t/ha)*
Almond	0.46 (HP)-1.80 (J&K)	1.13	1.86 (J&K)
Apple	1.54 (Arunachal Pr.) – 11.26 (J&K)	8.22	11.26 (J&K)
Kiwi fruit	1.20 (West Bengal) – 10.45 (Manipur)	3.15	10.45 (Manipur)
Peach	1.18 (HP) – 17.93 (Punjab)	6.33	17.93 (Punjab)
Pear	1.93 (Arunachal Pr.)-23.40 (Punjab)	7.05	23.40 (Punjab)
Pecan nut	0.54 (HP)	0.54	0.54 (HP)
Plum	1.59 (HP) -17.61 (Punjab)	3.62	17.61 (Punjab)
Walnut	0.53 (HP) – 3.31 (J&K)	2.79	3.31 (J&K)

Only seven commodities made a largest volume of imports (97.91%), which includes apple (47.05%) followed by almonds (28.12%), olives (7.24%), kiwi fruit (5.37%), walnut (3.86%), pears (3.72%) and pistachio nut (2.55%). In terms of value, 96.48% of the foreign exchequer spent towards the imports of only 5 commodities which includes almonds (51.00%) followed by apples (16.28%), olives (14.57%), pistachio nuts (8.45%), kiwi fruits (3.15%) and walnuts (3.03%). However, the maximum exported commodities in terms of value are only three commodities which include apple (94.20%) followed by walnut (2.42%) and almond (1.40%) accounting for a total of 98.02% imports (Table 7 & Figure 2).

During 2022, the growth rate in import and export commodities were assessed based on the previous year data (2021). In earlier years the import quantities were significantly very high, but in the representative year, imports have been slightly reduced in the commodities which are causing loss of foreign exchequer. As a result, there is a marginal decrease in imports and a slight increase in exports has been recorded (Table 8). The maximum imported commodities include almonds, apples, walnuts, kiwi fruit, olive and pistachio nuts. Except for olives, the rest of the commodities were reduced in term of volume as well as value. This a step towards the *Atmnirbhar Bharat*. However, the demand for olives is still on the higher side, particularly olive oil which has increased many folds in the year 2022. In rest of the commodities, the growth was found insignificant in terms of quantity and value. The export of apples has taken new dimensions, which has increased for fresh fruits as well as apple juice. Apple is the only potential commodity that can be exploited on large scale through quality fruit production, strengthening of the infrastructure and streamlining of the market linkage and collaboration. Kiwi fruits, peaches and apricots are also having a bright future for meeting the domestic demand as

Table 6: State-wise area, production, productivity and percentage share under different temperate fruits in India during 2021-22 (PIB, 2022). Values in brackets are indicated as percentage shares.

Crop	*Parameters*	*JK*	*HP*	*Kerala*	*Nag-aland*	*Tamil Nadu*	*Telen-gana*	*UK*	*Aruna -chal Pradesh*	*Mani-pur*	*Mizo-ram*	*Sikkim*	*w Bengal*	*Haryana*	*Punjab*	*CHG*	*MP*	*Maha-rashtra*	*Total*
Almond	Area ('000 ha)	5.46 (53.16%)	4.80 (46.74%)	0.01															10.27
	Production ('000 MT)	9.81 (81.55%)	2.22 (18.45%)																12.03
	Productivity (t/ha)	1.80	0.46	0															1.13
Apple	Area ('000 ha)	168.570 (53.64%)	115.02 (36.60%)	0	0.24			25.98 (8.27%)	4.44 (1.41%)										314.25
	Production ('000 MT)	1898.59 (73.47%)	611.90 (23.68%)	10	1.78	10	10	64.88 (2.67%)	6.83										2584.01
	Productivity (t/ha)	11.26	5.32		7.42			2.50	1.54										8.22
Kiwi fruit	Area ('000 ha)		0.20 (3.91%)		0.30 (5.87%)				3.56 (69.67%)	0.29 (5.68%)	0.30 (5.87%)	0.41 (8.02%)	0.05 (0.98%)						5.11
	Production ('000 MT)	0.30 (1.86)	0.72 (4.47%)		1.69 (10.49%)				7.11 (44.13%)	3.03 (18.81%)	1.03 (6.39%)	2.17 (13.47%)	0.06						16.11
	Productivity (t/ha)		3.60		5.63				2.00	10.45	3.43	5.29	1.20						3.15
Peach	Area ('000 ha)	2.50 (13.05%)	4.90 (25.57%)	0.01	0.26 (1.61%)	0.07		8.28 (43.22%)	0.05			0.14 (0.73%)		0.33 (1.72%)	2.62 (13.67%)				19.16
	Production ('000 MT)	7.60 (6.27%)	5.80 (4.78%)	0.03	1.77 (1.46%)	0.40		52.86 (43.61%)	0.07			0.33		5.38 (4.44%)	46.98 (38.76%)				121.22
	Productivity (t/ha)	3.04	1.18	3.00	6.81	5.71		6.38	1.40			2.36		16.30	17.93				6.33
Pear	Area ('000 ha)	14.16 (32.29%)	6.65 (14.50%)		0.20 (0.46%)	0.66 (1.44%)		13.25 (30.22%)	0.29 (0.66%)			1.66 (3.79%)		0.27 (0.62%)	4.34 (9.90%)	2.12 (4.83%)	0.25 (0.57%)		43.85
	Production ('000 MT)	81.53 (26.38%)	19.52 (6.32%)	0.01	2.06 (0.67%)	9.91 (3.21%)		73.78 (23.88%)	0.56 (0.18%)			4.14 (1.34%)		4.54 (1.47%)	101.57 (32.87%)	8.58 (2.78%)	2.82 (0.91%)		309.02
	Productivity (t/ha)	5.76	2.94		10.30	15.02		5.57	1.93			2.49		16.81	23.40	4.05	11.28		7.05

Pecan	Area ('000 ha)	0.91 (100%)											0.91
	Production ('000 MT)	0.49 (100%)											0.49
	Productivity (t/ha)	0.54											0.54
Plum	Area ('000 ha)	4.28 (17.92%)	8.90 (37.27%)	0.44 (1.84%)	0.38 (1.59%)	9.08 (38.02%)	0.04		0.08	0.51 (2.14%)		0.16 (0.67%)	0.01	23.88
	Production ('000 MT)	16.82 (19.46%)	14.16 (16.39%)	2.77 (3.21%)	5.52 (6.39%)	34.84 (40.31%)	0.14 (0.16%)		1.25 (1.45%)	8.98 (10.39%)		1.91 (2.21%)	0.03	86.42
	Productivity (t/ha)	3.93	1.59	6.30	14.53	3.84	3.50		15.63	17.61		11.94	3.00	3.62
Walnut	Area ('000 ha)	80.73 (78.01%)	4.26 (4.12%)			17.76 (17.16%)	0.74 (0.72%)							103.49
	Production ('000 MT)	267.16 (92.57%)	2.27 (0.79%)			18.76 (6.50%)	0.42 (0.15%)							288.61
	Productivity (t/ha)	3.31	0.53			1.06	0.57							2.79

well as export to other countries through proper planning and management from farm level to market intelligence.

Plant Genetic Resources of Temperate Fruits

Temperate fruit crops including pome fruits (apple, pear & quince), stone fruits (peach, plum, nectarine, apricot & cherry), nut crops (walnut, almond, hazelnut, pecan & pistachio), minor fruits (olive, kiwi fruit, persimmon, berries etc) are being maintained at NAGs. Backup of germplasm is being taken up at ICAR-NBPGR, New Delhi in the form of dormant buds through cryopreservation. About 200 accessions of apple are being maintained in the field genebank of each ICAR Institutes, *viz.*, ICAR-NBPGR Regional Station, Shimla (241 acc.); YSPUHF Regional Horticultural Research and Training Station, Mashobra (238 acc.); ICAR-CITH, Srinagar (~200 acc.; 7 species); IARI, Shimla; GBPUAT, Pantnagar; SKUAST, Srinagar. Thirty accessions of Malus varieties, including Red Delicious and rootstocks, are being conserved as *in vitro* cultures at National Genebank, ICAR-NBPGR, New Delhi. Dormant bud cryopreservation has been emphasized to have a cost-effective back up of the germplasm growing in the field gene banks. A large collection of pears is being maintained in the field gene banks of ICAR-CITH, Srinagar (35) NBPGR Regional Station, Shimla (87); YSPUHF Regional Horticultural Research and Training Station, Mashobra (63); SKUAST, Srinagar and GBPUAT, Pantnagar. In addition, 73 accessions of exotic pears procured from USA are being conserved *in-vitro* at National Genebank, ICAR-NBPGR. In addition to apple and pear, these Institutions also maintain and conserve germplasm of other crops like peach, plum, cherry, apricot etc. Germplasm of walnut and almond is mainly being maintained and conserved at ICAR-CITH, Srinagar. More than 20 accessions of *Rubus* spp. are being maintained in the filed gene banks of ICAR NBPGR Regional Station Shimla and Bhowali. In addition, 62 exotic accessions of blackberry and 21 accessions of blueberry procured from National Clonal Germplasm Repository, Corvallis, USA are being maintained *in vitro* at National Genebank, ICAR-NBPGR, New Delhi (Dar *et al*., 2018; Dhillon and Rana, 2003; Hassan *et al.,* 2018; Madhu *et al.,* 2023).

Germplasm Introduction and Exchange

Introduced crops are either directly used as varieties (primary introduction) or used in breeding for improving quality, productivity and imparting resistance (Secondary introduction). The NBPGR has been instrumental in introducing many new varieties like 'Red Delicious' apple, 'Bartlett' pear, 'Elberta' peach, 'Santa Rosa' plum, & 'Thompson Seedless' grapes, etc. (Singh, 2010). In apple, introduction of varieties and rootstocks is the continuous process because new varieties are being developed with better quality leading to their higher demands and acceptability. In 2009, varieties like 'Golden Delicious

Table 7: Import and export of horticultural commodities during 2022 (FAOSTAT, 2022)

Commodity	*Import*				*Export*			
	Quantity ('000 MT)	*% Share*	*Value (1000 USD)*	*% Share*	*Quantity (MT)*	*% Share*	*Value (1000 USD)*	*% Share*
Almond in shell	233746	27.322	967648	48.398	316.64	0.563	1610	0.563
Almond shelled	6810.45	0.796	52096	2.606	473.12	0.841	3023	0.841
Almond (Total)	240556.4	28.118	1019744	51.004	789.76	1.404	4633	1.404
Apple juice	38.46	0.004	35	0.002	2.51	0.004	1	0.004
Apple juice conc	10006.46	1.170	11180	0.559	106.45	0.189	215	0.189
Apples	392482.9	45.876	314345	15.722	52892.13	94.003	21346	94.003
Apple (total)	402527.8	47.050	325560	16.283	53001.09	94.197	21562	94.197
Apricot	759.41	0.089	1560	0.078	1.86	0.003	3	0.003
Apricot dried	5649.19	0.660	17066	0.854	71.42	0.127	331	0.127
Apricot (Total)	6408.6	0.749	18626	0.932	73.28	0.130	334	0.130
Cherries	1462	0.171	9148	0.458	12.18	0.022	6	0.022
Chestnut	0.31	0.000	1	0.000	14.77	0.026	52	0.026
Cranberries	860.3	0.101	5331	0.267	4.56	0.008	6	0.008
Currants	117.68	0.014	106	0.005	256.53	0.456	207	0.456
Hazelnut in shell	0.14	0.000	2	0.000	1.01	0.002	8	0.002
Hazelnut shelled	328.08	0.038	2382	0.119	9.15	0.032	66	0.016
Hazelnut (Total)	328.22	0.038	2384	0.119	10.16	0.018	74	0.018
Kiwi fruit	45935.79	5.369	63051	3.154	134	0.238	169	0.238
Olive pomace oil	3111.99	0.364	7435	0.372	2.05	0.004	6	0.004
Olive oil	53784.07	6.287	275629	13.786	40.26	0.072	214	0.072
Olives	0.08	0.000	1	0.000	0.49	0.001	0	0.001
Olive preserved	5079.63	0.594	8179	0.409	37.88	0.067	100	0.067
Olive (Total)	61975.77	7.244	291244	14.567	80.68	0.143	320	0.143
Peach nectarine	259.46	0.030	421	0.001	2.28	0.004	12	0.004
Pears	31834.34	3.721	32518	1.626	152.11	0.270	295	0.270
Persimmon	38.33	0.004	104	0.005	44.38	0.079	18	0.079
Pistachio in shell	21842.24	2.553	168903	8.448	28.17	0.050	249	0.052
Plums	6210.03	0.726	6008	0.300	201.32	0.358	68	0.358
Plum dried	2124.39	0.248	4878	0.244	15.93	0.028	79	0.028
Plum (Total)	8334.42	0.974	10886	0.544	217.25	0.386	147	0.386
Quince	0.01	0.000	0	0.000	0.2	0.059	0	0.000
Raspberries	9.72	0.001	75	0.004	72.36	0.129	207	0.129
Sour cherry	1.9	0.000	16	0.001	0.23	0.000	0	0.000
Strawberry	37.92	0.004	335	0.017	10.02	0.018	14	0.018
Walnut in shell	30798.25	3.600	50907	2.546	383	0.681	883	0.681
Walnut shelled	2204.59	0.258	9694	0.485	979.37	1.741	4396	1.741
Walnut (total)	33002.84	3.858	60601	3.031	1362.37	2.421	5279	2.421
Total	855534.07		1999360.00		56266.38		33584.00	

Reinders', 'Granny Smith', 'Gale Gala', 'Red Chief,' 'Camspur Spur' *etc* were introduced. In 2013, 'Super Chief Sandidge', 'Fuji Aztec', 'Gala Red Lum', 'Golden-Clone B', and 'Red Velox' were introduced and now more emphasis is given on introduction of new colored strains of 'Gala' like 'Gala Schinico Red', 'Gala T-Rex', 'Gala Dark Baron', 'Gala Nerissimo' etc and colour strains of 'Delicious' group like 'King Roat', 'Scarlet Spur-II', 'Jeromine', 'Zad-1', 'Adams' etc. Introduction

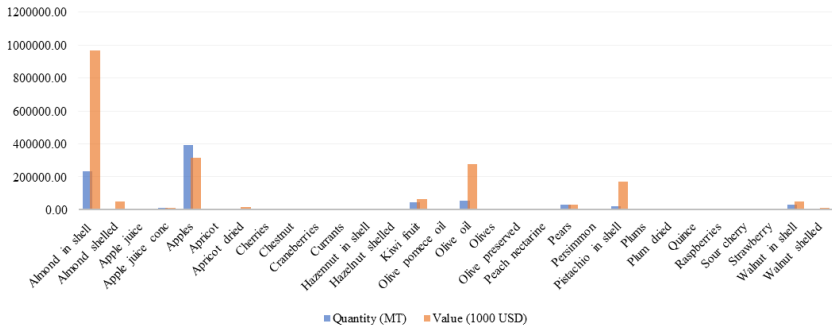


Figure 2: Imports of the temperate fruits and nut crops including value added products in India during 2022

Table 8: Growth in import and export of the temperate fruit commodities during (FAO, 2022)

Commodity	*Imports*		*Exports*	
	Quantity (%)	*Value (%)*	*Quantity (%)*	*Value (%)*
Almond in shell	6.06	12.00	-19.50	-15.26
Almond shelled	-57.80	-54.46	165.32	153.18
Apple juice	-75.30	-64.28	1294.44	-
Apple juice conc	-43.94	-40.56	-37.67	-44.87
Apples	-10.02	-16.71	82.07	48.80
Apricot	61.03	116.06	33.81	-25.0
Apricot dried	26.33	33.25	69.20	80.87
Cherries	122.42	98.09	461.12	100
Chestnut	34.78	-75.0	-36.0	-30.0
Cranberries	149.14	196.99	19.06	-14.28
Currants	488.4	100	-33.99	-40.85
Hazelnut in shell	-96.5	-89.47	910.0	-
Hazelnut shelled	25.86	14.68	9.15	34.69
Kiwi fruit	-31.70	-8.70	14.71	14.96
Olive pomace oil	-34.20	-8.37	540.63	100
Olive oil	531.99	575.51	-0.40	6.46
Olives	-52.94	-50.0	22.5	-
Olive preserved	39.18	32.18	1219.86	1150
Peach nectarine	-22.02	24.92	1100	1100
Pears	27.88	21.89	57.94	69.54
Persimmon	-1.72	4.0	28.64	63.64
Pistachio in shell	-20.65	-18.64	-48.29	-47.57
Plums	35.27	44.42	-24.27	-20.0
Plum dried	77.66	284.70	-89.58	-27.52
Raspberries	68.75	29.31	24.76	11.29
Sour cherry	-97.34	-97.25	-	-
Strawberry	74.26	87.15	-56.75	-65.85
Walnut in shell	-18.87	-31.02	-45.50	-43.17
Walnut shelled	-22.48	-23.47	-30.73	-36.44

of new strains of 'M-9' rootstock like 'M9-T337', 'M9-T339', 'M9-Pajam-1' etc has been initiated since 2013 and are being introduced on large scale. In cherry, self-fruitful varieties ('Lapins', 'Stella' *etc*) and clonal rootstocks are being imported by development departments, SAUs and other research Institutions. In almond more emphasis will be given on import of self-fruitful ('Independence', 'Shasta', 'Tuono' *etc*) & late blooming varieties ('Tardy Nonpareil', 'Ferralise', 'Ferragnese' *etc*) for commercialization and breeding programmes. In walnut, lateral bearing varieties ('Chandler', 'Fernor' etc) with respective pollinizer combinations ('Franquette', 'Fernette' *etc*) are being introduced on large scale for replacement of existing non-descriptive varieties to enhance yield and quality. Introduction of new varieties on large scale need quality testing to rule out the possibility of introduction of any pest or disease, therefore PEQ facilities at Srinagar (J &K); Mukteshwar (Uttarakhand) and Dirang (Arunachal Pradesh) have been established by ICAR under ICAR-Central Institute of Temperate Horticulture, Srinagar as Nodal Agency.

Breeding for Introgression and Development of Desirable in Commercial Varieties

Programmes for improvement in crops like apple, pear, almond and walnut have already been initiated by ICAR-CITH, Srinagar in 2009. Hybridization programme in apple for introgression of scab resistance in commercial apple cultivars and indigenous apple cultivar 'Ambri' has led to development of four hybrids ('Pride', 'Priame', 'Ammol' & 'Golden Snow') with desirable traits. 'Pride' ('Prima' x 'Red Delicious') and 'Priame' ('Prima' x 'Ambri') are scab resistant hybrids with better fruit quality traits than any existing scab resistant variety available in the world (Mir *et al.,* 2017; 2020). 'Ammo'l ('Ambri' x 'Mollies Delicious') is the coloured early maturing 'Ambri' derivative with excellent fruit quality traits like aroma, colour and extended shelf life. 'Golden Snow' ('Golden Delicious' x 'Snow Drift') is hybrid with pollinizer ability possessing excellent fruit quality traits like high TSS, lusture, creamy colour, resistance to russeting etc. Similarly breeding in pear for developing good quality, low chill and disease resistant varieties have been initiated in 2018. In walnut, hybridization programme

Table 9: Target traits and sources for breeding programmes in temperate fruits and nuts

Crop	*Trait*	*Gene*	*Source*	*Breeding strategy*
Apple	Scab resistance	Vf (Rvi6)	Prima, *M. floribunda*	MAB/ Cisgenics
	Fire blight resistance	Dm-1	*M. floribunda*	Cisgenics
	Alternaria resistance	Alt-1	*M. seiversii*	Cisgenics
	Precocity	TFL	Not known	Genome editing
	Columnar nature	Co	Wijcik	MAB
	Wooly apple aphid resistance	Er	Northern Spy	Cisgenics
	Rosy apple aphid resistance	Smh	*M. robusta*	Cisgenics
	Rosy curling aphid resistance	Sd	*Malus robusta*, 'McIntosh	Cisgenics/MAB
Pear	Scab resistance	Rvn/Rvi1	*Pyrus ussuriensis*, Bartlett (Williams), Beurre Hardy	MAB
	Pear psylla resistance	Py/Rvp1	Karamanka, Jerisbasma, Vodenjac	Hybridization /MAB
Walnut	Lateral bearing	L	Chandler, Fernor	Hybridization/MAB
	Precocity	Jrhd1	Not known	MAB
Almond	Self-fruitfulness	Sf	Independence, Shasta, Tuono	Hybridization/MAB
	Late blooming	Lb	Tardy Nonpareil, Ferragnese, Ferralise	Hybridization/MAB
	Sweet kernel	Ma/Sk	Prunus fenzliana	Cisgenics
Cherry	Self-fruitfulness	Sf	Stella, Sweetheart, Lapins	Hybridization/MAB
Apricot	Sweet kernel	Ma/Sk	*Prunus brigantina*	Cisgenics

of introgression of lateral bearing and nut quality traits has been taken up by different institutions including ICAR-CITH, Srinagar, SKUAST-K, Srinagar etc. For almond improvement hybridization programmes for traits like self-fruitfulness and late blooming are going on (Table 9).

Nutritional Strength of Temperate Fruits for Nutritional Security

Indian Himalayan region is rich in diversity in *Rubus*, *Ribes*, *Docynia*, *Cydonia*, *Myrica* and *Elaegnus* minor temperate fruits. These fruit crops are brought to Himalayan region for thousands of years not only survived but got established in the hills, leading to evaluation of new varieties. These species have been naturalized and some important selection can be evolved from few of them for exploitation. These fruit crops have already been in use by hill peoples and significantly contributed to the economy of tribal farmers. These fruit crops are excellent source of various nutrients, vitamins and antioxidants. The *Rubus* and *Ribes* are already been exploited in the developed countries and rated on top ten fruits available at global level based on maximum antioxidants. Initiatives for their collection, introduction and popularization is required to harness their immense nutritional potential for nutritional security of the country in future (Table 10).

Berries like blueberry, black berry and strawberries are well known for their high flavonol and anthocyanin contents, as well as elevated antioxidant activities by the oxygen radical absorbance capacity assay. Pears contain catechin (flavanol), caffeic, chlorogenic, and gallic acid (phenolic acids), as well as arbutin (glucoside) which are highly beneficial for human health. Apples are reportedly high in polyphenolic antioxidants, although these are reportedly high in the peels in comparison to the pulp. An apple a day keeps doctor away is used to dictate the nutraceutical properties of apple. Phenolic antioxidant activities have been shown to chelate and stabilize divalent cations, inhibit lipoxygenase, and scavenge free radicals (Ozcan *et al*. 2014). Furthermore, flavonoids, phenolic acids, and tannins have been shown to be anticarcinogenic and antimutagenic. Noroozi *et al*. (1998) reported the synergistic protective effects of l-ascorbic acid and flavonoids against oxidative DNA damage of lymphocytes. However, the absorption and bioavailability of some phytochemicals, such as anthocyanins, is reportedly low, while their metabolism is not implicit (Wu *et al*. 2002). Furthermore, the antioxidant capacity of some fruit extracts, such as strawberries, has been shown to be positively related to their antiproliferative activities. Like phenolic compounds, carotenoids are plant secondary metabolites with numerous functions in both plant and human physiology. In temperate fruits the concentrations as well as the interactions of carotenoids and chlorophyll are known to be responsible for the red, orange, and yellow coloration. Although apples are generally known to be low in carotenoids, it has been shown that carotenoids are high at the onset of development in the fruits but are lost as they mature.

Use of Crop Wild Relatives

The cultivated apple, *Malus domestica* Borkh., is a diploid or triploid species with a haploid set of 17 chromosomes and a genome size of approximately 600 Mb. Apple cultivation

Table 10: Temperate fruits are rich source of nutraceutical compounds

Nutraceutical factors	*Nutraceutical rich fruit crops*
Flavonoids (Anthocyanidins): Cyanidin 3-glycosides, Malvidin, Delphinidin, Pelargonidin	Blue berries, black berries, cranberry, raspberry, black currant, black grape, strawberries, cherries, plums, pomegranate
Flavanols: Morin, Procyanidins Prodelphinidins, Catechin, Epicatechin and their gallates	Apricots, apples, grapes, peaches, pears, plums, berries, cherries
Anthoxanthins (Flavonols): Myricetin, Fisetin, Quercetin, Kaempferol, Isorhamnetin	Cherry, apples, apricots, grapes, plums, berries, currants, cherries,
Phenolic acids: Chlorogenic acid, Ferulic acid, p-coumaric acid Ellagic acid, Gallic acid	Peach, cider, Strawberry, raspberry, grape, pomegranate, blueberry, cranberry, pear, cherry, apple
Tannins: Catechin, Epicatechin polymers, Ellagitannins, Proanthocyanidins, Tannic acids	Pomegranate, walnuts, peach, olive, plum, grape seeds apple, strawberries, raspberries, blackberry,

and production constitute one of the major fruit-producing industries addressing markets worldwide. However, climatic changes introduce a series of environmental stressors which challenge apple yield and fruit quality. Apple breeding could greatly benefit from apple wild relatives to face the challenge from adverse environmental conditions and biotic and abiotic stressors. For example, wild relatives, *Malus floribunda*, *Malus baccata,* and *Malus micromalus,* have been used to pyramid apple scab and powdery mildew resistance genes into progeny. Assessment of a broad range of wild Malus germplasm over the last 30 years has revealed ample potential sources of resistance to a multitude of diseases. Similarly, apple wild relatives in Malus collections have been evaluated and shown to possess traits related to fruit quality as well as abiotic stress resilience, such as cold hardiness and drought tolerance. In addition, investigations on the molecular basis of stress tolerance have indicated a key role for a DREB2 (dehydration-responsive element-binding factor 2) homologue in response to drought, cold, and heat in two highly drought-tolerant wild apple relatives, *Malus sieversii* and *M. prunifolia*. Likewise, *Diacylglycerol kinase* (*DGK*) genes were found to exhibit marked upregulation in response to drought and salt stress in *M. prunifolia*. Moreover, the deciphering of the cold-tolerant wild apple *Malus baccata* genome identified cold-responsive genes (*COR*) that will be useful in marker-assisted selection in breeding programs. Collectively, the wild relatives of any temperate crop like apple, pear, cherry etc provide an important genetic resource for incorporating resilience in cultivated varieties (Mir *et al.,* 2017b; Rana *et al.,* 2007; Verma *et al.,* 2023).

Varietal Wealth with Improved Fruit Quality and Higher Productivity

In true sense the temperate fruit crops have been commercially exploited in Europe, America and Australia where the work on improvement is in very advanced stage and were able to evolve several high yielding varieties having better quality and resistance to biotic and abiotic stresses. The new superior introductions from advance countries are now slowly replacing old varieties resulting in drastic changes in the production scenario of temperate fruit production (Kumar *et al.,* 2013; Lal *et al*., 2022; Sharma *et al*., 2004; Verma et al., 2013). The details of old varieties and new improved types grown in different states are given in Tables 11 and 12. In apple, during the last 50 years more than three hundred genotypes of apple have been introduced in India from Australia, Canada, Denmark, Germany, Israel, Italy, Netherlands, Russia, Switzerland, USA, and U.K., and have been tried and tested. Among various types the delicious group of cultivars predominates the apple market. The important varieties of apple in different types/groups are enumerated below.

Superior varieties

Oregon Spur, Rich a Red, Starkrimson, Red Chief, Well Spur, Hardeman, Gala Selection, Spartan, Gloster, Stark Spur, Top Red, Vance Delicious, Gold Spur, Silver Spur, Lal Ambri,

Color mutants

Vance Delicious, Top Red, Skyline Supreme.

Low chilling cultivars

Tropical Beauty, Mayaan, Michal, Schlomit, Chaubattia Princess and Chaubattia Anupam.

Early cultivars

Benoni, Irish Peach, Early Shanburry, Fanny

Juice making cultivars

Lord Lambourne, Granny Smith, Ellington Pippin.

Scab resistant cultivars

Priscilla, Sir Prize, Mac Free, Freedom, Coop-12, Coop-13, Firdaus, and Shireen.

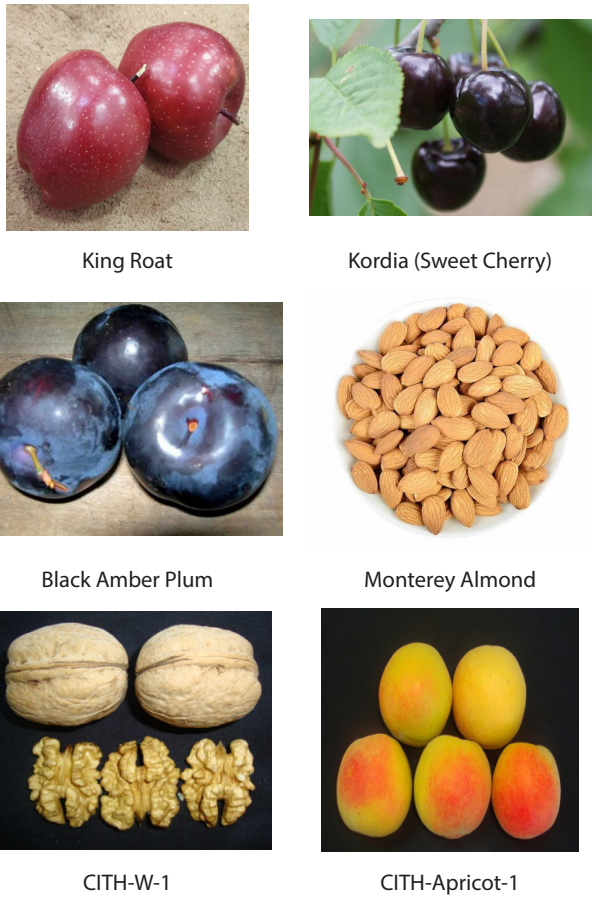
Table 11: Promising cultivars of pome, stone and nut fruits identified for commercial cultivation in different states

Fruits	*J & K*	*H.P.*	*Uttarakhand*
Apple	Oregon Spur, Rich a Red, Starkrimson, Red Chief, Well Spur, Hardeman, Gala Selection, Spartan, Gloster, Stark Spur, Top Red, Vance Delicious, Gold Spur, Silver Spur, Lal Ambri, Skyline Supreme, Red Delicious, royal Delicious, mollies Delicious	Oregon Spur, Rich a Red, Starkrimson, Red Chief, Well Spur, Hardeman, Top Red, Vance Delicious, Gold Spur, Silver Spur, Vance Delicious, Royal Delicious, Tydeman's Early, Mollies Delicious, Red delicious, Golden Spur, Michal	Oregon Spur, Rich a Red, Starkrimson, Red Chief, Well Spur, Early Shan burry, Chaubattia Princess, Fanny, Benoni, Red Delicious, Starking Delicious, Rymer, Buckingham, Mollies Delicious
Pear	Max Red Bartlett, William, Red Bartlett, Starking, Early China, Laxton's Superb, Bartlett, Flemish Beauty, Conference, Kashmiri Nakh, Doyenne-du-Comice, Anjou, Fertility, Vicar of Wakefield.	China, Bartlett, Max Red Bartlett, Flemish Beauty, Manning's Elizabeth, Winter Nellis	Thumb Pear, Doyenne du Comice, Victoria, William's Bartlett, Beurre Hardy, Flemish Beauty
Apricot	New Castle, Kaisha, Early Shipley, Suffaida, Charmagaz, Shakarpara, Frogmore Early, Gillgati Sweet, Amba, Moorpark, Nari, Halman, Rakchey Karpo Narmo, Afgani, Tokpopa, Koban	Kaisha, Nugget, Castle, Saffaida, Charmagaz	Charmagaz Kaisha, Moorpark, Turkey, St. Ambrose
Plum	Methley, Kelsey, Red Beauty, Santa Rosa, Sweet Early, Satsuma, Burbank, Frontier, Mariposa, Duerret, Grand Duke, Stanley, Tilton	Kelsey, Santa Rosa, Titron, Satsuma, Mariposa	Jamuni, Kelsey, Santa Rosa, Titron
Peach	Red Haven, Star Red Gold, July Elberta, Sun Haven, JH Hale, Quetta, Florida Sun, Florida Red, Snow Queen (Nectarine), Cresthaven (Nectarine), Red June, Crawford Early, Alexander	Alton, July Elberta, JH Hale, Sharbati, Shan-e-Punjab, Burbank	Sharbati Saffaida, Flordasun, Shan-e-Punjab, Paradelux, Crawfold Early, July Elberta
Sweet Cherry	Bigarreau Noir Grosse (Misri), Guigne Pourpeara Pecoce (Awal), Bigarreau Napoleon (double) Black Heart, Guigne Pourpeara Prece, Guigne Noir Gross, Guigne Noir Hative, Bigarreau Napoleon, Bigarreau Noir Grosse, Stella, Compact Stella, Van and Bing	Black Tartarian, Napoleon, Sue Sam, Lambert, Bing	Bedford Prolific, Black Heart, Governor's Wood

Table 12: Shift in the varietal profile from traditional to modern planting systems

Crop	1st generation varieties (1900 to 1990)	2nd generation varieties (1990 to 2020)	3rd Generation Varieties (2020 onwards) (Fig. 3)
Apple	Red Delicious, Golden Delicious Jonathan, King of Pippin, Yellow Newton, Irish Peach, American Mother, Queens Apple, Rome Beauty, Scarlet Siberian Karry Pippin, Chumure, Baldwin, White Doted Red. Benoni, Razakwari	Starkrimson, Mollies Delicious, Oregon Spur, Red Chief, Top Red, Vance Delicious, Silver Spur, Rich a Red, Super More Gold. Lal Ambri, Red Gold, Sunheri, Cooper IV	Jeromine, King Roat, Gala Scarlet, Red Velox, Scarlet Spur-II, Super Chief, Redlum Gala, and Auvi Fuji, Mema Mester, Schinco Red Gala, Devil Gala, Burge Red, Bingo Gala, Cosmic Crisp, Red Delicious Fenzad, Gala Star, Gala Fenzam, Gala Fenplus, Gala T Rex
Pear	Doyne Bosc, Gent, Drauard, Fertility, Beureu Hardy, China Pear	Bartlett, Chinese Sandy Pear (Kashmiri Nakh), Vicar of Wing Field, Conference	Eden, Forelle, Vermont, Conference, Dor Eden
Cherry	Mishri, Double, Makhmali, Awal, Tontal	Van, Stella, Bing, Reinear, Compact Stella, Lapins, Sweet heart, Regina, Bing	Kordia, Regina, Aeko, Adana, Maxima, Sweetheart, Bing Stucato, Sonata, Samba, Royal Helen, Sofia, Rocket, Royal Tioga
Plum	Sharp's Early, Formosa, Wickson, Satsuma, Burbank, Blue Imperatrice, Prune-D	Santa Rosa, Grand Duke, Burbank, Green Guage.	Angeleno, Yellow, Pink, Black, Red, Santa Rosa, Satsuma, Black Amber
Peach	Worlds Earliest, Peshawari, July Elberta, Elberta, Quetta	July Elberta, Elberta, Quetta, Pardelux	Henry, Fortynier, Topaz, June Pride, Fairtime, Snow Giant, Fantasia, Red Gold, Honey Kist, Garnem
Apricot	Charmagz, Kaisa, Farmer Early, Gilgiti Sweet, Amba, Quetta	Charmagaz, Kaisha, Gilgiti Sweet, Halman, Rakshey Karpo, Tokpopa, Shakarpara, Nari, Afgani	CITH A-1, 2, 3

Almonds	Seedling origin (unknown varieties)	IXL, Merced, Non Pareil, Makhdoom, Shalimar, Waris, Primorskij,	Non Pareil, Monterey, Carmel, Aldrich, Yorizane, Royal Rosa
Walnut	Seedlings (unknown varieties)	Hamdan, Suleiman, Partap, Govind and Seedling Selections from Kashmir.	CITH Walnut 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, Chandler, Franquette, Ferner



King Roat | Kordia (Sweet Cherry) | Black Amber Plum | Monterey Almond | CITH-W-1 | CITH-Apricot-1

Figure 3: 3rd generation fruit crop varieties with better fruit quality traits and higher yield.

Hybrids

Lal Ambri (Red Delicious x Ambri), Sunehari (Ambri x Golden Delicious), Amred (Red Delicious x Ambri), and Chaubatia Anupam & Chaubatia Princess (Early Shanburry x Red Delicious) developed in India.

Improved Rootstocks for Temperate Fruit Crops

Temperate fruits and nut crops are grown on seedling origin rootstocks. This resulted in the low productivity of fruits and nut crops. These seedling trees have long juvenile period and start bearing after 6 to 7 years in pome and stone fruits and 8-10 years in walnuts with the result, growers got discouraged as they have to wait for long period for their commercial bearing (Tsering Dolkar *et al.,* 2018). But during last 4 to 5 decades a good number of clonal rootstocks have been identified and developed in advanced countries having very short juvenile period (2–3 years) with resistant to biotic and abiotic stresses in various crops and have been recommended for grafting and budding of elite varieties in place of traditional seedling rootstocks, but in India they are yet to be exploited commercially. However, in the advance countries the grafted plants on clonal rootstocks have revolutionized the fruit industry. In view of the importance of these clonal rootstocks and to commercialize their use particularly for high density orcharding and for overcoming biotic and abiotic stresses, their multiplication and distribution has been given a priority and are being multiplied but on very limited scale both by Research Organizations and State Development Departments. Some of the commercially important rootstocks of various crops which are under multiplication along with their salient features is given in Table 13.

Application of Biotechnology in Temperate Fruit Improvement

Plant biotechnological approaches have opened unprecedented opportunities in the field of 'hi-tech' concepts of research with the aim to confront different biotic and abiotic stresses (Lal and Verma, 2022). Since the horticulture is one of the most priority sector, intensive and diversified research on different aspects by employing biotechnological tools can play a vital role in developing improved varieties and their multiplication. Considering the thrust on quality planting material production and distribution of superior cultivars and rootstocks of temperate fruits, micro propagation is one of the best options for achieving the goal. In USA and European countries commercial micro propagation has been developed as an industry but research and development on micro propagation in India, though started late, has progressed to & some extent and many institutions are actively involved in extensive research activities for standardizing protocols for all type of horticultural crops including temperate fruits. Apart from production aspects, screening for quality standards of tissue cultured plants, their stability and potential in the field, identification and incorporation of various elite genes in the existing genotypes for quality as well as biotic-abiotic stress tolerance and human resource development are some of the most important areas for bringing improvement in temperate fruits and have been given priority. To bring improvement in temperate fruits, particularly, apple and walnut, the ICAR and DBT have identified some thrust areas and funding different institutions in temperate region. The

Table 13: Promising rootstocks identified

S. No.	*Crop*	*Rootstocks*	*Salient features*
1	Apple	EMLA 111/ MMIII	Suit to drought prone areas
		EMLA.7	Suit to sloppy, virgin lands, semi vigorous
		EMLA.106/MM.106	Suit to sloppy, and less clay soils, semi vigorous
		EMLA 9/M9	For high density planting with assured irrigation and deep fertile soils, very dwarf
		M 779	For hilly areas of Uttarakhand and H.P.
2	Pear	Quince-A	Standard rootstocks, semi vigorous
		BA .29C	Standard rootstocks, semi vigorous
		Quince - C	Very dwarf
		Quince - B	Semi vigorous
3	Apricot	Apricot seedling	Vigorous, drought tolerant and compatible
		Peach seedling	Suitable for dry and light soils
4	Peach	Peach seedling	Vigorous and compatible
		Gf-557 & gf-677	Drought tolerance
		Siberian-C, Rubia	Dwarf
5	Plum	Wild peach × Apricot seedling	Seedling are vigorous
		Myrobalan-B, Myrobalan-29C, Myrobalan-GF-31, Marigona-2621, GF-8/1	Clonal and semi vigorous, compatible rootstocks
		Pixy × St. Julian. K	Dwarfing rootstocks
		Peach ×Apricot seedlings	Semi vigorous
6	Cherry	Colt	Semi dwarf
		F-12/1	Vigorous
		Mazzard and Mahaleb	Vigorous
7	Almond	Apricot, peach and almond seedlings	Vigorous
		Peach and almond hybrids GF-557×GF-677	Semi dwarfing, good for high density
8	Walnut	Walnut seedlings	Vigorous

Table14: Leading organizations involved in standardization and dissemination of technology on micro propagation of temperate fruits in India

Institution	*Major activities in biotechnology/tissue culture*
Dr. Y.S. Parmer University of Horticulture and Forestry, Solan, H.P.	Micro propagation of apple, peach, kiwi, strawberry and cherry.
Sher-e-Kashmir University of Agricultural Sciences and Technology (K), Srinagar.	Micro propagation of apple clonal root stock, walnut and cherry
University of Kashmir, Srinagar.	Tissue culture of walnut.
G.B.P.U.A.S.T., Pantnagar, Uttarakhand	Tissue culture of pear and peach.
The Energy Resources Institute, New Delhi	Tissue culture of apple and walnut.

activities and progress made in different institutes is detailed in Table 14.

Although, India stands next to China in production of fruits and vegetables, the contribution apple was just 2% to total world production as against 38% by China. In terms of productivity its position is dismal 68th. This warrants immediate short- and long-term biotechnological interventions. Considering the potential of this crop, and to meet growing demand of elite planting material and to bring genetic improvement, DBT in collaboration with ICAR Institutes and other Universities identified some priority areas and partner institutions to enhance productivity in the region (Table 15).

Low Chill Temperate Fruit Crops for Commercial Exploitation in India

Only those cultivars which have low chilling requirement and ability to tolerate high summer temperature should be selected (Bal, 2004; Bist and Yadav, 2004; Dennis, 1997; Dhatt, 2004; Kanwar and Singh, 2004; Mohammad, 2004; Sharpe, 1969; Weinberger, 1956). One of the most successful cultivars is 'Anna' apple, is now extensively grown in areas

Table 15: Priority areas and partner institutions for biotechnological interventions

Priority areas	*Partner Institutions*
Preparation of database on diversity of various cultivars	CITH, Srinagar, NBPGR
Genetic conservation *in-situ* conservation/evaluation	Kashmir University, Y.S. Parmar University, NBPGR, CITH, and IARI, Regional Centre, Amartara Cottage, Shimla
Identification of elite cultivars and rootstocks	CITH, Y.S. Parmar, University and RHRS, Mashobra
Micro propagation	TERI, CITH, Y.S. Parmar University and IHBT, Palampur
Certification for pathogens (viruses and others) and genetic fidelity • Development of diagnostic tools • Other pathogen diagnostics • Resistance to fungicides	IHBT, RHRS, Mashobra and Y.S. Parmar University, Regional Centre
Genetic improvement Short term: Identification of markers for resistance, temperature tolerance/low chilling requirement • Develop linkage maps • QTL maps • Develop mapping populations for breeding Long term- Development of transgenic for disease resistance shelf life / quality traits.	CCMB, Kashmir University, Jammu University, IHBT, TERI, IARI Centre Mashobra, IHBT, Palampur, Y.S. Parmar University and CITH

with limited chilling. The cultivars like 'Sharbati' peach; 'Titron' and 'Kala Amritsari' plum; 'Patharnakh', 'LeConte' and 'Baghugosha' pears became commercially popular in some parts of the subtropical India. A list of important low chill varieties of temperate fruits is mentioned in the table16 for reference purpose.

Current Challenges of the Temperate Fruit Industry

Challenges faced by temperate horticulture cultivation in India are mainly due to the unpredictable weather patterns, including frost, hail, and erratic rainfall, can damage crops and reduce yields.

Pest and disease pressure

Management of pests and diseases like apple scab and codling moth is crucial but challenging without effective control measures.

Limited technology access

Lack of access to modern agricultural technologies hampers productivity and efficiency in cultivation practices.

Infrastructure deficiency

Inadequate post-harvest facilities, storage, and transportation networks contribute to significant losses and reduced profitability.

Water scarcity

Water shortages, especially in regions relying on snowmelt for irrigation, pose challenges to maintaining optimal soil moisture levels.

Land degradation

Soil erosion and degradation threaten long-term productivity, particularly in hilly terrains.

Labour shortages

Seasonal labour shortages during critical stages like harvesting and pruning impact operations and increase costs.

Market instability

Fluctuating prices and lack of market information expose growers to financial risks and uncertainties.

Addressing these challenges requires comprehensive strategies focusing on technology dissemination, infrastructure development, sustainable practices, and market support to ensure the resilience and growth of temperate horticulture in India.

Expansion of cultivation area

There is untapped potential for expanding the cultivation area of temperate fruit crops by identifying and utilizing suitable lands in the Himalayan region. Terraced farming and orchard establishment on marginal lands can help optimize land use and increase production.

Crop diversification and adoption of new varieties

Introducing new varieties of temperate fruits that are better adapted to local conditions can diversify the fruit portfolio and reduce production risks. Research institutions and agricultural universities should focus on breeding high-yielding, disease-resistant cultivars suited to different agro-climatic zones.

Technology adoption

The adoption of modern agricultural practices, such as drip irrigation, fertigation, integrated pest management (IPM), and precision farming, can enhance productivity and resource use efficiency. Training and capacity-building

Table 16: Temperate fruits and their cultivars suitable for cultivation under subtropical climate

S. No.	*Fruit crop*	*Cultivars (*Chilling hours required; value given in bracket indicates the chilling requirement of the respective variety)*
1	Peach (*Prunus persica*)	FlordaGrande (100), Flordabelle (110), Flordared (110), Flordawon (110), FlordaPrince (150), FlordaGlo (150), Tropic Beauty (150), UF Beauty (200), Sunred (210), Flordabest (250), Early Amber (310), Flordasun (310), FlordaKing (350), Flordacrest (350), Gulfking (350), Desert Gold (350), Jewel (350), GulfCrimson (400), GulfPrince (400), Florda Home (400), Bonita (500), May Gold Su (500), GulfCrest (525), FlordaQueen (540), June Gold (650), Parbhat, Pratap, Sharbati, Safeda Early Cream, Saharanpur Prabhat, Shan-i-Punjab, Shaharanpur No. 6, Ranjit Bagh Early, Safeda, Shaharanpur Hybrid 3, Babcock,
2	Nectarine (*P. persica var. nucipersica)*	Sunbest (225), Sunraycer (250), UF Royal (250), UF Queen (250), Sunmist (275), Sundollar, (350), Suncoat (375), Sunred
3	Apple (*Malus domestica)*	Dorsett Golden (250), Anna (300), Tropic Mac (300), Tropic Sweet (300), 88-20 (375), Ein Scheimer (400), 60-39 (400), Tamma, Neomi, Tropic Beauty, Gallia Beauty, Winter Banana, Tame, Vered, HRM99
4	Pear (*Pyrus communis & P. pyrifolia*)	Patharnakh, Gola, Leconte, Keiffer, Smith, Baghugosha, China Pear, Pineapple, Baldwin, Tenn, Flordahome, Ayers Hood, Orient, Carnea, Tsu Li, Ya Li, *P. calleryana* (rootstock requires 400 chilling hours)
5	Strawberry (*Fragaria ananassa*)	Chandler, Tioga, Torrey, Selva, Belrubi, Fern, Pajaro
6	Plum (*Prunus salicina*)	Satluj Purple, Kala Amritsari, Jamuni Meeruti, Titron, Aloo Bokhara, Alucha Black, Titron Howe, Gulfruby, Gulfbeauty, Gulfblaze, Gulfrose
7	Apricot (*Prunus armeniaca*)	New Castle, Early Shipley, St. Ambroise, Benazir, NJ-13
8	Almond (*Prunus dulcis*)	California, Papershell, Hybrid 15, Pathick's Wonder, JKS-55, H-98, Achak (266), Desmayo Largueta (309), Ramillete (326), Marcona (435), Marta (478), Antoneta (514), Ferragnes (558)
9	Sweet Chery (*Prunus avium*)	Stella (200-250), Cristobalina, Temprona del Sot, Precoce de Bernard, Sunburst, Lapin, (Rootstocks - Gisela-5, Mahaleb)
10	Persimmon (*Diospyros kaki*)	Hachiya, Fuiju, Jiro, Hyakuma
11	Olive (*Olea europaea*)	Arbequina, Barnea, Frantoio, Koroneiki, Leccino, Picual, Coratina, Picholine
12	Blueberry *(Vaccinium angustifolium)*	Sharpblue (150), Emerald (200), Jewel (200), Windsor (225), Springhigh (225), Chaucer (400), Woodard (400), Brightwell (400), Climax (450), Tifblue (550), Powderblue (550)

programs should be conducted to educate farmers about the benefits of adopting advanced technologies.

Value addition and market development

Promoting value addition through processing, packaging, and branding of temperate fruits can create opportunities for higher returns and market penetration. Establishing fruit processing units, cold storage facilities, and marketing cooperatives can help reduce post-harvest losses and improve market access for farmers.

Sustainable practices and climate resilience

Implementing sustainable orchard management practices, such as organic farming, soil conservation measures, and water harvesting techniques, can enhance resilience to climate change and environmental degradation. Research on climate-resilient farming practices and crop insurance schemes can mitigate risks associated with climate variability and extreme weather events.

Opportunities in Temperate Fruit Industry

There are increasing opportunities in the temperate fruit industry in India mainly attributed due to higher productivity and farm income potential, huge market demand (domestic and international), Increasing awareness about nutritional value of fruits created round the year demand in every house hold, fast increasing economy improved the purchasing power, ddiversification and optimum utilization of resources/regions, opportunities for small holders, waste land utilization, resilience to climate change and carbon sequestration, scope of processing, packing, storage, value addition and other consumer oriented by-products. Some of priority areas are earmarked below in concise way-

- Higher productivity and farm income
- Huge market demand (domestic and international) due to large number of consumers within the country which has created negative trade deficit.
- Increasing awareness about nutritional value of fruits created round the year demand in every house hold.
- India is the fast-increasing economy resulted in the increase of purchasing power.
- Diversification and optimum utilization of resources/ regions.
- Opportunities for small as well as large holders
- Waste land utilization is only possible through growing

fruit crop trees.
- Fruit crops are comparatively more resilience to climate change and carbon sequestration.
- Larger scope of processing, packing, storage, value addition and transportation are the sectors to provide employment.
- Export and import of the of temperate fruits are a high-income generating sector.
- Employment generator: Need more skilled manpower
- Huge potential in nursery business

Strategies for Improving the Temperate Fruit Industry: A Way Forward Towards Self-reliance

Temperate fruit industry is very dynamic and going through a transformational change through adoption of technological innovation. These technologies are potential to achieve the ever-increasing demand of the domestic market as well as earning the foreign exchange (Kumar and Misger, 2012).

Use of high yielding varieties

New varieties with higher yield and improved fruit quality in temperate fruit and nut crops are the major input affecting the profitability at farm level. Adoption of suitable varieties under high, mid and low zones are pre-requisite for increasing the yield and producing quality fruits and assured supply in the market.

- Adoption of high density orcharding on clonal rootstocks in HDP. – 5 to 10-fold increase
- Diversification in fruit crops (Minor and unutilized fruits)
- Pollination management (apple, pear, plum, cherry, almond, walnut).
- Use of efficient irrigation including fertigation technologies. – inc. 30 to 40%
- Integrated nutrient management with focus on organic farming/biofertilizer application for eco-friendly nutrition as long-term strategy.
- Integrated pest management with focus on biological control & use of biopesticides
- Harvest management practices & post-harvest handling, processing, value addition and scientific storage.
- Production of true to type/certified quality planting material.
- Establishment of bud banks of superior genotypes
- Adoption of modern market management practices

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.02

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Documentation of Wild Edible Plants (WEPs) Consumption in North-Western Himalayas: The Untapped Genetic Resources for Ensuring Nutritional Security

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Abstract

The North-Western Himalayan region (NWHR) spread across Jammu & Kashmir, Himachal Pradesh, and Uttarakhand is a complex physiographical region consisting of glacier mountains, cold deserts, hot springs, and dense forests with unique biodiversity. The region is characterized by extreme weather, intense UV radiation, and low oxygen partial pressures limiting agriculture. Local communities have adapted to these conditions by relying on wild edible plants (WEPs) such as tubers, fruits, berries, and green leafy vegetables (GLVs) for nutrition and livelihood. However, in recent years, the consumption of WEPs and associated indigenous knowledge has been rapidly declining due to the adaptation of Western lifestyles and processed foods. In this context, the present work was taken up to survey and document various WEPs consumed in the NWHR. Nearly, 100 WEPs were recorded and are consumed in the form of curries, soups, sauces, cordials, and pickles. These WEPs contain myriad bioactive molecules such as carotenoids, phenolic acids, flavonoids, anthocyanins, anthraquinones, and terpenoids with therapeutic applications correlating to their traditional medicinal use. Some common uses of WEPs are against inflammation, gastro-intestinal disorders, infection, and hepatoprotection. The study emphasizes the importance of conserving and promoting WEPs for food security and potential therapeutic applications.

Keyboards: Wild edible plants, Bioactive molecules, Nutraceuticals, Phytopharmaceuticals, Value-added products.

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Received: 19/06/2024 **Revised:** 30/06/2024

Accepted: 25/08/2024

How to cite this article: Sharma K, S Gupta, V Srivatsan and SK Yadav (2024) Documentation of Wild Edible Plants (WEPs) Consumption in North Western Himalayas: The Untapped Genetic Resources for Ensuring Nutritional Security. *Indian J. Plant Genet. Resour.* 37(3): 404-424. **DOI:** 10.61949/0976-1926.2024.v37i03.02

Introduction

Nearly 90% of the calories in the human diet come from a few plant species, such as rice, wheat, maize, sugarcane, and potatoes, with cereals contributing to about 60% of the diet. These crops are water-intensive, have a high environmental footprint, and are vulnerable to environmental fluctuations and diseases (Dwyer *et al.,* 2022). Overreliance on these crops poses a significant threat to global nutritional security in the long run. With the global population expected to reach 9.7 billion by 2050, there is an urgent need to identify alternative crops to ensure nutritional security (Wijerathna-Yapa and Pathirana, 2022). Wild edible plants (WEPs) play a crucial role in meeting global dietary requirements. WEPs are indigenous species that grow and reproduce naturally in their habitats without human intervention or cultivation (Motti, 2022). They include green leafy vegetables (GLVs), fruits, nuts, berries, and tubers gathered from surrounding ecosystems. While 30,000 edible plants have been identified worldwide, only 7,000 species are consistently collected and consumed (Bacchetta *et al.,* 2016). WEPs are nutrient-dense and contain a wide range of bioactive molecules such as polyphenols, terpenoids, fatty acids, carotenoids, and

alkaloids with myriad health benefits (Ray *et al.,* 2020). They have been shown to help in recovering from malnutrition, including iron deficiency anemia and protein deficiency in rural communities (Knez *et al.,* 2023). Additionally, WEPs exhibit great genetic diversity, resilience to drought and changing climates, and resistance to pathogens and pests (Bacchetta *et al.,* 2016; Dwyer *et al.,* 2022). Therefore, WEPs have the potential to be a valuable source of future food, and there is a critical need to reintroduce them into human diets (Motti, 2022; Knez *et al.,* 2023).

Approximately 100 million people from 705 different ethnic communities in India rely on WEPs for their livelihood. These communities, mainly tribal and rural, produce a variety of value-added products from WEPs, such as juices, jams, pickles, and wines (Mishra *et al.,* 2021). In India, 1403 WEPs from 44 families have been identified as commonly consumed, with leafy shoots and fruits being the most consumed parts (Ray *et al.,* 2020). WEPs are particularly prevalent in mountainous regions like the Indian Himalayan region (IHR), which is known for its rich biodiversity and unique cultural practices centered around agro-pastoralism and WEP consumption (Thakur *et al.,* 2017; Hegde *et al.,* 2023). The North-Western Himalayan region (NWHR) spread across Jammu & Kashmir, Himachal Pradesh and Uttarakhand is a complex physiographical region consisting glacier mountains, cold deserts, hot springs and dense forests with unique biodiversity. The region is characterized by extreme weathers, intense UV radiation and low oxygen partial pressures limiting agriculture. Local communities have adapted to these conditions by relying on WEPs for nutrition and livelihood. Several authors have reported the use of WEPs as a source of bioactive molecules and essential nutrients from this region (Thakur *et al.,* 2017; Ray *et al.,* 2020; Pereira *et al.,* 2020; Hegde *et al.,* 2023). In recent years, there has been an overall consensus on the importance of WEPs and their conservation and value addition (Mishra *et al.,* 2021). Despite the growing recognition of WEPs, their consumption, and associated indigenous knowledge are declining due to the influence of Western lifestyles and processed foods. Further, the region is significantly influenced by the tourist population, often creating a negative impact on the local ecosystem, especially the food and culinary diversity (Pereira *et al.,* 2020). This trend poses a threat to biodiversity conservation and the preservation of traditional knowledge (Mishra *et al.,* 2021). In this context, we aimed to survey and document the understudied lesser-known genetic resources, i.e., WEPs in the North Western Himalayas across different seasons. Information such as the diversity of WEPs, plant parts used for edible applications, major bioactive molecules, and traditional medicinal uses have been recorded through extensive respondent surveys among the local populations. The study emphasizes the importance of conserving and promoting WEPs for food security and potential therapeutic applications. We envisage that comprehensive documentation and subsequent characterization would validate the traditional uses of these WEPs and promote their use as mainstream foods.

Materials and Methods

Study Area

The study area encompasses the North Western Himalayas comprising politically delineated states *viz*., Himachal Pradesh, Jammu & Kashmir (J&K) and Uttarakhand. Geographically the region is spread between 28° 43′-37° 05′ N latitude and 72° 40′ -81° 02′ E longitude covering an approximate area of 33 million ha. The representative study locations from each state and their and geographical coordinates are presented in Figure 1 and Table 1, respectively. The region is characterized with a tropical to temperate climate owing to the altitudinal variations ranging from 100 m to above 6000 m asl covering sub-tropical to cold temperate alpine zones. Geologically, the region comprises three ranges, the Greater Himalaya, the outer Himalaya and the lesser Himalaya. The mean rainfall in the region is approximately 800, 1200 and 1500 mm for Jammu & Kashmir, Himachal Pradesh and Uttarakhand, respectively. However certain regions of NWHR such as the Trans-Himalayan zone encompassing areas like Ladakh in J&K, Lahaul & Spiti in Himachal Pradesh, and Nelong valley of Uttarakhand are considered cold deserts with very low annual rainfall (~40 mm) and extreme temperatures ranging from -45°C in winters to 40°C in summers. Owing to the wide range of climatic conditions, the region is characterized by abundant plant diversity, particularly medicinal plants. The primary occupation of the tribal communities residing in the NWHR region is agro-pastoralism and primarily depends on the resources available from surrounding ecosystems.

Surveys

The work comprised field surveys, interactions with the locals of the study sites, data recording, analyses, and interpretation of the gathered information. Filed surveys were conducted between February 2022 to May 2022 in Himachal Pradesh, J&K and between November 2022 to January 2023 in Uttarakhand covering summer and winter seasons respectively. In the following year (2023), survey and data collection were conducted vice-versa, i.e., during winter months (Nov-Jan 2023) in Himachal Pradesh and J&K and summer months in Uttarakhand (Feb-April 2024). The study locations were shortlisted based on earlier reconnaissance surveys in a few representative sites. Intensive interviews such as door-to-door surveys and fieldwork were conducted at these sites (Table 1). Information such as age, gender, and literacy were recorded after taking the consent of the respondent. Information such as knowledge and use of WEPs were collected using structured interviews as described

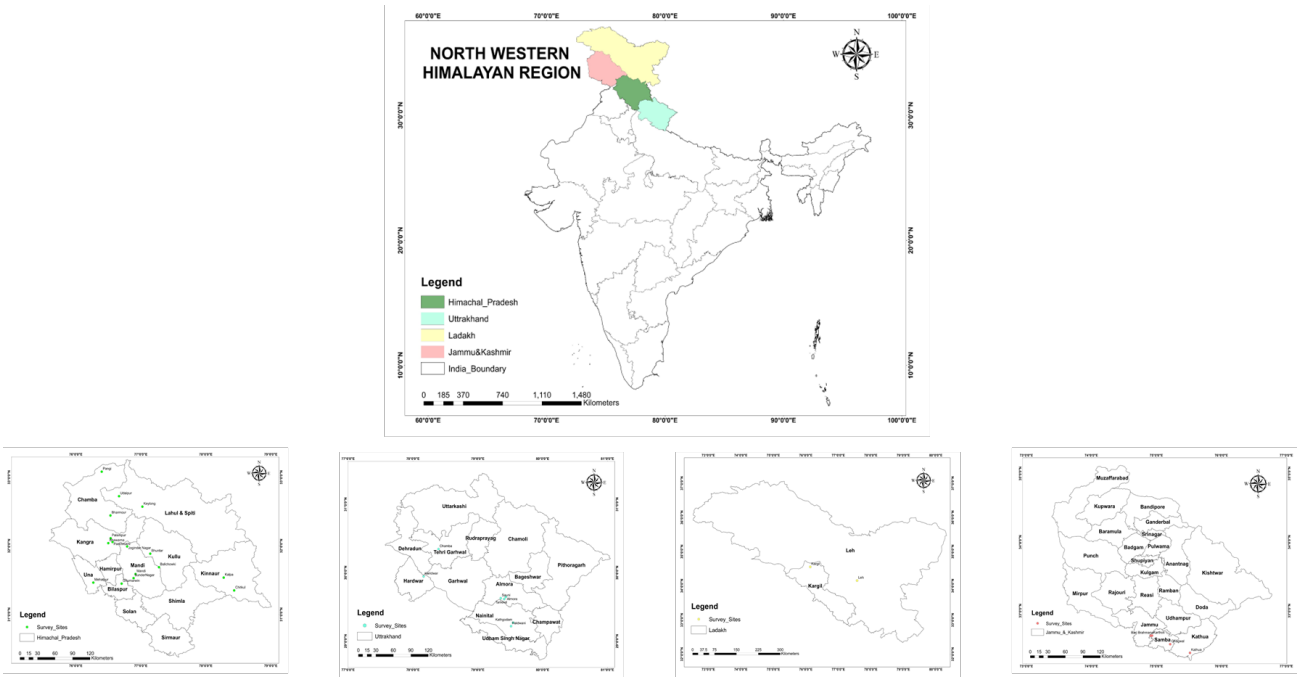

Figure 1: Location maps of study sites in the North Western Himalayan region

Table 1: Details of survey sites in the North Western Himalayan region

S. No.	*Name of the village*	*State*	*Latitude*	*Longitude*	*Altitude (m)*
1	Keylong	Himachal Pradesh	32.5710	77.0320	3080
2	Udaipur	Himachal Pradesh	32.7243	76.6651	2743
3	Bhuntar	Himachal Pradesh	31.8862	77.1455	2050
4	Balichowki	Himachal Pradesh	31.6886	77.2800	2000
5	Mandi	Himachal Pradesh	31.7087	76.9320	780
6	Sunder Nagar	Himachal Pradesh	31.5299	76.8889	1174
7	Joginder Nagar	Himachal Pradesh	31.9912	76.7899	1220
8	Ghumarwin	Himachal Pradesh	31.4491	76.7048	700
9	Pangi	Himachal Pradesh	32.9882	76.5303	2100
10	Bharmour	Himachal Pradesh	32.4428	76.5329	2100
11	Palampur	Himachal Pradesh	32.1109	76.5363	1355
12	Panchrukhi	Himachal Pradesh	32.0566	76.5647	1053
13	Bhawarna	Himachal Pradesh	32.0398	76.4997	1254
14	Mehatpur	Himachal Pradesh	31.4078	76.3435	393
15	Kalpa	Himachal Pradesh	31.5377	78.2754	2960
16	Chitkul	Himachal Pradesh	31.3508	78.4366	3450
17	Haridwar	Uttarakhand	29.9457	78.1642	314
18	Ranikhet	Uttarakhand	29.6434	79.4322	1869
19	Sauni	Uttarakhand	29.6278	79.3543	1679
20	Tarikhet	Uttarakhand	29.6141	79.4071	345
21	Haldwani	Uttarakhand	29.2183	79.5130	424
22	Kathgodam	Uttarakhand	29.2693	79.5441	554
23	Chamba	Uttarakhand	30.3455	78.3947	1524
24	Leh	Ladakh	34.1526	77.5771	3524

25	Kargil	Ladakh	34.5539	76.1349	2676
26	Kathua	Jammu & Kasmir	32.3863	75.5173	393
27	Kartholi	Jammu & Kasmir	32.6380°	74.9342°	340
28	Bari Brahmana	Jammu & Kasmir	32.6365°	74.9141°	340
29	Ghagwal	Jammu & Kasmir	32.5122	75.2129	370

by Thakur *et al.* 2017. Besides this, group discussions were held with locals in each site consisting mixed population of diverse age groups. The information on ethnic cuisines and ingredients utilized was primarily obtained from discussions with womenfolk while information on the availability of the WEPs, and their distribution was obtained from men. All the respondents were made aware of the purpose and nature of the study and data were recorded upon oral consent and agreement. The record of WEPs used by the local people such as parts used, and dishes prepared from the WEPs were collated based on household surveys (n = 524). The WEPs were categorized based on the purpose of use, such as vegetables, fruits, flavoring agents, raw food, and beverages (brew). The data on the usage of WEPs were further categorized season-wise *viz*., WEPs consumed in summer, winter, and rainy seasons. The information collated was evaluated for taxonomic diversity, species richness, and the plant part used for edible purposes (Table 2). The major metabolites identified in these WEPs were listed based on earlier published reports (Table 3).

Results

Wild Edible Plants and Their Consumption Pattern

Nearly 100 WEPs were identified to be consumed in the study region covering Himachal Pradesh, J&K and Uttarakhand. These 100 WEPs belonged to 51 different families; with members of Amaranthaceae (n = 8), Polygonaceae (n = 8), and Rosaceae (n = 8) being the predominant ones followed by Asteraceae members (n = 6). These were followed by Fabaceae, Aracaceae, Moraceae, and Eleagnaceae with 4 species in each of them being consumed. The rest of the families contained either one or two plants that are edible and consumed across the NWHR. In the majority of the cases, leaves and tender shoots (n = 43) was the predominant form of consumption as green leafy vegetables (GLVs) closely followed by fruits (n = 41), roots and tubers (n = 11), flowers and buds (n = 7), seeds (n = 4) and whole plant (n = 1) (Figure 2). Some of the common GLVs consumed in the NWHR, particularly Himachal Pradesh are *Amaranthus tricolor, Chenopodium album, Colacasia esculena, Nasturtium officinale, Brassica juncea, Zanthoxylum armatum, Urtica dioica, Portulaca oleracea, Oxalis latifolia, Rheum austral* are primarily used in the preparation of curries, sauces (chutney) and stuffed flat bread. In Uttarakhand, the following leaves are commonly utilized viz., *Boerhavia diffusa* L., *Antidesma montanum., Achyranthes aspera* L., *Polygonum aviculare* L., in addition to the aforesaid leaves that are consumed in Himachal Pradesh. Apart from its use as a food ingredient, the leaves of the aforesaid plants are primarily used in traditional medicine mainly for gastro-intestinal disorders, and for treating ulcers and infections (Thakur *et al.,* 2017). In the cold desert regions encompassing, Ladakh, Lahaul, and Spiti, a variety of wild leaves are consumed as food, medicine, and flavoring agent. *C. foliosum, Rumex hastatus, R. emodi,* and *Urtica tibetica* are commonly utilized leaves as vegetables. Leaves of *Allium jacquemontii, Murraya koennigii*, and *Mentha longifolia* are used as flavouring agents due to the presence of essential oils and aromatic compounds (Farzaei *et al.,* 2017).

The next form of WEP widely consumed are fruits and berries. These are consumed raw or cooked as vegetables or converted into a variety of products such as juices, jams, sauces, and pickles. Among wild fruits and berries, *Aegle marmelos*, *Artocarpus lacucha, Berberis sp. (B. aristate, B. asiatica)* DC., *Cornus capitata, Diospyros lotus, Ficus auriculata, Ficus palmata* (Wild Figs), *Myrica esculenta, Morus alba, Physalis peruviana, Punica granatum, Pyrus pashia, Ribes alpestere, Rubus sp. (R. elipticus, R. niveus), Prunus sp. (P. americana, P. mira), Hippophae rhamnoides* are few popular wild edible fruits from the NWHR. Among these fruits, seabuckthorn (*H. rhamnoides*), apricot (*P. americana*), pomegranate (*P. granatum*), and bael (*A. marmelos*) are valued highly owing to their medicinal properties (Bachheti *et al.* 2023).

Following leaves and fruits, tubers and roots are another important form of consumption of WEPs. Tubers of *Colacasia esculenta*, *Pueraria tuberosa, Typhonium diversifolium, Arisaema speciosum, Dioscorea sp.* (*D. bellophyla, D. bulbifera, D. oppositifolia*) are a few commonly consumed tubers. They are primarily used as vegetables for stuffing breads and used as curries and pickles. Apart from these, aerial parts of

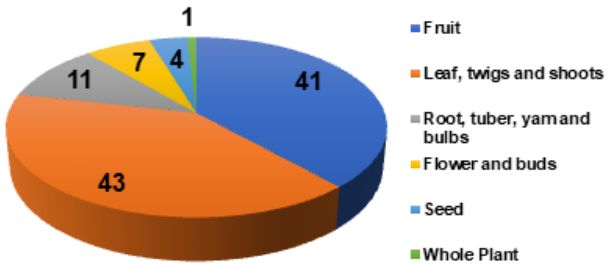

Figure 2: Statistics of different plant part used

several WEPs are primarily used as vegetables mainly curries. Flowers constitute a significant component of traditional foods in NWHR. The major seasonal flowers consumed are *Bauhinia variegeta, B. purpurea*, *Rhodeodendron arboreum*, *Viola odorata,* and *Bombax ceiba*. *Bauhinia* sp. (*B. variegeta* and *B. purpurea*) is used in the preparation of snacks (fritters) and stuffed flat breads. In addition, they have been used for treating infections and boosting immunity (Hegde *et al.,* 2023). Rhododendron sp. is used for the preparation of sauces and squash, cordial, and consumed during summers. They are primarily used as coolant and possess significant commercial value providing livelihood to the locals (Singh and Chatterjee, 2022). *V. odorata* flowers are dried and used as tea and preparation for decoction while *B. ceiba* flowers are used as a source of natural color and used for the treatment of anemia, haematuria, and hemorrhoids (Jain *et al.,* 2009).

Apart from Angiosperms, fiddlehead fern, *Diplazium* sp. (*D. esculentum* and *D. maximum*) are used as an important vegetable in the rainy season in Himachal Pradesh and Uttarakhand. The tender stalks of the fern are consumed as vegetables and used in curry preparations. Although not a plant, the locals consider it a plant (Sareen *et al.* 2021). Likewise, wild edible mushrooms, *Morchella esculenta* (Gucchi) and *Termitomyces* sp. (*T. heimii* and *T. microcarpus*) are commonly used as vegetables and preparation of curries across Himachal Pradesh, Uttarakhand and J&K (Atri *et al.,* 2019). A snapshot of various wild edibles distributed in the NWHR is presented in the Figure 3.

Bioactive Molecules from WEPs

Apart from their use as vegetables and raw foods, WEPs possess excellent bioactive properties owing to the presence of myriad bioactive molecules. The major class of bioactive molecules are phenolic acids, flavonoids, anthocyanins, terpenoids, carotenoids, anthraquinones, phenylethanoids and phenylpropanoids (Bhatt *et al.,* 2017; Bachheti *et al.,* 2023; Hegde *et al.,* 2023). The list of major classes of metabolites reported in the WEPs is presented in Table 3. The GLVS are a rich source of micronutrients, particularly iron, zinc and magnesium, and carotenoids, primarily lutein and beta carotene (Sarkar *et al.,* 2023). Fruits and berries are primarily rich sources of polyphenols. Some commonly detected metabolites in wild edible fruits from NWHR are 3-O-caffeoylquinic acid, 5-*O*-caffeoylquinic acid. Quercetin-3-*O*-glucoside, *p*-coumaric acid, 3-*p*-coumarylquinic acid, kaempferol glycosides, isorhamnetin, myricetin, catechins, gallic acid, and apigenin glucosides (Hegde *et al.,* 2023; Bachheti *et al.,* 2023). These polyphenols have been attributed with a wide range of bioactive properties viz., antioxidant, anti-inflammatory, hypocholesterolaemia and cardioprotective, and anti-cancerous (Pereira *et al.,* 2020). Some high-value and commercially important molecules from WEPs in NWHR are quercetin-3-O-glucoside from

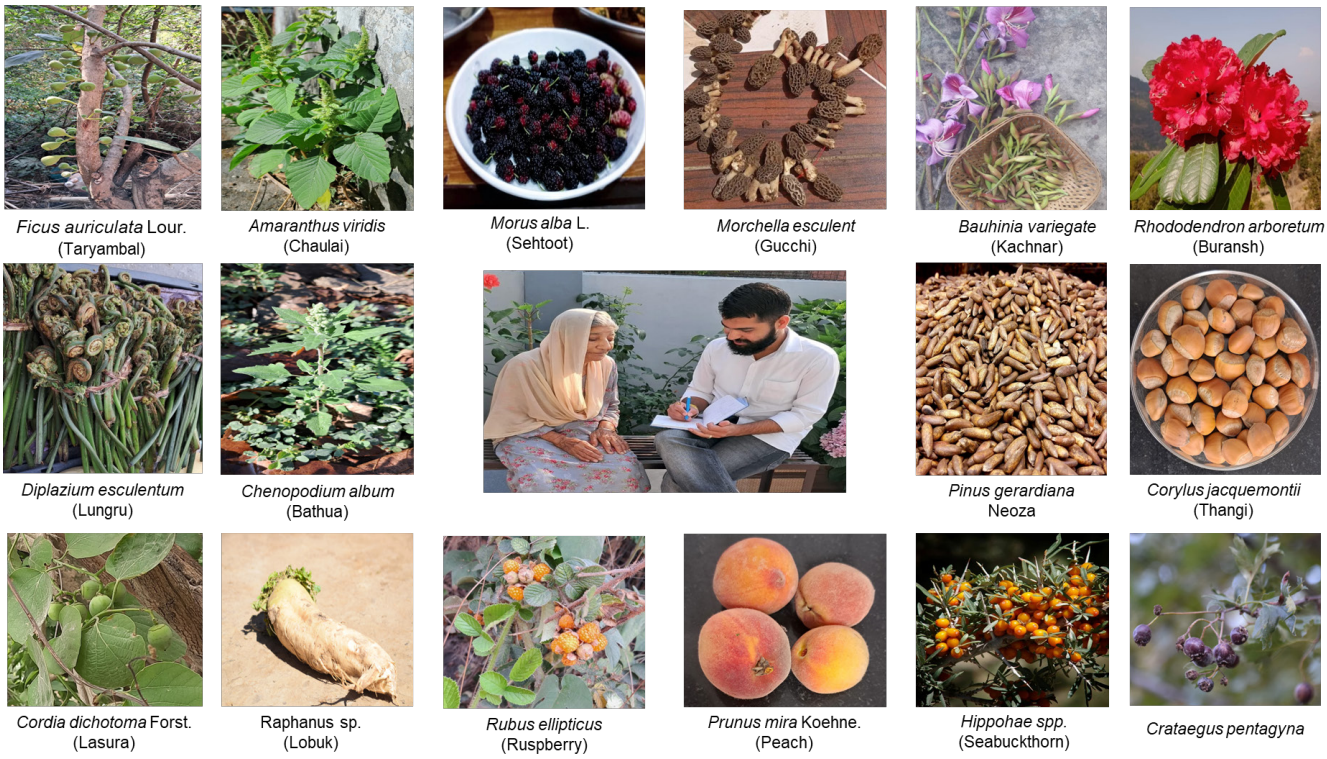

Figure 3: Photographs of wild edible plants consumed in North Western Himalayan region

Table 2: Wild edible plants (WEPs) consumed in the North Western Himalayan Region

S. No.	*Botanical name*	*Local name*	*Family*	*Part used*	*Method of consumption*
Himachal Pradesh					
Summer season					
1	*Rhododendron arboreum* Sm.	Buransh	*Ericaceae*	Flower	Chutney, juices and cordial
2	*Bauhinia variegeta* L.	Kachnar	Fabaceae	Buds and flowers	Fritters and kachru (Stuffed Indian flat bread)
3	*Cordia dichotoma* Forst.	Lasura	Boraginaceae	Raw fruits	Vegetable, pickle
4	*Amaranthus viridis* L.	Chulai	Amaranthaceae	Leaf	Leafy vegetable, curries
5	*Ficus palmata* Forssk	Fegra	Moraceae	Fruit	Ripe fruit, Vegetable curries
6	*F. auriculata* Lour.	Taryambal	Moraceae	Fruit	Ripe fruit, Vegetable curries
7	*Artocarpus lacucha* Buch.-Ham.	Dheu	Moraceae	Fruit	Ripe fruit, Vegetable curries
8	*Viola odorata* L.	Banfsa	Violaceae	Flower	Flavouring agent to tea
9	*Sechium edule* (Jacq.) Swartz	Lonku	Cucurbitaceae	Fruit	Vegetable curries
10	*Fagopyrum dibotrys* (D.Don) Hara	Kathu	Polygonaceae	Leaf and seeds	Leafy Vegetable curries
11	*Morchella esculenta* (L.) Pers.	Gucchi	Morchellaceae	Arial part	Vegetable curries
12	*Aegle marmelos* Correa.	Bael or wood apple	Rutaceae	Fruit	Ripe fruit, marmalade
13	*Berberis aristata* DC.	Kasmale	Berberidaceae	Fruit	Ripe fruit
14	*Carissa spinarum* L.	Garne or Conkerberry	Apocynaceae	Fruit	Ripe fruit
15	*Morus alba* L.	Wild toot or Shehtoot	Moraceae	Fruit	Ripe fruit, chutney
16	*Myrica esculenta* Buch-Ham. Ex D. Don	Kaphal	Myricaceae	Fruit	Ripe fruit
17	*Phyllanthus emblica* L.	Amla	Phyllanthaceae	Fruit	Ripe fruit, chutney, juice and pickle
18	*Rubus ellipticus* Sm.	Aakhe or Yellow Himalayan Raspberry	Rosaceae	Fruit	Ripe fruit
19	*Ziziphus mauritiana* Lamk.	Ber or Indian Jujube	Rhamnaceae	Fruit	Ripe fruit
20	*Fragaria indica* Andr.	Wild Strawberry	Rosaceae	Fruit	Ripe fruit, juice
21	*Prunus armeniaca* L.	Apricot	Rosaceae	Fruit	Ripe fruit, juice and jam
22	*B. asiatiica* Roxb. ex DC.	Indian/Asian Barberry	Berberidaceae	Fruit	Ripe fruit
23	*Crataegus pentagyna* Waldst. & Kit. ex Willd	Black Fruit Hawthorn	Rosaceae	Fruit	Ripe fruit
Rainy season					
24	*Colocasia esculenta* (L.) Schott	Patrode	Araceae	Leaf	Patrode, leafy vegetable curry
25	*Diplazium esculentum* (Retz.) Sw.	Lungru	Athyriaceae	Fern	Vegetable curry
26	*Portulaca oleracea* L.	Kulfa	Portulacaceae	Twigs	Leafy vegetable curry
27	*Termitomyces microcarpus* (Berk. & *Broome) R. Heim, Mem*.	Tatmor/Bhatoliyan	Lyophyllaceae	Arial Part	Vegetable curry, pickle
28	*Crataegus songarica* K. Koch	Van-Sangli or Ramjag	Rosaceae	Fruit	Ripe fruit
29	*Elaeagnus umbellate* Thumb.	Chinder	Elaeagnaceae	Fruit	Ripe fruit
30	*Pyrus pashia* Buch.-Ham ex D.Don	Kainth	Rosaceae	Fruit	Ripe fruit, pickle and marmalade

31	*Ribes alpestre* Wall. ex. Decne.	Chalendra or Asian gooseberry	Grossulariaceae	Fruit	Ripe fruit
32	*Rubus niveus* Thunb.	Akhe or Hill Raspberry	Rosaceae	Fruit	Ripe fruit
33	*Viburnum mullaha* Buch.-Ham ex. D. Don	Ghenu or Himalayan Viburnum	Adoxacea	Fruit	Ripe fruit
34	*Corylus jacquemontii Decne*.	Himalayan Hazelnut	Betulaceae	Fruit	Nuts, oil extraction
35	*Murraya koennigii* L.	Gandhelu or Metha Neem	Rutaceae	Fruit	Ripe fruit
36	*Elaeagnus umbellate* Thunb.	Ghain, Chindar	Elaeagnaceae	Fruit	Ripe fruit
Winter season					
37	*Brassica juncea* L.	Mustard Leaf	Brassicaceae	Leaf	Leafy vegetable curry, fritters and kachru (stuffed indian flat bread)
38	*Chenopodium album L.*	Bathua	Amaranthaceae	Twigs	Leafy vegetable curry, fritters and kachru (stuffed indian flat bread)
39	*Momordica dioica* Roxb.	Ban Karela	Cucurbitaceae	Fruit	Vegetable curry
40	*Colocasia esculenta* (L.) Schott	Colocasia tubers	Araceae	Tuber	Vegetable curry and pickle
41	*Cornus capitata* Wall. ex Roxb.	Tharbal or Himalayan strawberry tree	Cornaceae	Fruit	Ripe fruit
42	*Diospyros lotus* L.	Amlook or Date plum	Ebenaceae	Fruit	Ripe fruit
43	*Physalis peruviana* L.	Rasbhary	Solanaceae	Fruit	Ripe fruit
44	*Pinus gerardiana* Wall. ex D.Don	Neoza	Pinaceae	Fruit	Nuts, oil extraction
45	*Punica granatum* L.	Wild Pomegranate (Darhu)	Punicaceae	Fruit	Chutney
46	*Prunus mira* Koehne.	Pit Aaru (Smooth Pit peach)	Rosaceae	Fruit	Ripe fruit and jam
47	*Solanum nigrum* L.	Kali Makoi or Black Nightshade	Solanaceae	Fruit	Ripe fruit
48	*Olea ferruginea* Royle	Indian Olive	Oleaceae	Fruit	Ripe fruit
49	*Flacourtia indica* (*Burm. f.) Merr*.	Indian Plum or Governor's plum	Salicaceae	Fruit	Ripe fruit
Uttarakhand					
Summer season					
50	*Achyranthes aspera* L.	Chaff- flower	Amaranthaceae	Leaf, seed	Leafy vegetable curry
51	*Elaeagnus latifolia* L.	Khasi Cherry or Bastard oleaster	Elaeagnaceae	Fruit	Ripe fruits
52	*Bombax ceiba* L.	Semal	Bombacaceae	Flower	Vegetable curry and chutney
53	*Agave americana* Linn.	Ramban	Asparagaceae	Shoots	Vegetable curry
54	*Asparagus filicinus* Buch.-Ham.ex D.Don	Kairua	Asparagaceae	Shoots	Vegetable curry
55	*Dioscorea bulbifera* Linn.	Genthi	Dioscoreaceae	Tuber	Vegetable curry and pickle
56	*Urtica dioica* L.	Bichchu ghas	Urticaceae	Leaf	Leafy vegetable curry
Winter season					
57	*Bauhinia purpurea* L.	Khair-wal	*Fabaceae*	Flower, buds and fruit	Flower and buds as vegetable curry Ripe fruit
58	*Boerhavia diffusa* L.	Punarnava	Nyctaginaceae	Leaf	Leafy vegetable curry

59	*Polygonum aviculare* L.	Jhangar/Wild Buckwheat	Polygonaceae	Twigs	Leafy vegetable curry
60	*Pueraria tuberosa* DC.	Bilikand	*Fabaceae*	Tuber	Vegetable curry
Rainy season					
61	*Antidesma montanum* Blume	Amli	Phyllanthaceae	Leaves and fruit	Chutney and pickle
62	*Costus speciosus* (Koen ex. Retz) Sm.	Keu	*Costaceae*	Tuber	Vegetable curry
63	*Phytolacca sp.*	Jarag twigs	Phytolaccaceae	Twigs	Leafy vegetable curry
64	*Arisaema speciosum* Mart.	Bankh	Araceae	Tuber	Vegetable curry
65	*Chaerophyllum villosum* Wall. Ex DC.	Ganziadi	Apiaceae	Rhizome	Vegetable curry
66	*Dioscorea glabra* Roxb.	Tarur	Dioscoreaceae	Arial root yam	Vegetable curry
67	*Typhonium diversifolium* Wall. Ex Schott	Rugi	Araceae	Tuber	Vegetable curry
Jammu & Kashmir					
Summer season					
68	*Allium cepa* var. proliferum	Tree Onion/Praan Praand	Amaryllidaceae	Shoots, bulb	Flavouring agent and vegetable
69	*Celosia argentea* L.	Moval	Amaranthaceae	Leaf	Flavouring agent
70	*Malva sylvestris* Linn.	Soochal	Malvaceae	Leaf	Leafy Vegetable curry
71	*Nasturtium officinale* R. Br.	Nagbabur	Brassicaceae	Leaf	Leafy Vegetable curry
72	*Orobanche alba* steph.	Subzgul	Orobanchaceae	Whole plant	Vegetable
73	*Polygonum alpinum* All.	Tsokladar	Polygonaceae	Leaf	Leafy Vegetable curry
74	*Taraxacum officinale* Weber	Hand	Daisy family Asteraceae	Leaf	Leafy Vegetable curry
Rainy season					
75	*Amaranthus retroflexus* L.	Ganhaar/Redroot pigweed	Amaranthaceae	Seeds	Flavouring agent
76	*Amaranthus spinosus* Linn.	Charleree	Amaranthaceae	Leaf	Leafy vegetable curry
77	*Angelica glauco* Edgew.	Chorak	Apiaceae	Twigs and roots	Flavouring agent and leafy vegetables
78	*Commelina benghalensis* Linn.	Chura	Commelinaceae	Leaf	Leafy vegetable curry
79	*Medicago sativa* Linn.	Ispit	Fabaceae	Leaf	Leafy vegetable curry
80	*Polygonum aviculare* Linn.	Endrani	Polygonaceae	Leaf	Leafy vegetable curry
81	*Solanum nigrum* Linn.	Kainkothi	Solanaceae	Leaf	Leafy vegetable curry
Ladhak					
Summer Season					
82	*Saussurea gossypiphora* D.Don.	Ldums	Asteraceae	Leaf	Leafy vegetable curry
83	*Capparis spinosa* L.	Kabra	Capparaceae	Leaf and fruit	Leafy vegetable curry and pickle
84	*Chenopodium foliosum* Asch.	Sneou	Amaranthaceae	Leaf	Flavouring agent
85	*Sedum ewersii* Ledeb.	Churuppa	Crassulaceae	Twigs	Leafy vegetable curry
86	*Polygonum chinensis* L.	Jangli Palak	Polygonaceae	Leaf	Leafy vegetable curry
87	*Allium prezewalskianum* Regel.	Wild onion	Amaryllis	Shoots and bulb	Flavouring agent and vegetable curry
88	*Artemisia brevifolia* Wall. ex DC.	Kamchu	Asteraceae	Leaf	Flavouring agent

89	*Mentha longifolia* (L.) Huds.	Pholoing	*Lamiaceae*	Leaf	Flavouring agent
90	*Hippohae spp.*	Chharma or Seabuckthorn	Elaeagnaceae	Fruit, Leaf	Ripe fruit, chutney, juice and decoction
Rainy season					
91	*Carum carvi* L.	Caraway/Ambuk Konsnyot	Apiaceae	Leaf, seed	Flavouring agent
92	*Chenopodium botrys* L.	Sagani	Amaranthaceae	Leaf	Leafy vegetable curry
93	*Arnebi euchroma* (Royle ex Benth.) I.M.Johnst. A	Troma	Boraginaceae	Roots	Vegetable curry
94	*Crepis tectorum* L.	Remang	Asteraceae	Twigs	Leafy vegetable curry
Winter season					
95	*Fagopyrium esculentum Moench*	Tyat/Kuttu	Polygonaceae	Leaf	Leafy vegetable curry
96	*Rheum emodi* Wall	Lachu	Polygonaceae	Leaf	Leafy vegetable curry
97	*Lactuca sativa* L.	Dums	Asteraceae	Leaf	Leafy vegetable curry and flavouring agent
98	*Raphanus sp.*	Lobuk	Brassicaceae	Leaf	Chuney, pickle
99	*Lactuca dolichophylla* Kitam.	Khala	Asteraceae	Leaf	Leafy vegetable curry
100	*Oxyria digya* (L.) Hill	Lamanchu	Polygonaceae	Leaf	Leafy vegetable curry and eaten fresh

Bauhinia variegeta (Hegde *et al.,* 2023) cyanidin-3-O-glucoside from *Rhododendron arboreum* (Sendri *et al.,* 2022), berberine from *B. asiatica* and *B. aristata* (Chander *et al.,* 2017), naphthoquinone (shikonin) from *Arnebia euchroma* (Kumar *et al.,* 2021) polyunsaturated fatty acid such as alpha-linolenic acid and carotenoids from *Hippophae rhamnoides* (Wani *et al.,* 2016), apigenin derivatives from *Mentha longifolia* (Farzaei *et al.,* 2017), betalins from *Amaranthus* sp. (*A. tricolor and A. viridis*) (Hussain *et al.,* 2018). The structure of a few important bioactive metabolites identified in the WEPs distributed across the NWHR is presented in Figure 4. The motivation behind the consumption of WEPs among locals could be directly correlated with the lifestyle and environmental conditions they live in. High-altitude regions, specifically the cold desert regions of NWHR such as Ladakh, Lahaul, and Spiti are characterized by extreme cold climate, high UV irradiation, and hypobaric hypoxia (Bharti *et al.,* 2017). Such harsh living conditions are known to induce severe oxidative stress in the body and lead to the accumulation of reactive oxygen species (ROS) (Aranda-Rivera *et al.,* 2022). Oxidative stress is associated with several pathological conditions such as inflammation, neurological disorders, and cancer (Aranda-Rivera *et al.,* 2022). Several WEPs that are consumed in NWHR have been reported to counter oxidative stress owing to the presence of aforesaid bioactive molecules. For example, the widely consumed stinging nettle (*U. dioica*), and seabuckthorn (*H. rhamnoides*) contain strong antioxidants such as quercetin-3-O-glucoside, alpha-linolenic acid, β-carotene offering strong radioactive protection (Wani *et al.,* 2016). Similarly, other polyphenols such as apigenin and rutin derivatives are known to enhance endogenous antioxidant systems in the body and protect against radiation-induced damage (Choi *et al.,* 2014). The presence of antioxidant polyphenols in almost all the WEPs suggests the importance of these WEPs in maintaining the health of the locals. Certain medicinal herbs unique to cold desert regions have been used by the locals such as the leaves and shoots of *Rhodiola heterodonta*, *Potentilla ansernia,* and *Hippophae* sp. for the preparation of brews and tea (Chen *et al.,* 2023). *Rhodiola* contains phenylethanoids and phenylpropanoid metabolites such as salidroside and aromatic molecules such as tyrosol that have been reported to possess neuroprotective functions under hypoxic conditions (Li and Chen, 2017).

Challenges and Future Prospects in the Consumption of WEPs in NWHR

Although the WEPs play an important role in the subsistence of the local people, their consumption prevalence and traditional knowledge behind their utilization are slowly declining due to several reasons. One of the major factors affecting the continued consumption of WEPs among locals is urbanization and adaptation to modern lifestyle. In addition, the availability of packaged food and high

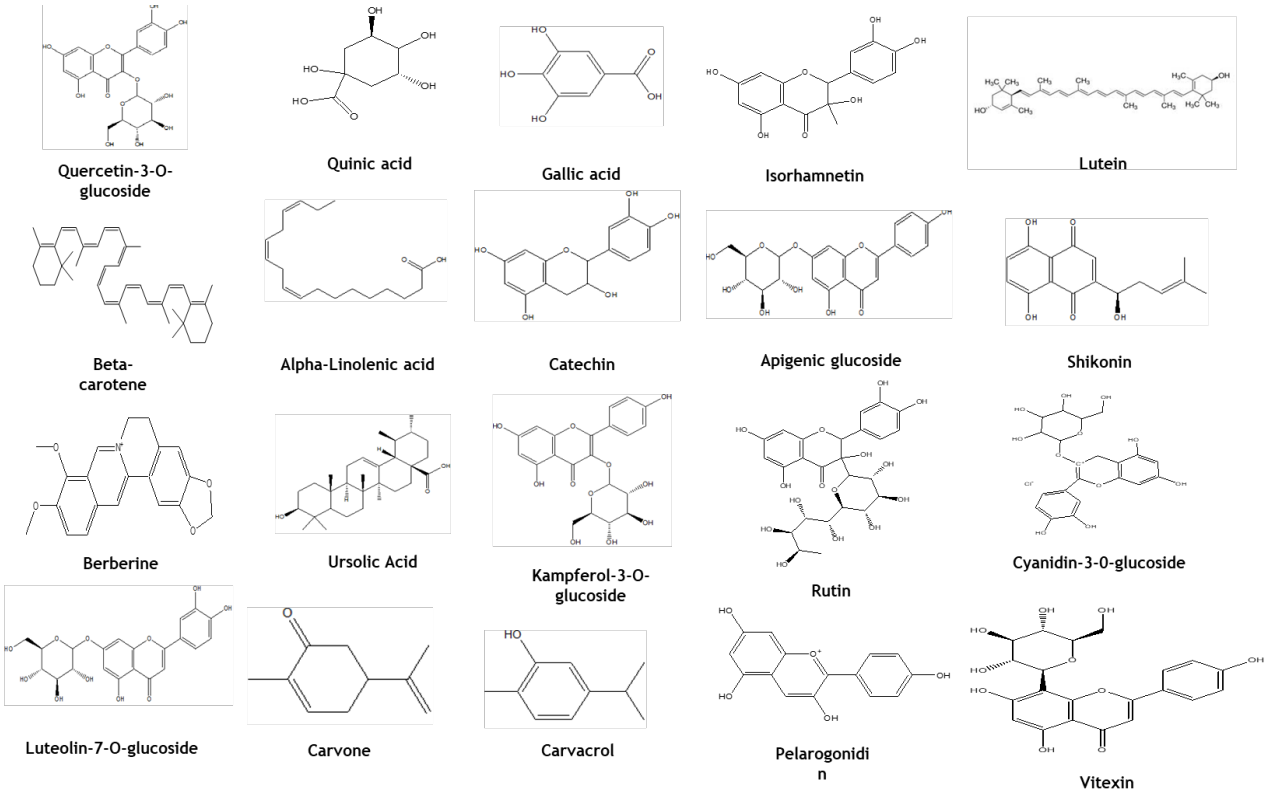

Figure 4: Major bioactive molecules in present in the WEPs distributed in the North Western Himalayan region

Table 3: Major metabolites and bioactive molecules

S. No.	*Latin name of the WEP*	*Major metabolites*	*Bioactive molecules*	*References*
1	*Rhododendron arboreum* Sm.	Flavonoids, flavonoid glycoside, organic compounds	Quercetin-3-rhamnoside, Rutin, Coumaric acid, naringenin and taxifolin	Kumar *et al.* 2019
2	*Bauhinia variegeta* L.	Flavonoid glycosides	Kaempferol-3-*O*-glucosyl-7-*O*-glucoside, kaempferol-3-*O*-rutinoside, kaempferol-3-*O*-glucoside, kaempferol-3-*O*-robinoside, quercetin-3-*O*rhamnoside, quercetin-3-*O*-glucosyl-7-*O*-glucoside, and quercetin-3-*O*-rutinoside, apigenin, myricetin, and luteolin	Hegde *et al.* 2023
3	*Cordia dichotoma* Forst.	Flavonoids polyphenols, tannins, and alkaloids	Kaempferol, quercetin and isorhamnetin	Raghuvanshi *et al.* 2022
4	*Amaranthus viridis* L.	Flavonoids, carotenoids, organic compunds	β-carotene and lutein, Kaempferol, kaempferol 3-O-β-glucoside, kaempferol 3-O-β-diglucoside, kaempferol-3-O-arabinoglucoside, quercetin, quercetin 3-O-xylosylglucoside, quercetin-3- O rhamnoglucoside, 2,4-Di-tert-butylphenol, Dioctyl phthalate	Poonia and Upadhayay, 2015
5	*Ficus palmata* Forssk	Alkaloids, tannins, flavonoids, terpenoids, cardiac glycosides	NR	Joshi *et al.* 2014
6	*F. auriculata* Lour.	Alkaloids, Saponins, glycosides, phytosterol, resins, phenols, tannins, diterpenes, Flavonoids	Quercetin, epigallocatechin	Mehra and Tandon, 2021
7	*Artocarpus lacucha* Buch.-Ham.	Flavonoids, phenols, saponins, tannins and coumarins	Kaempferol, Rutin, Quercetin, Luteolin7Oglucoside	Pertiwi *et al.* 2024

8	*Viola odorata* L.	Phenylpropanoids, stigmastanes, fatty alcohols, fatty acid and fatty acid ester	Eugenol, gamma-sitosterol, tetradecanoic acid, hexadecanoic acid, octacosanol, Octadecanoic acid, methyl ester	Jasim *et al.* 2018
9	*Sechium edule* (Jacq.) Swartz	Phenolic acid, flavonoids, alkaloids	Hydrobenzoic acids (galic, protocatechuic, syringic, p-hydroxybenzoic), hydroxycinnamic acid (cafeic, ferulic, p-coumeric, clorogenic), flavones, apigenin, Flavanonols (quercetin, myricetin, rutin) flavonones (naringenine), cucurbitane α-Amyrin, cycloartenol, β-amyrin, 24-methylenecycloartanol	Gavia-García *et al.* 2023
10	*Fagopyrum dibotrys* (D.Don) Hara	Flavonoids, phenols, terpenes, steroids, triterpenoids	Quercetin, rutin, catechins, catechin, epicatechin, benzoic acid, 3,4-dihydroxy benzoic acid, gallic acid, succinic acid, syringic acid, ferulic acid, glutinone, glutinol, 3α,21β-dihydroxy-olean-12-ene, olean-12-ene-3β,7β,15α,28-tetraol, ursolic acid, 3α-hydroxy-urs-12,15-dien, hecogenin, β-sitosterol, *N*-butanol-β-d-furan methylglycoside, *n*-butyl-β-d-fructopyronoside, β-daucosterol, daucosterol	Zhang *et al.* 2021
11	*Morchella esculenta* (L.) Pers.	Flavonoids, phenolic compounds, steroids	Flavones, flavonoids, quercetin, benzoic acid, cinnamic acid, gallic acid, phydroxybenzoic acid, Phydroxybenzoic acids, Protocatechuic acid, Vanillic acid, Sterol, Ergosterol	Singh *et al.* 2022
12	*Aegle marmelos* Correa.	Polyphenols, coumarins Tannins, alkaloids, pectin, phenolic acids, organic acids, flavonoids, tocopherols, carotenes	Alloimperatorin, zanthotoxol, imperatorin, xanthotoxol, isoimperatorin, umbelliferone, marmelide, scopoletin, marmelosin, scopolentin, marmesin, psoralen-a, scoparone, marmin, methyl ether, psoralen, 4,7,8-trimethoxyfuroquinoline, Skimminianine, aegelenine, halfordinol, aegeline, ethyl cinnamate, aegelinosides A, ethyl cinnamamide, aegelinosides B, dictamine, fragrine, gallic acids, p-coumaric acid, 2,3-dihydroxy benzoic acid, vanillic acid, chlorogenic acid, rutin	Sharma *et al.* 2022
13	*Berberis aristata* DC.	Alkaloids, berberine, palmatine, columbamine, quercetin	Berberamine, Aromoline, Jatrorrhizine, Oxyberberine, Tetrahydropalmatine, Oxycanthine, Lupeol, Oxycanthine	Jahan *et al.* 2022
14	*Carissa spinarum* L.	Polyphenols, flavonoids	Syringic acid, Resveratrol, Chlorogenic acid, Epicatechin, Myricetin, Quercetin, Luteolin, Apigenin	Nazareth *et al.* 2021
15	*Morus alba* L.	Flavonoids, polyphenol, anthocyanins, terpenes, carotenoids, and alkaloid	Quercetin (Quercetin 3-O-rutinoside, Quercetin 3-O-glucoside, Quercetin3-O-galactoside), Kaempferol (Kaempferol 3-O-glucoside, and Kaempferol 3-O-rutinoside), Guinic acid, Rutin, Catechin, Cyandin-3-glucoside, Chlorogenic acid, Gallic acid, Ferulic acid, p-coumaric acid, o-coumaric acid, Cinnamic acid, and Caffeic acid	Zhou *et al.* 2022
16	*Myrica esculenta* Buch-Ham. Ex D. Don	Tanins, phenolic acid, flavonoids, terpens, triterpenoids, steroids	Catechin, Gallic acid, Chlorogenic Acid, Coumaric acids, Gallic acid, Ferulic acid, 1-ethyl-4-methylcyclohexane, Myo-inositol, methyl-d-lyxofuranoside, 2-furancarboxyaldehyde, 2,5-furandionedihydro-3-methylene, furfural, oxirane	Kabra *et al.* 2019
17	*Phyllanthus emblica* L.	Phenolic acids, flavonoids, Tannins, alkaloids	Hydroxybenzoic acids (4-hydroxybenzoic acid, coumaric acid, gallic acid, protocatechuic acid, syringic acid, vanillic acid, flavonols, flavones, flavanones, and flavan-3-ols, Kampferol, quercetin, apigenin, luteolin, myricetin, ellagitannins, Ellagic acid, phyllantine and phyllantidine	Gul *et al.* 2022
18	*Rubus ellipticus* Sm.	Polyphenols, flavonoids, anthocyanins, tannins, terpenoids	Quercetin, rutin, Quercetin 3-O-glucuronide, Phloridzin, Epicatechin, Epigallocatechin, Chrysin, Cyanidin, Pelargonidin, Malic acid, Ellagic acid, Chlorogenic acid, Citric acid, Ascorbic acid, Quinic acid, m-Coumaric acid, p-Coumaric acid, β-Carotene Gallic acid, Catechin	Lamichhane *et al.* 2023

19	*Ziziphus mauritiana* Lamk.	Cyclopeptid alkaloids, sterols, flavonoid, terpenoids	Berberine, quercetin, kaempferol, sitosterol, stig-masterol, lanosterol, diosgenin, 2α-aldehydo-A (1)-norlup-20(29)-en-27, 28-dioic acid (zizyberanal acid), Zizyberanone, Zizyberanalic acid, Ursolic acid, Colubrinic acid, Alphitolic acid, 3-O-cis-p-coumaroyl alphitolic acid, 3-O-trans-pcoumaroyl alphitolic acid, Betulinic acid, Betulonic acid, 3-O-cis-pcoumaroyl maslinic acid, 3-O-trans-p-coumaroyl maslinic acid, Oleanolic acid, Oleanonic acid, Quercetin 3-O-rutinoside, Quercetin 3-O-robinobioside, Quercetin 3-O-galactoside, Quercetin 3-O-glucoside, Quercetin 3-O-rhamnoside, Quercetin 3-O-pentosylhexoside, Quercetin 3-O-6-malonylglucoside, Quercetin 3-O-malonylglucoside, Luteolin 7-O-6-malonylglucoside, Luteolin 7-O-malonylglucoside, Myricetin 3-O-galactoside, Naringenin triglycoside	Prakash *et al.*, 2021
20	*Fragaria indica* Andr.	Phenolics, phenolic acid, flavonoids, tannins, ellagic acid, glycoside, flavonols, proanthocynidins and benyl derivatives	NR	Bahukhandi *et al.* 2023
21	*Prunus armeniaca* L.	Organic acid, carotenoids, polyphenols, carotenoids, polysachharides	β-carotene, β-cryptoxanthin, γ-carotene, Lycopene, Chlorogenic, Neochlorogenic acids, Catechin, Epicatechin, Rutin, Pectin	Erdogan-Orhan and Kartal, 2011
22	*Berberis asiatiica* Roxb. ex DC.	Alkaloids, tannins, flavonoids, Terpenoids, sterols	Berberine, Berbamine, Palmatine, Columbamine, Jatrorrhizine, and Oxyacanthine	Semwal *et al.* 2023
23	*Crataegus pentagyna* Waldst. & Kit. ex Willd	Phenolics, proanthocyanidins flavonoid glycosides,	Quercetin, Isoquercetin, Rutin, Hyperoside, Epicatechin, Chlorogenic acid, Protocatechuic acid, gallic acid, caffeic acid, and chlorogenic acid, coumaric acid, chlorogenic acid, caffeic acid, ferulic acid, quercetin 3-O-glucoside (isoquercetin), quercetin, quercetin 3-O-rutinoside (rutin), (-)-epicatechin, kaempferol 3-O-glucoside, hyperoside, apigenin, cyanidin 3-O-glucoside, luteolin and procyanidins B1 and B2	Taleghani *et al.* 2024
24	*Colocasia esculenta* (L.) Schott	Alkaloid, flavonoid, tannin, glycoside	Tarin, Vicenin-2, iso-vitexin, iso-vitexin 3′-O-glucoside, vitexin X′-O-glucoside, iso-orientin, orientin-7-O-glucoside, luteolin 7-O-glucoside	Sharma *et al.* 2020
25	*Diplazium esculentum* (Retz.) Sw.	Alkaloids, flavonoids, glycosides, phenolic, tannins, terpenoids, steroids	Pentadecanoic acid, β-sitosterol, neophytadiene, α-linolenic acid, methylpalmitate, diisobutylphthalate, phytol and 10,12 hexadecadien-1-ol	Semwal *et al.* 2021
26	*Portulaca oleracea* L.	Flavonoid, alkaloids, terpenoids, fatty acid	Kaempferol, apigenin, luteolin, myricetin, and quercetin, N-trans-feruloyltyramine, dopa, dopamine, noradrenaline, omega-3 fatty acids	Iranshahy *et al.* 2017
27	*Termitomyces microcarpus* (Berk. & *Broome) R. Heim, Mem*.	Phenolic compounds, flavonoids	Tannic acid and gallic acid, gentisic acid, and protocatechuic acid, pyrogallol vanillic acid, syringic acid, pcoumaric acid, caffeic acid, ferulic acid, cinnamic acid, myricetin, kaempferol, quercetin,	Mitra *et al.* 2016
28	*Crataegus songarica* K. Koch	Phenols, flavonoids, anthocyanin	NR	Gania *et al.* 2014
29	*Elaeagnus umbellate* Thumb.	Polyphenols, anthocyanins	Lycopene, lutein, phytoene, phytofluene, β-cryptoxanthin, β-carotene, and α-cryptoxanthin	Gamba *et al.* 2020
30	*Pyrus pashia* Buch.-Ham ex D.Don	Sterols, triterpines	β-sitosterols, β-sitosterol-3-D glucoside, Lupeol	Ali and Juyal, 2018
31	*Ribes alpestre* Wall. ex. Decne.	Flavonoids	NR	Sun *et al.* 2021
32	*Rubus niveus* Thunb.	Polyphenols, flavonoids	NR	Moreno-Medina *et al.* 2018
33	*Viburnum mullaha* Buch.-Ham ex. D. Don	Polyphenols, flavonoid	Acetyl salicyclic acid, Clorogenic acid, Dihydroquercetin, Dihydrorobinetin, Dihydromyricetin, 2-isoprenylemodin, Rutin, Cosmosiin hexaacetate, Pectolinarin, Eriodictyol, Iriginol hexaacetate, Theaflavin, Epicatechin-pentaacetate, Lomatin, Peucenin	Singh *et al.* 2017

34	*Corylus jacquemontii Decne*.	Tannins, carotenoids, polyphenols	Apigenin, Dimethyl ellagic acid, Quercetin rhamnoside, Quercetin hexoside, Kaempferol rhamnoside	Kumar *et al.* 2016
35	*Murraya koennigii* L.	Flavonoids, phenolics, organic acid	Chlorogenic acid, Catechin, Rutin, Myricetin	Aroor *et al.* 2023
36	*Elaeagnus umbellate* Thunb.	Polyphenols, organic acids, monoterpenes,	Limonene, phellandrene, sabinene, terpinene, terpinolene citric, malic, oxalix, quinic, succinic, and tartaric	Gamba *et al.* 2020
37	*Brassica juncea* L.	Phenolic acids, flavonoids and glucosinolates, carotenoids	Sinigrin, Glucoiberin, progoitrin, glucoraphanin, gluconapin, 4-hydroxyglucobrassicin, glucoerucin, glucobrassicin, 4-methoxyglucobrassicin, gluconasturtiin, and neoglucobrassicin, β-carotene, lutein, violaxanthin, and neoxanthin	Frazie *et al.* 2017
38	*Chenopodium album L.*	Flavonoids	Kaempferol, kaempferol 3-O-βglucoside, kaempferol 3-O-β-diglucoside, kaempferol-3-Oarabinoglucoside, quercetin, quercetin 3-O-xylosylglucoside, and quercetin-3- O rhamnoglucoside	Poonia and Upadhayay, 2015
39	*Momordica dioica* Roxb.	Alkaloids, steroids, triterpenoids, saponins	Momordicin, lectins, β-sitosterol, saponin glycosides, ursolic acid, hederagenin, oleanolic acid, α-spinasterol, stearic acid, gypsogenin, momodicaursenol, 3β-o-benzoyl11-oxo-ursolic acid, 3β-o-benzoyl-6-oxo-ursolic acid, and 3o-β-D-glucuronopyranosyl gypsogenin	Talukdar and Hossain, 2014
40	*Colocasia esculenta* (L.) Schott	Polyphenols, polysaccharides	1-O-feruloylD-glucoside, 3, 5-DiCQ acid, vitexin, isovitexin, cyanidin-3-glucoside, luteolin-7-O-rutinoside, vicenin-2; caffeic acid, cyanidin-3-rhamnoside, chlorogenic acid, quercetin and hyperoside, Tarin, taro-4-l polysaccharide, taro polysaccharides 1 and 2 (TPS-1/TPS-2), A-1/B-2 α-amylase inhibitors, monogalactosyldiacylglycerols (MGDGs), and digalactosyldiacylglycerols (DGDGs)	Ribeiro *et al.* 2020
41	*Cornus capitata* Wall. ex Roxb.	Anthocyanin, flavonoid, phenolic acid, triterpenoid	NR	Badoni *et al.* 2024
42	*Diospyros lotus* L.	Polyphenols, flavonoids	Gallic acid, Catechin, Epicatechin Chlorogenic, Vanillic acid, Caffeic acid, Syringic, p-coumaric acid, Ferulic acid, Salicylic acid, sinapic acid, Quercetin-3-glucoside, Protocatechuic acid, Myricetin, 3,4-dihydroxybenzoic acid, Quercetin, 4-hydroxybenzoic acid, Salicylic acid, and Resveratrol	Hassan *et al.* 2022
43	*Physalis peruviana* L.	Phenolic acids, flavones, flavonols, flavanones, orthodipheols, anthocyanins	Campesterol, β-sitosterol, Stigmasterol	Puente *et al.* 2010
44	*Pinus gerardiana* Wall. ex D.Don	Phenolic acid, Phytosterol	Lycopene, Catechin, Oleic acid, Campesterol, Oleic acid, Gallocatechin, Linolenic acid, β-sitosterol	Singh *et al.* 2021
45	*Punica granatum* L.	Flavonoids, phenolic acids, ellagitannins, gallotannins	Apigenin, Tricetin, Luteolin, Kaempferol, Quercetin, Myricetin, Gallic acid, Ellagic acid, Ellagic acid pentoside, Ellagic acid-arabinoside, Ellagic acid rhamnoside, Brevifolincarboxylic acid, p- coumaric acid, Galloyl-HHDP-glucoside, Digalloyl-glucoside	Yisimayili and Chao, 2022
46	*Prunus mira* Koehne.	Flavonoids	NR	Ying *et al.* 2019
47	*Solanum nigrum* L.	Polyphenols, alkaloid	4 steroidal alkaloid glycosides, Solamargine, Solasonine, α and β- solanigrine	Wang et al., 2017
48	*Olea ferruginea* Royle	Polyphenols, quinones, flavonoids, Catechins, coumarins, terpenoids	NR	Bachheti *et al.* 2014
49	*Flacourtia indica* (*Burm. f.) Merr*.	Organic acid, flavonoids	Caffeic acid, ferulic acid and p-coumaric acid	Ndhala *et al.* 2007

50	*Achyranthes aspera* L.	Alkaloids, saponins, tannins, flavonoids, glycosides, steroids, Phenolic acids	27-cyclohexyheptacosan-7-ol, 16-hydroxy-26-methyl heptacosan-2-one, 17-pentatriacontanol, Isobetanin and betanin, eupatorin, chrysin, quercetin and kaempferol, 6-prenyl apigenin, bisdesmosidic saponin, sapogenin, β-sitosterol and spinasterol, gallic acid, vanillic acid, ferulic acid, isoferulic acid, protocatechuic acid, syringic acid, salicylic acid, gentisic acid, p-coumaric acid, trans-cinnamic acid, p-hydroxybenzoic acid, chlorogenic acid, sinapic acid and caffeic acid	Raju *et al.* 2022
51	*Elaeagnus latifolia* L.	Terpenoids, Triterpenoids, Anthraquinones	NR	Bachheti *et al.* 2014
52	*Bombax ceiba* L.	Flavonoids, alkaloids, phenolic acid, xanthones	Kaempferol, isorhamnetin, quercetin, and herbacetin Scopolamine, protocatechuic acid, esculetin, isomangiferin, mangiferin, isovitexin, vitexin, rutin, chlorogenic acid, methyl chlorogenate, vanillic acid, quercetin, fraxetin, palmitic acid, ethyl palmitate, β-sitosterol	Yasien *et al.* 2022
53	*Agave americana* Linn.	Phenols, flavonoids, phytosterols, and saponins	Quercetin, isorhamnetin, kaempferol, glycosylated derivates ellagic acid glycoside, Apigenin, p-coumaric acid, puerarin, Cantala-saponin-1	Bermúdez-Bazán *et al.* 2021
54	*Asparagus filicinus* Buch.-Ham.ex D.Don	Saponins and flavonoids	Filicinin A and B, Filiasparoside A and B, Aspafilioside C, Aspafilisine, kaempferol, quercetin, and rutin	Sobhy *et al.* 2022
55	*Dioscorea bulbifera* Linn.	Naphthofurans, Flavonoids, Steroids and steroid derivative	Diosbulbin, Daucosterol, β-sitosterol, Kaempferol-3,5-dimethylether, Caryatin, Myricetin, Kaempferol, Diosgenin, Quercetin, Stigmasterol, Pennogenin	Kundu *et al.* 2021
56	*Urtica dioica* L.	Flavonoids, Phenolic acids	Amentoflavone, apiin, apigenin, apigenin 7-O-*b*-D-glucoside, baicalin, baicalein, catechin, epicatechin, epigallocatechin gallate, chrysoeriol, genestein, isorhamnetin, kaempferol, keampferol 3-O-*b*-D-glucoside, luteolin, luteolin 7-O-*b*-D-glucoside, myrecetin, naringenin, quercetin, quercetin 3-O-*b*-D-glucoside, quercetin 3-O-*b*-D-galactoside, rutin, vitexin, Gallic acid, vanillic acid, syringic acid, protocatechuic acid, gentisic acid, Cinnamic acid, caffeic acid, p-coumaric acid, ferulic acid, chlorogenic acid, sinapic acid	Devkota *et al.* 2022
57	*Bauhinia purpurea* L.	Flavonoids and phenolic compounds	Flavone glycosides, dimeric flavonoids, 6-butyl-3-hydroxy flavanone, amino acids, phenyl fatty ester, lutine and β-sitosterol, B. purpurea lectin (in seeds)	Negi *et al.* 2012
58	*Boerhavia diffusa* L.	Tannins, flavonoids, alkaloids, glycosides, steroids, terpenoids, phenolic compounds	Quercetin 3-O-(2″-rhamnosyl)-robinobioside D-pinitol, fructofuranose, β-d-glucopyranose,	Juneja *et al.* 2020
59	*Polygonum aviculare* L.	Flavonol glucuronides	Myricetin 3-O-β-D-glucuronide, quercetin 3-O-β-D-glucuronide, isorhamnetin 3-O-β-D-glucuronide and kaempferol 3-O-βD-glucuronide	Granica *et al.* 2013
60	*Pueraria tuberosa* DC.	Alkaloids, carbohydrates, steroids, glycosides, tannins, terpenoids, flavonoids, coumarins and anthocyanidins	Puerarin, daidzein, genistein, phytosterols (β-sitosterol, stigmasterol, p-coumaric acid, arachidonic acid, eicosanoic acid, hexadecanoic acid, tetracosanoid acid,	Maji *et al.* 2014
61	*Antidesma montanum* Blume	Tannins, polyphenols, flavonoids, saponins and steroid glycosides	9-octadecenoic acid, n-hexadecanoic acid, and 9,12-octadecadienoic acid, carpusin, geraniin, antidesmin A, lupeolactone	Ismail *et al.* 2019
62	*Costus speciosus* (Koen ex. Retz) Sm.	Alkaloids, glycosides, steroids, phenolics, flavonoids, tannins, terpenoids, and saponins	Curcumin, curcuminoids, aliphatic hydroxyl ketones, triterpenes, starch mucilage, oxa-acid, fatty acid, abscisic acid, corticosteroids, tigogenin	Maji *et al.* 2020
63	*Phytolacca sp.*	Saponin, flavones, phytosterols	Esculentosides, phytolaccosides, cochliophilin A and α-spinasterol	Bailly, 2021
64	*Arisaema speciosum* Mart.	NR	NR	
65	*Chaerophyllum villosum* Wall. Ex DC.	Phenolic compounds, monoterpenes	Carvacrol methyl ether, thymol methyl ether, myristicin, γ-terpinene, p-cymene	Joshi, 2013

66	*Dioscorea glabra* Roxb.	Steroidal saponins, flavonoid, polyphenols, allantoin	Rutin, quercetin	Wang *et al.* 2023
67	*Typhonium diversifolium* Wall. Ex Schott	NR	NR	
68	*Allium cepa* var. proliferum	Flavonoid, organosulfur compounds, polyphenols and organic acids	Kuwanon K, ferulic acid, rhamnazin, leucopelargonidin and xanthomicrol	Zhou *et al.* 2020
69	*Celosia argentea* L.	Phenols, flavonoids, anthocyanins, diterpenes, saponins, cyclic-peptides, phenols, tannins	Isoflavones, latlancuayin, lutin, epigallocatechin, gallic acid, caffeic acid, rosmarinic acid, quercetin, triterpenoid saponins (celosin A-G, celosin I-II and celosin H-J, cristatain), Cycpeptide (morodin, celogentin A –K and celogenamide A)	Thorat, 2018
70	*Malva sylvestris* Linn.	Flavonoids, terpenoid, phenols, coumarin	Gossypetin 3-sulphate-8-O-β-$_D$-glucoside (gossypin), hypolaetin 3′-sulphate, 3-O--dglucopyranosyl-8-O-β-$_D$-glucuronopyranoside, hypolaetin 4′-methyl ether 8-O-β-$_D$-glucuronopyranoside, hypolaetin 8-O-β-$_D$-glucuronopyranoside, isoscutellarein 8-O-β-$_D$-glucuronopyranoside, malvone, 4-hydroxybenzoicacid, 4-methoxybenzoicacid, 4-hydroxy-3-methoxybenzoicacid, 2-hydroxybenzoic acid, 4-hydroxy-2-methoxybenzoic acid, 4-hydroxybenzyl alcohol, 4-hydroxydihydrocinnamic acid, 4-hydroxy-3methoxydihydrocinnamic acid, 4-hydroxycinnamic acid, ferulic acid, tyrosol, 7-hydroxy-6methoxycoumarin (scopoletin) and 5,7dimethoxycoumarin	Gasparetto, 2012
71	*Nasturtium officinale* R. Br.	Alkaloids, flavonoids, saponins, terpenoids/steroids, glycosides, tannins, glucosinolates	Gluconasturtin, gallic acid derivative, ferrullic acid derivative, proanthocynidin B1, p-coumaric acid derivative, apigenin, phydroxybenzoic acid, sinapic acid, p-coumaric acid, caftaric acid, quercetin-3- (cafferoyldiglucoside)-7glucoside, kaempferol-3-(caffeoyl diglucoside)- 7-rhamnoside, caffeoylmalic acid, coumaric acid derivative, β-carotene, 2-phenylethyl isothiocyanate, 4-phenylbutyl isothiocyanate, pulegone, sec-butyl isothiocyanate	Al-Snafi, 2020
72	*Orobanche alba* steph.	Terpenoids, organic acids and their derivatives	Linalool, geraniol, nerol, (Z)-iso-citral, geranylacetate, neral, neryl acetate, p-menthone, Pinocamphone, limonene, γ-terpinene, p-cymene, 1,8-cineol, α-copaene, Isobornyl-2-methyl-butyrate, δ-cadinene, Trans-caryophyllene, β-bourbonene, Caryophyllene oxide, Manool, Linoleic acid, Linolenic acid, Hexadecanoic acid, Palmitic acid, Myristic acid,	Shi *et al.* 2020
73	*Polygonum alpinum* All.	Flavonoids	Quercetin 3-*O*-arabinofuranoside, quercetin 3-*O*-β-glucuronopyranoside, quercetin 3-*O*-a-rhamnopyranosyl (1→6)-b-glucopyranoside, quercetin 3-*O*-β-galacturonopyranoside, quercetin 3-*O*-β-glucopyranoside, kaempferol 3-*O*-b-galactopyranoside, quercetin 3-*O*-β-galactopyranoside, and myricetin 3-*O*-β-galactopyranoside	Demirezer *et al.* 2006
74	*Taraxacum officinale* Weber	carotenoids; flavonoids, phenolic acids, sesquiterpene lactones, sterols, triterpenes	Quercetin, chrysoeriol, luteolin-7-glucoside, cafeic acid, chlorogenic acid, chicoric acid, taraxinic acid, taraxacoside, 11β,13-dihydrolactucin, ixerin D, taraxacolide-O-β-glucopyranoside, taraxasterol, β-sitosterol, stigmasterol, α-amyrin	Napoli and Zucchetti, 2021
75	*Amaranthus retroflexus* L.	Flavonoids, alkaloids, sesquiterpenes, phenolic acids, *O*-prenylated phenylpropanoids	Rutin and quercetin, amaranthine, ferulic acid, umbelliferone apigenin, boropinic acid, 4 -geranyloxyferulic acid (GOFA), 7-isopentenyloxycoumarin, auraptene, and umbelliprenin	Fiorito *et al.* 2017
76	*Amaranthus spinosus* Linn.	Betalains, hydroxycinnamates, saponins, steroids and flavonoids	Rutin, quercetin, amaranthine, isoamaranthine, hydroxycinnamates, quercetin and kaempferol glycosides, 7-p-coumaroyl, apigenin, 4-O-β-D-glucopyranoside, α-xylofuranosyl uracil, β-D-ribofuranosyl adenine and β-sitosterol glucoside	Tanmoy *et al.* 2014
77	*Angelica glauco* Edgew.	Terpene hydrocarbons, coumarins, phthalides	α-phellandrene, β-pinene, thujene, β-caryophyllene, γ-terpinene, β-bisabolene, germacrene D, trans-carveol, β-caryophyllene oxide, nerolidol, decursin, decursinol angelate, bergapten, phthalides ((*E*)- and (*Z*)-ligustilides, (*Z*)-butylidene phthalide	Kumar *et al.* 2022

78	*Commelina benghalensis* Linn.	Polyphenols, flavonoids, tannins, and alkaloids	Salicylic acid, p-coumaric acid, 8-hydroxyquinoline, caffeic acid, quinolones, catechol, resorcinol, tannic acid, chlorogenic acid n-octacosanol, n-triocotanol, stigmasterol, campesterol, hydrocyanic acid, beta-sitosterol and campesterol	Ghosh *et al.* 2019
79	*Medicago sativa* Linn.	Saponins, flavonoids	Triterpenic pentacyclic glycosides, zanhic acid, medicagenic acid, glucuronic acid, glycosides apigenin, luteolin, chrysoeriol, tricin and methyltricetin, medicarpin, melilotocarpan E, isoflavane millepurpan	Rafińska *et al.* 2017
80	*Polygonum aviculare* Linn.	Flavonoids	Quinic acid, quercitrin, myricetin, epicatechin, ellagic acid, kaempferol, iso-rhamnetin	Pawłowska *et al.* 2023
81	*Solanum nigrum* Linn.	Alkaloids, flavonoids, tannins, saponins, glycosides, coumarins, phytosterols	Solamargine, Solasonine, α and β- solanigrine, tigogenin, solasodine, solanine, sapogenin, diosgenin, tigogenin, solanidin, uttronin A, uttroside-A	Saleem *et al.* 2009
82	*Saussurea gossypiphora* D.Don.	Steroids, tannins, flavonoids, phenolics, saponins	Apigenin and luteolin	Mishra *et al.* 2021
83	*Capparis spinosa* L.	Flavonoid, polyphenol, alkaloids	Leaves: Rutin and quercertin Fruit: Capparine A, capparine B, flazin, guanosine, 1H-indole-3-carboxaldehyde, 4-hydroxy-1H-indole-3-carboxaldehyde, apigenin, kaempferol, thevetiaflavone, capparisine A, capparisine B, capparisine C, Tetrahydroquinoline acid	Zhang and Ma 2018
84	*Chenopodium Foliosum* Asch.	Phenolic compounds, monoterpenoid, sesquiterpenoids	Limonene, α-terpinene, γ-isomer, p-cymene, Carvacrol, thymol, α-pinene, camphor, β-caryophyllene	Kokanova-Nedialkova *et al.* 2009
85	*Sedum ewersii* Ledeb.	NR	NR	
86	*Polygonum chinensis* L.	Flavonoids, anthraquinones, phenylpropanoids, proanthocyanidines, coumarin, phenolic compound	1,2-benzenedicarboxylic acid, squalene, mono(2-ethylhexyl) ester, 8-methyloctahydrocoumarin	Ezhilan and Neelamegam, 2012
87	*Allium prezewalskianum* Regel.	NR	NR	
88	*Artemisia brevifolia* Wall. ex DC.	Phenolic acids, flavonoids c	chlorogenic acid, caffeic acid, coumaric acid, catechin and picein	Nataraj *et al.* 2022
89	*Mentha longifolia* (L.) Huds.	Flavonoids, ester flavonoid, phenol, monoterpene, terpenoid	Apigenin-7-o-glucoside, Luteolin 7-o-glucoside, Isoorientin Eriodictyol-7-rutinoside, Rosmarinic acid, Tricetin 3′-o-glucoside 5′-o-rhamnoside, Carvone, 1,8- cineole, Pulegone, Menthol, Menthone, Piperitenone oxide, Sabinene	Farzaei *et al.* 2017
90	*Hippohae rhamnoides* L.	Phenolics, flavonols glycosides	Aglycones quercetin, Isorhamnetin, Myricetin, Kaempferol, I-3-O-glucoside-7-O-rhamnoside, I-3-O-rutinoside, I-3-O-β-sophoroside-7-O-α-rhamnoside, I-3-Oglucoside, Q-3-O-glucoside, Q-3-Orutinoside, Q-3-O-sophoroside-7-O-rhamnoside	Wani *et al.* 2016
91	*Carum carvi* L.	Flavonoids	Carvacrol, Carvone, α-pinene, limonene, γ-terpinene, linalool, carvenone, and p-cymene	Sachan *et al.* 2016
92	*Chenopodium botrys* L.	Terpenes	Camphor, δ-3-carene, fenchone, linalool, menthone, nerol, β-pinene, pulegone, terpineol-4 and thujone) and sesquiterpenes (β-elemene, elemol and β-eudesmol)	Morteza, 2015
93	*Arnebi euchroma* (Royle ex Benth.) I.M.Johnst. A	Naphthoquinone, purpurin	Shikonin, alkannin, shikometabolin H, epoxyarnebinol, and iso-hexyl-naphthopurpurin	Chawla, 2021
94	*Crepis tectorum* L.	NR	NR	
95	*Fagopyrium esculentum Moench*	Flavonoids, phenolic compounds, fagopyritols, triterpenoids,	Rutin, quercetin, orientin, vitexin, isovitexin, isoorientin, (′)-Epicatechin, (′)-epicatechin-3-O-p-hydroxybenzoate, (′)-epicatechin-3-O-(3,4-di-Omethyl)-gallate, (+)-catechin-7-O-glucoside, phenylpropanoids, olean-12-en-3-ol, urs-12-an-3-ol	Jing *et al.* 2016

96	*Rheum emodi* Wall	Anthraquinone	1,8-dihydroxyanthraquinones, rhein, aloe emodin, emodin, emodin glucosides, chrysophanol glucosides, Sulfemodin 8 O Glucoside, chrysophanol and physcion, Revandchinone 1, 2,3,4	Zargar *et al.* 2011
97	*Lactuca sativa* L.	Organic acids, alkaloids, terpenoids, phenolic compounds	Hydroxybenzoic, hydroxycinnamic acid, glycosylated quercetin, luteolin, lactucin, apigenin	Yang *et al.* 2018
98	*Raphanus sp.*	NR	NR	
99	*Lactuca dolichophylla* Kitam.	NR	NR	
100	*Oxyria digyna* (L.) Hill	Flavonol	5, 7, 3′-trihydroxy-4-methoxyflavanone-7-O-(2»-O-beta -D-glucopyranosyl)-alpha -L-rhamnopyranoside and 5, 7, 2′, 3′, 4′-pentahydroxyflavone-8-C-glucopyranoside, Vitexin, Orientin, Hesperidin, Quercetin-3-O-beta-D-glucopyranoside and Stigmasterol	Ahmad *et al.* 2022

revenue through the cultivation of cash crops have resulted in a significant reduction in the utilization of WEPs, rather than the inclination (Thakur *et al.,* 2017). Upon survey, it was observed that locals were more inclined towards the sale of the WEPs for hard cash instead of consuming themselves, similar to the observation of Thakur *et al.* 2017; Chacha *et al.* 2022. From a scientific standpoint of view, the lack of *ex-situ* conservation, domestication strategies, and management practices would endanger the continued availability of WEPs. However, there is an urgent need to promote the domestication of underutilized WEPs owing to several benefits they offer, namely reduced carbon footprint in their production owing to lower fertilizer inputs, climate and pest resilience, multiutility use of single crop as food, fodder, fibre, and fuel.

Strategies for Introducing WEPs into Mainstream Agriculture

Although there is very limited knowledge of the conservation strategies for WEPs, efforts are being made towards their domestication to bring more diversity to our diet. Some potential strategies for domestication could be (i) captive cultivation of endangered WEPs and reintroducing them in natural populations, (ii) intercropping with cash crops, (iii) identification of soil microorganisms that promote WEP's growth and introducing them in their domestication, (iv) introducing drought resilient WEPs in degraded and dry lands and other novel environments, (v) use of new generation techniques such as high throughput phenomics, next generation sequencing, genome-wide association studies (GWAS), interactome big data analysis and machine learning for understanding the behaviour of WEPs under stress environments and utilizing the data for domestication process (Krug *et al.,* 2023).

Conclusion

The present work reiterates the importance of WEPs in bringing dietary diversity to humans. Dependence on fewer number of crops have resulted in significant volatility in crop yields impacting economies on a global scale. In addition, the high environmental footprints and vulnerability to pest and pathogenic attacks make these crops unsustainable for the future. Underutilized WEPs can offer a sustainable alternative to these crops and NWHR possess a great diversity of WEPs. In the present study, nearly 100 WEPs were identified and characterized for their consumption pattern season-wise in the NWHR. Green leafy vegetables and fruits were the predominant forms of WEP consumption. The health benefits derived from these WEPs are discussed through their phytochemical composition, polyphenols and terpenoids were the predominant class of molecules present across the groups responsible for their bioactive properties. The WEP consumption and environmental conditions such as that of cold desert regions are highly correlated. There is an urgent need for devising strategies to domesticate these WEPs. Use of novel technologies such as high throughput phenomics, next generation sequencing, genome wide association studies (GWAS), interactome big data analysis and machine learning would augment the conservation strategies for these unique WEPs. Introduction of underutilized genetic resources such as WEPs would enhance the regional food security and improve the health and well-being of the population.

Acknowledgments

The authors thank the Department of Science and Technology for funding under the Science and Heritage Research Initiative (SHRI) vide DST/TDT/SHRI-11/2021 (G).

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.03

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Genotypic Screening and Seed Treatment Studies for Improving Seed Germination and Vigor in Quinoa

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Abstract

Quinoa (*Chenopodium quinoa* Willd) - a potential pseudocereal native to the Andean region of South America is known as "mother grain" as it is rich source of high-quality proteins, lipids, minerals and vitamins. The germplasm lines of quinoa available with Punjab Agricultural University (PAU), Ludhiana, possessed a low germination percentage under laboratory and field conditions. The present study was aimed to screen 50 promising genotypes of quinoa for germination parameters, i.e., germination percentage, seedling vigor index (SVI) I and II, mean germination time and speed of germination using "between-paper" method under controlled conditions in the laboratory. One genotype, namely EC-896071, recorded the highest germination, i.e., 83.8%, followed by genotype EC-896076, which had 70.5% germination. Other genotypes which exhibited germination higher than 40% were EC-896063 (53.3%), EC-896081 (53%), EC-507739 (43.8%) and EC-896091 (42.5%). The above-mentioned six quinoa genotypes *viz.,* EC-507739, EC-896063, EC-896071, EC-896076, EC-896081 and EC-896091 were selected for seed treatment studies in order to enhance the germination and seedling vigor. Hydropriming for 2 hours recorded the highest improvement in mean germination time, speed of germination, germination percentage, SVI I and II and this time duration was standardized for other seed treatments also. Seeds were also primed with different chemicals *viz*., magnesium nitrate (0.5%), potassium nitrate (0.5%), potassium dihydrogen phosphate (0.5%), zinc sulfate (0.5%), kinetin (5 ppm); and scarified with 5% H_2SO_4 for 10 minutes and hot water (35°C) for 15 minutes. A comparison of hydropriming with all other treatments revealed that hydropriming for 2 hours is the best treatment for improving germination and seedling vigor of quinoa genotypes.

Keywords: Germination, Quinoa, Seed priming , Seed scarification, Vigor.

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Received: 26/02/2024 **Revised:** 18/07/2024

Accepted: 22/07/2024

How to cite this article: Singh R, N Kaur, G Khosla, S Sharma and RK Gill (2024) Genotypic Screening and Seed Treatment Studies for Improving Seed Germination and Vigor in Quinoa. *Indian J. Plant Genet. Resour.* 37(3): 425-432. **DOI:** 10.61949/0976-1926.2024.v37i03.03

Introduction

Chenopodium quinoa Willd., commonly known as quinoa, is a tetraploid traditional crop domesticated by the Incas and Indian cultures in the Altiplano region of the Andes in South America, dating 5000 to 3000 BC. Throughout the history of the Inca civilization, quinoa was considered to be a sacred food. During the Incas (pre-Columbian America), armies were fed a mixture of quinoa and fat, which was known as "war balls" due to their high nutritional value (Graf *et al*., 2015). Quinoa is an annual herbaceous plant belonging to the Amaranthaceae family. It is a pseudocereal crop, not a true cereal grain, as it is a dicotyledonous plant, while cereals are monocotyledonous. In quinoa seeds, reserve food is stored in a large central perisperm, one to two-cell layered endosperm and peripheral embryo (Prego *et al*., 1998). Quinoa seeds have a high nutritive value than most cereal grains and contain high content of essential amino acids such as lysine and high-quality proteins along with fats, carbohydrates, minerals and vitamins, and are free of gluten (Bhargava *et al*., 2006; Melini and Melini, 2021). The production of gluten-free foods from pseudocereals holds significance for individuals with celiac disease, ensuring a nutrient-rich diet (Villaluenga *et al.,* 2020). Quinoa also gained importance

in agriculture because of its huge genetic variability and its ability to tolerate predominant adverse environmental factors *viz.* soil salinity, frost, drought, or marginal soils (Hinojosa *et al.,* 2018; Stoleru *et al.,* 2019).

According to the Food and Agricultural Organization (FAO) of the United Nations, quinoa has an ideal balance of amino acids than any other grain. Quinoa has been integrated into the diet of astronauts by the National Aeronautics and Space Administration (NASA). It has emerged as a new potential crop for NASA's Controlled Ecological Life Support System (CELSS) due to the balanced and unique amino acid composition of this miracle grain (Sharma *et al*., 2021). Apart from beneficial components, quinoa grains also contain some anti-nutritional factors such as saponins, tannins, phytic acid and trypsin inhibitors. The saponins that cause bitterness are present in the outer layer, i.e., the pericarp of the seed, which can be removed through de-hulling, polishing and washing of the seed (Melini and Melini, 2021).

Quinoa seeds have porosity in the integuments, which enables them to easily gain or lose moisture from the environment, leading to loss of viability. Storage of quinoa seeds for longer duration under ambient conditions has been reported to increase the deterioration of seeds (Strenske *et al*., 2017). Seed priming is a pre-sowing soaking treatment to fasten the imbibition of water and start pre-germinative metabolic processes, consequently reducing the mean germination time and improving the germination percentage (Lutts *et al*., 2016). Seed hydropriming refers to controlled hydration, leading seeds to a physiologically active state by activating their metabolic processes partially without initiating actual seed emergence. Hydropriming treatment gets the seed into the first germination phase, in which metabolic activities are initiated (Pill and Necker, 2001). Other priming treatments include halopriming, osmopriming, hormopriming, nutripriming, *etc*.

Chenopodium quinoa germplasm, available with the Department of Plant Breeding and Genetics, PAU, Ludhiana, was observed to possess a low germination percentage. Therefore, present study was undertaken to screen the quinoa genotypes to identify genotypes having higher germination and optimum seedling vigor. Selected genotypes were also subjected to hydropriming and other seed treatments for improving their germination and early seedling growth.

Material and Method

Laboratory experiments were conducted in the Seed Physiology Laboratory, Office of Director (Seeds), Punjab Agricultural University, Ludhiana, Punjab, during 2022-2023. Fresh seeds of 50 genotypes acquired by Punjab Agricultural University, Ludhiana, from Regional Research Station, NBPGR, Shimla, were used in present study and their origin is given in Table 1. The seeds were stored at 4°C before evaluating them for seed quality parameters. These 50 quinoa genotypes were screened for germination parameters, *i.e.,* germination percentage, seedling length (cm), fresh weight of seedlings (g), seedling vigor index (SVI) I and seedling vigor index II. One hundred seeds of each genotype per replication were evaluated for germination using the between-paper method at a constant temperature of 20°C in a BOD incubator. On 7^{th} day, the final count was recorded and seedling length (root and shoot length) was measured using a centimeter scale. Fresh weight of 10 seedlings was measured using an electronic balance. Six best-performing genotypes were subjected to hydropriming for different durations for the selection of best hydropriming duration. The seeds were also primed with different chemicals *viz.*, magnesium nitrate (0.5%), potassium nitrate (0.5%), potassium dihydrogen phosphate (0.5%), zinc sulphate (0.5%), kinetin (5 ppm); and scarified with 5% H_2SO_4 for 10 minutes and hot water (35°C) for 15 minutes in order to improve their germination (%), SVI I and II. Data on the following observations were recorded:

Germination (%)= The seeds germinated during the germination period were counted and the total number of seeds germinated was divided by the total number of seeds sown and the result was expressed in percentage.

SVI I was calculated by using the following formula proposed by Abdul-Baki and Anderson (1973):

SVI I = Germination (%) x average seedling length (cm)

SVI II was calculated using the following formula proposed by Huang *et al*.(2018):

SVI II = germination (%) x fresh weight of 10 seedlings (g)

Mean germination time (MGT) of the quinoa genotypes was calculated using the following equation suggested by Ellis and Roberts (1981):

$$MGT = \Sigma(D \times N)/\Sigma N$$

Where N is the number of seeds germinating on that particular day, counted from the beginning of germination and represented by D.

The summation of the ratios resulted by dividing the daily count of the seeds germinated to the number of days to germinate was used to calculate the speed of germination (AOSA,1983):

Speed of germination = (g1/d1) +(g2/d2) +…+ (gn/dn)

Where g1, g2….gn are the number of newly germinated seeds on 1, 2… nth day respectively. d1, d2…dn refer to 1, 2… n^{th} day, respectively.

Alpha(α)-amylase activity of the quinoa seeds was measured following the 3,5-dinitro-salicylic acid method

(Murata *et al*., 1968). Quinoa seeds (0.1 g) were mixed with 2 mL of phosphate buffer and left at 4°C for 1-hour. After homogenization using mortar and pestle, contents were centrifuged at 10000 rpm for 15 minutes. The supernatant was taken and used for estimation of α-amylase activity. The supernatant (0.1 mL) was taken into the test tube. 0.5 mL of 1% starch was added into a test tube and incubated at room temperature for 15 minutes. After that, added 1-mL of DNS reagent to each test tube and kept in a water bath for 5 minutes at 100°C. The reaction was stopped by adding 0.5 mL of 40% potassium-sodium tartrate solution. Cooled the test tubes and then added 2.5 mL of distilled water. Absorbance was noted at 560 nm using a spectrophotometer (Systronics UV-VIS Spectrophotometer 117).

Statistical Analysis

The experiment was laid out in a completely randomized design (CRD) with four replications per genotype and critical difference values were calculated by analysis of variance (ANOVA) and Tukey's b test was applied to further analyze the differences using Minitab Software version 17.

Result and Discussion

Germination and SVI

The performance of 50 genotypes based on germination percentage is summarised in Figure 1. There were significant differences in germination percentage among various quinoa genotypes. There was only one genotype namely EC-896071 which exhibited germination higher than 80%. Likewise, there was only one genotype EC 896076, which exhibited germination higher than 70%. Four genotypes, namely EC-896063, EC-896081, EC-507739, EC-896091 had germination in the range of 40 to 60%. Most of the genotypes (32) exhibited germination in the range of 20 to 40% and 12 genotypes had germination lesser than 20%. SVI I of quinoa genotypes varied widely between 116 and 1239.8 (Figure 2). EC-896071 genotype exhibited SVI I higher than 1200 followed by the genotype EC-896076, which had SVI I higher than 900, which may be attributed to their higher germination percentage (83.8 and 70.5%, respectively) and longer seedlings (14.8 cm). Four genotypes, namely EC-896063, EC-896081, EC-507739 and EC-896110, had SVI 1 between 600 and 900. Likewise, both of the above-mentioned genotypes, EC-896071 (20.36) and EC-896076 (15.24) exhibited higher values of SVI II in the range of 15-25 (Figure 3). Five genotypes, namely EC-896063, EC-896091, EC-896081, EC-507739 and EC-896089, had seedling vigor index II in the range of 10 to 15. Chaganti and Ganjegunte (2022) observed that germination varied among the tested quinoa genotypes from 72.2 to 94.4%. Manugade *et al*. (2023) observed that SVI I varied among the tested quinoa genotypes from 634.14 to 1088.

Mean germination time (MGT) of various quinoa

Table 1: Origin of 50 quinoa genotypes used in the study

S. No	*Genotype*	*Origin*
1	IC-411824	Jammu & Kashmir, India
2	IC-411825	Jammu & Kashmir, India
3	EC-507738	United States of America (USA)
4	EC-507739	United States of America (USA)
5	EC-507741	United States of America (USA)
6	EC-507742	United States of America (USA)
7	EC-507743	United States of America (USA)
8	EC-507744	United States of America (USA)
9	EC-507746	United States of America (USA)
10	EC-507747	United States of America (USA)
11	EC-507748	United States of America (USA)
12	EC-507749	United States of America (USA)
13	EC-507767	United States of America (USA)
14	EC-896060	United States of America (USA)
15	EC-896061	United States of America (USA)
16	EC-896062	United States of America (USA)
17	EC-896063	United States of America (USA)
18	EC-896064	United States of America (USA)
19	EC-896069	United States of America (USA)
20	EC-896071	United States of America (USA)
21	EC-896072	United States of America (USA)
22	EC-896076	United States of America (USA)
23	EC-896077	United States of America (USA)
24	EC-896078	United States of America (USA)
25	EC-896079	United States of America (USA)
26	EC-896081	United States of America (USA)
27	EC-896085	United States of America (USA)
28	EC-896088	United States of America (USA)
29	EC-896089	United States of America (USA)
30	EC-896091	United States of America (USA)
31	EC-896094	United States of America (USA)
32	EC-896095	United States of America (USA)
33	EC-896097	United States of America (USA)
34	EC-896098	United States of America (USA)
35	EC-896099	United States of America (USA)
36	EC-896105	United States of America (USA)
37	EC-896109	United States of America (USA)
38	EC-896110	United States of America (USA)
39	EC-896111	United States of America (USA)
40	EC-896114	United States of America (USA)
41	EC-896115	United States of America (USA)
42	EC-896201	United States of America (USA)
43	EC-896203	United States of America (USA)
44	EC-896208	United States of America (USA)

45	EC-896210	United States of America (USA)
46	EC-896211	United States of America (USA)
47	EC-896213	United States of America (USA)
48	EC-896246	United States of America (USA)
49	EC-896275	United States of America (USA)
50	EC-896276	United States of America (USA)

genotypes ranged between 1.04 and 2.52. EC-896276 genotype recorded the lowest mean germination time followed by genotypes EC-896071 and EC-896203, respectively (Figure 4). The germination speed of various quinoa genotypes ranged between 3.33 and 24.17. EC-896071 genotype had the fastest speed of germination followed by genotypes EC-896201 and EC-896203, respectively (Figure 5). Parsons (2012) reported that seed germination in the Amaranthaceae family starts in less than 24 hours; the majority of seeds start germinating in less than 2 hours after imbibition in quinoa. Another study reported that seeds germinate rapidly, leading to radicle protrusion in 6 to 10 hours after the imbibition in quinoa (Makinen *et al*., 2014).

Seed Treatments

Based on germination parameters, six quinoa genotypes, namely, EC-507739, EC-896063, EC-896071, EC-896076, EC-896081 and EC-896091, were selected for undertaking hydropriming and other seed treatment studies. Mean germination time of quinoa genotypes recorded the lowest value when hydroprimed for 2 hours. Quinoa genotypes also recorded the highest germination speed when hydro primed for 2 hours. The interaction effect between genotypes and priming treatments was non-significant with reference to mean germination time and speed of germination (Table 2). In five quinoa genotypes *viz*., EC-507739, EC-896063, EC-896076, EC-896081 and EC-896091, hydropriming for 2 hours resulted in the highest enhancement in germination percentage. Only in one genotype, namely EC-896071, the highest enhancement in germination percentage was recorded due to 8 hours hydropriming, which was, however, statistically at par to control, 2 and 4 hours hydropriming. Like germination, SVI I and SVI II of the tested six genotypes recorded the highest increment due to 2 hours hydropriming (Table 3). From this study, 2 hours soaking of seed was kept as the standardized duration for other seed treatment studies *viz*., magnesium nitrate (0.5%), potassium nitrate (0.5%), potassium dihydrogen phosphate (0.5%), zinc sulphate (0.5%) and kinetin (5 ppm). The seeds were also scarified with 5% H_2SO_4 for 10 minutes and hot water (35°C) for 15 minutes.

A comparison of hydropriming with different seed treatments revealed that hydropriming for 2 h recorded the highest germination percentage followed by seed priming with 5 ppm kinetin (Table 4). The interaction effect

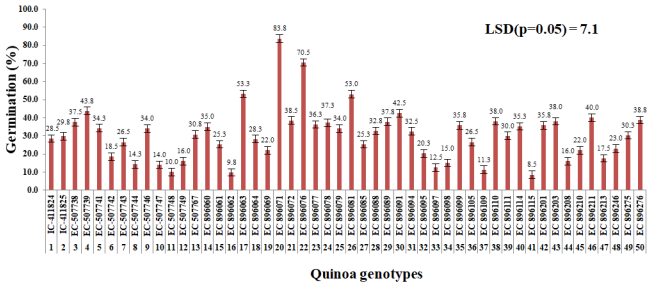

Figure 1: Germination percentage of 50 quinoa genotypes

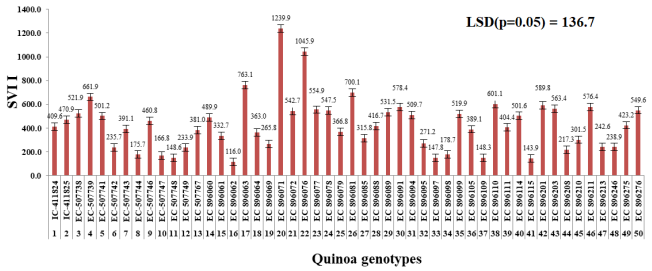

Figure 2: Seedling vigor index I (SVI I) of 50 quinoa genotypes

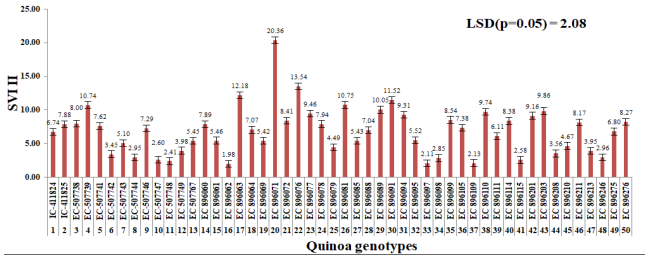

Figure 3: Seedling vigor index II (SVI II) of 50 quinoa genotypes

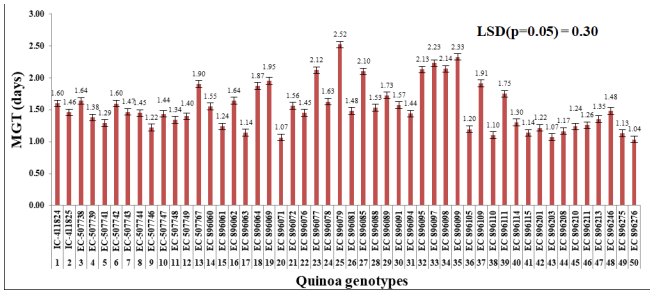

Figure 4: Mean germination time of 50 quinoa genotypes

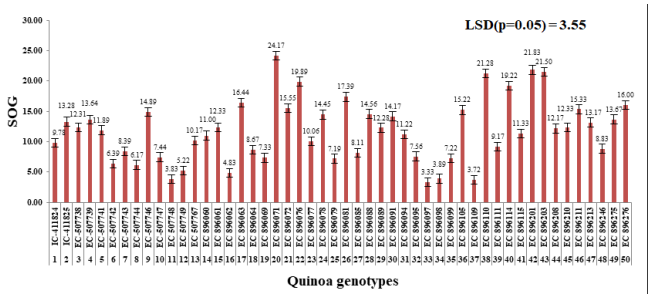

Figure 5: Speed of germination (SOG) of 50 quinoa genotypes

Table 2: Effect of hydropriming for different durations on mean germination time and speed of germination in selected quinoa genotypes

		Duration of hydropriming			
Genotypes	*Control (non-primed)*	*2 hours*	*4 hours*	*8 hours*	*Mean*
Mean germination time (days)					
EC-507739	$1.26^{a} \pm 0.04$	$1.05^{a} \pm 0.03$	$1.15^{a} \pm 0.03$	$1.20^{a} \pm 0.05$	1.16^{a}
EC-896063	$1.21^{a} \pm 0.03$	$1.08^{a} \pm 0.02$	$1.16^{a} \pm 0.02$	$1.24^{a} \pm 0.06$	1.17^{a}
EC-896071	$1.10^{a} \pm 0.05$	$1.06^{a} \pm 0.01$	$1.08^{a} \pm 0.03$	$1.13^{a} \pm 0.02$	1.09^{a}
EC-896076	$1.14^{a} \pm 0.02$	$1.11^{a} \pm 0.03$	$1.13^{a} \pm 0.04$	$1.15^{a} \pm 0.03$	1.13^{a}
EC-896081	$1.28^{a} \pm 0.15$	$1.16^{a} \pm 0.06$	$1.16^{a} \pm 0.03$	$1.25^{a} \pm 0.13$	1.21^{a}
EC-896091	$1.26^{a} \pm 0.10$	$1.19^{a} \pm 0.04$	$1.21^{a} \pm 0.12$	$1.22^{a} \pm 0.04$	1.22^{a}
Mean	1.21^{a}	1.11^{a}	1.15^{a}	1.20^{a}	
Speed of germination					
EC-507739	$16.7^{e-i} \pm 0.61$	$20.2^{a-f} \pm 1.74$	$16.7^{e-i} \pm 16.6^{i}$	$16.6^{e-i} \pm 0.31$	17.5^{ab}
EC-896063	$16.9^{c-i} \pm 0.34$	$17.0^{c-i} \pm 0.29$	$16.8^{d-i} \pm 15.3$	$15.3^{f-i} \pm 0.83$	16.5^{b}
EC-896071	$21.7^{a-d} \pm 0.78$	$22.3^{a} \pm 0.17$	$20.5^{a-e} \pm 20.3$	$20.3^{a-e} \pm 1.17$	21.2^{a}
EC-896076	$19.7^{a-g} \pm 1.02$	$22.1^{ab} \pm 0.61$	$21.8^{abc} \pm 19.8$	$19.8^{a-f} \pm 1.53$	20.9^{a}
EC-896081	$16.3^{e-i} \pm 0.55$	$17.6^{a-i} \pm 1.25$	$17.3^{b-i} \pm 17$	$17.0^{c-i} \pm 0.76$	17.0^{b}
EC-896091	$14.1^{hi} \pm 1.39$	$18.8^{a-h} \pm 0.97$	$14.8^{ghi} \pm 13$	$13.0^{i} \pm 0.58$	15.1^{b}
Mean	17.6^{a}	19.7^{a}	18.0^{a}	17.0^{a}	

Values with different superscripts vary significantly (p <0.05).

Table 3: Effect of hydropriming for different durations on germination percentage, seedling vigor index I and seedling vigor index II in selected quinoa genotypes

		Duration of hydropriming			
Genotypes	*Control (non-primed)*	*2 hours*	*4 hours*	*8 hours*	*Mean*
Germination (%)					
EC-507739	$42.7^{hij} \pm 2.3$	$46.3^{f-j} \pm 1.2$	$44.3^{g-j} \pm 0.9$	$39.3^{j} \pm 0.7$	43.2^{e}
EC-896063	$54.0^{d-g} \pm 2.6$	$61.3^{cde} \pm 0.7$	$57.3^{def} \pm 0.7$	$58.7^{de} \pm 1.8$	57.8^{c}
EC-896071	$84.0^{a} \pm 1.0$	$82.7^{a} \pm 1.8$	$82.3^{a} \pm 1.9$	$85.7^{a} \pm 3.2$	83.7^{a}
EC-896076	$70.7^{bc} \pm 4.7$	$80.0^{ab} \pm 2.9$	$63.3^{cd} \pm 2.6$	$60.3^{cde} \pm 2.7$	68.6^{b}
EC-896081	$53.7^{d-h} \pm 1.3$	$60.7^{cde} \pm 0.7$	$51.7^{e-i} \pm 0.9$	$43.7^{g-j} \pm 1.2$	52.4^{cd}
EC-896091	$42.3^{ij} \pm 1.5$	$51.3^{e-i} \pm 0.7$	$43.7^{g-j} \pm 3.0$	$41.3^{ij} \pm 1.3$	44.7^{de}
Mean	57.9^{ab}	63.7^{a}	57.1^{ab}	54.8^{b}	
SVI I					
EC-507739	$577.1^{ij} \pm 37.4$	$665.5^{ghi} \pm 9.8$	$595.0^{ij} \pm 9.4$	$495.5^{j} \pm 11.8$	583.3^{d}
EC-896063	$776.3^{fgh} \pm 23.7$	$862.2^{ef} \pm 43.1$	$777.8^{fgh} \pm 25.7$	$777.9^{fgh} \pm 23.4$	798.5^{bc}
EC-896071	$1204.8^{ab} \pm 6.1$	$1340.2^{a} \pm 8.7$	$1184.8^{bc} \pm 10.3$	$1254.1^{ab} \pm 24.7$	1246.0^{a}
EC-896076	$953.3^{de} \pm 54.1$	$1042.9^{cd} \pm 48.4$	$857.8^{ef} \pm 38.6$	$796.5^{fg} \pm 29.6$	912.6^{b}
EC-896081	$679.6^{ghi} \pm 8.2$	$883.9^{ef} \pm 20.9$	$629.5^{hij} \pm 35.8$	$533.8^{ij} \pm 5.0$	681.7^{cd}
EC-896091	$588.1^{ij} \pm 35.4$	$677.8^{ghi} \pm 8.9$	$542.8^{ij} \pm 39.6$	$498.2^{j} \pm 13.3$	576.7^{d}
Mean	796.5^{b}	912.1^{a}	764.6^{b}	726.0^{b}	
SVI II					
EC-507739	$11.26^{efg} \pm 1.06$	$12.36^{d-g} \pm 0.66$	$10.53^{efg} \pm 0.38$	$8.29^{g} \pm 0.19$	10.61^{d}
EC-896063	$14.60^{cde} \pm 0.71$	$16.93^{bc} \pm 1.18$	$13.78^{c-f} \pm 0.23$	$13.96^{c-f} \pm 1.34$	14.82^{bc}
EC-896071	$22.54^{a} \pm 0.21$	$24.32^{a} \pm 0.2$	$21.72^{a} \pm 0.77$	$23.63^{a} \pm 1.6$	23.05^{a}
EC-896076	$16.67^{bc} \pm 0.86$	$20.4^{ab} \pm 0.31$	$16.42^{bcd} \pm 0.67$	$13.05^{c-f} \pm 0.72$	16.63^{b}
EC-896081	$13.06^{c-f} \pm 0.29$	$15.98^{cd} \pm 0.59$	$11.69^{efg} \pm 0.66$	$10.09^{fg} \pm 0.03$	12.70^{cd}
EC-896091	$11.6^{efg} \pm 1.59$	$14.13^{c-f} \pm 0.09$	$11.45^{efg} \pm 0.42$	$10.6^{efg} \pm 0.24$	11.94^{cd}
Mean	14.95^{ab}	17.35^{a}	14.26^{b}	13.27^{b}	

Values with different superscripts vary significantly (p<0.05).

Table 4: Effect of different priming and scarification treatments on germination percentage, SVI I and SVI II in selected quinoa genotypes

Genotypes	*Control (non-primed)*	*Hydropriming*	*$Mg(NO_3)_2$*	*KNO_3*	*KH_2PO_4*	*$ZnSO_4$*	*Kinetin*	*5% sulphuric acid treatment*	*Hot water treatment (15 minutes)*	*Mean*
		2 h	*0.5%*	*0.5%*	*0.5%*	*0.5%*	*5ppm*	*10min*	*35°C*	
Germination (%)										
EC-507739	$39.7^{tu} \pm 0.3$	$46.3^{p-u} \pm 1.2$	$37.3^{u} \pm 0.7$	$40.3^{stu} \pm 1.2$	$46.3^{p-u} \pm 0.9$	$52.7^{k-r} \pm 0.7$	$49.5^{o-t} \pm 0.3$	$50.0^{n-t} \pm 0.6$	$49.7^{o-t} \pm 2.3$	45.8^{d}
EC-896063	$50.3^{m-t} \pm 0.9$	$61.3^{h-l} \pm 0.7$	$60.3^{i-o} \pm 1.2$	$63.3^{g-k} \pm 1.8$	$55.7^{j-p} \pm 1.2$	$45.3^{p-u} \pm 0.7$	$61.0^{h-m} \pm 0.6$	$45.0^{p-u} \pm 1.5$	$53.7^{k-q} \pm 1.2$	55.1^{c}
EC-896071	$80.7^{abc} \pm 1.5$	$82.7^{ab} \pm 1.8$	$84.3^{a} \pm 1.2$	$77.3^{a-e} \pm 0.7$	$75.7^{a-f} \pm 2.0$	$73.0^{b-g} \pm 2.1$	$83.0^{ab} \pm 0.6$	$77.3^{a-e} \pm 3.7$	$78.7^{a-d} \pm 0.3$	79.2^{a}
EC-896076	$65.3^{f-j} \pm 1.8$	$80.0^{abc} \pm 2.9$	$68.0^{d-i} \pm 2.3$	$71.3^{c-h} \pm 0.7$	$71.3^{c-h} \pm 0.7$	$66.3^{f-j} \pm 3.0$	$73.0^{b-g} \pm 1.7$	$75.3^{a-f} \pm 1.8$	$66.7^{e-i} \pm 1.8$	70.8^{b}
EC-896081	$51.3^{l-r} \pm 0.3$	$60.7^{h-n} \pm 0.7$	$54.3^{k-q} \pm 1.2$	$55.7^{j-p} \pm 1.9$	$54.3^{k-q} \pm 4.1$	$50.7^{l-s} \pm 4.7$	$48.0^{p-u} \pm 0$	$53.7^{k-q} \pm 1.9$	$60.7^{h-n} \pm 2.9$	54.4^{c}
EC-896091	$42.7^{r-u} \pm 1.8$	$51.3^{l-r} \pm 0.7$	$44.7^{q-u} \pm 1.3$	$43.7^{q-u} \pm 0.3$	$42.7^{r-u} \pm 1.8$	$46.8^{p-u} \pm 2.6$	$50.0^{n-t} \pm 4.6$	$49.3^{p-t} \pm 1.8$	$38.0^{u} \pm 1.2$	45.5^{d}
Mean	55.0^{b}	63.7^{a}	58.2^{ab}	58.6^{ab}	57.7^{ab}	55.8^{ab}	60.8^{ab}	58.4^{ab}	57.9^{ab}	
SVI I										
EC-507739	$505.0^{u} \pm 14.2$	$665.5^{n-u} \pm 9.8$	$497.4^{u} \pm 10.4$	$576.5^{q-u} \pm 8.6$	$604.7^{p-u} \pm 17.9$	$840.2^{g-n} \pm 6.8$	$598.7^{q-u} \pm 19.5$	$734.9^{k-s} \pm 26.6$	$734.0^{k-s} \pm 51.9$	631.7^{cd}
EC-896063	$704.8^{l-t} \pm 13.3$	$862.2^{f-m} \pm 43.1$	$796.8^{h-o} \pm 4.9$	$839.7^{g-n} \pm 21.5$	$761.0^{l-q} \pm 11.7$	$704.1^{l-t} \pm 16.6$	$759.1^{i-r} \pm 17.6$	$626.6^{o-u} \pm 18.4$	$747.9^{j-r} \pm 25.0$	749.7^{cd}
EC-896071	$1170.0^{abc} \pm 22.2$	$1340.2^{a} \pm 8.7$	$1163.3^{abc} \pm 29.1$	$1115.6^{bcd} \pm 15.6$	$1097.1^{bcd} \pm 35.3$	$1167.5^{abc} \pm 33.5$	$1099.7^{bcd} \pm 32.0$	$1166.8^{abc} \pm 70.6$	$1238.2^{ab} \pm 4.1$	1189.5^{a}
EC-896076	$932.1^{d-j} \pm 30.8$	$1042.9^{c-f} \pm 48.4$	$901.8^{e-k} \pm 57.1$	$990.1^{c-g} \pm 16.4$	$985.7^{c-g} \pm 6.0$	$1076.5^{b-e} \pm 39.0$	$938.1^{d-i} \pm 6.8$	$1102.9^{bcd} \pm 21.0$	$983.4^{c-h} \pm 7.5$	1010.2^{b}
EC-896081	$695.2^{m-t} \pm 18.8$	$883.9^{f-l} \pm 20.9$	$787.4^{i-p} \pm 25.7$	$762.5^{i-q} \pm 12.3$	$706.0^{l-t} \pm 63.5$	$730.3^{k-s} \pm 92.1$	$601.6^{p-u} \pm 2.1$	$737.7^{k-s} \pm 11.6$	$853.3^{g-n} \pm 63.1$	759.6^{c}
EC-896091	$555.7^{stu} \pm 18.2$	$677.8^{m-u} \pm 8.9$	$595.4^{q-u} \pm 24.7$	$571.4^{r-u} \pm 5.9$	$557.2^{stu} \pm 33.8$	$673.1^{n-u} \pm 45.4$	$638.6^{o-u} \pm 65.9$	$636.3^{o-u} \pm 18.6$	$521.5^{tu} \pm 14.6$	624.6^{d}
Mean	760.5^{b}	912.1^{a}	790.4^{ab}	809.3^{ab}	785.3^{ab}	865.3^{ab}	772.6^{ab}	834.2^{ab}	846.4^{ab}	
SVI II										
EC-507739	$9.03^{r} \pm 0.15$	$12.36^{j-r} \pm 0.66$	$10.64^{o-r} \pm 0.26$	$10.22^{pqr} \pm 0.40$	$11.8^{k-r} \pm 0.09$	$14.83^{g-n} \pm 0.82$	$11.27^{m-r} \pm 0.33$	$13.23^{i-q} \pm 0.18$	$13.50^{i-p} \pm 1.03$	11.67^{c}
EC-896063	$11.84^{k-r} \pm 0.70$	$16.93^{e-i} \pm 1.18$	$15.37^{g-m} \pm 0.59$	$14.38^{g-o} \pm 0.57$	$13.4^{i-p} \pm 0.79$	$13.37^{i-p} \pm 0.29$	$15.10^{g-n} \pm 0.86$	$11.05^{n-r} \pm 1.18$	$13.03^{i-r} \pm 0.51$	13.72^{c}
EC-896071	$21.55^{a-d} \pm 0.67$	$24.32^{ab} \pm 0.2$	$24.88^{a} \pm 0.18$	$22.09^{a-d} \pm 1.41$	$19.7^{c-f} \pm 1.05$	$21.28^{a-d} \pm 0.88$	$21.73^{a-d} \pm 0.21$	$20.25^{b-e} \pm 0.52$	$22.44^{abc} \pm 0.20$	22.16^{a}
EC-896076	$14.87^{g-n} \pm 0.11$	$20.4^{b-e} \pm 0.31$	$16.68^{e-i} \pm 0.35$	$15.69^{f-k} \pm 0.68$	$16.7^{e-i} \pm 0.63$	$20.78^{a-e} \pm 0.72$	$16.83^{e-i} \pm 0.70$	$18.44^{c-g} \pm 0.14$	$17.98^{d-h} \pm 0.18$	17.43^{b}
EC-896081	$12.01^{j-r} \pm 0.30$	$15.98^{f-j} \pm 0.59$	$14.24^{h-p} \pm 0.53$	$13.20^{i-q} \pm 0.58$	$12.4^{j-r} \pm 1.21$	$14.07^{h-p} \pm 2.00$	$11.73^{k-r} \pm 0.32$	$13.08^{i-r} \pm 0.11$	$15.44^{g-l} \pm 1.39$	13.54^{c}
EC-896091	$10.13^{pqr} \pm 0.76$	$14.13^{h-p} \pm 0.09$	$13.3^{i-q} \pm 0.25$	$11.08^{n-r} \pm 0.39$	$11.4^{l-r} \pm 0.39$	$13.41^{i-p} \pm 0.59$	$13.30^{i-q} \pm 1.26$	$13.66^{i-p} \pm 0.12$	$9.20^{qr} \pm 0.26$	12.08^{c}
Mean	13.24^{b}	17.35^{a}	15.85^{ab}	14.44^{ab}	14.27^{ab}	16.29^{ab}	14.99^{ab}	14.95^{ab}	15.27^{ab}	

Values with different superscripts vary significantly ($p<0.05$).

Table 5: Effect of different priming and scarification treatments on α-amylase activity (mg maltose min^{-1} g^{-1}) in selected quinoa genotypes

Genotypes	*Control*	*Hydropriming*	*$Mg(NO_3)_2$*	*KNO_3*	*KH_2PO_4*	*$ZnSO_4$*	*Kinetin*	*5% sulphuric acid*	*Hot water*	*Mean*
		2 h	*0.50%*	*0.50%*	*0.50%*	*0.50%*	*5ppm*	*10min*	*35°C*	
EC-507739	$9.23^{m-o} \pm 0.23$	$9.46^{l-o} \pm 0.19$	$9.70^{k-o} \pm 0.24$	$9.45^{l-o} \pm 0.07$	$10.45^{i-m} \pm 0.13$	$9.76^{k-o} \pm 0.17$	$9.51^{k-o} \pm 0.08$	$9.66^{k-o} \pm 0.18$	$9.99^{k-o} \pm 0.13$	9.69^{c}
EC-896063	$10.18^{i-o} \pm 0.11$	$10.57^{i-l} \pm 0.1$	$11.29^{g-j} \pm 0.24$	$10.56^{i-l} \pm 0.18$	$10.74^{h-k} \pm 0.33$	$10.27^{i-n} \pm 0.08$	$9.87^{k-o} \pm 0.27$	$10.00^{k-o} \pm 0.32$	$10.28^{i-n} \pm 0.08$	10.42^{c}
EC-896071	$14.13^{ab} \pm 0.26$	$14.84^{a} \pm 0.23$	$14.30^{ab} \pm 0.25$	$14.08^{ab} \pm 0.28$	$13.53^{bcd} \pm 0.31$	$13.99^{ab} \pm 0.14$	$14.33^{ab} \pm 0.11$	$14.36^{ab} \pm 0.24$	$14.06^{ab} \pm 0.27$	14.18^{a}
EC-896076	$13.76^{abc} \pm 0.30$	$14.02^{ab} \pm 0.38$	$13.83^{ab} \pm 0.15$	$14.31^{ab} \pm 0.35$	$13.38^{b-e} \pm 0.23$	$13.87^{ab} \pm 0.17$	$13.64^{abc} \pm 0.18$	$13.70^{abc} \pm 0.12$	$13.47^{b-e} \pm 0.22$	13.78^{a}
EC-896081	$12.21^{efg} \pm 0.25$	$12.54^{c-g} \pm 0.2$	$12.38^{d-g} \pm 0.03$	$12.56^{c-f} \pm 0.31$	$11.48^{f-i} \pm 0.14$	$11.99^{fgh} \pm 0.11$	$12.02^{fg} \pm 0.13$	$12.04^{fg} \pm 0.13$	$11.95^{fgh} \pm 0.16$	12.13^{b}
EC-896091	$8.99^{o} \pm 0.20$	$9.67^{k-o} \pm 0.12$	$10.27^{i-n} \pm 0.01$	$9.18^{no} \pm 0.39$	$9.13^{no} \pm 0.34$	$9.58^{k-o} \pm 0.16$	$9.70^{k-o} \pm 0.07$	$9.65^{k-o} \pm 0.32$	$9.73^{k-o} \pm 0.14$	9.55^{c}
Mean	11.42^{a}	11.85^{a}	11.96^{a}	11.69^{a}	11.45^{a}	11.58^{a}	11.52^{a}	11.57^{a}	11.58^{a}	

Values with different superscripts vary significantly ($p<0.05$).

between genotypes and treatment was significant. In three genotypes *viz*., EC-896076, EC-896081 and EC-896091, hydropriming for 2 hours recorded the highest germination; while in genotype EC-896071, seed priming with 0.5% magnesium nitrate recorded the highest germination. In genotype EC-896063, 0.5% potassium nitrate recorded the highest germination; however, in genotype EC-507739, 0.5% zinc sulphate recorded the highest germination.

Hydropriming for 2 hours also recorded the highest SVI I and II. The interaction effect between genotypes and treatments was significant for both the vigor indices (Table 4). In genotypes EC-896063, EC-896081 and EC-896091, hydropriming for 2 hours recorded the highest SVI I and II. Genotype EC-507739 recorded the highest SVI II when primed with 0.5% zinc sulphate closely followed by scarification with 5% sulphuric acid and hot water at 35°C. In genotypes EC-896071 and EC-896076, SVI II recorded the highest value when primed with 0.5% magnesium nitrate and 0.5% zinc sulphate, respectively which were closely followed by hydropriming for 2 hours.

Alpha- amylase activity recorded the highest value when seeds were treated with 0.5% magnesium nitrate which was statistically at par to 2 hours hydropriming (Table 5). The interaction effect between genotypes and treatments was significant w.r.t. α- amylase activity. In genotype EC-896071, hydropriming for 2 hours recorded the highest enhancement in α-amylase activity which could be responsible for higher germination and vigor indices of this quinoa genotype (Table 4). In genotype EC-896091, priming with 0.5% magnesium nitrate recorded the highest α-amylase activity which was, however, statistically at par to 2 hours hydropriming. Priming with 0.5% potassium nitrate recorded the highest enhancement in α-amylase activity in genotypes EC-896081 and EC-896076 which was statistically at par to 2 hours hydropriming. Seed priming activates α-amylase which hydrolyses the starch reserves, giving rise to α-maltose and α-glucose sugars that provide energy to the developing embryo during early seedling growth (Pujadas and Palau, 2001; Pawar and Laware, 2018). Hydropriming has been reported to enhance α-amylase activity in many cereals, including wheat and maize (Wattanakulpakin *et al*., 2012; Chakraborty and Bose, 2020).

Gayathri and Reddy (2018) observed that seed priming with 1% KH_2PO_4 and hydropriming for 6 h increased germination percentage in quinoa variety IC-411724, while in present study, the highest improvement in germination percentage was achieved by hydropriming for 2 hours. Musa *et al*.(2014) reported that hydropriming of amaranth seeds for 2 hours resulted in a significant enhancement of germination. Hydropriming for 12 hours and priming with 1% potassium nitrate has been reported to be the optimum priming technologies in beetroot and spinach, respectively, which are also the members of family Amaranthaceae

(Nirmala and Umarani, 2008; Kulsumbi *et al*., 2020).

Conclusion

Germination varied widely between 8.5 and 83.8% among the tested quinoa genotypes; only one genotype, EC-896071, exhibited germination higher than 80% and another genotype EC-896076 exhibited germination higher than 70%. These identified quinoa genotypes also possessed higher values of SVI I and II as compared to other tested genotypes. Thus, genotypes EC-896071 and EC 896076 can be utilized in the breeding programs for the development of varieties possessing higher germination and early seedling vigor. Quinoa seeds may also be hydro primed for 2 hours to achieve enhancement in germination and vigor indices.

Acknowledgments

The authors thank Punjab Agricultural University, Ludhiana for providing the necessary research facilities.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.04

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Morphological Characterization of Lemon Grass Genotypes under Semi-Arid Conditions of Haryana

RK Arya*, Vipan Kumar, PK Verma and Pawan Kumar

Abstract

Many aromatic plants are under cultivation in the Indian subcontinent and lemongrass is one of the most important aromatic plants. It is used in flavoring cold drinks, in scented soaps, shampoos and detergents, and as a fragrance in cosmetics, creams and perfumes. The present study was conducted for morphological characterization of 33 genotypes of lemongrass during two successive years, 2022 and 2023, at the Research area of Medicinal, Aromatic and Potential Crops Section (GPB), C.C.S. Haryana Agricultural University, Hisar. The results on the morphological characterization of lemongrass revealed that most of the genotypes in lemon grass were semi-spreading to compact type, tall to medium in height, with broad and green leaves having light purple leaf sheath color and medium in leaf length and tillers. About 27 genotypes were non-flowering and only six genotypes (NLG-1, Chirharit, RRL-16, Karishna, CKP-25 and OD-58) were able to bear flowering. On the basis of one or more morphological characters, each genotype is different from others.

Keywords: Lemongrass, *Cymbopogon flexuosus*, Morphological characterization, Aromatic plants.

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Received: 07/01/2024 **Revised:** 24/03/2024

Accepted: 18/06/2024

How to cite this article: Arya RK, V Kumar, PK Verma and P Kumar. (2024). Morphological Characterization of Lemon Grass Genotypes under Semi-Arid Conditions of Haryana. *Indian J. Plant Genet. Resour*. 37(3): 433-438.
DOI: 10.61949/0976-1926.2024.v37i03.04

Introduction

Many aromatic plants are under cultivation in the Indian subcontinent and lemongrass is one of most important aromatic plants. Lemon grass has mainly two types, i.e., *Cymbopogon flexuosus* (East Indian/Malabar), and *C. citratus* (West Indian). East Indian lemon grass is native to India and mainly cultivated in Kerala, A.P., Karnataka, T.N., Maharastra and U.P. West Indian lemongrass is native to Ceylon (Yadav *et al*., 2012). Lemongrass oil yield per plant was found to be higher under sulfate-dominated salinity than chloride-dominated salinity at comparable EC levels. Improvement in oil yield per plant was found with the aging of plants (Kumari and Varshney, 2012).

Lemongrass is commercially cultivated in Guatemala, India, China, Paraguay, Shri Lanka, England, Indonesia, Africa, Central America and Southern America for its essential oil. The quality of lemongrass oil is chiefly governed by the 'citral a' and 'citral b' contents, the compounds responsible for lemon flavor. This lemon flavor is commercially utilized in flavoring cold drinks, in scented soaps, shampoos and detergents, as a fragrance in cosmetics, creams and perfumes (Singh 2010 & Singh *et al*., 2024). It is also utilized to ride off the unpleasant odors in several industries. Lemongrass oil is used for making skin care creams as it has germicidal properties (Arya *et al*., 2021a). Spent lemongrass is used as a fuel, good raw material for paper manufacturing and excellent manure after compositing. As a medicinal plant, lemongrass has been considered a carminative and antimicrobial.

In addition to this, lemongrass green leaves or dried leaves are also popularly utilized as green tea or herbal tea (Behl *et al*., 2022). The bioactive compound 'Citral' extracted from the oil also used as an additive in alcoholic beverages, baked goods and confectionaries products (Kumar *et al*., 2024). Cital is also used as a base material to synthesize vitamin A and is also used in aromatherapy (Yadav *et al*., 2012). Wider adaptability and morphological stability is an important criteria to improve the herbage yield, and quality of oil and economic products. It is always desirable that a good yielding clone must be stable over different locations. Keeping in view the above points of economic importance and increasing demand for essential oils produced from lemongrass, the present study was undertaken with the objective of characterizing the lemongrass for morphological identification of genotypes or varieties.

Materials and Methods

The present study was conducted on the characterization of lemongrass genotypes during two successive years 2022-2023, at the Research area of MAP Section (GPB), CCS Haryana Agricultural University, Hisar in randomized block design. For present study 33 genotypes of lemongrass *viz*., Chirtarit, Krishana, NLG-1, GRL-1, NLG-2, NLG-3, NLG-4, NLG-5, NLG-6, NLG-7, NLG-8, NLG-9, NLG-10, OD-19, OD-23, OD-58, NLG-84, NLG-118, OD-388, RRL-16, HL-1, HL-2, HL-3, HL-4, HL-5, HL-6, HL-7, HL-8, HL-9, HL-10, HL-11, HL-12, CKP-25 (Table 1). All the good agronomic practices were followed as suggested by Arya *et al*., 2018. The data were recorded on ten randomly selected plants in each genotype in each replication in each year. The observations were recorded on plant morphological traits, i.e., growth habit (compact, semi-compact, semi-spreading or spreading), leaf sheath color (white, light purple or dark purple), leaf width (narrow or broad) seems to be most important and stable diagnostic plant features followed by plant height (tall, medium, dwarf), leaf length, leaf angle, leaf color, tillers per plant, flowering habit and flower color etc.

Table 1: Lemongrass genotypes collected from different sources

S. No.	*Genotypes*	*Source*
1.	Krishana	Pantnagar (UK)
2.	Chirharit	Pantnagar(UK)
3.	GRL-1	Pantnagar(UK)
4.	NLG-1	Faizabad (UP)
5.	NLG-2	Faizabad (UP)
6.	NLG-3	Faizabad (UP)
7.	NLG-4	Faizabad (UP)
8.	NLG-5	Faizabad (UP)
9.	NLG-6	Faizabad (UP)
10.	NLG-7	Faizabad (UP)
11.	NLG-8	Faizabad (UP)
12.	NLG-9	Faizabad (UP)
13.	NLG-10	Faizabad (UP)
14.	NLG-118	Faizabad (UP)
15.	NLG-84	Faizabad (UP)
16.	OD-23	Odakalli (Kerala)
17.	OD-388	Odakalli (Kerala)
18.	OD-19	Odakalli (Kerala)
19.	OD-58	Odakalli (Kerala)
20.	RRL-16	Jammu (JK)
21.	HL-1	Hisar (Haryana)
22.	HL-2	Hisar (Haryana)
23.	HL-3	Hisar (Haryana)
24.	HL-4	Hisar (Haryana)
25.	HL-5	Hisar (Haryana)
26.	HL-6	Hisar (Haryana)
27.	HL-7	Hisar (Haryana)
28.	HL-8	Hisar (Haryana)
29.	HL-9	Hisar (Haryana)
30.	HL-10	Hisar (Haryana)
31.	HL-11	Hisar (Haryana)
32.	HL-12	Hisar (Haryana)
33.	CKP-25	Jammu (JK)

Results and Discussion

Due to the non-availability of cultivated varieties for commercial cultivation of lemongrass, generally farmers of Haryana cultivate the open-pollinated varieties or locally adapted accessions of lemongrass as like other aromatic grasses. Therefore, morphological characterization on the basis of some morphological descriptors is the first step to developing the standard procedure to help the plant breeders in the early identification of potential cultivars. Among the morphological traits, plant type (compact or spreading), leaf sheath color (white or purple), leaf width seem to be the most important and stable diagnostic plant features, followed by plant height, leaf length, leaf angle, leaf color, tillers, flowering habit, etc.

On the basis of plant phenotypic observations recorded as per the morphological descriptors, a key for the identification of available genotypes was prepared, which is depicted in Figure 1(A-G). According to the lemongrass descriptor's key traits, all the genotypes were differentiated from each other.

Out of 33 genotypes used in the present study, on the basis of growth habit, 12 (Chirharit, NLG-1, NLG-3, NLG-4, NLG-5, NLG-6, NLG-8, NLG-9, HL-2, HL-3, OD-388) genotypes were of compact type, ten semi-spreading (Krishna, NLG-2, NLG-10, NLG-84, GRL-1, OD-23, HL-1, HL-7, HL-10, HL-12), seven semi-compact (NLG-7, NLG-19, OD-58, HL-4, HL-9,

Compact

Semi-compact

Semi-spreading

Spreading

A. Growth habit

Tall

Medium

Dwarf

B. Plant height

Very high

High

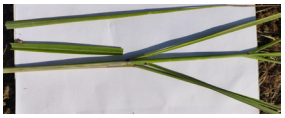
Medium

Low

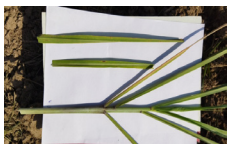
C. Tillers per plant

Light purple

Purple



Light green



Green

D. Leaf sheath color

Long

Medium

Short

E. Leaf length

Broad

Narrow

F. Leaf width

Non-flowering

Flowering

G. Flowering behavior

Figure 1 (A-G.): Morphological variability for different traits in lemon grass

HL-11, CKP-25) and remaining four (NLG-118, HL-5, HL-6, HL-8) were spreading type. On careful visualization of Table 2, it was noticed that the genotypes were classified as compact and semi-spreading types were further divided in tall and medium, while semi-compact was divided into tall, medium, and dwarf, but spreading types were restricted to medium and dwarf types only. On the basis of plant height, there were three groups, i.e., tall (Chirharit, NLG-3, NLG-5, NLG-6, NLG-8, NLG-9, NLG-7, OD-58, HL-9, HL-11, Krishna, NLG-10, OD-23, HL-1, HL-12, NLG-1), medium (NLG-4, OD-388, RRL-16, HL-2, HL-3, CKP-25, OD-19, GRL-1, NLG-2, NLG-84, HL-7, HL-10, HL-8, NLG-118) and dwarf (HL-4, HL-5, HL-6). In the same fashion, Yadav *et al*., 2013 in raya, Shahaji *et al*., 2020 in wheat and Arya *et al*., 2021b in cowpea characterized morphologically the different genotypes for their identification and differentiation purposes.

In the present study, sufficient variability was observed for the number of tillers per plant, and all the genotypes were grouped into four categories, i.e., very high, high, medium and low. Only one genotype, CKP-25 revealed profuse tillering, and only ten genotypes (Chirharit, NLG-9, HL-9, Krishna, NLG-10, HL-12, NLG-1, HL-8, OD-58, GRL-1) with high tillering and majority (20) of genotypes (NLG-2, NLG-3, NLG-5, NLG-6, NLG-7, NLG-8, NLG-118, NLG-84, OD-23, OD-388, OD-19, RRL-16, HL-1, HL-3, HL-4, HL-5, HL-6, HL-7, HL-10, HL-11) with medium tillering, and with low tillering only two genotypes (NLG-4, HL-2) were observed. Likewise, differences in tillering among rice genotypes were reported by Mani and Kumar (2018). For leaf sheath color character, majority of genotypes (18) revealed light purple color *viz*., Chirharit, NLG-3, NLG-5, NLG-6, NLG-9, NLG-7, OD-58, HL-9, CKP-25, Krishna, NLG-10, OD-23, HL-12, GRL-1, NLG-2, HL-5,

Table 2: Frequency distribution with some important traits of 33 genotypes/varieties of lemon grass

Plant descriptor	*Range of expression*	*Frequency*	*Genotypes/varieties*
Growth habit	Compact	12	Chirharit, NLG-1, NLG-3, NLG-4, NLG-5, NLG-6, NLG-8, NLG-9, HL-2, HL-3, OD-388
	Semi-compact	7	NLG-7, NLG-19, OD-58, HL-4, HL-9, HL-11, CKP-25
	Semi-spreading	10	Krishna, NLG-2, NLG-10, NLG-84, GRL-1, OD-23, HL-1, HL-7, HL-10, HL-12
	Spreading	4	NLG-118, HL-5, HL-6, HL-8
Plant height	Tall	16	Chirharit, NLG-3, NLG-5, NLG-6, NLG-8, NLG-9, NLG-7, OD-58, HL-9, HL-11, Krishna, NLG-10, OD-23, HL-1, HL-12, NLG-1
	Medium	14	NLG-4, OD-388, RRL-16, HL-2, HL-3, CKP-25, OD-19, GRL-1, NLG-2, NLG-84, HL-7, HL-10, HL-8, NLG-118
	Dwarf	3	HL-4, HL-5, HL-6
Tillers/plant	Very high	1	CKP-25,
	High	10	Chirharit, NLG-9, HL-9, Krishna, NLG-10, HL-12, NLG-1, HL-8, OD-58, GRL-1,
	Medium	20	NLG-2, NLG-3, NLG-5, NLG-6, NLG-7, NLG-8, NLG-118, NLG-84, OD-23, OD-388, OD-19, RRL-16, HL-1, HL-3, HL-4, HL-5, HL-6, HL-7, HL-10, HL-11,
	Low	2	NLG-4, HL-2,
Leaf sheath color	Light purple	18	Chirharit, NLG-3, NLG-5, NLG-6, NLG-9, NLG-7, OD-58, HL-9, CKP-25, Krishna, NLG-10, OD-23, HL-12, GRL-1, NLG-2, HL-5, HL-6, NLG-118
	Purple	5	NLG-8, HL-11, OD-19, NLG-84, NLG-1
	Light green	6	NLG-4, OD-388, RRL-16, HL-4, HL-7, HL-8
	Green	4	HL-2, HL-3, HL-1, HL-10,
Leaf length	Long	4	NLG-5, NLG-9, HL-9, HL-12,
	Medium	21	Chirharit, NLG-3, NLG-8, NLG-7, Krishna, NLG-10, OD-23, NLG-2, NLG-118, HL-11, OD-19, NLG-1, OD-388, HL-7, HL-2, HL-3, HL-1, NLG-6, OD-58, CKP-25, GRL-1,
	Short	8	NLG-4, NLG-84, RRL-16, HL-4, HL-5, HL-6, HL-8, HL-10,
Leaf width	Broad	28	Chirharit, NLG-5, NLG-3, NLG-9, NLG-8, NLG-7, HL-9, Krishna, NLG-10, OD-23, HL-12, NLG-2, HL-5, HL-6, NLG-118, HL-11, OD-19, NLG-84, NLG-1, NLG-4, OD-388, RRL-16, HL-4, HL-7, HL-8, HL-2, HL-3, HL-1,
	Narrow	5	NLG-6, OD-58, CKP-25, GRL-1, HL-10,
Flowering habit	Non-flowering	27	NLG-5, NLG-3, NLG-9, NLG-8, NLG-7, HL-9, NLG-10, OD-23, HL-12, NLG-2, HL-5, HL-6, NLG-118, HL-11, NLG-84, NLG-4, OD-388, HL-4, HL-7, HL-8, HL-2, HL-3, HL-1, NLG-6, OD-58, GRL-1, HL-10,
	Flowering	6	Chirharit, Krishna, NLG-1, OD-19, RRL-16, CKP-25,

HL-6, NLG-118, only five genotypes were under purple color (NLG-8, HL-11, OD-19, NLG-84, NLG-1), only six genotypes in light green category (NLG-4, OD-388, RRL-16, HL-4, HL-7, HL-8) and only four genotypes (HL-2, HL-3, HL-1, HL-10) were green in sheath color. Similar findings were also reported in sorghum by Shafiqurrahaman *et al*. (2022).

The grouping of genotypes on the basis of leaf length revealed that only four genotypes exhibited long leaves, i.e., NLG-5, NLG-9, HL-9, HL-12 and maximum (21) genotypes were under the medium group (Chirharit, NLG-3, NLG-8, NLG-7, Krishna, NLG-10, OD-23, NLG-2, NLG-118, HL-11, OD-19, NLG-1, OD-388, HL-7, HL-2, HL-3, HL-1, NLG-6, OD-58, CKP-25, GRL-1) and only eight genotypes was categorized under short leaf group (NLG-4, NLG-84, RRL-16, HL-4, HL-5, HL-6, HL-8, HL-10). On the basis of leaf width, all 33 genotypes were categorized only in two groups, i.e., broad and narrow bearing genotypes. In the present investigation, the majority of genotypes (28) were categorized as broad leaf genotypes, namely, Chirharit, NLG-5, NLG-3, NLG-9, NLG-8, NLG-7, HL-9, Krishna, NLG-10, OD-23, HL-12, NLG-2, HL-5, HL-6, NLG-118, HL-11, OD-19, NLG-84, NLG-1, NLG-4, OD-388, RRL-16, HL-4, HL-7, HL-8, HL-2, HL-3, HL-1 opposite to this, only five genotypes (NLG-6, OD-58, CKP-25, GRL-1, HL-10) were grouped as narrow leaf genotypes. Similar findings were also reported by Singh (2010) in lemon grass, Shahaji *et al*. (2020) in durum and Veluru *et al*. (2023) in rose. Bhosale *et al*. (2021) also reported significant variability for leaf characters in anjan grass.

Generally, all the flowering bears flowers according to their flowering season and under a set of environmental

conditions. If any plant species or variety/genotype does not receive the required environmental condition, it does not come in flowering. In the present investigation, out of 33 genotypes, only six genotypes were found able to bear flowering and remaining 27 genotypes were not come in flowering and grouped as non-flowering (NLG-5, NLG-3, NLG-9, NLG-8, NLG-7, HL-9, NLG-10, OD-23, HL-12, NLG-2, HL-5, HL-6, NLG-118, HL-11, NLG-84, NLG-4, OD-388, HL-4, HL-7, HL-8, HL-2, HL-3, HL-1, NLG-6, OD-58, GRL-1, HL-10). Similar differences were reported by a different worker in sugar cane under north Indian conditions due to differences in their thermal and photoperiod requirements of the genotype. Moreover, the precision of the above morphological descriptors characterization may be enhanced through electro-phonetic studies in the future. But, for this precise study advanced laboratory techniques are required (Singh, 2010).

Conclusion

It may be concluded on the basis of morphological characterization of lemongrass that most of the genotypes studied were tall to medium in plant height, semi-spreading to compact type with broad and green leaf having light purple leaf sheath color and medium in leaf length and tillers. Only six genotypes, *viz*., NLG-1, Chirharit, RRL-16, Karishna, CKP-25 and OD-58, were found able to bear flowering and the majority of genotypes (27) were unable to flower. The morphological characterization in lemongrass was found effective in making differentiation among genotypes under investigation.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.05

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Phenotypic Diversity of Maize Landraces from North-Western India and Exploring their Potentiality

Jyoti Kumari*, Shivani Sharma, Sherry R Jacob, Ram Kumar Sharma, Preeti Jakhar, Sapna Langyan, Ishwar Singh, KS Hooda and Ashok Kumar

Abstract

Collection of local landraces is essential for preserving the genetic variability and their evaluation and utilization through plant breeding provide economic benefits to the farmers and mankind. The present study aimed to evaluate the diversity present in the maize collections of North-Western (NW) regions of India on the basis of agro-morphological traits. About 294 diverse accessions collected from remote areas of the North-Western region (Rajasthan and Gujarat) were evaluated for 26 agro-morphological descriptor traits for two consecutive years, 2015 and 2016. Based on qualitative traits, the predominance of pink tassel anther, glume color and silk color green, droopy and leathery leaves and yellow-colored kernels were found in the collected accessions. These accessions had wide variability for green cob yield/plant, tassel branching, leaf width, number of ears per plant and ear height. Boxplot analysis revealed that accessions of Rajasthan had relatively higher mean values for leaf length, leaf width, ear width and 100-seed weight, whereas accessions from Gujarat were early maturing. The cluster analysis based on the phenotyping data divided 294 accessions into six classes and the spatial diversity of accessions in biplot clearly depicted that the accessions of Rajasthan had more diversity in comparison to those from Gujarat. Multi-trait specific accessions (IC331107 with high ear length and width, kernel rows and number; IC280465, early maturing with less plant and ear height; IC331144 and IC470443 with earliness and bold seededness) could be selected for further research and utilization in breeding and genetics studies.

Keywords: Maize landraces, Characterization, Genetic resources, Diversity analysis, North-Western India

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Received: 15/04/2024 **Revised:** 14/06/2024

Accepted: 26/06/2024

How to cite this article: Kumari J, S Sharma, SR Jacob, RK Sharma, P Jakhar, S Langyan, I Singh, KS Hooda and A Kumar (2024) Phenotypic Diversity of Maize Landraces from North-Western India and Exploring their Potentiality. *Indian J. Plant Genet. Resour.* 37(3): 439-446. **DOI:** 10.61949/0976-1926.2024.v37i03.05

Introduction

Maize (*Zea mays* L.) is the third most important food crop after rice and wheat, having diverse uses as human food, animal feed, fodder and industrial products. Globally, maize is known as a queen of cereals owing to its highest genetic yield potential and is one of the cereal crops that can be grown in different seasons, ecologies and altitudes. Maize has high variation for kernel types like normal yellow/white grain corn, sweet corn, baby corn, popcorn, waxy corn, high amylase corn, high oil corn, quality protein maize, etc. It is considered a *Kharif* crop since 80% of its sown area is under cultivation in the *Kharif* season. In terms of area and production, the USA is the largest producer of maize in the world. The cultivation of maize in India is practiced in 9.86 m ha with the production of 32.42 m tonnes and 3.29 tonnes ha^{-1} productivity (https://agriwelfare.gov.in/en/StatHortEst). Among Indian states, Karnataka has the highest area and production under maize (1.59 m ha and 5.22 m tonnes) followed by Madhya Pradesh (1.40 m ha and 4.57 m tonnes). Among other states, Maharashtra (1.29 m ha and 3.53 m tonnes), Rajasthan (0.95 m ha and 2.04 m tonnes) and Bihar (0.66 m ha and 2.52 m tonnes) has the major share in area and production (Agricultural Statistics at a Glance, 2022).

The maize crop is considered to be domesticated in Southern Mexico from teosinte (*Z. mays* L. subsp. *parviglumis*) between 6000 to 10,000 years ago (Matsuoka *et al*., 2002). It further spread to other parts of the world and got adapted to diverse climates and soil types such as the deserts and the high elevations of the mountains. Grant and Wellhausen (1955) studied the racial diversity of maize in India and observed extensive variability in plant, tassel and ear characteristics in the North-Eastern (NEH) region and North-western highlands of India. Mukherjee *et al.* (1971) reported that the varieties of Northern Plains and Peninsular India resembled Mexican and Columbian germplasm.

Morphological characterization is a pre-requisite for the assessment, description and classification of germplasm collections to enhance their use in maize breeding (Prasanna and Sharma, 2005; Wasala *et al.,* 2013; Kumari *et al*., 2017). The importance of phenotyping maize landraces from India and other countries has been highlighted in various studies (Salazar *et al*., 2016; Kumari *et al.,* 2017; Islam *et al.,* 2020; Nelimor *et al*., 2020). The National Genebank of India (NGB) housed in ICAR National Bureau of Plant Genetic Resources (NBPGR) conserves around 11,094 maize accessions comprising both indigenous and exotic collections. Of these, 331 accessions have been collected from Rajasthan and 181 accessions from Gujarat as landraces and local collections over the years. These regions fall in arid and semi-arid regions, having fragile ecosystems and receiving very less rainfall. Different forms of diversified uses of maize are found in the west and central plains of India. It is used as corn soup, *daliya*, roasted cob, popped kernel, corn oil, forage/fodder, wafers/*papad, sattu* and *chapatti*/flatbread. Some of the local cultivars/landraces grown in the western plain region of India included the flint types, Doodhmogar and Sameri, known for early maturity and drought tolerance; Gulla and Chandan with drought tolerance and Sathi, with insect-pest resistance trait (Pandey *et al.,* 2015). Dhillon *et al*. (2005) reported some promising landraces from the North-Western (NW) region as Sathi local from Punjab with heat and drought tolerance, very early maturity, excellent yield and high adaptability, Basi local and Dausa local from Rajasthan with multiple traits like excellent yield characters, drought tolerance trait and wider adaptability. This untapped valuable diversity needs to be collected, conserved, systematically evaluated and effectively utilized. Therefore, the present study was undertaken to characterize and evaluate the landraces and local collections from Rajasthan and Gujarat for agro-morphological traits and, to analyze phenotypic diversity among the accessions collected and to identify the trait-specific germplasm for utilization in maize improvement.

Materials and Methods

About 294 accessions conserved in the National Gene Bank (NGB), comprising 190 accessions from Rajasthan and 104 from Gujarat, were used for characterization and evaluation purposes in this study (Supplementary Table 1, Figure 1). The accessions from Gujarat were collected from the districts of Amreli, Banaskantha, Baroda, Bharuch, Dahod, Godhra, Jamnagar, Junagadh, Narmada, Panchmahal, Sabarkantha, Surat, Vadodara and Vijay Nagar. Similarly, from Rajasthan, the collections belonged to remote villages in the districts of Ajmer, Alwar, Banswara, Baran, Bharatpur, Bhilwara, Bundi, Chittorgarh, Dausa, Dungerpur, Jaipur, Jodhpur, Jhalawar, Jhunjhunu, Karauli, Kota, Pali, Pratapgarh, Rajsamand, Sawai Madhopur, Sirohi, Tonk and Udaipur. The altitude of the collection site varied from 13 m above sea level (Surat) to 300 m above sea level (Dahod) in Gujarat.

These accessions were evaluated in Augmented Block Design at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, during *Kharif* 2015 and 2016 with four checks HQPM-1, Bio9637, Jawahar Pop Corn and Pusa Composite 3 randomized in each 15 blocks of size 40, with the last block as an incomplete block. Each experiment comprised a row plot with a row length of 4 m and row-to-row spacing as 75 cm. The experimental farm is situated at a latitude of 28°40′ N and longitude of 77°12′ E and an altitude of 228.6 m above the mean sea level (Arabian Sea). The mean annual rainfall of Delhi during the crop season was 650 mm and annual temperature ranged between 12 and 32°C. The data were recorded for 26 agro-morphological descriptors as per the minimal descriptors and descriptor's states developed by ICAR-NBPGR (Mahajan *et al.,* 2000). The 15 agronomic characters included days to tassel, days to silk, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), leaf length (cm), leaf width (cm), tassel branching, number of kernel rows/ear, number of kernels/rows, days to maturity, number of ears/plant, grain weight (g) and green cob yield/plant (g). The 11 qualitative characters undertaken in this study were early plant vigor, tassel texture, tassel anther glume color, silk color at emergence, leaf color, leaf orientation, leaf pubescence, leaf texture, grain texture, grain size and kernel color.

Analysis of variance (ANOVA) for the individual year was carried out as per the augmented design and then the adjusted mean of both years was subjected to combined analysis after ascertaining the homogeneity of error variance using Bartlett's test (Arsham, 2010). Adjusted mean values for each trait were used for further analyses. Boxplot was generated for 15 quantitative traits to compare the performance of accessions from both states. Genetic diversity analysis was performed using a hierarchical algorithm with Euclidean distances and Ward's method of minimum variance for clustering the accessions. Principal component analysis (PCA) was carried out based on a phenotypic correlation matrix for the 15 descriptors. Each principal component was calculated by taking a linear combination of an Eigenvector of the correlation matrix with a variable. The biplot based on two principal components

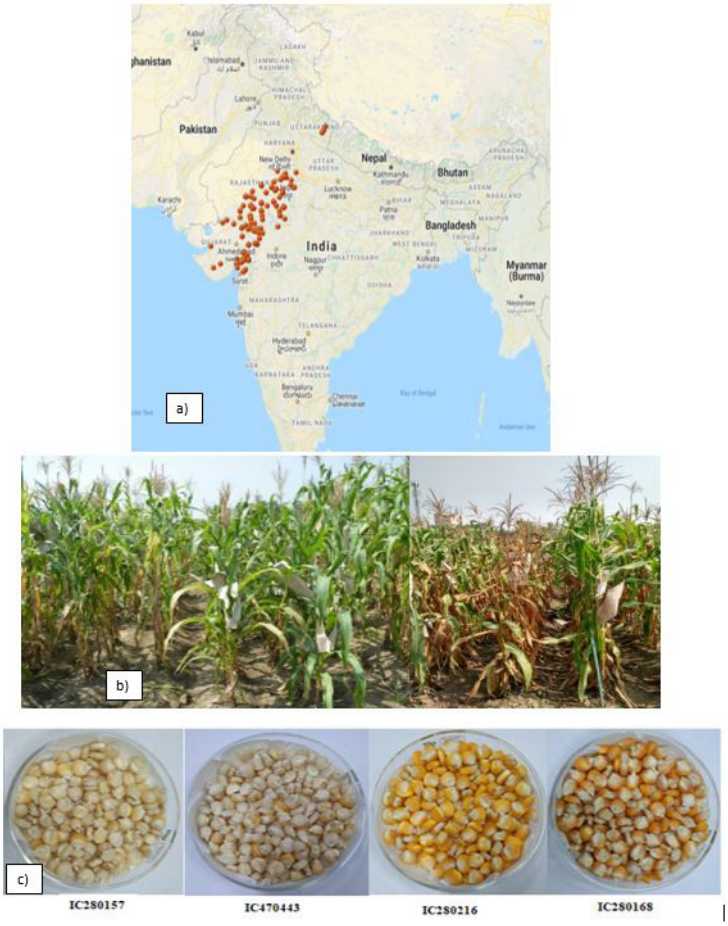

Figure 1: a) GIS map depicting collection area of maize accessions, b) Field view showing early maturing accession; c) Maize accessions with high grain weight

was also generated to depict the two-dimensional view of accession scores as well as the loading of characters. ANOVA was estimated using SAS 9.3, whereas Boxplot, frequency distribution, clustering and PCA were performed using JMP 15 software.

Results

Agro-morphological Characterization

Characterization for qualitative traits describes the accessions about their distinctiveness, uniqueness and specific traits. The frequency distribution of some qualitative traits (early plant vigor, tassel texture, silk color, leaf color, leaf pubescence, leaf texture, grain texture, grain size, kernel color) are depicted in Figure 2. Agro-morphological characterization for silk and tassel-related traits revealed that the majority of the accessions had pink tassel anther glume color (185), followed by light purple (83), green (23) and purple color(3); however, tassel glume base color was absent in 293 accessions. The silk color at emergence was pink in 174, while green in 115 accessions. Tassel texture was either medium or lax except 18 accessions with dense type. For leaf color, the majority of them were green (136) and dark green color (91). Leaf orientation was found to be erect in 53 while drooping in 238 accessions. Another trait, leaf pubescence, was present in 50 accessions. For leaf texture, 121 accessions had leathery texture, followed by 116 as normal and, 213 accessions had medium leaf width and 78 had narrow leaf width. For kernel traits, yellow-colored kernels (160) were predominant, followed by white (60). Most of the accessions had either indented or round type grain shapes. Grain size, the important parameter for yield determinant, was medium in the majority of the accessions. However, bold size was recorded in six accessions from Rajasthan, namely, IC280216, IC280435, IC280169, IC280212, IC437070 and IC470443. The ear shape was cylindrical with an intermediate husk cover and regular kernel row arrangement in most of the accessions.

Phenotypic Variability and Identification of Trait-specific Germplasm

Analysis of genetic variability and diversity in maize collections of specific regions is of utmost importance to know the prevalence of specific traits in the landraces. We observed sufficient variation for all 15 quantitative traits (Table 1 and Supplementary Figure 1). Days to tassel

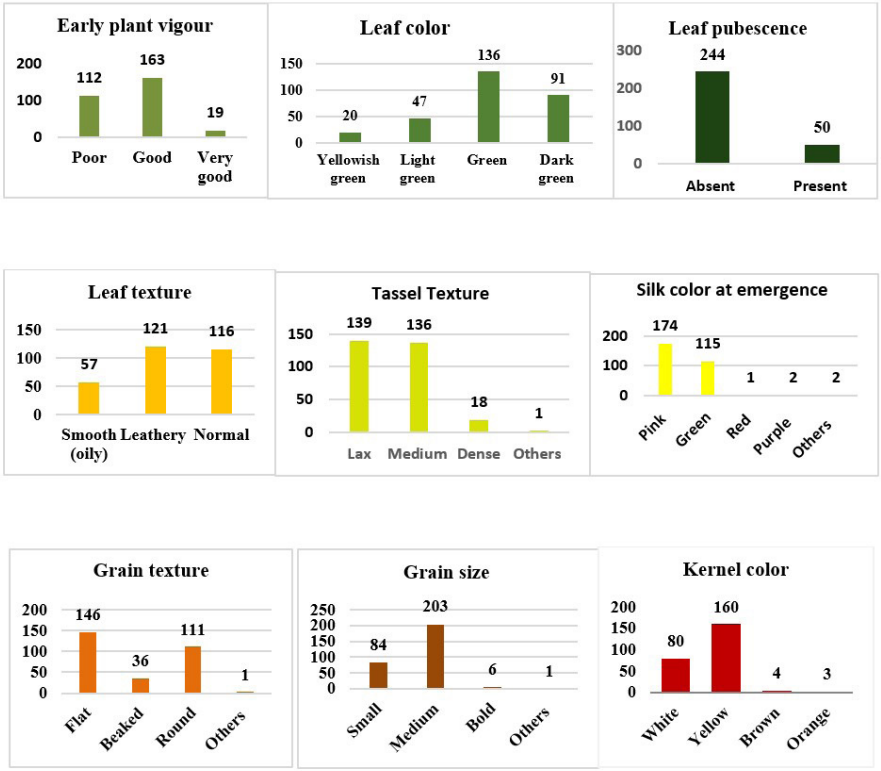

Figure 2: Frequency distribution for nine qualitative traits in maize accessions

varied from 41.5 to 73 days with a mean value of 53.37 days; days to silk varied from 45 to 75 days with mean value of 6.69 days; grain yield/plant showed a range from 50 to 390 g with an average of 175.11 g; tassel branching varied between 12.60 to 38 with a mean value of 20.83; plant height ranged from 141.10 to 239.25 cm with a mean value of 200.44 cm; ear height ranged from 73.60 to 149.5 cm with mean value of 105.28 cm; a number of ears/plants ranged from 1.15 to 2.45 with mean of 1.61. Leaf length varied from 54.80 to 105.30 cm with a mean value of 86.16 cm and leaf width ranged from 6 to 12.90 cm with a mean value of 9.36 cm. These accessions matured between 80.50 to 98.11 days with a mean value of 89.65 days. Among ear traits, ear length varied between 10.25 to 21.80 cm with a mean value of 15.61 cm, ear width ranged from 2.30 to 4.90 cm with a mean value of 3.50 cm, kernel rows/cob ranged between 8.95 to 16, with a mean value of 12.74; a number of kernels/row varied between 19.70 to 41.30 with range of 29.79 and 100-grain weight varied between 14.15 to 31.40 g with average of 20.82 g.

Boxplot analysis revealed that accessions from Rajasthan showed a wider range of variability than that of Gujarat for traits days to tassel, days to silk, tassel branching, ear height, leaf width, ear width and 100 seed weight. Similarly, accessions from Gujarat showed more variation than Rajasthan for green cob yield/plant, numbers of ears/plant, ear length, and number of kernel rows and for traits like plant height, leaf length and number of kernels per row, accessions from both states showed similar range of variability (Supplementary Figure 2).

Promising maize germplasm was identified for different traits (Table 1), such as, for green cob yield per plant, IC331150, IC337022, IC325844, IC280180, IC313646, IC325961, IC331147, IC325856 (>310.00 g). For 100-seed weight, IC280216, IC470443, IC280168, IC280157, IC273359, IC331144 (>27 g) were found promising. Maize accessions IC331141, IC331144 and IC280167 had tasseling and silking in less than 45 days and IC280465, IC449437 and IC344701 came in maturity in about 80 days. High kernel numbers per row, *i.e.*, more than 38, were found in accessions IC331205, IC273356, IC337035, IC331107, IC437070, IC280182, IC337025, IC470459. We also identified accessions with multiple traits, namely IC331107 (Medium plant height, long and wide ear, high number of kernel rows and kernels per row) and IC280465 (earliness and medium plant height), IC331144 and IC470443 (earliness and seed weight). These promising germplasms were validated in replicated trial during *Kharif* 2017 and 2018, consecutively for two years.

Multivariate Analysis

Correlation analysis was carried out among 15 quantitative parameters as shown in Supplementary Table 2. Days to tasseling showed a positive correlation with days to silking

Table 1: Mean and range of traits studied and trait-specific germplasm identified in maize collections

Traits	*Range*	*Mean ± SE*	*Trait specific germplasm*
Days to tasseling	41.50–73.00	53.37 ± 0.45	IC331144(Guj), IC331153(Guj), IC280167(Raj), IC331141(Guj), IC330939(Raj), IC280465(Raj), IC470443(Raj), IC280406 (Raj) (<45.00)
Days to silking	45.00–75.50	56.69 ± 0.23	IC331141(Guj), IC331144(Guj), IC280167(Raj), IC330939(Raj), IC331153(Guj), IC280465(Raj), IC470443(Raj), IC280405(Raj) (<48.50)
Green cob yield/plant	50.00–390.00	175.11 ± 3.27	IC331150(Guj), IC337022(Guj), IC325844(Raj), IC280180(Raj), IC313646(Raj), IC325961(Guj), IC331147(Guj), IC325856(Raj) (>310.00)
Tassel branching	12.60–38.00	20.83 ± 0.19	IC280429(Raj), IC325961(Guj), IC280421(Raj), IC331198(Guj), IC280422(Raj), IC337023(Guj), IC337022(Guj) (>28.00)
Plant height (cm)	141.10–239.25	200.44 ± 1.02	IC344658(Guj), IC280168(Raj), IC280465(Raj), IC331107(Guj), IC280445(Raj), IC77602(Raj), IC337090(Guj), IC344794(Guj) (<166.00)
Ear height (cm)	73.60–139.45	105.28 ± 0.66	IC82002(Guj), IC280426(Raj), IC344658(Guj), IC77602(Raj), IC280444(Raj), IC280465(Raj), IC280461(Raj), IC449432(Raj) (<83.45)
No. of ears per plant	1.15–2.45	1.61 ± 0.01	IC81998(Guj), IC273353(Raj), IC280164(Raj), IC273346(Raj), IC330966(Guj), IC331193(Guj), IC273358(Raj), IC280415(Raj) (>2.00)
Leaf length (cm)	54.80–105.30	86.16 ± 0.52	IC337006(Guj), IC280212(Raj), IC298557(Guj), IC280200(Raj), IC82089(Raj), IC310656(Raj), IC81991(Guj) (>102.60)
Leaf width (cm)	6.00–12.90	9.36 ± 0.07	IC280431(Raj), IC280157(Raj), IC280429(Raj), IC273338(Guj), IC280165(Raj), IC280174(Raj), IC280408(Raj), IC325876(Raj) (>10.80)
Days to maturity	80.50–98.11	89.65 ± 0.18	IC280465(Raj), IC449437(Raj), IC344701(Guj), IC344716(Guj), IC280405(Raj), IC280459(Raj), IC280462(Raj), IC449432(Raj) (<82.00)
Ear length (cm)	10.25–21.80	15.61 ± 0.09	IC333328(Guj), IC331107(Guj), IC337042(Guj), IC313643(Raj), IC331205(Guj), IC337038(Guj), IC330965(Guj), IC331093(Guj) (>19.00)
Ear width (cm)	2.30–4.90	3.50 ± 0.02	IC280450(Raj), IC77611(Guj), IC331107(Guj), IC280429(Raj), IC337439(Guj), IC331205(Guj), IC337024(Guj), IC331118(Guj) (<4.00)
No. of kernel rows	8.95–16.00	12.74 ± 0.07	IC331107(Guj), IC331098(Guj), IC273342(Guj), IC280161(Raj), IC391316(Raj), IC82089(Raj), IC336989(Guj), IC337022(Guj) (>15.00)
No. of kernels/row	19.70–41.30	29.79 ± 0.20	IC331205(Guj), IC273356(Raj), IC337035(Guj), IC331107(Guj), IC437070(Raj), IC280182(Raj), IC337025(Guj), IC470459(Raj) (>37.92)
100 Seed weight (g)	14.15–31.40	20.82 ± 0.15	IC280216(Raj), IC470443(Raj), IC280168(Raj), IC280157(Raj), IC273359(Raj), IC331144(Guj), IC437070(Raj), IC273332(Guj) (>25.40)

(0.97**), days to maturity (0.75 **), green cob yield/plant (0.30**), leaf length (0.20**) and grain weight (0.29**). Days to silking had a positive association with yield per plant (0.29**), leaf length (0.22**), days to maturity (0.77**) and grain weight (0.31**). Yield per plant showed a positive correlation with leaf length (0.16**) and days to maturity (0.32**). Tassel branching showed a positive correlation with leaf width (0.36**) and ear width (0.23**). Plant height was positively associated with ear height (0.79**), leaf length (0.17**) and days to maturity (0.17**), whereas ear height showed a positive correlation with leaf length (0.18**), leaf width (0.17**), days to maturity (0.16**), ear length (0.17**) and ear width (0.17**). Leaf length showed positive correlations with leaf width (0.25**), days to maturity (0.22**), ear length (0.16**), ear width (0.24**) and grain weight (0.26**), while leaf width had a positive correlation with ear length (0.31**), ear width (0.32**), number of kernel rows (0.19**) and grain weight (0.19**). Ear length showed positive correlations with ear width (0.45**), number of kernel rows (0.23**), number of kernels/row (0.61**) and grain weight (0.35**), whereas ear width had a positive correlation with the number of kernel rows (0.54**), number of kernels/row (0.35**) and grain weight (0.42**).

Genetic diversity analysis was performed using hierarchical cluster analysis with Ward's method. All the accessions were grouped into six clusters comprising 46, 80, 20, 73, 38 and 40 accessions, respectively (Supplementary Figure 3). Among all the clusters, cluster 2 was the largest and cluster 3 was the smallest one. Cluster I comprised accessions with high grain weight with high numbers of ears per plant, whereas cluster III comprised early maturing accessions. Cluster IV had accessions with high yield per plant, leaf length, ear length, ear width and number of kernels per row, while cluster V had accessions with high leaf width and number of kernel rows. Cluster VI comprised accessions having tall plant height and ear height (Supplementary Table 3).

The PCA based on correlation was used to study interrelationships among the different parameters and their contribution to the overall variability. The first five

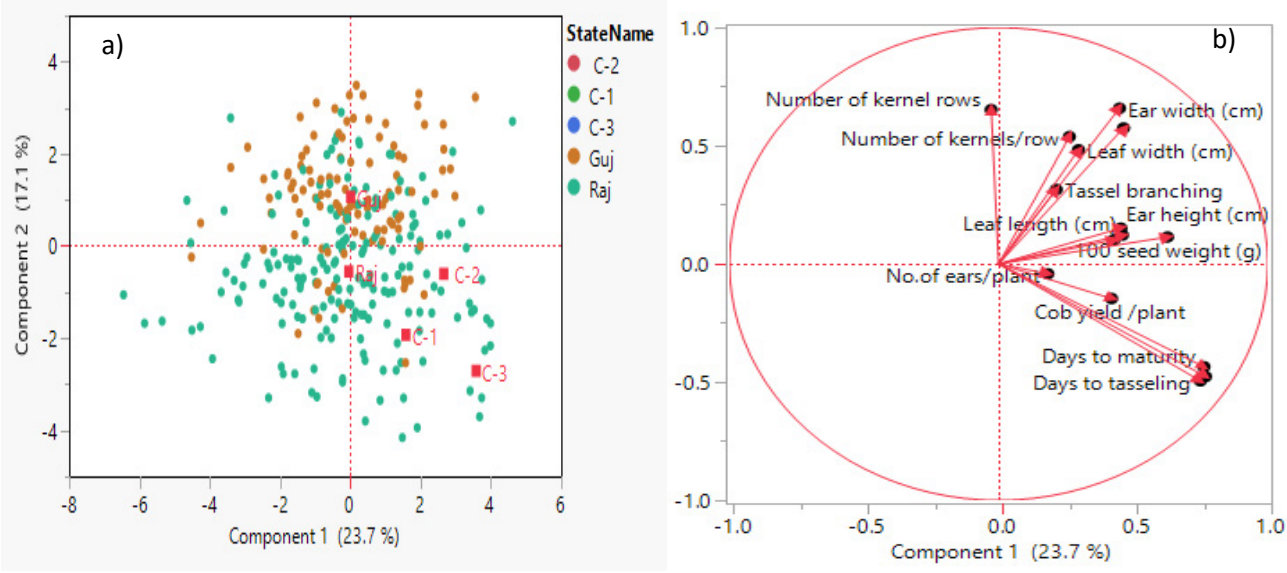

Figure 3: Principal component biplot showing the distribution of maize accessions: a) Genotype biplot; b) Trait biplot

components provided major summary of data and explained 67.49% variance in maize germplasm. The first principal component (PC I) accounted for 23.72% of the variation and was mainly contributed by days to silking, days to tasseling, days to maturity and 100-grain weight. The second principal component accounted for 40.78% of variation and was mainly contributed by ear width, number of kernel rows, number of kernel/rows and ear width (Supplementary Table 4). Two-dimensional principal components plots displayed significant variation in accessions from both states, with visible intra-state diversity (Figure 3). However, some accessions from adjoining districts or from the inter-state boundary area are overlapping, which might be due to the gene flow resulting from cross-pollinating behavior of maize.

Discussion

Characterization and evaluation of any landrace is the primary step to gaining knowledge about the specific traits of the germplasm accession collected for conservation and further utilization in breeding programs. Evaluation of genetic resources for specific traits is essential for finding new sources of donor for target traits and their introgression into elite lines for specific breeding purposes. The maize accessions from this fragile ecosystem of NW India had mainly pink tassel anther glume color, absence of tassel glume color base, pink or green silk color, medium or lax tassel texture, green and dark green leaf color, drooping leaf orientation, absence of leaf pubescence and leathery or normal leaf texture and medium leaf width. With regard to kernel traits, these accessions had majorly yellow colored kernels followed by white, indented or round type grain shape and medium grain size. However, large-size grain was recorded in six accessions from Rajasthan, namely, IC280216, IC280435, IC280169, IC280212, IC437070 and IC470443. Ear shape was cylindrical with intermediate husk cover and regular kernel row arrangement in most of the accessions, which meant that farmers preferred these types during selection on their farmland. The phenotypic evaluation of maize landraces was reported by earlier researchers in various countries, including Canada (Azar *et al.* 1997), Turkey (Ilarslan *et al.* 2002), Mexico (Pressoir and Berthaud 2004), India (Prasanna and Sharma 2005, Kumar *et al.,* 2015 and Kumari *et al.*, 2017) and China (Wei *et al.* 2009).

Positive correlation among days to tasseling and silking with green cob yield/plant, leaf length and grain weight suggested more time is required for biological growth and photosynthate accumulation in plants. Similarly, a positive association of leaf length and leaf width with ear length, ear width and grain weight was observed, which is due to the role of larger leaf area in translocation of photosynthates from source to sink. Ear length showed a positive association with ear width, number of kernel rows, number of kernels/row and grain weight. Thus, for enhanced maize yield, medium-maturity germplasm with large leaf size and ear length should be preferred. Similar kind of association between grain yield, 100-seed weight, ear girth and ear length have been reported previously (Selvaraj & Nagarajan, 2011; Jambagi & Wali, 2016).

Knowledge of the extent and pattern of genetic diversity within germplasm accessions, particularly collections of a specific region, is important for effective future collection, development of conservation strategies and efficient use of these genetic resources (Frankel *et al.* 1995). Ecological characteristics of any region influence the genotypic constitution of landraces during domestication. Genetic diversity provides breeders with basic germplasm material for crossing programs and broadening of genetic base. Here, the cluster analysis revealed a sufficient level of variability in

the maize germplasm and accessions from a diverse group, such as groups 3 and 6 for plant and ear height and groups 1 and 3 for tasselling and silking, which can be used in the hybridization program. Cluster analysis used by Gouesnard *et al.,* 1997 Sharma *et al*., 2010 Kumar *et al*., 2015; Kumari *et al*., 2017 and Goyanka *et al*., 2021 also differentiated maize landraces based on morpho-agronomic characters.

In this study, the principal component biplot supported the result obtained by cluster analysis. The first five components provided a major summary of data and explained most of the variation in maize germplasm. The first principal component was mainly contributed by days to silking, days to tasseling, days to maturity and 100-grain weight. The two-dimensional principal components plot showed good variation in accessions from both states, with overlapping in accessions from adjacent locations across the state boundaries due to gene flow caused by cross-pollination. Several researchers used principal component analysis to analyze diversity patterns in maize germplasm (Mohammadi and Prasanna, 2003; Angelo *et al.,* 2008; Lu *et al.,* 2009). Semagn *et al.* (2012) in their study obtained three groups among 450 germplasm based on PCA using 1065 SNPs and principal component analysis supported the clustering pattern.

Being a crop with varied uses, maize has immense potential to be utilized as feed, fodder, food and various industrial uses. Hence, there is a need to search for novel germplasm that can be used directly as a product or indirectly through further improvement. This study led to the identification of unique germplasm for specific traits like green cob yield per plant (IC331150, IC337022, IC325844), early tasseling and silking less than 45 days (IC331144, IC331153, IC280167), early maturity, high kernel number per row (IC331205, IC273356, IC337035), kernel rows (IC331107, IC331098, IC273342), ear length (IC333328, IC331107, IC337042) and grain weight (IC280216, IC470443). The accessions with multiple traits (IC331107 with high ear length and width, kernel rows and number; IC280465, early maturing with less ear height; IC331144 and IC470443 with earliness and bold seededness) were also identified for further use in a breeding program. Therefore, evaluation of the untapped gene pool of maize is necessary to find out the variation present and to promote their conservation and utilization.

Acknowledgments

We sincerely thank all the farming communities across the NW region who have been conserving the germplasm on farms, explorers for collecting valuable genetic resources and the Director, ICAR-National Bureau of Plant Genetic Resources, New Delhi, for providing infrastructure facility to carry out the research.

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Supplementary Files

https://ispgr.in/public/site/supplementary-files/2600-supplementary-file.pdf

P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.06

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Assessment of Genetic Variability and Correlation in Pointed Gourd (*Trichosanthes dioica* Roxb) Genotypes for Yield and Yield Attributing Traits

Shyam Raj Singh*, Shailendra Rajan, Dinesh Kumar, KK Srivastava and VK Soni

Abstract

This study aimed to evaluate the nature and extent of genetic variability and relationships among key yield-attributing traits in pointed gourd (*Trichosanthes dioica* Roxb). A broad spectrum of variability was observed across selected genotypes for all traits assessed. The minimal disparity between genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) across traits suggests a lesser influence of environmental factors on these plant traits, indicating the potential effectiveness of selection based on phenotypic performance. High estimates of heritability, coupled with substantial genetic advances for fruit yield per plant (g), vine length, and number of fruits per vine, suggest the presence of additive genes, facilitating selection processes. Fruit yield per plant exhibited significant positive correlations with average fruit weight, fruit circumference, fruit length, fruit width, vine length, number of internodes per vine, and female flower length at both genotypic and phenotypic levels. Moreover, there was a notable positive direct effect by average fruit weight, vine length, number of internodes per vine, intermodal length, female flower length, fruit width, and number of primary branches, along with their significant positive correlation with yield. Considering their high heritability and genetic advance, these traits emerge as crucial components contributing to fruit yield, suggesting a need for greater emphasis on them during yield improvement programs in pointed gourd.

Keywords: Correlation, Heritability, Genetic advance, Path analysis, Pointed gourd.

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Received: 19/01/2023 **Revised:** 18/04/2024

Accepted: 21/06/2024

How to cite this article: Singh SR, S Rajan, D Kumar, KK Srivastava and VK Soni (2024) Assessment of Genetic Variability and Correlation in Pointed Gourd (*Trichosanthes dioica* Roxb) Genotypes for Yield and Yield Attributing Traits. *Indian J. Plant Genet. Resour.* 37(3): 447-453. **DOI:** 10.61949/0976-1926.2024.v37i03.06

Introduction

Pointed gourd (*Trichosanthes dioica* Roxb.) stands out as a perennial, dioecious vegetable cherished for its nutritional and medicinal merits within the Cucurbitaceae family. Its cultivation spans approximately 20,000 hectares in India alone, yielding around 310,000 metric tons with a productivity rate of 14.89 t/ha (NHB 2018-19). Flourishing in tropical and subtropical climates, major producing states encompass Bihar, West Bengal, Odisha, Chhattisgarh, Assam, and Uttar Pradesh. This versatile vegetable finds its way into various culinary delights, from vegetable curries to pickles, owing to its enduring market presence and high demand fueled by its unique medicinal properties. Documented benefits include aiding digestion, acting as a diuretic and laxative, invigorating the heart and brain, and ameliorating circulatory disorders by regulating cholesterol levels while enriching vitamin, protein, and mineral content (Malek, 2009; Swamy, 2022).

Despite its significance, the widespread adoption of pointed gourd faces a bottleneck in low productivity, primarily attributed to the dearth of high-yielding varieties. As India serves as one of the primary centers of origin for *T. dioica* Roxb. (Chandra *et al*., 1995), the fruit exhibits a wide spectrum of variability in shape, size, color, quality, and bearing characteristics (Hazra and Ghose, 1999).

Consumer and grower preferences lean towards green, fleshy fruits with soft seeds and high yields. To address this gap between potential and actual yields, there's an exigency for genetic restructuring in pointed gourd, focusing on consumer-preferred attributes such as appealing creamy flesh, green fruit, and fewer soft seeds.

The diverse genetic reservoir of parental lines harbors promising allelic variations for novel combinations. Understanding the genetic variability across various traits is pivotal for identifying suitable genes to enhance crop genetic behavior (Nwangburuka *et al*., 2011). Genetic diversity plays a vital role in meeting the multifaceted goals of plant breeding, encompassing increased yield, uniformity, desired quality, and resistance to biotic and abiotic stresses. Hence, a systematic comprehension of genetic diversity in targeted traits is a potent tool for breeding programs tailored to specific conditions. Previous studies have focused on accessions collected from surveys (Chandra *et al*., 1995; Debata *et al*., 2017) or identified important genotypes (Jena *et al*., 2017; Verma, *et al*., 2017; Pramila *et al*., 2023). This study marks the first attempt to explore the population resulting from crosses among different ecotypes from subtropical India, including parents used in its population development. The significance of this endeavor lies in recognition of the diverse genetic reservoir inherent in parental lines, which harbors promising allelic variations for novel combinations

However, the intricacies of horticultural specifications in pointed gourd present breeders with limited avenues for improvement, given that yield is a complex trait influenced by multiple components. Direct selection solely based on yield performance proves ineffectual. Thus, comprehending variability within available germplasm and unraveling the associations between yield and various component characters are imperative for targeted enhancements (Chotaliya and Kulkarni, 2017).

In this context, statistical tools emerge as indispensable aids in estimating variability. Heritability is a predictive tool for gauging the reliability of phenotypic values, guiding breeders in selecting characters with high heritability. It determines to what extent the environment impacts yield by determining genotypic and phenotypic yield and yield components of diverse crop genotypes (Ullah *et al*., 2012). Genetic progress is the quantity of heritable genes gained in a character under a certain selection pressure. High genetic progress, as well as high heritability estimates, provides the best conditions for selection. Genetic advance provides insights into the expected progress resulting from selection within populations. Characters with high heritability can quickly progress by using simple selection. Heritability, on the other hand, has been explored and shown to be of no practical value without the involvement of genetic advancements. The coefficient of variation depicts the degree of variability present in many different traits, but it does not include the heritable component. A correlation study can also provide trustworthy and helpful information about the selection type, scope, and direction. Correlation analysis delineates associations, while path analysis disentangles causative factors and their relative importance. Leveraging these tools empowers breeders to grasp the associations between independent and dependent variables; thus guiding crop improvement endeavors through selecting component traits (Singh *et al*., 2017). Against this background, this study endeavors to elucidate the nature and extent of genetic variability across a diverse set of genotypes sourced from various regions across India, coupled with heterotic selections and aims to identify traits exhibiting significant genetic variability and high heritability, providing valuable insights for genotype selection and breeding programs.

Materials and Methods

The research spanned two consecutive years, from 2019 to 2021, and took place at the experimental farm of ICAR-Central Institute for Subtropical Horticulture Rehmankhera, Kakori, Lucknow specifically within block I. Positioned between 26º 45' to 27º 10' N latitude and 80º 30' to 80º 5' E longitude, with an elevation of 123 m above sea level, the experimental site provided an ideal environment for studying pointed gourd genotypes. A diverse set of genotypes sourced from West Bengal, Bihar, and Uttar Pradesh and heterotic selections bred at ICAR-CISH were meticulously studied over two consecutive years and sourced from different regions across India. To ensure uniformity and reliability in the experimental setup, each genotype's rooted plants (cuttings) were transplanted in October 2018. Planting was done with a spacing of 2 x 1 m in rows, maintaining a female-to-male ratio of 9:1, a configuration commonly used to optimize pollination and fruit set in pointed gourd cultivation. The experiment was laid out in a randomized block design with three replications.

The soil of the experimental plot was identified as loamy, indicating a balanced mixture of sand, silt, and clay, which is typically favorable for plant growth. With a pH of 6.8 and an electrical conductivity of 0.36 Sm^{-1}, the soil provided adequate nutrients and conductivity for robust plant development. Cultural practices were meticulously implemented throughout the experiment to ensure consistent growth and phenotypic expression of the pointed gourd traits under study. Plants were trained using a curtain system, a common practice in vine crops like pointed gourd, to maximize sunlight exposure and facilitate air circulation, which is crucial for optimal growth and yield.

Data collection was conducted systematically, with observations recorded from five randomly selected plants in each plot and replication. A comprehensive set of traits was measured, including vine length, number of internodes

per vine, internodal length, number of primary branches per plant, female flower length, fruit length, fruit width, fruit circumference, average fruit weight, and fruit yield per plant. These traits were chosen based on their relevance to plant growth, development, and yield potential.

Statistical analysis of the data was carried out using analysis of variance following the guidelines outlined by Panse and Sukhatme (1967). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formulas provided by Burton and De Vane (1953). Additionally, heritability (broad sense) and genetic advance as a percentage of means were computed following the protocols outlined by Allard (1960) and Johnson *et al*. (1955), respectively.

Results and Discussion

With the exception of the length of the female flowers and the circumference of the fruit, the analysis of variance that was carried out for the experiment design revealed a considerable amount of variation among the thirty genotypes of pointed gourd across all of the parameters examined. This variability can be traced to the many sources of genetic material and environmental effects, the primary factors that shape the phenotype. The considerable prevalence of variability shows that there are ample options for selection to increase yield in pointed gourd species (Table 1).

The average vine length was 790.78 cm, with a range that extended from 382.67 to 1527.33 cm. Similarly, the number of internodes present in each vine ranged from 35.00 to 105.33, with a mean value of 77.93. Intermodal lengths varied from 6.75 to 15.17 cm, with 10.18 cm being the average. Other characteristics, such as the number of primary branches, the length of the female flower, the length of the fruit, the breadth of the fruit, the circumference of the fruit, the average weight of the fruit, and the amount of fruit produced by each plant, were found to exhibit a broad range of variance (Table 2). These differences highlight the genetic diversity among genotypes, showing the possibility for yield improvement through breeding programs that incorporate a variety of parental lines.

The GCV and the PCV provide insights into the variability of traits within pointed gourd genotypes. As shown in Table 2, a comparison of GCV and PCV values reveals the relative contributions of genetic and environmental factors to trait variation. The characteristics, including vine length, the count of internodes per vine, and internodal length (cm), demonstrate a range of GCV values from 27.42 to 18.49%. This variability underscores the substantial genetic diversity among genotypes, pointing to a predominant influence of genetic factors on these traits.

In contrast, traits like fruit width (cm) and circumference (cm) display relatively lower GCV values than their PCV values. This indicates a stronger influence of environmental factors on the variation observed in these traits. Moreover, traits with high GCV values, such as average fruit weight (g) and fruit yield per plant (g), suggest significant genetic variability among genotypes for these economically important traits. This variability presents opportunities for selection and breeding programs to improve yield and fruit quality in pointed gourd. Overall, comparing GCV and PCV values provides valuable insights into the relative contributions of genetic and environmental factors to trait variation, guiding breeders in identifying traits with higher genetic potential for improvement in pointed gourd genotypes.

Local germplasm is a rich resource that may be used to breed robust cultivars (According to Yadav *et al*., 2013; Singh *et al*., 2014). This is especially true when adapting to specific climatic zones, which can help mitigate environmental concerns connected with climate change. The GCV and the PCV are two estimates that can be utilized to evaluate the degree of variability among specific physical characteristics. There appears to be a limited amount of environmental influence on the expression of horticultural traits, as indicated by the proximity between the phenotypic and genotypic coefficients of variation. When compared to genotypic coefficients, phenotypic coefficients that are larger imply that environmental factors have an impact on the expression of traits. The study conducted by Jena *et al*. (2017) showed that some characteristics, including fruit production per plant, average fruit weight, number of primary branches, and vine length, demonstrated large coefficients of variation. These characteristics are considered economically significant and offer a significant potential for improvement through selection.

Table 1: Mean square of different traits in pointed gourd genotypes

Source of variation	*Degree of freedom*	*Vine length*	*Number of internodes/ vine*	*Inter nodal length*	*No. of Primary branches/ vine*	*Female flower length*	*Fruit length*	*Fruit diameter*	*Fruit circumference*	*Average Fruit weight*	*Fruit yield /plant*
Replications	2	15199.19	5.59	1.81	9.79	0.171	0.350	0.240	0.307	2.54	38119945.701
Genotypes	29	149548.61**	624.15**	12.48**	81.95**	0.865	7.309*	0.562	5.070*	617.56 **	513260851.225**
Error	58	8454.63	1.04	1.46	4.95	0.181	0.103	0.012	0.108	0.59	16838203.541

** Significant at 1% level
*Significant at 5% level

Table 2: Range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advances (GA) in pointed gourd

Traits	*Range*		*Mean*	*Genotypic variance (%)*	*Phenotypic variance (%)*	*Phenotypic coefficient variation (%)*	*Genotypic coefficient variation (%)*	*Heritability in broad sense (%)*	*Genetic advance (%)*
	Min	*Max*							
Vine length (cm)	382.67	1527.33	790.78	47031.32	55486.00	29.788	27.425	84.76	411.30
Number of internodes per vine	35.00	105.33	77.93	207.70	208.74	18.540	18.494	99.50	29.61
Inter nodal length (cm)	6.75	15.17	10.18	3.67	5.13	22.269	18.839	71.57	3.34
No. of primary branches/plant	6.33	21.67	13.19	25.66	30.62	41.954	38.411	83.82	9.56
Female flower length (cm)	5.17	7.33	6.07	0.23	0.41	10.540	7.872	55.78	0.74
Fruit length (cm)	5.97	12.28	9.30	2.40	2.50	17.021	16.667	95.89	3.13
Fruit width (cm)	2.39	4.40	3.55	0.18	0.20	12.462	12.068	93.78	0.85
Fruit circumference (cm)	9.17	15.40	12.16	1.65	1.76	10.918	10.577	93.86	2.57
Average fruit weight (g)	22.38	81.46	45.40	205.66	206.24	31.634	31.589	99.72	29.50
Fruit yield /plant (g)	504.00	4923.07	1787.36	165474215.89	182312419.44	38.178	36.372	90.76	1275.81

Traits such as vine length (cm), number of internodes per vine, and average fruit weight (g) demonstrate high heritability values, exceeding 80%. This suggests that a substantial proportion of the observed variation in these traits is attributable to genetic factors rather than environmental influences (Table 2). Conversely, traits like female flower length (cm) and inter nodal length (cm) exhibit relatively lower heritability estimates, indicating a stronger influence of environmental factors on their expression. Furthermore, traits with high heritability estimates, such as fruit yield per plant (g) and fruit length (cm), present promising opportunities for targeted selection and breeding efforts to improve yield and fruit quality in pointed gourd genotypes.

Overall, the heritability estimates provide breeders with valuable insights into the genetic control of traits, guiding the selection of superior genotypes with desirable characteristics for further breeding programs.

Heritability estimates help predict a section of traits since they indicate the dependability of phenotypic values for selection purposes. The combination of high heritability and developments in genetics supports the existence of additive gene effects, particularly in characteristics such as the number of fruits produced by each vine, the length of the vine, and the number of fruits produced by each plant. This suggests that there is the possibility of achieving genetic advantages through selection.

The correlation between traits and yield in pointed gourd genotypes is crucial for understanding their potential impact on overall productivity. Table 3 shows significant correlations with fruit yield per plant (g) for several traits. Vine length (cm) displays a positive correlation with fruit yield per plant at both genotypic (G: 0.4564) and phenotypic (P: 0.469) levels. This suggests that longer vines may increase fruit yield in pointed gourd.

Fruit length (cm) also exhibits a notable positive correlation with fruit yield per plant, with genotypic (G: 0.600) and phenotypic (P: 0.559) coefficients indicating a strong association. Longer fruits may thus contribute to higher yields in pointed gourd genotypes. Additionally, fruit circumference (cm) demonstrates a significant positive correlation with fruit yield per plant, showing genotypic (G: 0.883) and phenotypic (P: 0.777) coefficients. This implies that fruits with larger circumferences may contribute positively to overall yield. These correlations highlight the importance of considering vine length, fruit length, and fruit circumference to enhance yield in pointed gourd genotypes. Breeders and researchers can leverage this information to prioritize traits that positively influence yield during selection and breeding programs.

There is a possibility that pleiotropic gene action or linkage is responsible for the associations that exist between various trait components. Insights into the overall and genetic relationships between desired features

Table 3: Genotypic (G) and phenotypic (P) coefficient correlation estimation among the traits of pointed gourd genotypes

Traits		Vine length (cm)	Number of internode per vine	Inter nodal length (cm)	No. of primary branches/vine	Female flower length(cm)	Fruit length (cm)	Fruit diameter (cm)	Fruit circumferenc (cm)	Average fruit weight (g)	Fruit yield/ plant (g)
Vine length (cm)	G	1	0.651**	0.683**	0.160**	-0.149	0.038	-0.089	-0.081**	-0.182	0.456**
	P	1	0.603**	0.733**	0.128**	-0.069	0.032	-0.070	-0.078**	-0.164	0.511**
Number of internodes per vine	G		1	-0.086	0.168	-0.047**	0.032**	-0.352**	0.133**	-0.072	0.347**
	P		1	-0.068	0.152	-0.043**	0.033**	-0.342**	0.132**	-0.072	0.334**
Inter nodal length (cm)	G			1	0.062	-0.112	0.129	0.172**	-0.221**	-0.159	0.280**
	P			1	0.039	-0.015	0.103	0.155**	-0.192**	-0.129	0.373**
Number of primary branches/vine	G				1	-0.386**	-0.494	-0.363**	-0.516**	-0.638**	-0.476**
	P				1	-0.285**	-0.427	-0.334**	-0.464**	-0.588**	-0.423**
Female flower length (cm)	G					1	0.225**	-0.191	0.405	0.312**	0.256**
	P					1	0.168**	-0.100	0.245	0.233**	0.207**
Fruit length (cm)	G						1	0.291**	0.584**	0.653**	0.598**
	P						1	0.289**	0.580**	0.639**	0.559**
Fruit width (cm)	G							1	0.526**	0.574**	0.409**
	P							1	0.549**	0.592**	0.430**
Fruit circumference (cm)	G								1	0.834**	0.683**
	P								1	0.808**	0.628**
Average fruit weight (g)	G									1	0.777**
	P									1	0.7441**

*Significant at 5% level
** significant at 1% level

Table 4: Estimates of direct (bold) and in direct of significant traits on yield pointed gourd

Characters	*Vine length*	*Number of internodes per vine*	*Inter nodal length*	*No. of primary branches/vine*	*Female flower length*	*Fruit length*	*Fruit diameter*	*Fruit circumference*	*Average fruit weight*	*Fruit yield/ plant (g)*
Vine length (cm)	**0.3087**	0.201	0.211	0.0495	-0.0458	0.012	0.028	0.056	0.4564	0.469
Number of internodes per vine	0.1814	**0.279**	-0.024	0.0468	-0.013	0.009	-0.098	-0.020	0.347	0.347
Inter nodal length (cm)	0.1539	0.182	**0.226**	0.0139	-0.0252	0.029	0.039	-0.036	0.28	0.280
No. of primary branches	0.0001	0.000	0.000	**0.0003**	-0.0001	0.000	0.000	0.000	-0.476	0.476
Female flower length (cm)	-0.0169	-0.005	-0.013	-0.0440	**0.114**	0.026	-0.022	0.036	0.2556	0.256
Fruit length (cm)	-0.0016	-0.001	-0.006	0.0215	-0.0098	**-0.044**	-0.013	-0.029	0.598	0.600
Fruit width (cm)	-0.0050	-0.020	0.010	-0.0203	-0.0107	0.016	**0.056**	0.033	0.43	0.430
Fruit circumference (cm)	0.0105	-0.017	0.029	0.0670	-0.0527	-0.076	-0.071	**-0.108**	0.777	0.883
Average fruit weight (g)	-0.1746	-0.069	-0.152	-0.6108	0.2989	0.626	0.567	0.958	**0.4564**	0.777

Residual effect -0.128

can be gained through phenotypic and genotypic correlations, respectively. According to Debate *et al*. (2017), fruit production per plant displayed substantial positive relationships with various characteristics, including fruit weight, fruit circumference, fruit length, and vine length. These correlations indicate the significance of these characteristics as factors that contribute to productivity. According to Khan *et al*. (2009), Verma *et al*. (2017), and Jena *et al*. (2017), selection strategies ought to give priority to characteristics that have high positive associations with fruit yield. Some examples of such characteristics include fruit weight per plant and vine length.

The analysis of path coefficients makes it possible to divide correlation coefficients into two categories: direct and indirect impacts of independent factors on the variable that is being studied (the dependent variable). The fruit yield that each plant produced was regarded as the dependent variable in this investigation, whereas the other characteristics were deemed to be independent factors (Table 4). The intricate interrelationships between characteristics were further underlined by indirect impacts that occurred through a variety of channels. Positive contributions to fruit yield per plant were also made by characteristics such as fruit length, fruit circumference, and female flower length. These contributions were made indirectly through a variety of cellular pathways.

Overall, the fruit's average weight, the vine's length, the number of internodes on each vine, and the length of the fruit were essential components for increasing yield in a pointed gourd. The variation in genotypic path coefficients suggests that incorporating new traits into pointed gourd breeding programs in subtropical climates could lead to enhanced fruit yield.

Conclusion

The analysis indicates significant variability among pointed gourd genotypes, offering ample selection opportunities for yield enhancement. Traits like vine length and average fruit weight exhibit considerable genetic variability, while high heritability estimates suggest predominant genetic influence. Positive correlations between traits like vine length, fruit length, and fruit circumference with yield per plant underscore their importance. Path coefficient analysis highlights the significance of traits like average fruit weight and vine length in yield enhancement of pointed gourd. Leveraging genetic diversity and understanding trait associations could improve pointed gourd yield, particularly in subtropical climates.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.07

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Unraveling the Hidden Patterns of Genetic Diversity in Oat (*Avena sativa* L.) Accessions: Insights from Novel Hybrid Hierarchical K-means Clustering

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Abstract

Avena sativa is primarily grown as a food crop but also serves as a valuable feed for livestock. Oat is a versatile and nutritious grain with a range of health benefits, making it a popular choice for consumers and a valuable crop for agricultural production. In pursuit of crop improvement, cluster analysis is an analytical approach that allows researchers to uncover underlying patterns and structures within a dataset. Eventually, this aids in identifying exemplary genotypes for improved yield attributes. The present study involved a meticulous examination of phenotypic data of 62 oat genotypes taken during *Rabi* 2019-20 at CCS Haryana Agricultural University, Hisar, Haryana. A novel and superior technique, hybrid hierarchical K-means, was employed for enhanced outcomes in comparison to traditional hierarchical and K-means clustering methods. Among the four distinct clusters formed, cluster I exhibited the highest count of genotypes. Additionally, cluster I had the lowest intra-cluster distance and the highest group mean, implying the presence of additive gene action and favorable combinations of alleles for yield-related traits, respectively. Clustering offers breeders the advantage of focusing their efforts on representative genotypes within each cluster, thereby accentuating the efficiency of resource allocation and the management of breeding materials. Promising genotypes from the most diverse clusters can act as parents for hybridization programs. The research will enhance our understanding of oat genetics and facilitate the development of superior cultivars. Ultimately, this will help optimize yields and meet the growing demand for this nutritious crop.

Keywords: Clustering, Diversity, Forage, Heterosis, H-K-means, Oat.

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Received: 22/12/2023 **Revised:** 04/04/2024

Accepted: 01/07/2024

How to cite this article: Chawla R, M Jattan , DS Phogat, A Sharma and M Redhu (2024) Unraveling the Hidden Patterns of Genetic Diversity in Oat (*Avena sativa* L.) Accessions: Insights from Novel Hybrid Hierarchical K-means Clustering. *Indian J. Plant Genet. Resour.* 37(3): 454-459. **DOI:** 10.61949/0976-1926.2024.v37i03.07

Introduction

Oat (*Avena sativa*) belonging to family Poaceae is regarded as a prominent multifunctional cereal owing to its inherent versatility (Prates and Yu 2017, Chawla *et al.,* 2021). It sets itself apart from other cereals due to a plethora of unparalleled benefits, rendering it highly coveted and favored by a substantial multitude of individuals (Ahmad *et al.,* 2014). Oat covers a worldwide production of 23.3 million metric tons (USDA, 2023). The worldwide oats market experienced growth from $6.67 billion in 2022 to $7.13 billion in 2023, reflecting a compound annual growth rate (CAGR) of 7.0%. Oats are known for their adaptability to diverse climatic conditions and can be cultivated in a wide range of regions around the world (Isidro-Sanchez *et al.,* 2020). The crop possesses attributes that render it highly valuable for both human alimentation and animal fodder (Chawla *et al.,* 2022). As a livestock feed, it offers a combination of nutritional composition, digestibility and palatability that makes it an excellent choice for a variety of animals (Ross *et al.,* 2004; Nikolaudakis, 2016). The non-commercial character of forage crops and the generation of fodder with minimal inputs from deteriorated & marginal land results in a substantial disparity between the availability & demand of fodder (Singh *et*

al., 2022a). The aforementioned circumstances underscore the criticality of conducting research on forage crops in order to address this disparity effectively (Surje and De, 2014; Krishna *et al.,* 2014). Furthermore, achieving high yield despite its health benefits, remains a challenge majorly due to low genetic potential, weed competition, inadequate agronomic practices and limited investment in breeding programs (Gorash *et al.,* 2017; Yang *et al.,* 2023). Addressing these factors through improved genetics, increased research & investment can help optimize oat yields and meet the growing demand for this nutritious cereal crop.

To enhance the progress of any breeding program, it is imperative to systematically assess the available materials to identify diverse lines suitable for hybridization programs (Kiran *et al.,* 2023; Krishna *et al.,* 2014). Cultivars possessing enhanced yield potential, along with the ability to thrive at elevated altitudes beyond the existing climatic thresholds for arable farming, have the potential to alleviate the strain caused by overgrazing and deforestation (Arora *et al.,* 2021). Crop germplasm serves as a reservoir of genetic diversity that can be utilized for crop improvement programs. Different studies have highlighted the importance of genetic diversity assessment in crop plants and the recent analytical perspectives & advancements in crop breeding (Govindaraj *et al.,* 2015).

In this research, multivariate analysis was employed to expedite the identification of promising heterotic combinations suitable for harnessing diverse improved cultivars. Clustering analysis serves as a valuable tool in crop breeding, providing breeders with a systematic and data-driven approach to understand & exploiting the genetic diversity within crop populations (Mohammadi and Prasanna, 2003). By leveraging the insights gained from clustering analysis, breeders can make effective decisions, optimize breeding strategies and ultimately develop improved crop varieties with enhanced traits & productivity. This paper employs a novel and unconventional methodology for clustering analysis, i.e., hybrid hierarchical K means clustering, presenting an improved and distinctive approach. Following a comprehensive assessment of diverse oat genotypes, this investigation substantially facilitated the discernment of the most promising genotypes for yield attributes (Kaur *et al.,* 2018). As a result, this study will make a substantial contribution toward the significant attainment of food and fodder security.

Materials and Methods

Plant Material and Experimental Details

The research consists of 62 oat genotypes, including 3 checks (OS 6, JHO 851 and UPO 212) that were procured from diverse regions across the country (Supplementary Table 1). The study was undertaken at the Research Farm Area, Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (Haryana) (latitude 29^0 10′ North and longitude 75^0 46′ East with an altitude of 215.2 m above the mean sea level) during *Rabi* 2019-20. The trial was conducted in an augmented design with seven blocks, each having three checks. Each genotype was sown in three rows of 3 m length each.

Data Recording

The data on phenotypic traits were collected from five randomly chosen vigorous plants for each genotype except for DFF and DM, which was on a plot basis. The data was recorded at 50% flowering stage and their mean value was taken. A total of 13 phenotypic traits were evaluated including PH- Plant height (cm), TPL- Number of tillers/plant, NOL- Number of leaves/plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield/plant (g), DMY- Dry matter yield/plant (g), DFF- Days to 50% flowering, DM- Days to maturity, SY- seed yield/plant (g), TW- Test weight (1000 seed weight in g).

Statistical Analysis

Initial hierarchical cluster analysis was performed using the methodology proposed by Ward, 1963. The k-means algorithm initiates by selecting a random set of observations as the initial cluster centers. However, the final clustering outcome is highly dependent on this initial random selection, potentially yielding different results with each computation. To mitigate this issue, a solution called hybrid hierarchical k-means clustering (k-means) has been devised, combining the strengths of hierarchical clustering and traditional k-means methods. By incorporating both approaches, k-means offers enhanced scalability, flexibility, interpretability, cluster compactness and outlier handling. These advantages render hkmeans a valuable and applicable technique for clustering analysis across diverse domains. R studio software, version 26.0 (R Core Team, 2020) was used for analysis. All the graphs were drawn using the same software. The inter and intra-cluster distances were calculated on the basis of Euclidean distance while considering the mean values of various traits as cluster mean values.

Results and Discussion

Despite the considerable genetic variability indicated by the mean sum of squares for all traits, the analysis of variance alone does not provide a comprehensive explanation for the extent of genetic diversity observed. Understanding and harnessing genetic divergence greatly contribute to the invaluable enhancement of crops (Kumari and Jindal, 2019). The presence of a substantial multitude of clusters serves as evidence of ample diversity among the oat genotypes. Upon examination of the phenotypic data acquired from 62 oat genotypes, a comprehensive analysis led to the formation

of a total of four distinct clusters. The clustering pattern unveiled that cluster I had the highest count of genotypes, comprising 28 genotypes, while cluster IV emerged as the second largest cluster, encompassing 14 genotypes. Additionally, cluster II comprised 11 genotypes, whereas cluster III constituted the smallest count, comprising nine genotypes (Table 1). The maximum inter-cluster distance was exhibited between clusters II and III (5.93) followed by clusters II and IV (5.89). On the contrary, the least inter-cluster was demonstrated between clusters I & II. The highest intra-cluster distance was manifested by cluster II, while the minimum intra-cluster distance was showcased by cluster I (Table 2). Cluster I exhibited the most elevated mean values for economic traits, including seed yield (15.8), green fodder yield (177.5) and dry matter yield (35.8). Additionally, this cluster demonstrated the highest mean values for other attributes, namely PH (147.8), TPL (11.0), NOL (59.3), LW (2.6), DFF (115.0) and DM (145.3) (Table 3). Moreover, it was observed that the cluster mean values for these traits within cluster I exhibited a statistically significant superiority over the general mean value derived from the population of 62 oat genotypes. Cluster III had the highest mean values of NOS and DFF, whereas cluster IV had the highest mean value for LL. Poonia and Phogat, 2017 found similar findings where cluster 1 had the highest mean values for GFY, DMY and PH.

In hk-means clustering, the algorithm initially applies hierarchical clustering to the dataset, which involves creating a hierarchical structure of clusters based on similarity measures. This hierarchical structure is represented in visual presentation as a dendrogram. Four distinct clusters emerge; visually differentiated by different colors as illustrated in Figure 1. Furthermore, after generating the initial clustering hierarchy, the algorithm applies the k-means clustering approach to refine the clusters. The k-means algorithm assigns each data point to the nearest centroid and updates the centroids iteratively until convergence. This step helps to optimize the cluster assignments and improves the compactness & separation of the resulting clusters. This is presented in the form of a cluster plot having 4 distinct groups (Figure 2). The cluster membership in this plot has been adjusted and refined compared to the dendrogram, resulting in distinct and improved groupings.

Cluster III exhibited a minimum number of genotypes, signifying a constricted genetic foundation. It is characterized by their shared ancestral origin and diminished relatedness to the genotypes belonging to other clusters. Inter-cluster distance helps in identifying distinct clusters harboring divergent characteristics (Paw *et al.,* 2020). This in turn, aids in the meticulous selection of the diverse genotypes. Breeding programs frequently aspire to forge hybridizations between genetically distant clusters to instill novel traits, augment genetic diversity and foster the development of superior cultivars, as corroborated by the study conducted by Bhandari *et al.,* (2017). Clusters II and III exhibited the greatest

Table 1: Clustering details of 62 oat genotypes based on D^2 statistics

Cluster number	*Genotypes*
I	OS 6, UPO 212, HFO 1116, HFO 1117, HFO 1118, HFO 1121, HFO 1122, GP 65, GP 298, HFO 424, HFO 902, HFO 903, HFO 1013, HFO 1016, HFO 1109, HFO 1111, HFO 1112, HFO 1113, HFO 1114, HFO 1115, KENT, RO-11-2-2, JHO 2006-1, OL 1766-2, HFO 1107, HFO 1105, OL 125, OL 1861
II	JHO 851, GP 192, GP 492, HFO 1123, OL 1874-2, NDO-1, PLP-1, RO-11-2-6, JHO 99-1, JO-1, HFO 1106
III	HFO 529, GP 580, HFO 607, GP 68, GP 158, HFO 1101, HFO 1104, HFO 1108, OL 1869-1
IV	HFO 611, HFO 707, GP 781, HFO 806, HFO 818, GP 875, HFO 901, HFO 915, HFO 917, HFO 1003, HFO 1005, HJ 8, OS 403, JHO 822

Table 2: Intra and inter-cluster distance based on average Euclidean D^2 values

	I	*II*	*III*	*IV*
I	3.53	4.87	5.48	5.00
II	4.87	4.62	5.93	5.89
III	5.48	5.93	3.84	5.30
IV	5.00	5.89	5.30	4.49

Diagonal values indicate intra-cluster distance

Table 3: Cluster mean and general mean values of 13 phenotypic traits in 62 oat genotypes

Traits	*I*	*II*	*III*	*IV*	*General mean*
PH	147.8	145.6	124.6	143.3	143.0
TPL	11.0	7.0	8.6	8.1	8.1
NOL	59.3	36.2	43.3	42.2	42.3
LL	49.9	49.8	45.4	55.6	50.9
LW	2.6	2.2	2.2	2.2	2.2
PL	31.3	33.7	23.4	32.6	31.8
NOS	66.6	59.2	74.1	60.4	62.4
GFY	177.5	131.5	119.7	150.9	143.1
DMY	35.8	24.4	21.3	28.8	27.1
DFF	115.0	113.8	115.0	110.6	113.2
DM	145.3	141.3	143.0	137.2	140.9
SY	15.8	9.3	12.8	12.9	11.7
TW	32.9	32.4	27.0	37.2	33.2

Note: The values shown in bold are the highest cluster mean values for the respective traits

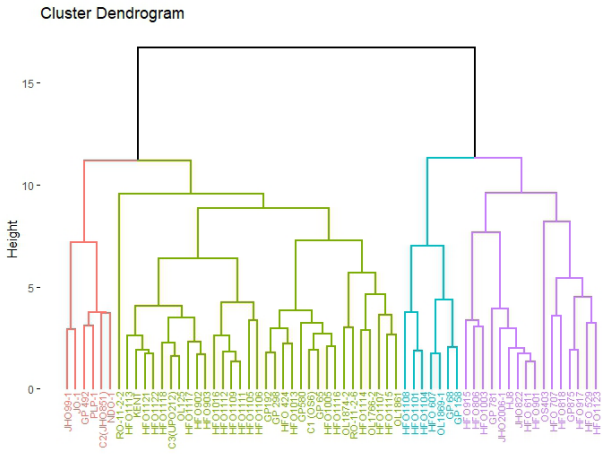

Figure 1: Dendrogram based on initial clustering (hierarchical) of 62 oat genotypes for thirteen phenotypic traits

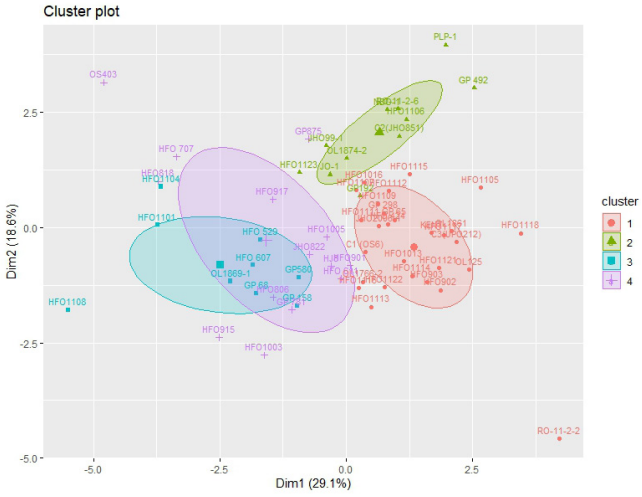

Figure 2: K means cluster plot inferred from final clustering (K means clustering). Refined genotypes which led to final cluster membership

inter-cluster distance, indicating significant dissimilarity between them. Within cluster II, the genotype JHO 851 is a multi-cut check. While genotype HFO 1108 present within cluster III showed the highest GFY and DMY among all 62 genotypes. The cross-breeding of these genotypes has the potential to yield highly heterotic hybridization, akin to the effective implementation observed in the pedigree method. Similarly, second most distant clusters were II and IV. In cluster IV, HFO 707 & HFO 818 were high yielding genotypes for GFY and OS 403 & GP 781 were high seed yielding genotypes. Henceforth, genotypes from these two clusters act as potent source of diverse yet good performing parents required for hybridization (Poonia *et al.,* 2020). Intra-cluster distances, by measuring the genetic similarity within clusters can indicate the extent to which additive genetic effects govern the observed phenotypic variation (Chakravorty *et al.,* 2012). When genotypes within a cluster exhibit small intra-cluster distance, it suggests that they share a high degree of genetic similarity and likely they possess similar combinations of additive alleles. This indicates the presence of strong additive gene action, as the phenotypic variation within the cluster can be attributed to the additive effects of genes that are relatively fixed within the cluster (Carroll *et al.,* 2015). Understanding the extent of additive gene action is crucial in breeding programs and genetic improvement efforts. The highest intra-cluster distance was seen for cluster II (4.62); indicating greater genetic diversity within the cluster. Kumari and Jindal, 2019 observed the highest intra-cluster distance to be 6.02, depicting genetic relation among genotypes. This implies that a wider range of genetic factors, including non-additive gene effects such as dominance and epistasis, influences the observed phenotypic variation. For instance, a study assessed 25 morphological traits and found varying degrees of differentiation, indicating a broad genetic base influencing these traits. It suggested that a wider range of genetic factors influences the observed phenotypic variation within the cluster of early Polish oat cultivars (Boczkowska *et al.,* 2014).

The mean values of traits within a cluster represent the average performance of genotypes within that cluster (Mohammadi and Prasanna, 2003). It provides quantitative evidence of the performance and potential of genotypes for specific traits (Singh *et al.,* 2022b). This average performance can provide insights into the genetic characteristics and potential of genotypes in terms of their ability to express desirable traits or exhibit tolerance to specific environmental conditions. Cluster I demonstrated superior mean values for GFY, DMY, SY, PH, TPL, NOL, LW, DFF and DM, which suggested that the genotypes within this cluster possessed genetic factors that contributed to high-yield performance. That the genotypes in this cluster had favorable combinations of alleles for these yield-related traits. Breeders can focus on genotypes within cluster I to develop cultivars with superior yield attributes. Furthermore, the general mean (for all 62 genotypes as a population) is also mentioned for comparison in Table 3. Cluster I exhibited not only the highest mean values for the aforementioned traits but also surpassed the overall mean. This offers breeders a valuable opportunity to avoid individual genotypic assessments and concentrate their endeavors on representative genotypes within each cluster. This enables them to administer the breeding material with enhanced efficiency and allocate resources in a more judicious manner.

Conclusion

The present study employed a more advanced approach, i.e., hybrid hierarchical k-means clustering to evaluate genetic diversity and performance for various yield contributing traits. The application of hybrid hierarchical k-means clustering combined the advantages of hierarchical and k-means methods. The analysis led to the categorization

of 62 oat genotypes into four distinct clusters, as visually depicted in the cluster plot. This plot provided a clear and concise representation of the clusters and their refined memberships. These results played a crucial role in identifying promising genotypes for future breeding programs. Furthermore, the assessment of inter-cluster distances results in emphasizing the potential of hybridization between genotypes of genetically distant clusters to introduce novel traits and enhance overall genetic diversity. Cluster II and III exhibited the greatest dissimilarity, while cluster I demonstrated the highest mean values for economic traits and outperformed the general mean. These findings provide breeders with valuable insights for crop improvement and cultivar development. The identification of distinct clusters, assessment of inter-cluster and intra-cluster distances and evaluation of mean values for traits provided valuable information for breeders to select superior genotypes, enhance genetic diversity and ultimately foster the development of improved oat cultivars.

Authors Contribution

Rukoo Chawla: Investigation, data collection, writing an original draft and statistical analysis. Meenakshi Jattan: Designing of experiments, supervision, guidance. D.S. Phogat: Contribution of experimental material, supervision and editing. Amit Sharma: Reviewing and improving. Mandeep Redhu: reviewing and editing.

Acknowledgment

For carrying out the research, the authors are grateful to the Director of Research, CCS Haryana Agricultural University, Hisar (Haryana).

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.08

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Variability in Morpho-physicochemical Traits and Selection of Superior Genotypes of Aonla (*Phyllanthus emblica* L.) from Northeast India

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Abstract

Aonla (*Phyllanthus emblica* L.), commonly known as Indian gooseberry, is of great importance due to its medicinal and nutritional value. The current investigation was carried out to study the morphological, physical, and biochemical characteristics of 84 aonla genotypes growing in the wild from Mizoram, Meghalaya, and Tripura states of Northeastern India. Variation was observed in the qualitative parameters (11 parameters) and significant to highly significant differences were observed in the quantitative parameters (22 parameters) among the studied genotypes. The fruit weight varied from 2.6 to 9.78 g, TSS from 7.67 to 18 °Brix, vitamin C from 206.3 to 1392.5 mg/100 g, titrable acidity from 1.7 to 4.9%, total sugar from 3.8 to 12.3%, phenol from 1022.80 to 4210.00 mg/100 g and protein from 2.1 to 6.2%. Six genotypes were found promising and they can be recommended for direct cultivation as well as for breeding programs. These selected genotypes can serve as valuable genetic resources for further research and development efforts.

Keywords: Ascorbic acid, Genetic resources, Indian gooseberry, Phenol, Morphology.

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Received: 16/04/2023 **Revised:** 24/07/2024

Accepted: 25/07/2024

How to cite this article: Rozar KP, S Kumar , R Sharma, N Hegde, KS Kumar and N Kumari (2024) Variability in Morpho-physicochemical Traits and Selection of Superior Genotypes of Aonla (*Phyllanthus emblica* L.) from Northeast India. *Indian J. Plant Genet. Resour.* 37(3): 460-466. **DOI:** 10.61949/0976-1926.2024.v37i03.08

Introduction

Wild aonla (*Phyllanthus emblica* L. family Phyllanthaceae), generally known as Indian gooseberry, is indigenous to India, Pakistan, China, Sri Lanka, Malaysia, and Southeast Asia (Parmar and Kaushal, 1982). Aonla is a rich source of vitamin C, amino acids, and minerals, which make the fruits very nutritious. Aonla is used for various ailments by Ayurveda, Siddha, Unani systems of India, Sri Lankan, Tibetan, and Chinese Systems of medicine. It is used as a healing option and immunity booster for respiratory disorders, heart disorders, scurvy, diarrhea and dysentery, aging, and hair tonic (Krishnaveni and Mirunalini, 2010). Its therapeutic potential is attributed to its antioxidant properties, high vitamin C content, and other beneficial compounds that contribute to its medicinal value across different cultures and traditional healing practices.

Aonla, found naturally in India, is widespread across various regions, including the Himalayas, Bihar, West Bengal, Odisha, Chota Nagpur, Deccan, Karnataka, and the Western Ghats (Rawat and Uniyal, 2003). Typically, wild aonla is found in mixed forests with rugged terrain, sometimes challenging to access. The northeastern part of India, especially in Lower Assam, Meghalaya, Mizoram, and Tripura, harbors a diverse genetic pool of aonla (Sankaran and Dinesh, 2020)

Aonla holds immense importance globally for its various health benefits. However, there is a need to understand and characterize the diverse genetic pool of aonla present in the Northeastern regions of India, particularly local aonla genotypes growing in

Figure 1: Distribution map of the 84 selected genotypes of aonla

Meghalaya, Mizoram, and Tripura. The study aims to assess the morpho-physical-biochemical properties of wild aonla genotypes from these regions to identify superior varieties suitable for cultivation and breeding programs. Additionally, the research seeks to contribute valuable insights from the conservation of genetic resources and inform future genetic improvement endeavors.

Material and Methods

Wild aonla trees were surveyed and a total of 84 aonla genotypes were selected for the study. A minimum of 100 m distance between the two genotypes was taken into consideration while selecting them. However, in cases where there was noticeable variation in morphological traits, the distance criterion was compromised to some extent to ensure a diverse sample. The 84 genotypes were sampled from the states of Mizoram, Meghalaya, and Tripura, comprising eight districts (32 genotypes) from Mizoram, five districts (20 genotypes) from Tripura and seven districts (32 genotypes) from Meghalaya. The sites ranged from 42 to 1447 m. amsl in elevation and latitude from 22°30'15'' to 25°54'59.56'' N, longitude 90°1'25.14'' to 93°21'54.38'' (Figure 1). The geographical details of the selected genotypes have been given in Supplementary file 1. The survey was done in July and August of 2019 and the fruits were collected in three phases: early harvest in October and November, mid-harvest in December 2019 and January 2020, and late harvest till March of 2020. The healthy fruits from each genotype were collected and transported immediately to the lab of the Forestry Department, Mizoram University, and kept in a deep freezer (-80°C) for further physicochemical characterization.

Phenotypic diversity of the germplasm was recorded based on quantitative and qualitative traits related to trees, leaves and fruits. Standard SOPs given by Mahajan *et al.* (2002) and guidelines for conducting DUS testing on Indian Gooseberry given by PPV & FRA (2014) have been followed. Matured leaves from the middle of tertiary branches were selected for the observations on the leaf. Each genotype was replicated three times to ensure the reliability and accuracy of the data. Within each replication, a sample of 20 fruits was collected for analysis. The physical parameters of the fruits were observed in terms of the fruits' shape, surface, stalk and stone shape. Vernier caliper measured fruits' length and diameter, and the weight was taken in on an electric weighing balance. The fruit stalks of diameter above 1-mm were considered thick and diameters below 1-mm were considered as thin stalks. The color of the fruits was

recorded with a visual evaluation of the color chart of the Royal Horticultural Society (RHS), London. The pulp of each fruit was weighed separately and the pulp percentages were worked out. Fruit pulp was dried in an oven at 70°C until a constant weight was achieved and moisture content was expressed in percentage. A hand refractometer was used to determine the total soluble solid (°Brix) and values were corrected to 20°C. Total phenolic content was analyzed as suggested by Ranganna (1986). Acidity was determined by titrating the fruit juice against 0.1N NaOH. Total sugar and reducing sugar were determined by the titration method (Lane and Eynon, 1923) and it was expressed in percentage. Ascorbic acid (mg/100 mL) was analysed as described by Ranganna (2004). In contrast, protein was estimated as per methods described by Lowry *et al.* (1951). The "Weighted-Ranged" method was modified to determine the promising aonla genotypes (Guleryuz *et al.*, 1998). Ascorbic acid content, phenolic content, pulp-stone ratio, TSS, total sugar, fruit weight, protein and yield were taken into consideration while giving the ranking.

Statistical Analysis

The data were subjected to ANOVA analysis by following a completely randomized design. Significance and non-significance differences between different treatments were determined by calculating the respective *F* value and comparing with the appropriate value of *F* at 5% probability level.

Results and Discussion

Morphological Characters of Aonla Trees and Fruits

In this study, a wide range of diversity was observed in the trees, leaves, and fruit traits of 84 aonla genotypes growing in NE India. Detailed morphological characters of the aonla genotypes are presented in Supplementary File 2, and the number and percentage of the genotypes' morphological characters are shown in Figure 2. The tree height of the genotypes studied ranged between 4.5 and 14.4 m. The highest tree height was recorded in CRR1 from Garo Hills, whereas the shortest was recorded in KYR5 from West Jaintia Hills. Among the genotypes studied, the tree group between 9 to 12 m accounted for 45.24% (38 genotypes), followed by the 6 to 9 m group, which accounted for 38.10%, the 12 to 15 m group at 11.90%, and the 3 to 6 m group at 4.76%. The highest tree girth was observed in TSP3 (196 cm), and the minimum girth was observed in WNG2 (20 cm). Girth between 25 to 30 cm. accounted for 65.71%, followed closely by 50 to 70 cm (34.52%), and girths below 25 cm accounted for only 4.76%. Late maturity (54) accounted for 64.29%, followed by mid (25) and early maturity (5), accounting for 29.76 and 5.95%, respectively, of the total genotypes studied. Of all the genotypes, 34 (40.48%) showed a spreading tree shape, followed by semi-spreading (33), which accounted for 39.29%, while erect and drooping contributed 13.10% (11) and 7.14% (6) of tree shape among genotypes (Supplementary Figure 1). 55.95% exhibited sparse foliage, and 44.05% exhibited dense foliage. Oblong (61 trees, 72.62%) leaf shape was recorded maximum, followed by oval (19.05%) and elliptical (8.33%). The average pinnate leaf size ranged from 0.9 (WNG2) to 2 mm (CRR1). The majority of the leaf apexes revealed an acute apex, accounting for 59.52% (50), while obtuse apexes accounted for 40.48% (34) (Supplementary Figure 2). Glabrous leaf surface was recorded to be dominant, which showed 95.24% (80), and moderately glabrous leaf surface showed 4.76% (4) (Supplementary Figure 3). Similarly, variations in morphological characters of aonla genotypes were also recorded by Singh *et al.* (2016) from northeastern regions of India and Singh *et al.* (2021) from semi-arid conditions.

Detailed fruit morphological characters of aonla genotypes are shown in Supplementary File 3, and their numbers and percentages are shown in Figure 3. Three types of fruit shapes were recorded, where flattened round accounted for 47.62%, round shape accounted for 42.86%, and triangular shape accounted for 9.52%. Of the total genotypes studied, 65 (77.38%) had a smooth fruit surface, and 17 (20.24%) had a rough surface. Among the genotypes, 54.76% had a thin stalk, and 45.24% had a thick stalk. Five types of stone shapes (Figure 4) were observed in the present study: round shape (32.14%), oval shape (28.57%), oval round shape (19.05%), triangular shape (17.86%), and flattened round (2.38%) as shown in Figure 3. All fruit colors fell under yellow-green with different shades, except for

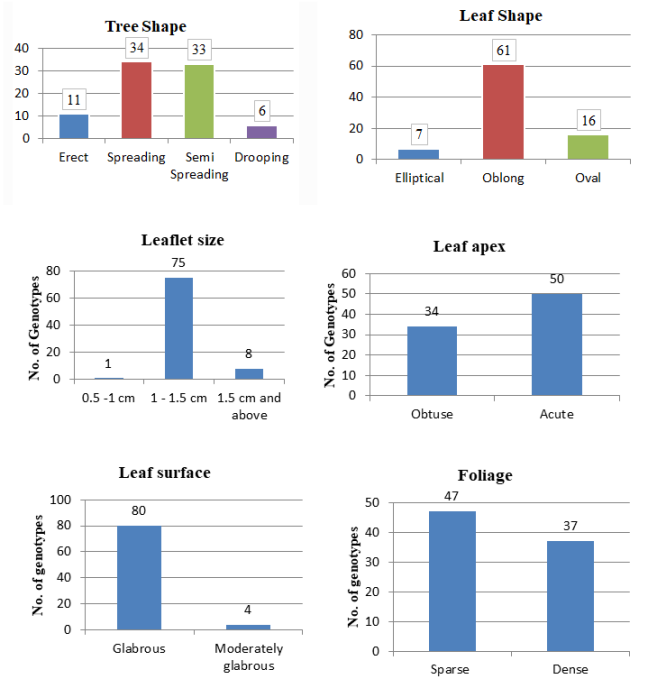

Figure 2: Frequency of aonla genotypes falling under different morphological categories

the MZU-1 sample, which showed an orange-red color. The highest percentage of fruit color was found to be yellow-green 153C and 145C, accounting for 17.86% each, followed by yellow-green 151A, accounting for 14.29%, while the lowest was found to be orange-red 35B (Supplementary Figure 4), accounting for only 1.19% of the total genotypes studied. These findings are in close proximity to the results reported by Rai et *al.* (1993) and Singh *et al.* (2016).

Physical Characters of Aonla Fruits

Aonla genotypes were found to be statistically different ($p < 0.05$) in the context of all studied fruit quality parameters. The result in Table 1 (Supplementary files 4, 5, and 6) revealed that the maximum average fruit length was recorded in JAINTIA1 (24.72) followed by TRA1 (24.6 mm) JAINTIA3 (23.54 mm), and the minimum was recorded in NGP13 (12.77 mm). Among the germplasms, the maximum diameter was recorded in JAINTIA1 (28.04 mm) successively by WNG3 (26.86 mm), subsequently by JAINTIA4 (25.77 mm), whereas the shortest diameter was observed in LTL1 (14.67 mm), The highest L-D ratio among the fruits was observed in WNG2 (1.2 mm) and the lowest ratio was observed in KLS3 with a ratio of 0.78. The highest L-D ratio observed in WNG2 was due to its typical shape where the pulp was found attached in the fruit's stalk. Our findings of fruit length and diameter are in agreement with other findings of Singh *et al.* (2016), who also reported variation in fruit length of aonla in the range of 12.6 to 25.3 mm and 12.7 to 21.00 mm, they also reported variation in fruit diameter ranged between 12.7 to 25.7 mm and 12.7 to 24.4 mm.

The fruit weight was observed maximum in genotype JAINTIA1 (10.71 g) subsequently, by UMR3 (9.99 g), WNG3 (9.78 g), while the minimum weight was observed in genotype LTL1 with 2.45 g only. These findings are consistent with previous research by Chiranjeevi *et al.,* (2018), who also documented variations in fruit physical parameters among different aonla varieties. Similarly, Chandra *et al.* (1998) observed variations in fruit physical parameters among aonla genotypes collected from the Garo Hills of Meghalaya, further supporting the observed diversity in fruit weight within the species. The variation in these fruits may be mainly due to its genetic constitution and the location where they were grown. From all the genotypes, the fruits from MAMIT-4 have the highest dry matter content (23.22%)

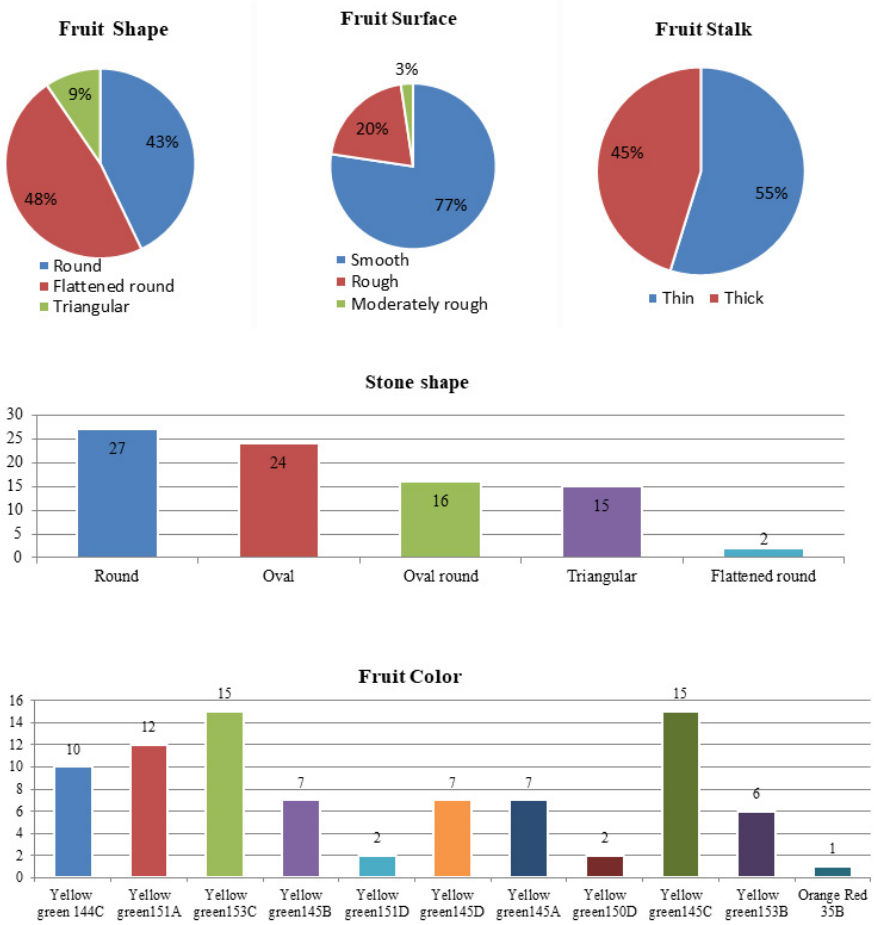

Figure 3: Fruit characteristics of *P. emblica* genotypes (n = 84)

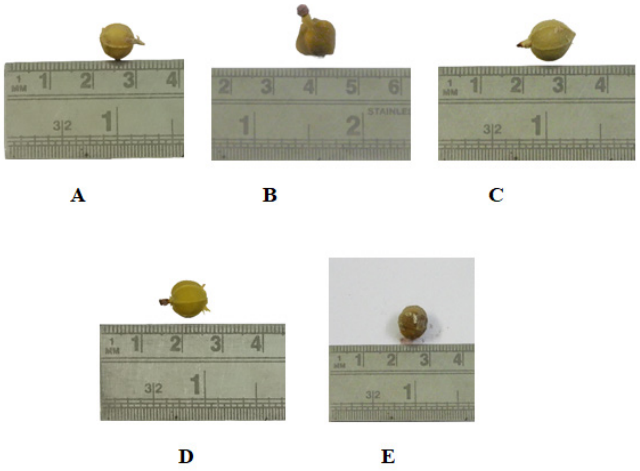

Figure 4: Stone shapes of aonla fruits: Round shape (A), Triangle shape (B), Oval shape (C) and oval round (D) and Flattened round (E)

followed by DACOPGKE (23.18%), whereas the lowest dry matter content was observed in CHITOKTE (14.09%). Kumar *et al.* (2013), Thakur *et al.* (2018) and Chandra *et al.* (2020) also reported similar values of aonla fruits.

Regarding pulp percentage, the maximum was observed in WNG3 with 92.91% followed by TSP5 (92.8%), while the lowest was recorded in CM7 with only 71.84%. Similarly, the maximum pulp-stone ratio was recorded in WNG3 (13.10) followed by TSP5 (12.89), minimum pulp-stone was recorded in CM7 (2.48). Pulp-to-stone ratio is a vital factor in identifying a superior genotype by breeders. These results align with previous studies conducted by Kumar *et al.* (2013), Hazarika and Laltluangkimi (2019) and Chandra *et al.* (2020).

In the present study the stone weight ranges from 0.28 to 1.54 g. The maximum value was recorded in SM1 (1.54 g) and minimum in TSP5 (0.28 g). Our result is in agreement with the findings of Chandra *et al.* (1998); Singh and Singh (2016) and Hazarika and Laltluangkimi (2019) from North-east India.

Significantly higher fruit yield of aonla genotype was recorded from TSP1 with 163.54 kg/tree followed by TSP2 with 152.35 kg/tree. While, the lowest yield was recorded from WNG3 with only 31.25 kg/tree. One possible explanation for the increase in production is that there are more fruits per determinate shoot. Our findings showed a higher yield as compared to aonla cultivar Balwan (85.33 kg/tree) recorded from Punjab by Aulakh *et al.* (2013). Variation in fruit yield of aonla was also reported by Pandey *et al.* (2016).

Biochemical Parameters of Aonla Fruits

Table 2 (Supplementary files 7, 8 and 9) reveals that the total soluble solid of the genotype ranged from 7.5° (KYR6) to 18 °Brix (SCH1). Among the studied germplasm, WNG2 was observed to have the highest titriable acidity (4.90) and the minimum was observed in UMR31 (1.65). TSS and acidity ratio ranged between 1.65 and 8.91, the maximum was

Table 1: Mean and range of physical attributes of fruits of aonla in different North-East states

State	*Number of trees*	*Fruit length (mm)*	*Fruit diameter (mm)*	*Ld ratio*	*Pulp (%)*	*Stone weight (G)*	*Pulp weight (G)*	*Pulp-stone ratio*	*Fruit weight (g)*	*Dry matter content (%)*	*Yield (kg/tree)*
meghalaya	32	19.12 (12.77–24.72)	20.96 (15.57–28.04)	0.91 (0.79–1.20)	87.90 (75.87–92.91)	0.71 (0.32–1.4)	5.5 (1.74–11.14)	8.08 (3.15–13.10)	5.969 (2.61–10.71)	18.78 (14.09–23.18)	57.23 (31.25–111.07)
Mizoram	32	17.23 (12.78–23.47)	19.24 (14.67–24.85)	0.9 (0.78–0.99)	85.64 (71.84–92.80)	0.66 (0.28–1.54)	4.21 (1.66–7.95)	6.94 (2.48–12.89)	4.63 (2.45–9.10)	19.12 (15.34–23.22)	75.86 (39.61–163.54)
Tripura	20	18.15 (15.30–20.80)	20.27 (16.97–23.13)	0.91 (0.81–1.01)	88.7 (81.38–91.77)	0.65 (0.44–0.96)	5.21 (3.16–6.86)	8.41 (5.16–11.22)	5.38 (3.58–7.61)	18.93 (16.26–23.07)	58.31 (32.66–100.39)
-											
$CD_{0.05}$		0.84	0.90	0.03	1.62	0.083	0.497	1.10	0.60	1.11	
-											
CV		5.24	5.09	4.30	1.15	7.628	6.191	8.82	12.80	3.62	

*CD and CV of each parameter are calculated for 84 genotypes combined

Table 2: Mean and range values of biochemical parameters of aonla fruits in different northeastern states

State	*TSS (°Brix)*	*Titriable acidity (%)*	*TSS : acidity*	*Ascorbic acid (mg/100g)*	*Total sugar (%)*	*Reducing sugar (%)*	*Non-Reducing sugar (%)*	*Phenol (mg/100 g)*	*Protein (%)*
Meghalaya	11.47 (7.50–17.50)	2.70 (1.65–4.90)	4.6 (2.11–7.66)	663.51 (180.00–1255.00)	8.15 (5.46–12.24)	5.13 (3.51–8.17)	3.28 (0.96–6.35)	1285.77 (687.73–3201.41)	3.92 (2.18–6.24)
Mizoram	12.36 (8.07–18.00)	2.78 (1.66–3.93)	4.69 (2.22–8.91)	686.42 (195.00–1393.00)	8.19 (4.96–11.33)	5.2 (3.43–6.53)	3.25 (0.80–6.28)	1331.6 (620.55–2598.16)	3.86 (2.31–6.13)
Tripura	11.56 (8.17–17.17)	2.93 (1.70–4.39)	4.17 (2.11–6.95)	753.93 (300.70–1176.00)	8.52 (3.90–13.05)	5.48 (2.47–9.10)	3.29 (1.10–5.59)	1605.38 (863.66–2979.61)	4.12 (2.48–5.58)
$CD_{0.05}$	0.89	0.28	0.57	39.63	0.79	0.39	0.81	100.13	0.51
CV	4.66	6.17	7.74	3.54	5.92	4.65	15.26	4.50	8.02

*CD and CV of each parameter are calculated for 84 genotypes combined

recorded from LTL1 and the minimum was recorded from both NKL1 and LCR1. These findings of aonla genotypes closely align with Singh and Singh (2016), Singh *et al.* (2016), and Hazarika and Laltluangkimi (2019). Accession MMT1 (1392.5 mg 100 g^{-1}) recorded the highest ascorbic acid and for the same least value was calculated in genotype KYR6 (180 mg 100 g^{-1}). More or less similar variation in Ascorbic acid was observed from the Garo Hills of Meghalaya, which ranged between 322.5 to 982.50 mg/100 g (Chandra *et al.,* 1998) from northeast India ranging between 375 to 1428.50 mg/100 mL (Singh and Singh, 2016; Singh *et al.,* 2016) and from Garhwal Himalaya, ranging between 191.13 mg 100 - 495.21 mg 100 g^{-1} (Naithani *et al*., 2020).

The total sugar of the genotype ranged from 3.89 to 13.05%, in which the maximum was observed in LCR1 and the minimum in SNM2. The average Total sugar was determined between 7.50 to 13.68% from 39 aonla genotypes (Singh *et al.,* 2016), between 3.2 to 6.0% (Kumar *et al.,* 2013). In the present study, it was also revealed that genotype LCR1 had a significantly higher level of reducing sugar (9.1%) and TURA1 had the highest non-reducing sugar (6.35%). However, the minimum reducing sugar was determined in SNM2 (2.47%) and the lowest non-reducing in LTL1 (0.8%). Some other researchers also recorded variations in reducing sugar and non-reducing sugars (Kumar *et al.,* 2013; Hazarika and Laltluangkimi, 2019).

Among all genotypes, polyphenol content as gallic acid equivalent was recorded as the maximum value in UMR-2 (320.41 mg/100 g) and MMT4 recorded the minimum value (620.55 mg/100 g) of phenol. Singh *et al.,* (2016) reported that there was a significant variation of phenolic content in Aonla genotypes selected from North East India, with the value range between 944.85 to 4969.50 mg. Kumar and Rao, (2011) also determined the phenolic content (Gallic acid equivalent) between 3505.61 to 6155.71 mg/100 mL of different aonla cultivars. Parveen and Khatkar (2015) reported that desi aonla had a low protein of about 2.12%. In this study average protein content in the selected genotype of fruit ranged between 2.18 to 6.24%, the highest in CHITOKTE and the lowest in GBD5 genotype. The variation in protein content among different genotypes was also reported by other researchers (Kafkas *et al.,* 2020).

Conclusion

This study provides a comprehensive overview of the morphological diversity present in aonla genotypes in Northeast India. KOLASIB, WNG-3, TPN-7, TSP-1, TSP-3 and TURA-4 (Supplementary Figure 5) are observed as promising genotypes on the basis of the "Weighted-Ranged" method. The findings of the study indicate a high degree of diversity in the morphological characters of aonla genotypes. These findings provide important information for the selection and breeding of aonla genotypes with desirable morphological traits. However, further studies are necessary to assess

the genetic diversity of these genotypes and understand the underlying molecular mechanisms that control these morphological characters. Such studies could facilitate the identification of key genes involved in morphological traits and enable the development of molecular markers for selecting desirable genotypes. Additionally, further research could investigate the relationship between morphological traits and aonla fruit quality attributes such as nutritional and medicinal properties. Overall, the study provides an important baseline for future research on aonla genotypes, which could facilitate the development of improved aonla cultivars with desirable morphological and quality traits. The study provides a valuable contribution to the understanding of aonla diversity in northern India and can aid in the development of a sustainable aonla production system.

Acknowledgment

The present study was supported by the Department of Biotechnology, Ministry of Science and Technology, New Delhi, India (BT/PR25115/NER/95/1024/2017)

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Supplementary Files

https://ispgr.in/public/site/supplementary-files/23-21-supplementary-files.pdf

P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.09

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Evaluation of Sesame Genotypes against Leaf Webber and Capsule Borer, *Antigastra Catalaunalis* (Duponchel) Resistance

S Omprakash*, C Narendra Reddy, M Swarna Sree, T Kiran Babu, M Sreedhar and D Padmaja

Abstract

Evaluation of sesame genotypes against leaf webber and capsule borer (*Antigastra catalaunalis)* was carried out under field conditions at the Regional Agricultural Research Station, Polasa, Jagtial, during late *kharif* 2018 and 2019. A total of 60 genotypes, along with a resistant check, SI-250 and a susceptible check, TC-25 were screened. During the two years of screening, none of the genotypes were highly resistant to *A. catalaunalis*. Seven sesame genotypes *viz*., JCS 3894, JCS 3884, JCS 3594, JCS 3265, JCS 3910, JCS 4018 and JCS 3605, were categorized as resistant and two genotypes, JCS 3755 and SI1052 showed highly susceptible reaction based on grading during the year 2018. The genotypes *viz.,* JCS 3894, JCS 3578, JCS 3593, JCS 3265, SI 9050, JCS 3981 and JCS 3605 showed resistant reactions in the year 2019 and none of the genotypes showed highly susceptible reactions against *A. catalaunalis.*

Keywords: Capsule borer, Genotypes, Grading, Leaf webber, Screening, Sesame.

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Received: 14/08/2023 **Revised:** 04/07/2024

Accepted: 16/07/2024

How to cite this article: Omprakash S, CN Reddy, MS Sree, TK Babu, M Sreedhar and D Padmaja (2024) Evaluation of Sesame Genotypes against Leaf Webber and Capsule Borer, *Antigastra Catalaunalis* (Duponchel) Resistance. *Indian J. Plant Genet. Resour.* 37(3): 467-472.
DOI: 10.61949/0976-1926.2024.v37i03.09

Introduction

Sesame, *Sesamum indicum* (L.) is the oldest oilseed crop of the world cultivated throughout India and considered as 'Queen of oilseeds' because of its superior oil quality. Among the several cardinal factors responsible for the low yield of sesame, damage by insect pests is considered as one of the vital factors causing substantial yield loss under field conditions. Among 67 insect pests damaging the sesame crop *viz.,* leaf webber and capsule borer (*Antigastra catalaunalis* Duponchel), gall fly (*Asphondylia sesami* Felt) were considered as major insect pests (Choudhary *et al*., 1986). The leaf webber and capsule borer (*A. catalaunalis*) feed on tender foliage by webbing the top leaves, feeding on flowers and boring into the pods (Narayanan and Nadarajan, 2005). This insect pest causes 10 to 70% infestation on leaves, 34 to 62% on flowers and 10 to 44% infestation on pods resulting about 72% loss in yield (Ahirwar *et al.,* 2010). Resistant varieties play a major role in integrated pest management (IPM) by reducing the insecticidal application against insect pests and improving the performance of natural enemies. Even a low level of resistance is also effective, which in turn reduces the number of sprays on crops and the cost of spraying (Srivastava, 1993). Therefore, it is important to identify genotypes. Knowledge of resistance mechanisms and associated factors is essential for the effective utilization of resistant sources in the crop improvement program. So, the use of resistant varieties is recognized as an environmentally safe and economically sound component of pest management. Insect-resistant varieties provide

pest control at no cost to farmers (Prem Kishore, 2001). So, the present investigation on "evaluation of sesame genotypes against leaf webber and capsule borer, *Antigastra catalaunalis* (Duponchel) resistance was taken up to identify resistant genotypes.

Materials and Methods

The investigation on screening of sesame genotypes against *A. catalaunalis* was carried out under field conditions at Regional Agricultural Research Station, Polasa, Jagtial (18°15′15.8″ N, 78°58′51.6″ E) during late *kharif* 2018 and 2019. A total of 60 genotypes along with resistant check, SI-250 and susceptible check, TC-25 were screened (Average weather of 33.2 (T maximum), 21.0 (T minimum), 90.56 (RH Morning), 66.11 (RH evening)). Each genotype was sown (30.08.2018 and 28.08.2019 in respective years) in 5 m row length with a spacing of 30 x 15 cm. Sesame genotypes were sown in three blocks and 20 genotypes were accommodated in each block along with resistant and susceptible checks. The intercultural operations as well as fertilizer application (N, P_2O_5 and K_2O @ 40, 20 and 20 kg ha^{-1}, respectively) were done as per recommendations. No plant protection chemicals were sprayed against insect pests and screening was done under natural field conditions only. Data on leaf webber and capsule borer *(A. catalaunalis*) infestation in different genotypes was recorded under field conditions during both *late kharif* 2018 and 2019 seasons. Observation of leaf, flower and capsule damage by *A. catalaunalis* was recorded on 10 designated plants at 30 days after sowing (leaf damage), 45 DAS (flower damage) and 60 DAS (capsule damage). The healthy and damaged leaf, flower and capsules were counted and finally percent leaf, flower and capsule damage was calculated. Further, the reaction of genotypes against *A. catalaunalis* was categorized by using 0 to 9 scale as suggested by Sridhar and Gopalan (2002) (Tables 1 and 2).

$$\text{Percent leaf/flower/capsule damage} = \frac{\text{No. of damaged leaves/flowers/capsules}}{\text{Total no. of leaves/flowers/capsules}} \times 100$$

Results and Discussion

Screening results of sesame genotypes during late *kharif* 2018 (Table 3) revealed that leaf damage ranged from 6.16 - 30.43%, flower damage 3.22 to 16.67% and capsule damage 2.06 to 9.05% among the screened genotypes. Out of 60 genotypes screened against *A. catalaunalis*, none of the genotypes recorded a highly resistant reaction. Seven genotypes *viz.,* JCS 3894, JCS 3884, JCS 3594, JCS 3265, JCS 3910, JCS 4018 and JCS 3605 were categorized as resistant, eighteen genotypes *viz.,* DT116, JCS 3886, JCS 3893, JCS 2477, RF2, JCS 3596, JCS 3593, JCS 2420, JCS 3202, TK4-22, GT 50, JCS 1020, SI 1125, ES 5, ES 15, ES 7, SI 9050 and JCS 3881 were categorized as moderately resistant, 33 genotypes *viz.,* GPC 13-12, JCS 3895, JCS 3889, JCS 3739, DT 112, JCS 3872, DT 97, JCS 3992, JCS 3898, JCS 3890, RF4, JCS 3578, JCS 3605, JCS 3599, JCS 3751, JCS 2611, JCS 2696, JCS 3287, DT 26, SI 72-A, SI 1036, NIC 8011, SI 253, KMR 14-A, ES-10, NIC 16226, SI 248, SI 885, PVT 224, JCS 3981, JCS 3880, JCS 2698 and JCS 4013 were categorized as susceptible and two sesame genotypes JCS 3755 and SI1052 showed highly susceptible reaction based on grading during the year 2018.

During the year 2019 same set of sesame genotypes (Table 4) was screened against *A. catalaunalis*. The leaf damage among sesame genotypes ranged from 5.78 to 21.12%, flower damage 1.64 to 13.33% and capsule damage 2.01 to 8.43. Among 60 sesame genotypes screened during 2019, none of the genotypes showed highly resistant reactions and seven entries *viz.,* JCS 3894, JCS 3578, JCS 3593, JCS 3265, SI 9050, JCS 3981 and JCS 3605 showed resistant reactions. The 21 sesame genotypes *viz.,* DT 116, JCS 3886, DT 97, JCS 3992, JCS 3893, JCS 3884, JCS 3596, JCS 2420, TK 4-22, GT 50, JCS 1020, ES-5, KMR 14-A, SI 248, ES-7, SI 885, JCS 3910, JCS 3881, JCS 2698, JCS 4018 and JCS 4013 showed moderately resistant reaction and 32 genotypes *viz.,* GPC 13-12, JCS 3895, JCS 3889, JCS 3739, DT 112, JCS 3755, JCS 3872, JCS 3898, JCS 3890, JCS 2477, RF4, RF2, JCS 3605, JCS 3599, JCS 3594, JCS 3751, JCS 2611, JCS 2696, JCS 3287, DT26, JCS 3202, SI 72-A, SI 1036, NIC 8011, SI 253, SI 1125, SI 1052, ES-15, ES-10, NIC 16226, PVT 224, JCS 3880 showed susceptible reaction against *A. catalaunalis.*

These results were in accordance with Panday *et al.* (2014), who reported that none of the entry was recorded as tolerant against *A. catalaunalis*. Mamta Devi Choudhary *et al.* (2018) who reported that, among 15 varieties of sesame against *A. catalaunalis* and, none were found

Table 1: Scoring method for evaluation of sesame genotypes against *A. catalaunalis*

Percent damage			
Leaf (A)	*Flower (B)*	*Pod (C)*	*Cumulative score (A+B+C) / 3*
0–10	0–5	0–2	1
10–20	5–10	2–4	3
20–30	10–15	4–6	5
30–40	15–20	6–8	7
>40	>20	>8	9

Table 2: Grading method for evaluation of sesame genotype against *A. catalaunalis*

Cumulative score	*Grade*	*Degree of resistance*
0–1.0	1	Highly resistant (HR)
1.1–2.0	3	Resistant (R)
2.1–3.0	5	Moderately resistant (MR)
3.1–5.0	7	Susceptible (S)
5.1–9.0	9	Highly susceptible (HS)

Table 3: Screening data and reaction of sesame genotypes against leaf webber and capsule borer *A. catalaunalis* during late *kharif* 2018

S. No.	*Genotypes*	*Leaf damage (%)*	*Score (a)*	*Flower damage (%)*	*Score (b)*	*Capsule damage (%)*	*Score (c)*	*Cumulative score ((a+b+c)/3)*	*Grade*	*Reaction*
1	GPC 13-12	11.08	3	10.89	5	7.25	7	5.0	7	S
2	JCS 3895	14.95	3	6.87	3	6.21	7	4.3	7	S
3	JCS 3889	16.16	3	8.14	3	4.65	5	3.7	7	S
4	JCS 3894	6.16	1	3.56	1	2.12	3	1.7	3	R
5	DT 116	13.16	3	6.78	3	3.94	3	3.0	5	MR
6	JCS 3739	10.13	3	9.12	3	6.10	7	4.3	7	S
7	DT 112	14.93	3	10.71	5	7.62	7	5.0	7	S
8	JCS 3886	18.51	3	8.06	3	3.47	3	3.0	5	MR
9	JCS 3755	14.86	3	16.53	7	7.57	7	5.7	9	HS
10	JCS 3872	18.09	3	8.66	3	7.38	7	4.3	7	S
11	DT 97	10.48	3	5.16	3	4.41	5	3.7	7	S
12	JCS 3992	21.19	5	6.90	3	3.94	3	3.7	7	S
13	JCS 3893	7.12	1	8.12	3	3.57	3	2.3	5	MR
14	JCS 3884	8.87	1	3.71	1	3.87	3	1.7	3	R
15	JCS 3898	13.21	3	6.00	3	6.59	7	4.3	7	S
16	JCS 3890	16.53	3	8.12	3	7.58	7	4.3	7	S
17	JCS 2477	16.25	3	9.12	3	3.22	3	3.0	5	MR
18	RF4	20.51	5	7.02	3	6.70	7	5.0	7	S
19	RF2	16.93	3	5.48	3	3.27	3	3.0	5	MR
20	JCS 3596	11.88	3	3.31	1	3.04	3	2.3	5	MR
21	JCS 3578	15.85	3	5.94	3	6.00	5	3.7	7	S
22	JCS 3605	17.83	3	6.19	3	7.14	7	4.3	7	S
23	JCS 3599	15.66	3	8.12	3	4.11	5	3.7	7	S
24	JCS 3594	7.27	1	3.08	1	2.98	3	1.7	3	R
25	JCS3751	18.89	3	8.66	3	5.16	5	3.7	7	S
26	JCS 3593	9.98	1	4.12	1	4.57	5	2.3	5	MR
27	JCS 2611	14.45	3	12.07	5	5.53	5	4.3	7	S
28	JCS 2696	26.01	5	10.00	3	7.66	7	5.0	7	S
29	JCS 3287	16.77	3	7.69	3	9.05	9	5.0	7	S
30	JCS 3265	8.96	1	3.22	1	2.06	3	1.7	3	R
31	DT 26	21.65	5	9.94	3	6.34	7	5.0	7	S
32	JCS 2420	13.25	3	6.68	3	3.73	3	3.0	5	MR
33	JCS 3202	13.35	3	3.81	1	4.56	5	3.0	5	MR
34	TK 4-22	10.30	3	4.24	1	3.70	3	2.3	5	MR
35	GT 50	11.69	3	4.32	1	2.26	3	2.3	5	MR
36	JCS 1020	11.41	3	6.56	3	3.35	3	3.0	5	MR
37	SI 72-A	14.06	3	10.77	5	7.14	7	5.0	7	S
38	SI 1036	16.15	3	16.67	7	5.90	5	5.0	7	S
39	NIC 8011	13.81	3	8.00	3	7.43	7	4.3	7	S
40	SI 253	20.16	5	7.43	3	7.17	7	5.0	7	S
41	SI 1125	12.50	3	3.73	1	3.80	3	2.3	5	MR
42	ES-5	16.06	3	6.40	3	3.57	3	3.0	5	MR
43	SI 1052	30.43	7	12.34	5	7.46	7	6.3	9	HS

Cont....

S. No.	Genotypes	Leaf damage (%)	Score (a)	Flower damage (%)	Score (b)	Capsule damage (%)	Score (c)	Cumulative score ((a+b+c)/3)	Grade	Reaction
44	KMR 14-A	24.52	5	8.45	3	3.88	3	3.7	7	S
45	ES -15	8.51	1	9.56	3	3.53	3	2.3	5	MR
46	ES-10	11.43	3	6.56	3	5.77	5	3.7	7	S
47	NIC 16226	12.23	3	8.16	3	5.61	5	3.7	7	S
48	SI 248	10.31	3	7.48	3	5.03	5	3.7	7	S
49	ES-7	14.17	3	3.68	1	2.76	3	2.3	5	MR
50	SI 885	17.63	3	6.28	3	5.63	5	3.7	7	S
51	SI 9050	12.42	3	4.70	1	3.31	3	2.3	5	MR
52	PVT 224	23.49	5	5.10	3	7.57	7	5.0	7	S
53	JCS 3981	8.89	1	7.23	3	6.33	7	3.7	7	S
54	JCS 3910	9.09	1	4.26	1	2.75	3	1.7	3	R
55	JCS 3881	8.11	1	7.59	3	3.77	3	2.3	5	MR
56	JCS 3880	24.22	5	7.87	3	5.63	5	4.3	7	S
57	JCS 2698	13.25	3	6.25	3	5.69	5	3.7	7	S
58	JCS 4018	9.88	1	4.62	1	3.82	3	1.7	3	R
59	JCS 3605	7.12	1	4.76	1	3.85	3	1.7	3	R
60	JCS 4013	18.04	3	11.11	5	3.06	3	3.7	7	S
	TC 25 (S. check)	28.12	5	12.39	5	8.11	9	6.3	9	HS
	SI 250 (R. check)	6.68	1	1.75	1	3.26	3	1.7	3	R

HR: Highly Resistant, R: Resistant, MR; Moderately Resistant, S: Susceptible, HS: Highly Susceptible

Table 4: Screening data and reaction of sesame genotypes against leaf webber and capsule borer *A. catalaunalis* during late *kharif* 2019

S. No.	Genotypes	Leaf damage (%)	Score (a)	Flower damage (%)	Score (b)	Capsule damage (%)	Score (c)	Cumulative score ((a+b+c)/3)	Grade	Reaction
1	GPC 13-12	12.48	3	6.27	3	7.71	7	4.3	7	S
2	JCS 3895	11.89	3	5.77	3	6.12	7	4.3	7	S
3	JCS 3889	14.55	3	13.33	5	6.48	7	5.0	7	S
4	JCS 3894	5.78	1	1.90	1	2.16	3	1.7	3	R
5	DT 116	12.18	3	5.63	3	3.90	3	3.0	5	MR
6	JCS 3739	16.09	3	8.94	3	6.78	7	4.3	7	S
7	DT 112	15.04	3	6.16	3	6.76	7	4.3	7	S
8	JCS 3886	9.92	1	7.14	3	3.92	3	2.3	5	MR
9	JCS 3755	19.31	3	10.12	5	5.15	5	4.3	7	S
10	JCS 3872	18.05	3	8.20	3	5.75	5	3.7	7	S
11	DT 97	10.08	3	6.38	3	3.21	3	3.0	5	MR
12	JCS 3992	18.18	3	6.98	3	3.76	3	3.0	5	MR
13	JCS 3893	13.56	3	6.80	3	2.88	3	3.0	5	MR
14	JCS 3884	12.50	3	4.92	1	5.49	5	3.0	5	MR
15	JCS 3898	13.76	3	6.00	3	7.76	7	4.3	7	S
16	JCS 3890	12.29	3	12.24	5	6.76	7	5.0	7	S
17	JCS 2477	19.12	3	8.49	3	4.06	5	3.7	7	S

Cont....

S. No.	Genotypes	Leaf damage (%)	Score (a)	Flower damage (%)	Score (b)	Capsule damage (%)	Score (c)	Cumulative score ((a+b+c)/3)	Grade	Reaction
18	RF4	19.88	3	11.92	5	6.00	5	4.3	7	S
19	RF2	12.70	3	6.06	3	4.41	5	3.7	7	S
20	JCS 3596	11.64	3	4.76	3	3.06	3	3.0	5	MR
21	JCS 3578	8.89	1	2.70	1	3.83	3	1.7	3	R
22	JCS 3605	12.50	3	12.73	5	5.32	5	4.3	7	S
23	JCS 3599	14.09	3	5.51	3	7.75	7	4.3	7	S
24	JCS 3594	10.12	3	6.82	3	4.08	5	3.7	7	S
25	JCS3751	20.00	3	9.82	3	8.79	9	5.0	7	S
26	JCS 3593	8.21	1	4.53	1	2.25	3	1.7	3	R
27	JCS 2611	15.05	3	7.55	3	6.86	7	4.3	7	S
28	JCS 2696	24.05	5	5.56	3	6.99	7	5.0	7	S
29	JCS 3287	20.00	3	9.43	3	8.43	9	5.0	7	S
30	JCS 3265	8.12	1	2.00	1	2.01	3	1.7	3	R
31	DT 26	22.10	5	7.02	3	6.78	7	5.0	7	S
32	JCS 2420	13.00	3	4.55	1	3.85	3	2.3	5	MR
33	JCS 3202	13.33	3	6.90	3	4.78	5	3.7	7	S
34	TK 4-22	12.74	3	3.12	1	2.33	3	2.3	5	MR
35	GT 50	18.20	3	4.76	1	4.69	5	3.0	5	MR
36	JCS 1020	13.21	3	3.64	1	3.77	3	2.3	5	MR
37	SI 72-A	20.00	3	12.32	5	8.00	7	5.0	7	S
38	SI 1036	12.96	3	11.63	5	6.00	5	4.3	7	S
39	NIC 8011	21.05	5	12.50	5	5.77	5	5.0	7	S
40	SI 253	20.49	5	8.33	3	4.13	5	4.3	7	S
41	SI 1125	17.02	3	10.26	5	7.02	7	5.0	7	S
42	ES-5	11.76	3	5.26	3	3.39	3	3.0	5	MR
43	SI 1052	19.12	3	6.78	3	5.70	5	3.7	7	S
44	KMR 14-A	11.93	3	3.85	1	3.45	3	2.3	5	MR
45	ES -15	14.16	3	10.92	5	5.08	5	4.3	7	S
46	ES-10	12.39	3	10.26	5	6.41	7	5.0	7	S
47	NIC 16226	9.57	1	11.32	5	6.67	7	4.3	7	S
48	SI 248	20.01	5	2.13	1	3.75	3	3.0	5	MR
49	ES-7	11.77	3	4.55	1	3.66	3	2.3	5	MR
50	SI 885	17.89	3	2.38	1	5.36	5	3.0	5	MR
51	SI 9050	7.09	1	4.20	1	3.51	3	1.7	3	R
52	PVT 224	21.12	5	5.36	3	7.41	7	5.0	7	S
53	JCS 3981	6.80	1	4.20	1	2.56	3	1.7	3	R
54	JCS 3910	10.12	3	1.67	1	3.16	3	2.3	5	MR
55	JCS 3881	13.11	3	6.00	3	3.06	3	3.0	5	MR
56	JCS 3880	17.32	3	14.12	5	7.86	7	5.0	7	S
57	JCS 2698	16.80	3	3.85	1	4.92	5	3.0	5	MR
58	JCS 4018	15.38	3	2.63	1	2.18	3	2.3	5	MR
59	JCS 3605	8.76	1	1.64	1	3.95	3	1.7	3	R

Cont....

S. No.	*Genotypes*	*Leaf damage (%)*	*Score (a)*	*Flower damage (%)*	*Score (b)*	*Capsule damage (%)*	*Score (c)*	*Cumulative score ((a+b+c)/3)*	*Grade*	*Reaction*
60	JCS 4013	19.60	3	6.32	3	3.31	3	3.0	5	MR
	TC 25 (S. check)	26.18	5	11.12	5	8.33	9	6.3	9	HS
	SI 250 (R. check)	7.62	1	5.06	3	1.28	1	1.66	3	R

HR: Highly Resistant, R: Resistant, MR; Moderately Resistant, S: Susceptible, HS: Highly Susceptible

immune. Present results were in agreement with Balaji and Selvanarayan (2009) who reported that among 140 sesame accessions evaluated against leaf webber and capsule borer *A. catalaunalis*, none of the accessions was rated highly resistant (HR), but 14 accessions were categorized as resistant (R), while 110 accessions were susceptible (S) and 16 accessions were highly susceptible (HS). These results were also in accordance with Karuppaiah and Nadarajan (2013) who reported that the two genotypes as moderately resistant with a score of 3 and grade 5. These findings in agreement with Mishra *et al*. (2016) reported, based on the cumulative scoring, 13 accessions and resistant check SI-250 were rated as resistant.

Based on two years of screening data, it was summarized that the sesame genotypes *viz.,* JCS 3824, JCS 3265 and JCS 3605 consistently showed resistant reactions in both years. So, these genotypes can be useful in resistant breeding programs.

Acknowledgment

The authors would like to thank Professor Jayashankar Telangana State Agricultural University for providing financial assistance.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.10

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Multivariate Analysis of Fodder Maize (*Zea mays* L.) Germplasm Lines under Temperate Niches

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Abstract

An experiment was conducted following randomised complete block design (RCBD) with three replications to assess the genetic variability among germplasm lines of fodder maize. A total of 16 traits were taken including yield and quality attributes. The statistical analysis of the data demonstrated existence of significant genetic variation among all the evaluated maize germplasm lines for each trait under study. The phenotypic coefficients of variation (PCV) estimates were invariably higher than their corresponding genotypic coefficient of variation (GCV) values thereby suggesting the environmental influence. Fresh leaf weight per plant exhibited high genotypic and phenotypic coefficient of variation. Selection of superior fodder maize germplasm lines based on their performance for green fodder yield per plant, grain yield per plant, fresh stem weight per plant and stem girth will be effective as these traits showed high heritability coupled with high genetic advance. Plant height, fresh leaf weight per plant and stem girth exhibited considerable direct effects, coupled with highly significant and positive correlation with green fodder yield per plant indicating true correlation between them, therefore, selecting these traits would greatly enhance green fodder yield per plant. Principal component analysis revealed that five out of 16 principal components recorded Eigen values greater than one and could explain 88.33% of the total variability. Based on PC1 scores, the germplasm lines KDFM-86, KDFM-79, KDFM-76 and KDFM-55 were identified as potential contributors of variability, which can be used in crossing programs to transfer key traits related to yield.

Keywords: Cluster analysis, Fodder, PCA, *Zea mays* L.

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Received: 05/11/2023 **Revised:** 24/06/2023

Accepted: 25/06/2024

How to cite this article: Bashir M, NS Khuroo, ZA Dar, A Wani, Z Rashid and AB Shikari (2024) Article Title. *Indian J.PlantGenet.Resour.*37(3):473-481.**DOI:** 10.61949/0976-1926.2024.v37i03.10

Introduction

Maize (*Zea mays* L.) is an important cereal crop belonging to the tribe Maydeae of the grass family Poaceea (Dhoot *et al.,* 2017). It is a dual purpose crop that produces kernels for human consumption as well as fodder for livestock (Borkhatariya *et al.,* 2022). It is considered an ideal forage because it grows quickly, produces high yields, is palatable, is rich in nutrients and helps to increase body weight and milk quality in cattle (Sattar *et al.,* 1994). Because of the size and dispersion of its foliage, maize is better than most other cereal crops at utilising sunlight being a C4 plant and develops more quickly (Warman, 2003). As fodder for livestock, maize is excellent, highly nutritive and sustainable (Hukkeri *et al.,* 1977, Iqbal *et al.,* 2006). Maize holds sufficient nutritional quality when we compare it to other non-leguminous fodders (Mahdi *et al.,* 2011).

India has the largest livestock population in the world and is the top producer of milk, accounting for 23% of global milk production. Despite India's largest livestock population and its global position with highest milk production, the productivity of Indian cattle is low compared to the global average and even lower than the European countries (Rajendra and Mohanty, 2004). Milk production is heavily reliant on the availability of high quality fodder. An insufficient supply of high quality feed and fodder is the primary factor lowering milch animal productivity in India

(Kumari *et al*., 2022). There is currently a net deficiency of 35.6% green fodder, 10.95% dry fodder and 44% concentrate feed materials in the country (Singh *et al.,* 2022).

Maize is commonly grown as a *Kharif* fodder in the north-western regions of India. Its quality is much better than sorghum and pearl millet, since both sorghum as well as pearl millet possess anti- quality components such as hydrocyanic acid and oxalate, respectively. Secondly, baby corn is ready for harvest approximately 2 months after sowing (Chaudhary *et al*., 2012). Maize contains high concentrations of protein and minerals and possesses high digestibility (Gupta *et al.,* 2004). It also possesses excellent ensiling characteristics as it contains sufficient quantities of soluble sugars required for proper fermentation (Allen *et al.,* 2003). On an average, it contains 9-10% crude protein (CP), 60 to 64% neutral detergent fibre (NDF), 38 to 41% acid detergent fibre (ADF), 23 to 25% hemi-cellulose, and 28 to 30% cellulose on the dry matter basis when harvested at milk to early dough stage (Kumar *et al.,* 2020).

The achievement of any programme aimed at improving crops is subjected to the nature and magnitude of genetic variability present in the quantitative and qualitative traits, as this increases the likelihood of identifying and selecting desirable types. The mean values, genotypic and phenotypic coefficient of variation, heritability, correlation coefficients and path coefficient analysis of the traits are some of the essential attributes that ascertain the potency of a breeding program. Multivariate analysis is the most popular approach for assessing the genetic diversity to study the pattern of variation and their genetic relationships within collections of germplasms. Principal component analysis and Cluster analysis are preferred tools and has made it possible to choose genetically diverse parents for breeding programme. The diversity analysis plays a crucial part in selecting divergent parents for hybridisation in order to maximize heterosis effectively. Based on the above consideration, a study was taken to evaluate the genetic diversity among fodder maize germplasm lines to select the best line that can be exploited in future maize breeding programme.

Materials and Methods

Experimental Material

A set of 48 fodder maize germplasm lines including three checks (African Tall, J-1006, Shalimar Fodder Maize-1) were used for evaluating yield and quality attributing traits. The experiment was laid out in randomised complete block design (RCBD) at experimental field of Division of Genetics and Plant Breeding, Faculty of Agriculture, Wadura, SKUAST-K during *Kharif,* 2022. Each genotype was sown in a 4 m row with an intra-row spacing of 15 cm and inter-row spacing of 30 cm. Recommended agronomic practices and plant protection measures were diligently followed during the crop period to raise a healthy and productive crop.

Observations Recorded

A total of 16 yield and quality contributing traits *viz.,* days to 50% tasseling, days to 50% silking, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), stem girth (cm), fresh leaf weight per plant (g), fresh stem weight per plant (g), leaf: stem ratio, green fodder yield per plant (g), dry matter yield per plant (g), grain yield per plant (g), crude protein (CP), acid detergent fibre (ADF) and neutral detergent fibre (NDF) were analysed.

Statistical Analysis

All the statistical analysis was carried out in R studio software (R studio Team, 2020). Analysis of variance was carried out using the 'Agricolae' package (de Mendiburu, 2015) of R studio. The various genetic parameters like phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability broad sense (h^2) and genetic advance (GA) along with correlation and path analysis were estimated using the 'Variability' package (Popat *et al.,* 2020). PCA and hierarchical UPGMA clustering were performed using 'Factoextra' package (Kaufman and Rousseeuw, 1990).

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance (Table 1) revealed that the mean sum of squares due to germplasm lines were highly significant for all the traits under study. This indicates the existence of substantial heterogeneity among the 48 fodder maize germplasm lines studied, with regard to all the analyzed characters and offers an opportunity for further study and assessment of variability parameters. Similar results of significant mean sum of squares due to genotypes for all the traits studied were observed by Mallikarjuna *et al.* (2011); Nataraj *et al.* (2014); Mani and Deshpande (2016); Shazia *et al.* (2017); Khan *et al.* (2018) and Vanjare *et al.* (2021). The notable findings revealed substantial genetic variation resulting from natural genetic variation or crossbreeding which can be exploited through selection.

Genetic Variability Study

High magnitude of PCV and GCV (>20%) were observed for fresh leaf weight per plant and grain yield per plant and lowest (<20%) for neutral detergent fiber as represented in Figure 1. In this study, PCV was found to be greater in magnitude than its corresponding GCV (Table 2) for all the analyzed characters indicating that the detected differences are both the product of genotype and environmental effect. However, the narrow range of differences suggests that environmental effects have a relatively minimal impact on the expression of these characters. Similar findings have been observed for PCV and GCV by Borad (1993) for fresh leaf weight per plant in sorghum, Dar *et al.* (2014) for days to 50 per cent tasseling, days to 50 per cent silking and grain yield per plant in maize; Kapoor and Batra (2015) for leaf width and

neutral detergent fiber in maize; Rathod *et al.* (2021) for days to 50 per cent tasseling , days to 50 per cent silking and leaf width in maize; Naharudin *et al.* (2021) for number of leaves per plant and neutral detergent fiber in maize.

Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance are usually more helpful than heritability alone in predicting the resultant effect for selecting the best genotypes. Figure 2 represents the Heritability and genetic advance value of different fodder traits. High magnitude of broad sense heritability with high magnitude of genetic advance as percent of mean was exhibited by fresh stem weight per plant, grain yield per plant, green fodder yield per plant and stem girth. Moderate magnitude of heritability with high genetic advance was exhibited by dry matter yield per plant and leaf:stem ratio. Above results indicate the presence of additive gene action and selection may lead towards improvement for these characters. Hence, it offers improved prospects for selecting maize plant material with these traits. These results are in agreement with Singh *et al.* (2017) for green fodder yield per plant in sorghum; Gayosso Barragan *et al.* (2020) for stem girth; Magar *et al.* (2021) for grain yield per plant; Rathod *et al.* (2021) and Pavithra *et al.* (2022) for stem girth and green fodder yield per plant in maize. Low heritability along with low genetic advance for the characters indicates the influence of environment upon these characters and selection would be ineffective in such cases.

Correlation and Path Coefficient Analysis

The correlation between all possible combinations among the characters was estimated at the genotypic level (Table 3). Genotypic correlation coefficients offer a means to quantify the genetic relationship between different traits, providing insights into which traits may be valuable for identifying more significant traits in a specific selection program. The correlation coefficients at the genotypic level obtained in the current investigation indicated that there were generally positive associations among the characters studied, which is beneficial for breeding high-yielding cultivars in fodder maize.

Green fodder yield per plant displayed a positive and highly significant correlation with dry matter yield per plant, plant height, fresh stem weight per plant, fresh leaf weight per plant, stem girth, number of leaves per plant, leaf length and leaf width but significant and positive correlation with crude protein, days to 50% silking, days to 50% tasseling and grain yield per plant. It indicated that an increase in any of these traits will increase green fodder yield per plant. A negative and non-significant correlation with leaf: stem ratio, acid detergent fiber and neutral detergent fiber were also observed. These findings are in agreement with the results of Icoz and Kara (2009) for green fodder yield and dry matter yield in maize; Kapoor and Batra (2015) for plant height, leaf length, leaf width and number of leaves per

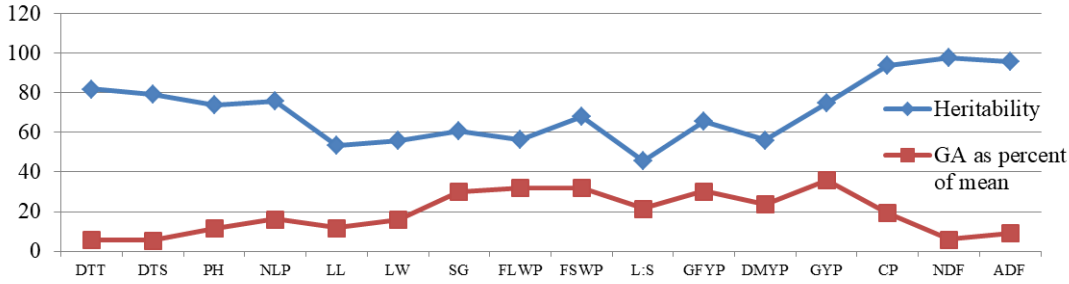
Table 1: Analysis of variance of 16 forage traits in fodder maize germplasm lines

Trait	DTT	DTS	PH	NLP	LL	LW	SG	FLWP	FSWP	L:S	GFYP	DMYP	GYP	CP	NDF	ADF
Replication	1.69	0.63	61.2	0.05	10.3	0.10	0.03	0.43	152.5	0.004	138.7	15.87	12.16	0.047	0.012	0.111
Genotype	18.70**	20.49**	782.33**	3.75**	172.72**	2.89**	0.33**	1210.3**	1873.6**	0.05**	5138.2**	263.56**	199.09**	1.65**	11.87**	13.17**
Error	1.28	1.66	82.6	0.36	39.0	0.60	0.05	248.3	255.4	0.01	764.8	54.3	20.11	0.03	0.09	0.18

Table 2: Estimates of PCV, GCV, heritability and genetic advance as percent of mean among 16 forage traits in fodder maize germplasm lines

Trait	*DTT*	*DTS*	*PH*	*NLP*	*LL*	*LW*	*SG*	*FLWP*	*FSWP*	*L:S*	*GFYP*	*DMYP*	*GYP*	*CP*	*NDF*	*ADF*
PCV	3.46	3.38	7.50	10.37	10.74	13.85	23.96	27.65	22.75	23.02	22.43	20.65	23.40	10.07	2.94	4.53
GCV	3.13	3.00	6.45	9.03	7.84	10.34	18.66	20.75	18.75	15.52	18.16	15.46	20.43	9.76	2.94	4.53
h^2	81.91	79.01	73.83	75.84	53.33	55.77	60.64	56.36	67.96	45.45	65.59	56.10	74.79	93.83	97.55	95.94
GAM	5.84	5.50	11.41	16.20	11.79	15.91	29.93	32.10	31.85	21.55	30.31	23.86	36.05	19.48	5.98	9.14

Figure 1: PCV and GCV values of different fodder maize traits



***Abbreviations:** **DTT** = Days to 50 per cent tasseling, **DTS** = Days to 50 per cent silking, **PH** = Plant height(cm), **NLP** = Number of leaves per plant, **LL** = Leaf length (cm), **LW** = Leaf width (cm), **SG** = Stem girth (cm) , **FLWP** = Fresh leaf weight per plant (g), **FSWP** = Fresh stem weight per plant (g), **L:S** = Leaf: stem ratio, **DMYP** = Dry matter yield per plant (g), **GYP**= Grain yield per plant (g), **CP** = Crude protein (%), **NDF** = Neutral detergent fiber (%), **ADF**=Acid detergent fiber (%), **GFYP** = Green fodder yield per plant (g)

Figure 2: Heritability and genetic advance values of different fodder maize traits

plant and neutral detergent fiber with green fodder yield in maize; Ali *et al.* (2015) for plant height with green fodder yield in maize; Alawe *et al.* (2020) for dry matter yield per plant with green fodder yield per plant in maize, Rathod *et al.* (2021) for plant height, number of leaves per plant, dry matter percent and crude protein with green fodder yield in maize. These results suggest that taller plants with wider, longer and more number of leaves, thicker stem and higher dry matter yield per plant would be helpful in improvement of green fodder yield per plant.

Correlation gives only the general relation between two variables, whereas path coefficient spits correlation into direct and indirect effects. Based on the data recorded, genotypic correlations were used to estimate path coefficients taking GFYP as a dependent variable (Table 4). The direct positive effect on green fodder yield per plant was exhibited by plant height, stem girth, fresh leaf weight per plant and leaf: stem ratio. Hence, direct selection for these traits could be practised for developing high green fodder yield maize germplasm lines. These results are in consonance with Srivas and Singh (2004); Icoz and Kara (2009); Kapoor and Batra (2015); Alawe *et al.* (2020); Rathod *et al.* (2021) and Borkhatariya *et al.* (2022) in maize.

UPGMA Cluster Analysis

Unweighted pair group method with arithmetic mean (UPGMA) is a type of hierarchical clustering in which a cluster tree (dendrogram) is created to represent data, where each group (or "node") is connected to two or more groups of descendants. Each node in the cluster comprises a collection of similar items; the group of nodes in the chart next to each other is connected. Clusters at one level join clusters at the next level upwards, using a degree of dissimilarity, the cycle continues till altogether nodes are in the tree, providing a pictorial snap of the data in the whole collection. UPGMA was used to divide the forty-eight germplasm lines into four groups, using Euclidean distance as the dissimilarity measure (Figure 3). The germplasm lines were not scattered

Table 3: Estimates of genotypic correlation coefficients among yield and quality attributing traits in fodder maize

Traits	*DTT*	*DTS*	*PH*	*NLP*	*LL*	*LW*	*SG*	*FLWP*	*FSWP*	*L:S*	*DMYP*	*GYP*	*CP*	*NDF*	*ADF*	*GFYP*
DTT	1.00	0.99**	0.21*	0.19*	0.09	0.08	0.16*	0.14	0.17*	-0.00	0.12	-0.07	-0.03	0.08	-0.04	0.17*
DTS		1.00	0.23**	0.19*	0.13	0.06	0.17*	0.14	0.18*	-0.01	0.14	-0.04	-0.03	0.06	-0.07	0.18*
PH			1.00	0.76**	0.64**	0.60**	0.80**	0.86**	0.90**	-0.02	0.82**	0.14	0.16	-0.10	-0.05	0.85**
NLP				1.00	0.33**	0.61**	0.55**	0.84**	0.64**	0.32**	0.75**	-0.06	-0.02	0.06	0.03	0.78**
LL					1.00	0.31**	0.65**	0.66**	0.67**	-0.02	0.72**	0.26**	0.25**	-0.04	0.03	0.72**
LW						1.00	0.29**	0.83**	0.39**	0.62**	0.61**	-0.02	0.12	-0.05	0.01	0.63**
SG							1.00	0.61**	0.98**	-0.44*	0.79**	0.30**	0.24**	-0.23*	-0.17*	0.78**
FLWP								1.00	0.71**	0.41**	0.87**	0.05	0.13	-0.00	0.03	0.80**
FSWP									1.00	-0.33**	0.93**	0.25**	0.22**	-0.20*	-0.14	0.84**
L:S										1.00	-0.05	-0.28**	-0.08	0.26**	0.23*	-0.01
DMYP											1.00	0.25**	0.21**	-0.11	-0.06	0.98**
GYP												1.00	0.37**	-0.20*	-0.34**	0.18*
CP													1.00	-0.28**	-0.18**	0.20*
NDF														1.00	0.83**	-0.13
ADF															1.00	-0.07
GFYP																1.00

Table 4: Estimates of genotypic path coefficients among yield and quality attributing traits in fodder maize

Traits	*DTT*	*DTS*	*PH*	*NLP*	*LL*	*LW*	*SG*	*FLWP*	*FSWP*	*L:S*	*DMYP*	*CP*	*NDF*	*ADF*	*'GFYP*
DTT	**-0.066**	0.050	0.067	-0.015	-0.004	-0.007	0.113	0.050	-0.003	-0.000	-0.007	0.00034	-0.0011	-0.0003	0.175*
DTS	-0.066	**0.050**	0.075	-0.015	-0.007	-0.005	0.120	0.053	-0.003	-0.004	-0.008	0.00036	-0.0009	-0.0005	0.187*
PH	-0.013	0.011	**0.455**	-0.060	-0.033	-0.053	0.353	0.280	-0.018	-0.004	-0.058	-0.0015	0.0015	-0.0004	0.856**
NLP	-0.012	0.009	0.246	**-0.079**	-0.017	-0.054	0.302	0.382	-0.013	0.073	-0.048	0.00027	-0.0009	0.0030	0.789**
LL	-0.006	0.006	0.208	-0.026	**-0.051**	-0.027	0.451	0.237	-0.013	-0.005	-0.046	-0.0023	0.0006	0.0003	0.724**
LW	-0.005	0.003	0.194	-0.048	-0.016	**-0.089**	0.201	0.299	-0.008	0.143	-0.039	-0.0011	0.0008	0.0010	0.634**
SG	-0.109	0.008	0.260	-0.043	0.033	-0.026	**0.590**	0.219	-0.020	-0.101	-0.057	-0.0022	0.0034	-0.0013	0.784**
FLWP	-0.009	0.007	0.270	-0.066	-0.034	-0.074	0.298	**0.408**	-0.014	0.084	-0.056	-0.0012	0.00013	0.00028	0.805**
FSWP	-0.011	0.009	0.260	-0.051	-0.035	-0.035	0.677	0.257	**-0.021**	-0.075	-0.059	-0.0020	0.0030	-0.0011	0.845**
L:S	0.000	-0.000	-0.006	-0.025	0.001	-0.056	-0.306	0.147	0.006	**0.229**	0.003	0.0007	-0.0038	0.0018	-0.019
DMYP	-0.008	0.007	0.297	-0.059	-0.037	-0.055	0.620	0.314	-0.019	-0.012	**-0.064**	-0.0020	0.1005	-0.0005	0.983**
GYP	0.005	-0.002	0.045	0.005	-0.013	0.002	0.208	0.020	-0.005	-0.064	-0.015	-0.0034	0.0030	-0.0027	0.181*
CP	0.002	-0.001	0.052	0.002	-0.013	-0.011	0.166	0.487	-0.004	-0.018	-0.013	**-0.0092**	0.0041	-0.0014	0.202*
NDF	-0.005	0.003	-0.033	-0.005	0.002	0.005	-0.163	-0.003	0.004	0.061	0.007	0.0026	**-0.0144**	0.0065	-0.132
ADF	0.003	-0.003	-0.018	-0.003	-0.002	-0.011	-0.120	0.012	0.003	0.054	0.004	0.0017	-0.0120	**0.008**	-0.074

* and ** Significant at 5 and 1 percent respectively

uniformly amongst the clusters. Cluster II was the biggest cluster with 17 germplasm lines followed by cluster IV (16 germplasm lines), cluster I (13 germplasm lines) and cluster III (2 germplasm lines).

There was a wider genetic diversity among genotypes of different clusters as the distances between clusters were greater than the distances within the clusters (Table 5). The intra-cluster distance ranged from 2.54 to 4.43. Cluster I had the greater intra-cluster distance (4.43) followed by cluster III (4.20), cluster II (4.19) and cluster IV (2.54).

The inter-cluster distance ranged from 5.17 to 7.43. cluster II and IV had the greatest inter-cluster distance (7.43) followed by cluster I and IV (6.69), cluster I and III (6.51), cluster II and cluster III (5.80), cluster III and cluster IV (5.24) and cluster I and cluster II (5.17).

Table 5: Intra and inter-cluster distances among four clusters

Cluster	*I*	*II*	*III*	*IV*
I	4.43	5.17	6.51	6.69
II		4.19	5.80	7.43
III			4.20	5.24
IV				2.54

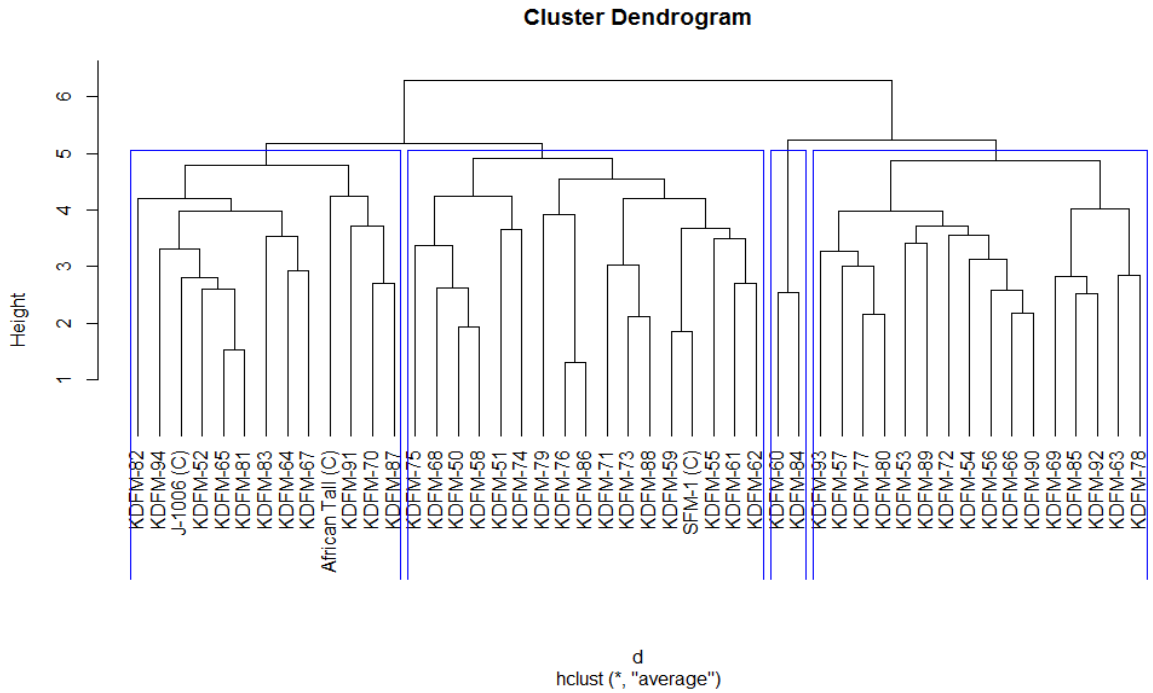


Figure 3: UPGMA dendrogram of 48 germplasm lines based on 16 yield and quality attributing traits

Principal Component Analysis (PCA)

Principal component analysis (PCA) is important for elucidating the primary contributor to total variance along each axis of differentiation. It is a data reduction technique used to concurrently describe the interrelationship among set of variables. PCA enables the visualization of distinctions among individuals, the identification of potential groups and finding relationships among individuals and variables. Its main objective is to determine the smallest set of components that can account for the highest proportion of total variability.

Principal component analysis was performed using yield and quality attributing traits in fodder maize germplasm lines including three checks. The analysis revealed that the number of principal components formed were equal to number of characters studied. The criteria followed for selecting the principal components to be included in further analysis was based on Eigen values of principal components. Out of 16, only 5 principal components (PCs) exhibited more than 1 Eigen value and showed 88.33% variability among the traits studied which was also reported by Muhammad *et al.* (2015); Jain and Patel (2016); Shazia *et al.* (2017); Mounika *et al.* (2018); Poonia *et al.* (2021) and Kifayat *et al.* (2022). The results showed that the first principal component, i.e., PC1 accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. PC1 accounted for 43.5% of total variability, whereas, PC2, PC3, PC4 and PC5 exhibited 15.4, 12.4, 9.5 and 6.7% respectively, for the traits under study (Table 6 and Figure 4).

Table 6: Eigen values, percent variability and cumulative percent variability for 16 principal components in fodder maize

Principal component	*Eigen value*	*Percentage of variance*	*Cumulative percentage (%)*
PC1	6.966	43.5	43.5
PC2	2.468	15.4	59.0
PC3	1.981	12.4	71.3
PC4	1.516	9.5	80.8
PC5	1.073	6.7	87.5
PC6	0.793	5.0	92.5
PC7	0.549	3.4	95.9
PC8	0.330	2.1	98.0
PC9	0.148	0.9	98.9
PC 10	0.110	0.7	99.6
PC11	0.043	0.3	99.9
PC12	0.011	0.1	99.9
PC13	0.007	0.0	100.0
PC14	0.003	0.0	100.0
PC15	0.001	0.0	100.0
PC16	0.000	0.0	100.0

Eigen loadings of $\pm$0.3 were considered as major contributory factors to the variations that were observed. The higher the loadings, regardless of sign, the more they will be discriminating between the accessions. PC1 accounted for the highest variation which was mainly due to the high positive vector loadings of plant height, number of leaves per plant, stem girth, fresh leaf weight per plant, fresh stem

Table 7: Contribution of various characters in different principal components

PCs	*DTT*	*DTS*	*PH*	*NLP*	*LL*	*LW*	*SG*	*FLWP*	*FSWP*	*L:S*	*GFYP*	*DMYP*	*GYP*	*CP*	*NDF*	*ADF (%)*
PC1	0.081	0.084	0.356	0.302	0.272	0.263	0.313	0.349	0.343	0.051	0.376	0.366	-0.062	0.046	-0.047	-0.034
PC2	0.027	0.016	0.008	0.193	0.007	0.258	-0.261	0.203	-0.197	0.484	-0.020	-0.032	-0.331	-0.114	0.438	0.443
PC3	-0.679	-0.678	-0.005	-0.003	0.065	0.127	-0.034	0.091	-0.025	0.130	0.029	0.057	0.102	-0.030	-0.125	-0.025
PC4	0.138	0.132	-0.038	0.050	-0.066	0.313	-0.260	0.133	-0.207	0.460	-0.061	-0.088	0.030	0.192	-0.469	-0.499
PC5	0.022	0.014	-0.062	-0.197	0.309	-0.023	-0.057	0.014	-0.065	0.098	-0.032	-0.003	0.414	0.762	0.191	0.233

*Abbreviations: DTT = Days to 50 per cent tasseling, DTS = Days to 50 per cent silking, PH = Plant height(cm), NLP = Number of leaves per plant, LL = Leaf length (cm), LW = Leaf width (cm), SG = Stem girth (cm) , FLWP = Fresh leaf weight per plant (g), FSWP = Fresh stem weight per plant (g), L:S = Leaf: stem ratio, GFYP = Green fodder yield per plant (g), DMYP = Dry matter yield per plant (g), GYP = Grain yield per plant (g), CP = Crude protein (%), NDF = Neutral detergent fiber (%), ADF = Acid detergent fibre (%)

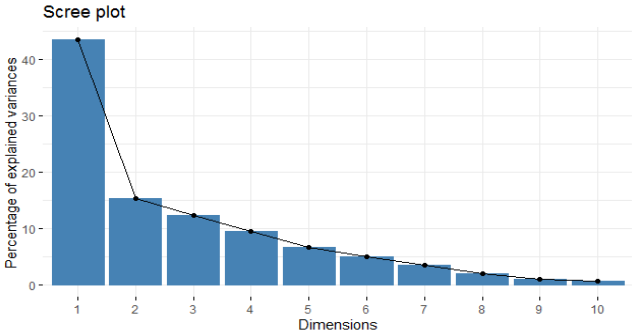


Figure 4: Scree plot

weight per plant, green fodder yield per plant and dry matter yield per plant. Hafiz *et al.* (2015) and Chikuta *et al.* (2015) reported a significant contribution from the first principal component towards overall variability while analyzing different traits.

The diversity in PC2 was due to positive loadings from leaf: stem ratio, neutral detergent fiber and acid detergent fiber. The diversity in PC3 was due to negative vector loadings from days to 50 per cent tasseling and days to 50 per cent silking. PC4 had positive vector loadings from leaf: stem ratio, leaf width and negative vector loadings from neutral detergent fiber and acid detergent fiber. PC5 had positive loadings from leaf length, grain yield per plant and crude protein. Similar results were reported by Avinash *et al.* (2016), Sinha *et al.* (2019) and Pavithra *et al.* (2022).

From this study, it was clear that the key yield-related traits are primarily represented in PC1 (Table 7). Consequently, germplasm lines falling within this principal component and having high PC scores should be targeted for the cultivation of high-yield varieties. Germplasm lines with the highest PC scores (KDFM-86, KDFM-79, KDFM-76, KDFM-55) in PC 1 are poised to serve as donors for the transfer of desired traits, as indicated by their trait contributions. Following hybridization, the careful selection of optimal recombinants in subsequent segregating generations might be fruitful for the development of high-yielding fodder maize lines.

The PCA biplot effectively reveals the inter-relationship among maize traits (Figure 5). The first two PC's were used to generate a biplot. Based on PC1 and PC2 green fodder yield per plant, dry matter yield per plant, plant height, fresh leaf weight per plant, fresh stem weight per plant, stem girth, number of leaves per plant, leaf: stem ratio, neutral detergent fiber and acid detergent fiber displayed notably extended vectors, suggesting the presence of substantial variation among germplasm lines. In simpler terms, these traits exhibit pronounced variation across the 48 germplasm lines investigated, suggesting their role as the most prominent discriminators within the studied data.

The PCA analysis organized the lines into groups that spread across all four quadrants, indicating significant variability in traits. The right top quadrant consisted of the germplasm lines KDFM-65, KDFM- 81, KDFM- 83, KDFM-84, KDFM-82, KDFM-71, KDFM-91, KDFM-87, KDFM-70, KDFM-76, J-1006 and African tall and were related to plant height, leaf length, fresh leaf weight per plant, number of leaves per plant, leaf: stem ratio, days to 50% tasseling and days to 50% silking. The right bottom comprised of germplasm lines KDFM-88, KDFM-73, KDFM-75, KDFM-62, KDFM-58, KDFM-50, KDFM-68, KDFM-61, KDFM-55, KDFM-59, KDFM-79, KDFM-86 and SFM-1 related to green fodder yield per plant, dry matter yield per plant, fresh stem weight per plant, stem girth, crude protein and grain yield per plant. The germplasm lines KDFM-67, KDFM-94, KDFM-52, KDFM-80, KDFM-77, KDFM-63, KDFM-72, KDFM-89, KDFM-78, KDFM-66, KDFM-93, KDFM-53 and KDFM-57 in left top quadrant were

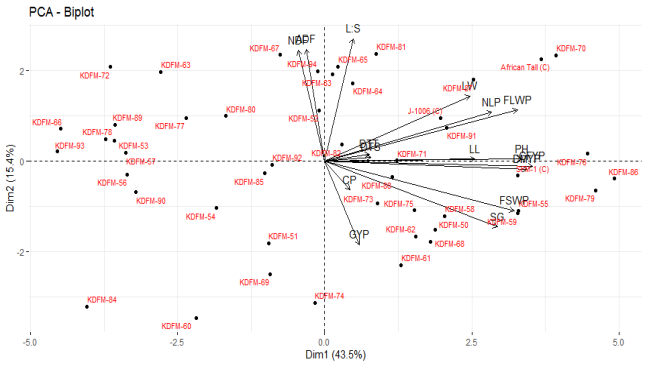


Figure 5: PCA Biplot

closely related to acid detergent fiber and neutral detergent fiber. The germplasm lines KDFM-56, KDFM-90, KDFM-92, KDFM-85, KDFM-54, KDFM-51, KDFM-69, KDFM-74, KDFM-84 and KDFM-60 showed no significant improvement for any trait as indicated by their positions on the axes devoid of trait arrows.

The biplot demarcated the germplasm lines with different traits explained by the first two dimensions. As a result, a breeder can easily estimate the genetic distance between genotypes, facilitating informed decisions for genotype selection. This is made possible by condensing multiple variables into the two primary principal components, analyzed simultaneously. Germplasm lines close to each other on the score plot are similar, while lines near the origin are distinctive, and those farther away are particularly extreme.

The cosine of the angle between the vectors of the two traits measures the degree of correlation similarity between them, considering their variation across different germplasm lines. The traits pair plant height and leaf length had an angle of zero, indicating a perfect correlation of +1. Traits of each group had acute ($<90^0$) angles between them, indicating they were positively correlated and their variation was similar, so each trait within a particular group can substitute for the other trait in the same group. The traits like leaf: stem ratio had a near-right angle with fresh stem weight per plant, indicating that variation of one trait was more or less independent of the other trait (near zero correlation). On the contrary, NDF and ADF had obtuse angle ($>90^0$) with green fodder yield per plant, indicating that their variation was in the opposite direction (negative correlation).

The biplot formed by the first two PC's grouped the 48 germplasm lines in a manner akin to UPGMA cluster analysis, utilizing the entire data from all the traits. This demonstrated that PCA is a dependable approach for pinpointing key traits that account for the most significant variations and serves as a reliable means to predict crucial traits that influence the clustering of distinct line. In this context, traits possessing substantial absolute values near unity within the first PC exert a more pronounced influence on clustering compared to those with lower absolute values nearer to zero. Hence, in the current study, the differentiation of genotypes into distinct clusters arose from the relatively substantial contributions of a few select traits, rather than minor contributions from each trait.

Conclusion

Analysis of diverse multivariate parameters revealed that the existing germplasm lines exhibit substantial variability across various yield components and quality traits. The strategic selection of these germplasm lines in future breeding programs holds promise for the development and release of cultivars with improved yield and quality characteristics.

Acknowledgment

The authors express their gratitude to the Division of Genetics and Plant Breeding, Faculty of Agriculture, SKUAST-Kashmir and DARS, Rangreth for their invaluable support and assistance.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.11

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Characterization and Utilization of Potential Genetic Resources for Improvement of *Citrullus lanatus* Under Desert Ecosystem

DK Samadia, AK Verma and Hanuman Ram*

Abstract

Mateera is an indigenous type of drought-hardy watermelon and is extensively grown with mixed cropping on sand-dunes landscape in the *Thar* Desert. Its tender and ripe fruits and seed kernels are liked by desert dwellers and sold at a high premium. Earlier, due to the absence of *mateera* varieties, farmers used heterozygous seeds collected from their own fields, which resulted in uninsured quality. From 1994 to 2012, diverse *Citrullus* germplasm was collected, evaluated, conserved, and utilized and intensive research work was carried out at ICAR-CIAH, Bikaner, Rajasthan, India. A close correspondence between PCV and GCV values with respect to characters under study indicated that the testing environment has very little influence on the expression of the attributes. Thus, selection based on phenotype can be effective with an equal probability of success. On the evaluation of a wide range of germplasm, it was found that standard watermelon genotypes failed to express their potential under high temperatures and rainfed conditions of arid regions. Thus, the use of indigenous and generated variability and the promotion of varieties from native germplasm is found to be beneficial. *Mateera* lines AHW-18 (IC-430201), AHW-19 (IC-430202), AHW-65 (IC-430208), AHW-108 (IC-430215), AHW-140 (IC-430225), AHW-RSS-1 (red seeded isolate from germplasm of Churu district) and AHW-BSM-1 (black seeded isolate from AHW-19) were found promising for use in breeding or trait-specific selections. The developed *mateera* varieties, *i.e.,* AHW-19 and Thar Manak are early in harvesting, producing better quality fruits and of multiple-use, and recommended for cultivation under resource constraints in a hot arid climate.

Keywords: *Citrullus*, Desert ecosystem, Drought-tolerant, Hot arid climate.

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Received: 15/02/2023 **Revised:** 07/08/2024

Accepted: 20/08/2024

How to cite this article: Samadia DK, AK Verma and H Ram (2024) Characterization and Utilization of Potential Genetic Resources for Improvement of *Citrullus lanatus* Under Desert Ecosystem. *Indian J. Plant Genet. Resour.* 37(3):482-493.**DOI:** 10.61949/0976-1926.2024.v37i03.11

Introduction

Indian sub-continent is rich in cucurbitaceous crop-plant diversity. The arid and semi-arid region of north-western India is endowed with a wide range of genetic variability, particularly *Citrullus* and *Cucumis* group of multiple-use attributes. Indigenous cucurbits *viz*., *kachri, kaakdia, mateera, tinda* and *tumba* are component crops of traditional farming, providing nutrition and income to the inhabitants of the desert ecosystem. *Mateera* is a drought-tolerant landrace of watermelon (*C. lanatus*) and is very useful to the growers for getting benefits from its tender and ripened fruits, seed kernels, and organic and rainfed crop commodities. *Tumba* or *Indrayan* or bitter melon (*C. colocynthis*) is non-edible and perennial, and fruits are used for pickling, medicine and seed oil. Third is tinda (*Praecitrullus fistulosus*) and is a popular vegetable for tender and dehydrated (*Phophalia*) fruits (Samadia and Pareek, 1998; Pareek *et al*., 1999; Samadia, 2007).

Entirely ripe fruits of *C. lanatus* are palatable as a febrifuge or antipyretic. Its fruit is a diuretic and can be used to treat kidney stones and dropsy. In case of diabetes and alcoholic toxicity, fruit peel is suggested. Watermelon is high in vitamins A and C, as well as vitamin B_6, beta-carotene, thiamine, and potassium (Mezzomo

and Ferreira, 2016; https://www.nal.usda.gov/human-nutrition-and-food-safety/nutrient-lists-standard-reference-legacy-2018). Watermelon juice reduces SOD activity and LDL cholesterol while increasing CAT activity and HDL cholesterol, disclosing that it has antioxidant properties (Georgina *et al*., 2011). The scented, sweet and red fruit of *Citrullus lanatus* is digestible and delicious. It has roughly 40% lycopene, a cancer-fighting antioxidant. Lycopene is easy to absorb without requiring high-temperature treatment and is relatively stable when stored and refrigerated. Watermelons should be hard and symmetrical, with no cuts or indications of strikes. It contains citrulline, a substance that helps to decrease blood pressure. Watermelon juice consumption has been associated with lower insulin resistance which is beneficial to fight against metabolic syndrome and type 2 diabetes (Xue *et al*., 2015).

Non-availability of trait-specific varieties suited to abiotic stressed production sites of the arid region is the prime limiting factor in promoting *mateera* and thus, a targeted work plan was made to improve quality fruit harvest. Intensive surveys were conducted in regional diversity zones and germplasm were collected, evaluated and categorized for the breeding program. Besides, generated progenies from selected germplasm and breeding material developed through identified parentage combinations were studied over the seasons and years to conclude the results of strategic research on varietal development are described in this paper.

Materials and Methods

Agro-climate of the Study Region

In India, Rajasthan (23º 3′–30º 12′ N and 69º 3′–78º 17′ E) is geographically very big state and much agro-climatic variability is reported *viz*., arid, semi-arid and dry sub-humid. All the experimental trials were conducted at ICAR-CIAH, Beechwal, Bikaner (28º 6′ N latitude and 73º 2′ E longitudes and altitude 223 m) and this area is under a hyper-arid zone of the Indian *Thar* desert. In arid farm-lands, high temperature (35–42ºC) during the *kharif* season, long drought spells (15–35 days) and the sandy soil creates an environment where very few vegetable crops reach to economic harvest under the rainfed situations and *mateera* is well known among them. Further, extremes of winter and summer seasons' temperature variability, as well as range, also determine the period of sowing and harvesting of *mateera*.

Germplasm Collection, Augmentation, Evaluation and Utilization

For the collection of regional diversity of *Citrullus*, surveys were conducted from 1994 and 2003 and it was in targeted variability pockets of arid, semi-arid and tribal areas of Rajasthan. Besides, collaborative collections were made with ICAR-National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Jodhpur. Maximum *mateera* variability was collected (178) from Bikaner, Churu, Nagour, Jodhpur, Barmer, Jaisalmer, Pali and Hanumangarh districts with desert ecology, rainfed and mixed cropping during Kharif. In contrast, watermelons (28 germplasm) were explored from Sikar, Jaipur, Tonk, Ajmer, Kota, Chittorgarh, Udaipur, Sirohi and adjoining districts with semi-arid climate and summer season cultivation. In addition, introduced and national watermelon genotypes (11 entries) were assembled from ICAR-NBPGR, New Delhi, Rajasthan Agricultural Research Institute, Durgapura (Jaipur), ICAR-Indian Institute of Horticultural Research, Bengaluru and ICAR-Indian Institute of Vegetable Research, Varanasi.

Over the years collected *Citrullus lanatus* diversity was evaluated in a phase manner. For characterization, 35 attributes related to growth, flowering, fruiting, maturity, fruit yield, quality and seed components were studied for all the material. Both *mateera* and watermelon germplasm were categorized based on the prioritized traits such as earliness, number of fruits, fruit quality and marketable yield under hot, arid climates. The watermelon varieties, hybrids, purified *mateera* material and developed lines were assessed over the seasons to understand their suitability for two-season cultivation. Therefore, each germplasm or breeding material was studied at least four times in rainy and summer and rainfed and irrigated situations. For evaluation of each germplasm or line, a single row of 25 m length was kept standard throughout the experimental trials and 50 plants/genotype/row were maintained. With the start of flowering, 12 plants were tagged in each genotype and four groups were made for recording observations. A wide range of data was generated from the germplasm (155 genotypes) and it was with varying seasons and production situations of 1995–1999 and 2000–2003 at Bikaner. Initially, the purified germplasm (Table 1) was short-listed based on performance and prioritized traits. Means of two-season data of the year 2003 of the short-listed genotypes were used for assessment of genetic variability components and means of four-season crop data were analyzed for comparative performance.

For the purification of *mateera* germplasm, promising genotypes were identified based on fruit quality traits and performance. After purification, *mateera* selections were compared with standard watermelon varieties for fruit quality and yield. Simultaneously, breeding for drought-tolerant *mateera* through hybridization was taken with the objectives of improving adaptive selections for acceptable flesh quality, higher sweetness, and cultivation under water stress and high-temperature conditions. The *mateera* selections (AHW-18, AHW-19 and AHW-65) and watermelon varieties (Sugar Baby, Durgapura Meetha, Charleston Local and Mahobobi) were used in hybridization breeding (single, diallel and bi-parental mating). Developed F_1, F_2, BC_1, BC_2

Table 1: Details of *Citrullus* germplasm initially purified at ICAR-CIAH, Bikaner

S. No.	*IC number*	*Accession/collector number*	*S. No.*	*IC number*	*Accession/collector number*
1	IC-430191	DKS/AHW/01	29	IC-430219	DKS/AHW/118
2	IC-430192	DKS/AHW/02	30	IC-430220	DKS/AHW/119
3	IC-430193	DKS/AHW/04	31	IC-430221	DKS/AHW/120
4	IC-430194	DKS/AHW/05	32	IC-430222	DKS/AHW/122
5	IC-430195	DKS/AHW/07	33	IC-430223	DKS/AHW/123
6	IC-430196	DKS/AHW/10	34	IC-430224	DKS/AHW/135
7	IC-430197	DKS/AHW/12	35	IC-430225	DKS/AHW/140
8	IC-430198	DKS/AHW/14	36	IC-430226	DKS/AHW/150
9	IC-430199	DKS/AHW/16	37	IC-278416	KCM/BKP-18
10	IC-430200	DKS/AHW/17	38	IC-278417	KCM/BKP-19
11	IC-430201	DKS/AHW/18	39	IC-315281	DPY-117
12	IC-430202	DKS/AHW/19	40	IC-315283	DPY-119
13	IC-430203	DKS/AHW/30	41	IC-315284	DPY-120
14	IC-430204	DKS/AHW/40	42	IC-315288	DPY-124
15	IC-430205	DKS/AHW/43	43	IC-315290	DPY-126
16	IC-430206	DKS/AHW/50	44	IC-315304	DPY-140
17	IC-430207	DKS/AHW/56	45	IC-315306	DPY-142
18	IC-430208	DKS/AHW/65	46	IC-315313	DPY-149
19	IC-430209	DKS/AHW/76	47	IC-315321	DPY-157
20	IC-430210	DKS/AHW/80	48	IC-315324	DPY-160
21	IC-430211	DKS/AHW/82	49	IC-315328	DPY-164
22	IC-430212	DKS/AHW/85	50	EC-420978	Mahobobi
23	IC-430213	DKS/AHW/93	51	EC-420977	Charleston
24	IC-430214	DKS/AHW/100	52	IC-0590087	Thar Manak
25	IC-430215	DKS/AHW/108	53	-	AHW RSS-1
26	IC-430216	DKS/AHW/110	54	-	AHW BSM-1
27	IC-430217	DKS/AHW/112	55	-	Sugar baby
28	IC-430218	DKS/AHW/115	56	-	Durgapura Meetha

and parents were studied for their performance as rainy and summer season crop during 1999-2003. Promising segregates were selected in F_2 and, further breeding work advanced and emphasis was given to individual plant selection based on the fruit flesh quality traits and adaptability under dryland climate. From 2004–2010, the most promising lines, selections, and varieties of *mateera* and watermelon were evaluated with the varying seasons and situations. Since fruit flesh quality, cracking-free, marketable yield and tolerance to arid conditions were prioritized components for *mateera*, therefore, long-term data were assessed in various formats to conclude the research work.

Results and Discussion

Indian sub-continent is a primary, secondary and an area of regional diversity for several vegetable significant plants. Based on survey studies, it is recorded that the types of vegetables found growing in the arid and semi-arid areas of north-western India are distinctly different due to the eco-adaptations and climatic variability. The *Aravalli* range separates the desert ecosystem into two parts, namely, the Western arid and semi-arid East, where a rich variability of *Citrullus* and *Cucumis* species exists. With the facts, systematic surveys in targeted pockets and crop-specific explorations were conducted in drylands and tribal areas of Rajasthan and Gujarat for the collection of wild and

Table 2: Important characters of short-listed germplasm of *Citrullus* utilized for genetic variability component studies under hot arid climate

Genotype	*Days to first male flower (DAS)*	*Node to first male flower*	*Days to first female flower (DAS)*	*Node to first female flower*	*Days to first harvest (DAS)*	*Marketable fruits/ plant (No.)*	*Fruit yield/ plant (kg)*	*Fruit weight (kg)*	*Fruit length (cm)*	*Fruit girth (cm)*
IC-278416 (KCM/BKP-18)	40.69	5.36	53.82	13.27	84.16	1.22	2.17	1.76	22.42	48.06
IC-278417 (KCM/BKP-19)	41.94	5.13	48.29	15.29	84.53	1.55	1.90	1.62	19.16	45.49
IC-315281 (DPY-117)	43.87	5.26	53.33	12.16	85.96	1.06	7.40	6.81	44.60	70.87
IC-315283 (DPY-119)	45.79	2.76	54.22	13.27	84.19	1.13	4.80	4.30	27.02	58.15
IC-315284 (DPY-120)	47.62	5.24	54.48	9.24	88.10	1.17	8.11	2.68	29.57	51.00
IC-315288 (DPY-124)	45.17	4.70	52.08	11.20	88.60	1.45	1.94	1.32	21.28	42.01
IC-315290 (DPY-126)	47.68	4.40	55.12	12.28	95.90	1.66	2.08	1.23	19.53	42.56
IC-315304 (DPY-140)	49.05	6.50	56.18	13.23	98.11	1.33	2.06	1.51	21.62	47.35
IC-315306 (DPY-142)	47.49	5.29	54.49	12.30	91.98	1.15	4.86	4.33	25.98	60.50
IC-315313 (DPY-149)	45.01	5.55	51.05	13.98	82.04	1.34	3.60	2.73	34.19	54.58
IC-315321 (DPY-157)	50.57	7.44	55.06	15.28	85.89	1.03	4.36	4.11	29.05	60.91
IC-315324 (DPY-160)	40.97	4.21	47.02	8.22	80.90	1.75	5.09	2.89	28.24	47.20
IC-315328 (DPY-164)	44.64	6.48	50.86	10.79	85.43	1.27	0.99	0.78	16.11	35.58
IC-430201 (DKS/AHW/18)	40.45	4.53	46.12	9.12	80.62	4.01	16.18	4.17	30.67	62.75
IC-430202 (DKS/AHW/19)	36.16	4.15	44.57	6.18	78.12	4.28	16.44	3.97	35.64	59.20
IC-430208 (DKS/AHW/65)	34.02	3.12	43.77	6.05	76.02	5.45	15.47	2.84	28.12	55.24
Durgapura Meetha	49.10	5.07	63.23	15.45	101.21	1.42	4.81	3.44	24.74	67.43
Sugar Baby	47.24	6.18	55.52	14.15	96.99	1.15	3.19	2.79	24.67	61.02
EC-420977 (Charleston)	47.99	7.12	59.75	11.16	106.01	1.25	6.38	5.05	34.97	54.55
EC-420978 (Mahobobi)	54.17	10.21	67.23	21.34	114.65	1.04	2.72	2.56	19.57	49.90
IC-0590087 (Thar Manak)	34.50	4.42	44.57	10.78	76.98	4.24	17.52	4.26	23.34	58.27
Mean	44.48	5.53	52.90	12.13	88.87	1.90	6.29	3.10	26.69	53.93
CV (%)	1.03	2.09	1.21	2.28	0.78	3.06	3.87	1.98	1.73	1.42
CD (5%)	0.75	0.19	1.05	0.45	1.14	0.09	0.40	0.10	0.76	1.26

Table 3: Important characters of short-listed germplasm of *Citrullus* utilized for genetic variability component studies under hot arid climate

Genotype	*Edible flesh thickness (cm)*	*Non-edible flesh thickness (cm)*	*TSS (^{0} Brix)*	*Vine length (m)*	*Branches/ plant (No.)*	*Number of seeds/fruit*	*Seed test weight (g)*	*Seed length (cm)*	*Seed width (cm)*
IC-278416 (KCM/BKP-18)	11.33	2.05	7.20	2.50	4.12	232.56	7.61	1.13	0.64
IC-278417 (KCM/BKP-19)	12.24	1.52	6.40	2.76	4.17	109.53	8.05	1.05	0.64
IC-315281 (DPY-117)	17.68	2.49	6.12	2.64	5.05	251.16	2.30	0.72	0.43
IC-315283 (DPY-119)	15.47	2.37	8.20	3.13	5.13	63.32	4.52	0.83	0.55
IC-315284 (DPY-120)	16.35	2.78	8.44	3.11	4.05	187.61	7.62	1.26	0.75
IC-315288 (DPY-124)	11.41	1.53	5.14	2.92	5.19	74.26	6.66	1.04	0.65
IC-315290 (DPY-126)	12.47	1.50	10.23	3.18	5.09	94.56	4.11	0.80	0.56
IC-315304 (DPY-140)	12.20	0.74	8.42	3.11	5.05	157.29	4.08	0.95	0.54
IC-315306 (DPY-142)	15.14	2.07	9.11	2.56	4.15	235.73	5.16	0.97	0.64
IC-315313 (DPY-149)	14.55	1.07	10.08	2.56	6.08	135.71	5.42	1.04	0.57
IC-315321 (DPY-157)	15.18	1.52	8.26	3.12	4.13	258.04	4.31	0.95	0.55
IC-315324 (DPY-160)	13.22	1.54	10.43	2.76	5.17	190.64	4.42	0.96	0.54
IC-315328 (DPY-164)	8.15	1.12	6.32	2.89	6.18	64.61	3.52	0.86	0.55
IC-430201 (DKS/AHW/18)	14.40	2.05	8.12	4.48	6.27	319.21	8.32	1.22	0.75
IC-430202 (DKS/AHW/19)	13.43	1.65	8.20	3.69	5.46	384.28	8.50	1.23	0.74
IC-430208 (DKS/AHW/65)	13.22	1.71	8.31	2.75	5.57	418.55	8.59	1.23	0.76
Durgapura Meetha	14.55	2.13	9.11	3.75	5.50	342.12	8.62	1.26	0.83
Sugar Baby	14.94	1.55	9.11	3.73	5.12	112.90	5.06	0.86	0.55
EC-420977 (Charleston)	13.20	2.13	8.06	2.84	5.18	284.51	5.08	0.94	0.52
EC-420978 (Mahobobi)	14.13	1.24	8.51	2.65	4.12	195.14	12.10	1.35	0.85
IC-0590087 (Thar Manak)	16.36	1.91	10.92	3.50	5.39	128.13	7.50	1.25	0.55
Mean	13.79	1.74	8.32	3.08	5.05	201.90	6.26	1.04	0.63
CV (%)	1.73	2.55	1.99	2.96	2.12	1.27	0.61	1.66	0.93
CD (5%)	0.39	0.07	0.27	0.15	0.17	4.23	0.06	0.02	0.01

semi-cultivated germplasm of cucurbits. A rich variability in *mateera*, watermelon, *tinda* and *tumba* was collected, evaluated, and utilized over the years (1994 to 2012) as *Citrullus* genetic resource (254 entries) and at present, 75 germplasm/breeding material is being maintained at ICAR-CIAH, Bikaner (Samadia and Haldhar, 2019).

The arid and semi-arid region of Rajasthan is endowed with a rich diversity in dessert and non-dessert forms of melons and has unique variability patterns in the areas of cultivation. Owing to drought-tolerating capacity, *mateera* is a specific landrace of desert ecosystems. It is grown rainfed in the kharif and its seeds are uniform and *khaki* in color. Other-side, watermelon is grown in a semi-arid region with irrigations during the summer season and seeds are much variable and it is mostly developed through introduced varieties. *Mateera* is widely grown on sand dunes, and following special *Bari* practices (micro-catchments) where about 1 L of water is poured at each seed-sowing point and it is in March month to harvest rainfed crop produce (Samadia and Pareek, 2001).

The existence of diversity in watermelon-type *mateera* is unique in the *Thar* desert, where it appears to have acquired drought-hardy characteristics. During the primary surveys, 178 *mateera* collections were studied and they showed great variability in economic characters *viz*., fruit shape (round, oval, oblong, cylindrical-long), fruit size (0.5–7.5 kg), flesh content, flesh firmness, flesh color (pink, whitish-pink or reddish), TSS (3–12^0 Brix), seed content and seed color. Besides, morphological variations were also recorded for vine length, branches, leaf size, shape, color and coating, flowering, and fruiting at production sites. The performance of two *mateera* lines (AHW-19 and AHW-65) was compared with watermelon cultivars (Arka Manik, Arka Jyoti, MHW-11 and NWM-102) with twelve irrigations and under the prevalent practice in a desert ecosystem. The practice is to add about one litre of water at sowing time and later crop is supported by conserved and rain-water. In this study, watermelon genotypes failed to produce any fruits, whereas *mateera* lines yielded about three fruits per vine. With irrigations, watermelon depicted 8 to 9^0 Brix TSS compared to 7 to 8^0 Brix in *mateera*. However, commercial cultivars were often damaged by cracking. Thus, primary studies revealed the potentiality to develop drought-tolerant varieties from the existing variability to provide better economic returns to the desert farmer (Samadia and Pareek, 1996).

Realizing the importance of multiple-use of *mateera* in the Indian desert and potentialities in its period of fruit availability (April to November), systematic improvement work was taken with the objectives to develop varieties for uniform quality production, including dessert-salad, loiya and high seeds. For this, a wide range of collected germplasm was evaluated and utilized in breeding and conserved at the national gene bank. On evaluation in 1995-96, collected *mateera* germplasm (155 accessions) exhibited enough variations for morphological components of vine, fruit, flesh quality and yield. A wide range was is recorded for important characters such as days to first male flower appearance (24.5–45.2 DAS), days to first female flower appearance (40.2–55.5 DAS), node to first female flower (5.4–18.5), number of fruit-set/plant (3.5–20.85), days to first harvest (72.5–110.5 DAS), number of fruits/plant (0.85–7.45), fruit length (10.32–40.50 cm), fruit girth (25.91–73.54 cm), fruit weight (0.50–8.55 kg), TSS (2.14–12.5^o Brix), number of seeds/fruit (155–965), vine length (2.20–6.50 m) and number of branches/plant (3.12–6.45). Much variability is recorded for fruit rind, stripes pattern, flesh color, content and seeds. Both collected and generated material was repeatedly studied for variability parameters and most of the attributes exhibited similar trends under the investigation, and the components of genetic diversity from twenty-one short-listed genotypes are described in Tables 2, 3, 4 and 5.

Analysis of the variance of short-listed germplasm revealed the existence of highly significant genotypic differences for most of the quantitative characters, depicting greater variability in experimental material. Days to the opening of flowers and fruit set are very important attributes for earliness under dryland conditions, and the first male and female flowers ranged from 34.02–54.17 and 43.77–67.23 from sowing, respectively. The node number of the first male and female flower appearance ranged from 3.12–10.21 and 6.05–21.34, respectively. Days to the first fruit harvest range were very high (76.02–114.65 DAS) and important trait for *mateera* and watermelon under arid conditions. The number of marketable fruits ranged from 1.03–5.45, and yield was 0.99–17.52 kg/plant. Wide variations for fruit characters, viz., weight (0.78–6.81 kg), length (16.11–44.60 cm) and girth (35.58–70.87 cm) were recorded among the tested genotypes depicting the greater scope of improvement. Similar trends were also recorded in round melon under hot arid climate (Samadia, 2007).

For PCV, GCV and other variability component studies, two seasons' data of the year 2003 of the short-listed genotypes, including checks, were used. The estimates of GCV and PCV indicated that there is ample scope for improvement in the crop targeted. In general, the estimates of PCV were higher than GCV for all the characters. The GCV, which provides a greater picture of the extent of genetic variability in the diversity, ranged from 11.28% for days to first fruit harvest to 85.23% for fruit yield/plant. The GCV estimates were considerably higher (>30%) for characters such as number of fruits/plant, fruit yield/plant, fruit weight, number of seeds/fruit and seed test weight, whereas it was moderate (>15%) for a node to the first male and female flower opening, fruit length, fruit girth, edible and non-edible flesh thickness, TSS, vine length, seed length and seed weight indicating better scope through selection. A

Table 4: Important characteristics of short-listed germplasm of *Citrullus* utilized for genetic variability component studies at ICAR-CIAH, Bikaner

Genotype	Fruit shape	Skin color	Flesh color	Seed coat color	Seed size	Fruit quality rating	Crop growth rating
IC-278416 (KCM/BKP-18)	Obovate	Light green stripes, clear	Light pink	Yellowish white	Big	C -Poor	Poor
IC-278417 (KCM/BKP-19)	Obovate	Light green stripes, clear	Light pink	Reddish	Big	C	Poor
IC-315281 (DPY-117)	Oblong	Light green stripes, very clear	Red	Light brown	Very small	C	Poor
IC-315283 (DPY-119)	Oval-round	Dark green stripes, not-clear	Pink	Brownish	Small	B - Medium	Medium
IC-315284 (DPY-120)	Obovate	Dark green stripes, clear	Red	Light brown	Big	B	Good
IC-315288 (DPY-124)	Oblong	Light green stripes, clear	Wp	Reddish	Big	C	Poor
IC-315290 (DPY-126)	Round	Light green stripes, clear	Red	Brown	Small	A - Good	Good
IC-315304 (DPY-140)	Round	Dark green stripes, clear	Light pink	Brown	Small	B	Medium
IC-315306 (DPY-142)	Oval-round	Dark green stripes, clear	Red	Brown	Small	A	Poor
IC-315313 (DPY-149)	Oval-round	Dark green stripes, clear	Pink	Brown	Small	B	Good
IC-315321 (DPY-157)	Oval-round	Dark green stripes, clear	Light pink	Brown	Small	C	Poor
IC-315324 (DPY-160)	Round	Dark green stripes, clear	Dark pink	Brown	Small	AA-Very good	Good
IC-315328 (DPY-164)	Round	Dark green stripes, not-clear	Light pink	Brown	Small	C	Poor
IC-430201 (DKS/AHW/18)	Obovate	Dark green stripes, clear	Pink	Brown khaki	Big	B	Good
IC-430202 (DKS/AHW/19)	Obovate	Dark green stripes, clear	Pink	Brown khaki	Big	B	Good
IC-430208 (DKS/AHW/65)	Round	Green stripes, not-clear	Pink	Brown	Big	B	Good
Durgapura Meetha	Round	Light green, non-stripes	Dark pink	Light brown mottled	Big	AA	Good
Sugar Baby	Round	Dark green stripes, non-clear	Red	Light brown	Small	AA	Good
EC-420977 (Charleston)	Oblong-long	Light green, non-stripe	Pink	Black brown	Small	B	Medium
EC-420978 (Mahobobi)	Round	Light green stripes, clear	Light pink	Light brown	Big	C	Medium
IC-0590087 (Thar Manak)	Oblong	Dark green stripes, clear	Red	Blackish brown	Big	AA	Good

close correspondence between PCV and GCV values with respect to characters under study indicated that the testing environment has very little influence on the expression of the attributes. Thus, selection based on phenotype can be effective with an equal probability of success. Ram *et al.*, 2023 also reported the traits having narrow differences among GCV, PCV and broad sense heritability values, suggesting low effect of environment in snowball cauliflower. Very high heritability (broad sense) estimates values were obtained for all the characters in the present study and it suggested that these traits may generally be governed by additive gene action.

The genetic advance as a percent of the mean ranged from 23.22 for days to first harvest to 175.33 for fruit yield/plant. The high value of GA (> 50%) was obtained for the node to the first male and female flower, number of fruits/plant, fruit yield/plant, fruit weight, fruit length, non-edible flesh thickness, number of seeds/fruit and seed test-weight and thus, these traits are governed by additive gene action. High heritability values accompanied by high genetic advance were found for the node to first male and female flower, number of fruits/plant, fruit yield/plant, fruit weight, fruit length, non-edible flesh thickness, number of seeds/fruit and seed test-weight suggested that these traits are predominantly under the control of additive gene action. Hence, simple selection could be effective for the improvement of these traits.

Where: DFM- Days to first male flower (DAS), NMF- Node to first male flower, DFF- Days to first female flower (DAS), NFF- Node to first female flower, DFH- Days to first harvest (DAS), MF/P- Marketable fruits/ plant (No.), FY/P- Fruit yield/plant (kg), FW- Fruit weight (kg), FL- Fruit length (cm), FG- Fruit girth (cm), EFT- Edible flesh thickness (cm), NEF- Non-edible flesh thickness (cm), TSS (^{0} Brix), VL-Vine length (m), B/P- Branches/plant (No.), NS/F- Number of seeds/fruit, STW- Seed test weight (g), SL- Seed length (cm) and SW- Seed width (cm).

High heritability value coupled with low genetic advance (>25%) were obtained for days to the first male and female flower appearance and days to the first harvest were probably due to the non-additive type of gene action and direct selection for these characters will be less effective. The traits such as number of fruits/plant, fruit yield/plant, fruit weight, number of seeds/fruit and seed test-weight possessing high GCV, heritability and genetic gain could effectively be used in selection, as it has been suggested that characters with high heritability coupled with high genetic gain would respond to selection better than those with high heritability and low genetic gain. The high variability and heritability, along with high genetic advance expressed by the above-mentioned traits indicated that the genotypes can be tested in multi-location traits and selected as donors for these characters or used as a parents in the hybridization program.

The magnitude of genotypic correlation coefficients was slightly higher than their corresponding phenotypic correlation coefficients for all the traits, indicating a strong inherent association between various traits under study. The studies indicated that fruit yield/plant had a positive and significant correlation with the number of fruits/plant (0.887), number of seeds/fruit (0.596), vine length (0.503), seed length (0.492), fruit weight (0.491), fruit girth (0.473) and fruit length (0.441), and also with edible flesh thickness (0.398), branches/plant (0.352) and non-edible flesh thickness (0.344). Days to first male flower (-0.713), node to first male flower (-0.485), days to first female flower (-0.601), node to first female flower (-0.626) and days to first harvest (-0.516) had a negative and significant correlation with fruit yield/plant. Negative and significant association of days to the appearance of the male flower (-0.819), days to the appearance of the female flower (-0.710) and days to first harvest (-0.563) with a number of fruits/plant, which clearly indicated that early genotypes bear more number of fruits/plant.

Days to the first harvest had a positive and significant association with days to the first male flower (0.822), days to the first female flower (0.924), nodes to first male flower (0.732) and nodes to the first female flower (0.672) that indicates the mutual association of these characters for their expression. Fruit girth showed a positive and significant correlation with fruit weight (0.854), fruit length (0.685), edible flesh thickness (0.811), non-edible flesh thickness (0.520) and the number of seeds/fruit (0.554). Seed test weight had a positive and significant correlation with seed length (0.923), seed weight (0.890) and the number of seeds/fruit (0.372).

Path analysis (Table 6) revealed a positive direct effect on fruit yield/plant was maximum from the number of fruits/plant (2.088) followed by seed width (1.918), fruit length (1.617), seed length (1.566), days to first harvest (1.312) and node to first female flower (1.290). Similarly, the maximum negative direct effect showed by seed test weight (-3.387) followed by the number of seeds/fruit (-1.606), edible flesh thickness (-1.519), days to first male flower (-0.923), days to first female flower (-0.915) and branches/plant (-0.880) on fruit yield/plant. The number of fruits/plant had a positive effect on fruit yield/plant due to positive indirect effects via days to first male flower (0.750), days to first female flower (0.650), number of seeds/fruit (1.101), seed length (1.045), branches/plant (0.940), vine length (0.878), seed test-weight (0.838) and seed weight/fruit (0.674). Thus, it is suggested that for effective selection for higher yield in *Citrullus*, the number of fruits/plants is an important character. But it may slightly affect the fruit weight and size. Thus, a moderate balance has to be made for a medium number of fruits, fruit weight and size to obtain better results under dryland climate.

Table 5: Genetic variability components for various characters from short-listed *Citrullus* germplasm at ICAR-CIAH, Bikaner

Traits	*Min.*	*Max.*	*Mean*	*CD (5%)*	*ECV (%)*	*GCV (%)*	*PCV (%)*	*h^2 (%) (broad sense)*	*Genetic advance (GA)*	*Genetic gain (5%SI)*
DFM	34.02	54.17	44.48	0.75	1.03	11.80	11.81	99.74	10.80	24.28
NMF	3.12	10.21	5.53	0.19	2.09	26.95	26.98	99.80	3.07	55.47
DFF	43.77	67.23	52.90	1.05	1.21	11.36	11.38	99.62	12.36	23.37
NFF	6.05	21.34	12.13	0.45	2.28	28.38	28.41	99.78	7.08	58.41
DFH	76.02	114.65	88.87	1.14	0.78	11.28	11.29	99.84	20.63	23.22
MF/P	1.03	5.45	1.90	0.09	3.06	69.67	69.69	99.94	2.73	143.47
FY/P	0.99	17.52	6.29	0.40	3.87	85.23	85.26	99.93	11.04	175.53
FW	0.78	6.81	3.10	0.10	1.98	47.89	47.91	99.94	3.06	98.64
FL	16.11	44.60	26.69	0.76	1.73	25.43	25.45	99.85	13.97	52.35
FG	35.58	70.87	53.93	1.26	1.42	16.47	16.49	99.75	18.28	33.89
EFT	8.15	17.68	13.79	0.39	1.73	15.26	15.30	99.57	4.32	31.38
NEF	0.74	2.78	1.74	0.07	2.55	28.61	28.65	99.74	1.02	58.87
TSS	5.14	10.92	8.32	0.27	1.99	17.77	17.81	99.58	3.04	36.54
VL	2.50	4.48	3.08	0.15	2.96	16.30	16.39	98.91	1.02	33.39
B/P	4.05	6.27	5.05	0.17	2.12	13.77	13.83	99.21	1.43	28.27
NS/F	63.32	418.55	201.90	4.23	1.27	52.24	52.25	99.98	217.29	107.62
STW	2.30	12.10	6.26	0.06	0.61	37.51	37.51	99.99	4.84	77.26
SL	0.72	1.35	1.04	0.02	1.66	17.26	17.29	99.69	0.37	35.50
SW	0.43	0.85	0.63	0.01	0.93	17.96	17.97	99.91	0.23	36.98

Table 6: Path analysis (direct and indirect) for various characters in short-listed *Citrullus* germplasm at ICAR-CIAH, Bikaner

CHR	DFM	NMF	DFF	NFF	DFH	MF/P	FW	FL	FG	EFT	NEF	TSS	VL	B/P	NS/F	STW	SL	SW	FY/P (GR)
DFM	-0.923	-0.704	-0.827	-0.675	-0.759	0.756	0.092	0.172	0.052	-0.044	0.114	0.041	0.145	0.358	0.270	0.131	0.230	-0.009	-0.713
NMF	0.326	0.427	0.326	0.332	0.313	-0.250	-0.007	-0.080	-0.036	-0.008	-0.114	-0.045	-0.096	-0.156	-0.091	0.043	-0.012	0.010	-0.485
DFF	-0.820	-0.697	-0.915	-0.704	-0.845	0.650	0.009	0.152	-0.052	-0.073	-0.015	0.026	0.159	0.364	0.097	-0.074	0.048	-0.142	-0.601
NFF	0.943	1.003	0.994	1.290	0.867	-0.834	-0.151	-0.446	0.015	0.104	-0.308	-0.035	-0.282	-0.561	-0.451	0.208	-0.050	0.089	-0.626
DFH	1.079	0.961	1.212	0.882	1.312	-0.739	-0.110	-0.313	-0.069	-0.044	-0.173	0.021	-0.121	-0.411	-0.123	0.182	-0.034	0.221	-0.516
MF/P	-1.711	-1.222	-1.483	-1.350	-1.176	2.088	0.271	0.301	0.370	0.087	0.049	0.426	0.878	0.940	1.101	0.838	1.045	0.674	0.887
FW	0.002	0.000	0.000	0.003	0.002	-0.003	-0.028	-0.023	-0.024	-0.021	-0.017	-0.002	-0.002	-0.000	-0.013	0.004	0.002	0.005	0.491
FL	-0.301	-0.304	-0.268	-0.560	-0.386	0.233	1.315	1.617	1.109	0.994	0.751	0.023	0.062	0.274	0.834	-0.368	-0.200	-0.335	0.441
FG	-0.038	-0.057	0.039	0.008	-0.035	0.120	0.578	0.464	0.677	0.549	0.352	0.135	0.256	0.035	0.375	0.018	0.050	0.038	0.473
EFT	-0.072	0.029	-0.122	-0.123	0.051	-0.063	-1.168	-0.934	-1.232	-1.519	-0.882	-0.558	-0.283	0.315	-0.344	-0.022	-0.114	0.035	0.398
NEF	-0.085	-0.184	0.011	-0.164	-0.091	0.016	0.418	0.320	0.359	0.401	0.690	-0.052	0.092	-0.157	0.197	0.031	0.058	0.064	0.344
TSS	-0.012	-0.030	-0.008	-0.007	0.004	0.058	0.029	0.004	0.057	0.105	-0.021	0.287	0.060	0.030	0.016	0.011	0.048	0.002	0.254
VL	-0.020	-0.029	-0.022	-0.028	-0.012	0.054	0.019	0.005	0.048	0.024	0.017	0.027	0.129	0.056	0.028	0.025	0.032	0.034	0.503
B/P	0.341	0.323	0.351	0.383	0.276	-0.396	-0.021	-0.149	-0.045	0.182	0.201	-0.094	-0.384	-0.880	-0.064	0.142	0.056	0.084	0.352
NS/F	0.470	0.344	0.170	0.562	0.151	-0.847	-0.738	-0.828	-0.890	-0.363	-0.459	-0.094	-0.352	-0.117	-1.606	-0.599	-0.749	-0.755	0.596
STW	0.480	-0.342	-0.274	-0.546	-0.471	-1.359	0.514	0.771	-0.091	-0.050	-0.151	-0.132	-0.662	0.547	-1.263	-3.387	-3.128	-3.017	0.340
SL	-0.390	-0.046	-0.083	-0.060	-0.040	0.784	-0.155	-0.194	0.117	0.118	0.132	0.264	0.391	-0.100	0.730	1.447	1.566	1.341	0.492
SW	0.018	0.045	0.298	0.133	0.324	0.619	-0.376	-0.397	0.108	-0.044	0.178	0.015	0.515	-0.184	0.902	1.708	1.642	1.918	0.262

Table 7: Comparative characters of high-quality fruit-yielding *mateera*- 'Thar Manak' with parents

Character	*Parental varieties*		*Developed variety*
	Mateera AHW-19	*Sugar baby*	*Thar manak*
Days to first female flower (DAS)	44.5	55.2	38.5
Node number to first female flower	7.1	14.2	12.7
Days to first harvest (DAS)	76.5	97.5	75.5
Number of marketable fruits/plant	4.29	1.14	3.45
Marketable fruit yield/plant (kg)	16.54	3.22	12.15
Fruit weight (kg)	3.85	2.83	3.25
Fruit length (cm)	35.5	24.1	22.5
Fruit girth (cm)	58.8	60.2	58.5
Edible flesh thickness (cm)	13.4	15.1	16.8
Non-edible flesh thickness (cm)	1.95	1.51	1.61
TSS (^{0} Brix)	8.12	10.15	10.82
Fruit characters	Oblong, dark green-green clear stripes; No fruit cracking	Round, green to dark green non-stripes rind; Severe fruit cracking	Oblong-round, dark green-green clear stripes on rind; No fruit cracking
Flesh characters	Pink, B-grade	Red, A-grade	Red, A-grade
Seed characters	High seed content, medium-sized and khaki color	High seed content, small-sized and mottled brown	Low seed content, very big sized and blackish

Figure 1: *Mateera* var. AHW-19

Figure 2: *Mateera* var. AHW-65

During characterization, *Citrullus lanatus* germplasm was categorized based on prioritized attributes and promising *mateera* lines viz., AHW-18 (IC-430201), AHW-19 (IC-430202), AHW-65 (IC-430208), AHW-108 (IC-430215), AHW-140 (IC-430225), AHW-RSS-1 (red seeded isolate from germplasm of Churu district) and AHW-BSM-1 (black seeded isolate from AHW-19) was selected for use in the breeding program. Among watermelons, Sugar Baby, Durgapura Meetha and Charleston Local were found to have the potential for flesh firmness and color under arid climates. For the first time, two *mateera* selections *viz.*, AHW-19 and AHW-65 released for immediate gains in 1998 and growers accepted it for uniform harvest under rainfed conditions. The utilization of *Citrullus* germplasm for the breeding program has been described and emphasized that native landraces would be useful under abiotic stressed conditions (Pareek and Samadia, 2002; Samadia *et al*., 2002 and Samadia and More, 2011).

However, two essential traits of commercial watermelon, *i.e.*, eye-appealing flesh quality and sweetness, were not materialized in *mateera* varieties developed by the institute (Figure 1 and 2). Therefore, intensive breeding work was carried out involving AHW-19, AHW-65, Sugar Baby, Durgapura Meetha, Charleston and Mahobobi. First, a large number of progenies were generated using selected parentage in combinations (F_1, F_2, BC_1, BC_2 and bi-parental) and evaluated. Simultaneously, requisite segregates isolated from F_2 to develop individual plant progeny and selfing precedes selection for generation advancement. Four prioritized traits such as flesh quality, earliness, tolerance to cracking and yield behavior under high temperature

Figure 3: *Mateera* var. Thar Manak

and abiotic stressed situations, were kept to screen the progenies.

The desirable progenies and their derivates were advanced over the years and evaluated both in the rainy and summer of 2000 to 2004. Fruit quality, fruiting behavior, reaction to cracking, insects and diseases were taken into consideration to screen the developed progenies. In F_6 generation, a few progenies of the cross combination of AHW-19 x Sugar Baby exhibited desirable trends for fruit flesh (color, firmness, content and TSS) and yield. After assessing fruit quality components among $F_{6/a}$ family, four blocks (F_6/a/3, F_6/a/7, F_6/a/9 and F_6/a/10) were developed and advanced for uniformity. On evaluation, these showed desirable trends for earliness, the number of marketable fruits/plants, fruit size, shape and flesh quality.

The fruit quality and yield components of advanced family F_6/a/10 were much superior and highly acceptable, depicting internally as good Sugar Baby and rind characters as *mateera* (Table 7). This was further advanced in isolation and open-pollinated progeny named F_6/a Thar Manak (Figure 3) and released in 2007. The developed variety is devoid of cracking and suitable for spring-summer and rainy-season cultivation under hot arid climates. Thus, the strategic research work in *Citrullus* was found effective in the conservation and utilization of native germplasm and also the development of breeding material for further benefits.

Conclusion

Breeding for improvement in fruit quality and productivity is a continuous nature of work to ensure genotypes for cultivation under high temperature, drought, and low rain and suitability to the organic or prolonged period of harvest. Because the present watermelon genotypes exhibit susceptibility to viruses and abiotic stresses. Based on long-term studies in germplasm utilization at ICAR-CIAH, Bikaner, future strategies were carved out for in-depth understanding and strengthening the activities: -

1. Utilization of the regional and national genetic resources of *mateera*/watermelon to breed marketable quality fruit-yielding genotypes for cultivation under high temperatures and varying production situations such as low-input, organic, rainfed, surface-covering protective technique as a mechanism of escaping severity of winter for short-spell and vertical harvesting, and
2. Utilization of Indigenous *mateera* germplasm to develop trait-specific/value-added genotypes such as *loiya* and seed-kernels for production under rainfed and abiotic stresses conditions, and its promotion through seed-chain owing to their regional preferences.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.12

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Association and Variability of Morphological, Yield and Yield Attributing Traits in Mung Bean [*Vigna radiata* (L.) Wilezek]

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Abstract

The efficacy of the selection process is greatly enhanced by using appropriate selection indices. The knowledge of the genetic variability and relationship among various traits affecting seed yield is essential for crop improvement. The present study was undertaken to evaluate 51 diverse genotypes of mungbean for the estimation of genetic variability, heritability & genetic advance, the correlation coefficient for eleven traits and their association level with yield. Results of the analysis of variance revealed significant differences for all the characters studied and, thereby offered an ample opportunity for selecting suitable genotypes with desired traits. High PCV and GCV were observed for seed yield per plant (56.05/47.60), primary branches per plant (40.27/32.38), pods per plant (36.31/32.93) and biological yield per plant (38.46/33.17) indicating the role of additive gene action in the expression of these characters. Analysis of correlation revealed that the magnitude of genotypic correlation coefficients was higher than the phenotypic correlation coefficients suggesting the existence of inherent association among the traits studied. High heritability was observed for plant height (0.89) followed by pods per plant (0.82) and seeds per pod ((0.81), indicating the less influence of environment on these characters. Seed yield was found to be positively correlated with primary branches per plant, number of pods per plant, number of seeds per pod and biological yield per plant. Path coefficient analysis revealed the importance of pods per plant and, the number of seeds per pod, while the highest negative direct effect was recorded for the harvest index.

Keywords: - Correlation coefficient, Mung bean, Path analysis, Variability.

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Received: 31/03/2023 **Revised:** 21/06/2024

Accepted: 20/08/2024

How to cite this article: Dar SA, MH Khan, J Hussain, NA Dar, BA Alie, S Mehvish, A Qayoom, A Khan and Uzma Fayaz (2024) Association and Variability of Morphological, Yield and Yield Attributing Traits in Mung Bean [*Vigna radiata* (L.) Wilezek] . *Indian J. Plant Genet. Resour.* 37(3): 494-501. **DOI:** 10.61949/0976-1926.2024.v37i03.12

Introduction

Pulses are an excellent option for dietary protein. Pulses, when used as food with other cereals, definitely meet the requirement of a balanced diet. Mung bean (*Vigna radiata* L.) is a vital and important pulse crop, also known as green gram, and is an excellent source of easily digestible proteins with low flatulence, which complements the staple rice diet in Asia. In India, it is the third most important pulse crop after chickpea and pigeonpea. It is grown mainly as a *kharif* season crop. However, its cultivation in rabi season is restricted to the eastern and southern parts of the country.

Seed yield in mung bean is a complex character like other crops, determined by various components. A clear knowledge of variability in various quantitative characters existing in the breeding material helps plant breeders select superior genotypes on the basis of different genetic parameters such as genotypic variation, heritability, genetic gain, etc, to understand the nature and magnitude of variation for the available plant characters. Hence it is necessary to estimate the relative amount of genetic and non-genetic variability exhibited by the traits under the study (Moose and Mumm, 2008). Yield is dependent on various characteristics and environmental conditions that exist during crop growth. It is,

therefore, essential to study the association of characters among themselves and with the yield of crops. Genotypic correlation provides a measure of genotypic association between two characters and helps to identify more useful relationships between characters. Indirect association becomes complex and important when a number of variables are included in the study of correlation. In such cases, a more defined technique as, path coefficient analysis, helps to find out the direct and indirect causes of character association. Every component character has a direct and indirect effect on yield. If correlation is due to direct effect, it reflects a true relationship and selection is practiced for such a character for improving the yield. In case if the effect is indirect through another component trait, the breeder has to select the latter trait through which the indirect effect is exerted. The presence of high variability in this crop offers much scope for its improvement. Hence, an attempt was made to assess the genetic variability, heritability, genetic advance, correlation and path analysis in respect to desirable traits in 51 genotypes of mung bean, which will help in the selection of promising lines for the further breeding program and to explore high yielding lines of mung bean.

Materials and Methods

The experiment was undertaken at the Research Farm of Division of Genetics and Plant Breeding (GPB), Faculty of Agriculture (FoA), Wadura, Sopore, Sher-e-Kashmir University of Agricultural Sciences and Technology Kashmir (SKUAST-K), to evaluate the 51 genotypes of mung bean for genetic variability with respect to yield and yield contributing traits (Table 1a) The experiment was laid out in randomized block design with three replications during 2021-22. Each genotype was sown at the spacing of 30 cm between rows and 10 cm between plants and about two seeds were dibbled at each hill to assure germination. A uniform standard plant population was maintained throughout the experiment. A standard recommended package of practices was followed to raise a good crop. Observations for all the traits (except days to 50% flowering and days to maturity) were recorded by taking ten randomly selected plants from each replication. Days to 50% flowering and days to maturity were computed on a plot basis. The data of 11 morphological traits *viz* days to maturity, number of branches per plant, plant height (cm), pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%) were recorded at the time of maturity, whereas observation on days to 50% flowering was recorded for different genotypes when they attained 50% flowering stage. Analysis of variance for the observations recorded on different traits was carried out as per the standard procedure of Box *et al.* (1978). Genotypic and phenotypic coefficients of variability were estimated according to Johnson *et al.* (1955). Heritability in a broad sense and Genetic advance were worked out as per the procedures of Burton and Dewane (1953) and Johnson *et al.* (1955), respectively. Estimation of phenotypic and genotypic correlation suggested by Fisher (1954) and Al-Jibouri *et al.* (1958). Path coefficient of variation was computed as per the method given by Dewey and Lu (1959).

Results and Discussion

Analysis of Variance and Mean Performance

Since, yield is governed by polygenes with small, similar and cumulative effects and highly influenced by the environment, selection based on yield alone is ineffective. The breeders apply indirect selection on yield through a selection of yield attributes with high heritability so that environmental influence can be minimized.

The mean sum of squares with respect to morphological traits has been given in (Table 1b). The results revealed that the mung bean genotypes differed significantly for all the traits *viz* days to 50% flowering, days to maturity, number of branches per plant, plant height (cm), pod length (cm), number of pods plant^{-1}, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%) indicating the presence of sufficient variability and all the genotypes differed from each other in respect of characters, which open a way for improvement in the material through selection. A similar finding was also reported by Bisht *et al.* (2014), Javed *et al.* (2014), Singh *et al.* (2012) and Srivastava and Singh (2012).

The mean performance of the genotypes showed a wide range of variability for all the parameters studied (Table 2). The range of variation was highest for plant height (cm) followed by biological yield per plant (g), number of pods per plant and the seed yield per plant (g). This may be due to the existence of diversity in genotypes evaluated, while the coefficient of variation was higher for seed yield and number of branches per plant, and medium to low values were observed for biological yield per plant (g), pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), harvest index (%), plant height (cm) and days to flowering and maturity. The coefficient of variation was low which indicated that most of the genotypes had average height and mass selection would be effective for shorter height. Similar finding was also reported by Ahmad *et al.* (2015), and Payasi (2015).

Coefficients of Variability

Genotypic and phenotypic coefficients of variability are of greater importance in determining the extent of variability present within germplasm. The value of the phenotypic coefficient of variation was observed to be higher than the genotypic coefficient of variation for all characters, indicating that the environment had an important role in

Table 1a: Passport information and pedigree of mung bean genotypes

S. No.	*Genotype*	*Pedigree*	*Originating centre*	*Area of adoption*
1	IPM 02-3	IPM 99-125×Pusa Bold 2	IIPR, Kanpur	NWPZ (DL, HR, HP, J&K, PN, RJ)
2	IPM 205-7	IPM02-1×EC398899	IIPR, Kanpur	SZ (AP, TN) CZ (MP, & GJ)
3	IPM-410-3	IPM03-1×NM1	IIPR, Kanpur	NWPZ/CZ (RJ, PN, HR, DL, HP, UK, J&K, MP, MH & GJ
4	PKV-AKM-4	BM 4×PS 7	PKV, Akola	CZ (MH, MP) SZ (KA, OD, TN)
5	Pat-Mung-5	Selection from VC 6368	GBPUA& T, Pantnagar	Uttar Pradesh
6	SML 832	SML 302 × Pusa Vishal	PAU, Ludhiana	Punjab
7	TMB 136	TM 98-80 × SML 668	BARC, Trombey	West Bengal
8	IPM-99-125 (Meha)	PM 3× AMP 36	IIPR, Kanpur	NWPZ (DL, HR, HP, J&K, PN, RJ)
9	RMG 268	R 288-8 × J 780	RARI, Dugapura	Rajasthan
10	ML 818	5145/87 × ML 267	PAU, Ludhiana	NWPZ (HR, PN, UP, UK)
11	PM 14-3	PM 6 × Pusa Ratna	GBPUAT, Pant Nagar	Uttarakhand
12	Samrat	ML 20/19 × ML 5	IIPR, Kanpur	NWPZ/CZ (RJ, PN, HR, DL, HP, UK, J&K, MP, MH & GJ
13	COGG-8	COGG 923 × VC6040	TNAU, Coimbatore	Tamil Nadu
14	EC581523 B	Exotic collection	-	-
15	HUM 16	Pusa Bold 1 × HUM 8	IARI, New Delhi	Uttar Pradesh, Bihar, West Bengal and Assam
16	EC581523	Exotic collection	-	-
17	IPM 02-14	IPM 99-125 × Pusa Bold 2	IIPR, Kanpur	SZ (AP, KN, TN, OD)
18	MH 421	Muskan × BDYR 2	CCSHAU, Hissar	NWPZ/CZ (DL, HR, RJ, W. UP)
19	MH 1-25	Asha × PDM 90-1	CCSHAU, Hissar	Haryana
20	SML 1817	PAU 911 × Mash 114	PAU, Ludhiana	Punjab
21	NDMZ 15-2	NDM 1 × Pant Mung -5	NDUAT, Kumarganj	UP, Uttrakhand
22	MH-1010	MH 98-1 × PDM 96-262	CCSHAU, Hissar	NEPZ & NWPZ (BH, HA, DL, JH, PB, RJ, UP, WB)
23	ML 2037	ML 818 × VC 6372-45-8-1	PAU, Ludhiana.	Punjab
24	MH 534	ASHAXBDYR-2	CCSHAU, Hissar	Haryana
25	KM 2241	Samrat × PDM 54	CSAU, Kanpur	NHZ (TR, MN, J&K, HP)
26	TMB 37	Kopergaon ×TARM 2	BARC, Trombey	West Bengal
27	Pusa Vishal	Selection from NK 92	IARI, New Delhi	NHZ (J&K, MN, TR)
28	MH 2-15	PDM116×Gujarat-1	CCSHAU, Hissar	NWPZ/CZ (DL, HR, RJ, W. UP)
29	SML 668	Selection from AVROC line NM 94	PAU, Ludhiana	Punjab
30	SML 1018	ML 613×BDYR-2	PAU, Ludhiana	Punjab
31	MH 929	RMG 268×UPM 98 1	CCSHAU, Hissar	Haryana
32	MH 925	PUSA VISHAL × ML 682	CCSHAU, Hissar	Haryana
33	MH 934	MH 96-1× 2KM 117	CCSHAU, Hissar	Haryana
34	MH 926	Rice bean × ML 1108/682	CCSHAU, Hissar	Haryana
35	MH 921	MH 96-1× 2KM 114	CCSHAU, Hissar	Haryana
36	MH 919	RMG-62 × UPM 98-1	CCSHAU, Hissar	Haryana
37	MH 539	MH 96-1×BDYR-1	CCSHAU, Hissar	Haryana
38	EC 30400	Exotic collection	-	-
39	EC 399223	Exotic collection	-	-

40	EC 470095	Exotic collection	-	-
41	EC 581523	Exotic collection	-	-
42	IPM 06-5	Mutant of EC 369223	IIPR, Kanpur	NWPZ (DL, HR, HP, J&K, PN, RJ)
43	TMB 131	Samrat × Kopergoan	BARC, Trombey	-
44	EC 393410	Exotic collection	-	-
45	GM 11-02	GM 9910 × Pusa Vishal	SDAU, S.K. Nagar	Gujarat
46	Pusa Ratna	VC 6368 × ML 267	IARI, New Delhi	NHZ (J&K, MN, TR)
47	Pusa 251552	Exotic collection	-	-
48	MH 560	ASHAXBDYR-1	CCSHAU, Hissar	Haryana
49	LGG 460	Lam M2× ML 267	ARS, Lam	Andhra Pradesh, Tamil Nadu, Eastern Uttar Pradesh
50	Pusa 9531	Selection from NM 9473	IARI, New Delhi	NHZ (J&K, MN, TR)

Table 1b: Analysis of variance (Mean Squares) for the eleven characters of mung bean genotypes

Source of variation	*df*	*Mean squares*										
		DFF	*DM*	*PH (cm)*	*PBPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*SYPP*	*BYPP*	*HI*
Replications	2	260.784	731.314	1730.693	3.549	117.849	12.414	8.471	0.042	41.700	228.629	29.166
Treatment	50	19.071**	23.038**	343.284**	1.985*	49.971**	13.223**	14.957**	2.033**	36.756**	137.251**	43.756**
Error	100	3.104	2.694	13.579	0.306	3.356	2.027	1.031	0.166	4.194	14.121	4.973

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP – number of Primary branches per plant, NPPP – Number of Pods per plant, PL - Pod length (cm), NSPP - Number of seeds per pod,100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%),

influencing the expression of these characters (Table 3). High PCV and GCV were observed for seed yield per plant (56.05/47.60), primary branches per plant (40.27/32.38), pods per plant (36.31/32.93) and biological yield per plant (38.46/33.17) indicating that improvement could be possible through the selection of these traits. Similar results were also reported by Panigrahi *et al.* (2014), and Suresh *et al.* (2010), while moderate PCV and GCV were recorded for pod length (28.98/23.33), seeds per pod (20.62/18.65) and 100-seed weight (17.75/15.77). The low PCV and GCV were recorded for days to 50% flowering (6.78/5.39) and days to maturity (4.34/3.67). Low to moderate GCV and PCV values indicated the influence of the environment on these traits and limited scope for improvement by selection. The results revealed that the genotypic coefficient of variation was close to that of phenotypic variation for days to 50% flowering, days to maturity and harvest index, indicating that the phenotypic coefficient of variation was largely due to genetic differences and less environmental influence. Similar results were also reported by Das and Baru (2015), (Raselmiah *et al.* (2016), More *et al.* (2016), Usharani *et al.* (2016) and Tabasum *et al.* (2010). However, a considerable difference was observed between GCV and PCV values for primary branches per plant and seed yield per plant, indicating a role of the environment in the expression of these traits.

Table 2: Range mean and co-efficient of variability for different traits of mung bean

Characters	Mean ± SE	Range	CV (%)
Days to 50% flowering	42.76 ± 0.19	38.00-47.00	4.12
Days to maturity	70.78 ± 0.18	65.67-75.66	2.32
Plant height (cm)	78.26 ± 0.44	61.00-114.00	4.71
Primary branches per plant	2.31 ± 0.47	1.33-3.66	23.95
Number of pods per plant	11.97 ± 1.06	6.67-23.00	15.30
Pod length (cm)	8.28 ± 0.06	5.97-11.70	17.19
Number of seeds per pod	11.55 ± 0.76	8.00-15.67	8.79
100 seed weight (g)	5.00 ± 0.15	4.17-6.83	8.15
Seed yield per plant (g)	6.92 ± 0.75	3.34-18.08	29.59
Biological yield per plant (g)	19.31 ± 2.25	9.63-40.33	19.46
Harvest index (%)	35.60 ± 2.42	30.95-45.99	6.26

Heritability and Genetic Gain

Heritability, in a broad sense, includes additive and epistatic effects; it is realized only when accompanied by genetic advances. However, GCV with heritability estimates would

Table 3: Estimation of genetic variability parameters for eleven characters in mung bean

Characters	σ^2g	σ^2p	*GCV (%)*	*PCV (%)*	$h^2_{(b)}$	*GA*	*GA as % of mean*
Days to 50% flowering	5.322	8.426	5.395	6.789	63.16	3.78	8.83
Days to maturity	6.781	9.475	3.679	4.349	71.57	4.54	6.41
Plant height (cm)	109.902	123.481	13.396	14.199	89.00	20.37	26.03
Primary branches per plant	0.560	0.866	32.386	40.278	64.65	1.24	53.64
Pods per plant	15.538	18.894	32.931	36.314	82.24	7.36	61.52
Pod length (cm)	3.732	5.759	23.331	28.983	64.80	3.20	38.69
Seeds per pod	4.642	5.673	18.654	20.622	81.83	4.01	34.76
100 seed weight (g)	0.622	0.788	15.778	17.758	78.94	1.44	28.88
Seed yield per plant (g)	10.854	15.048	47.609	56.057	72.13	5.76	83.29
Biological yield per plant (g)	41.043	55.164	33.177	38.463	74.40	11.38	58.95
Harvest index (%)	12.928	17.901	10.100	11.885	72.22	6.29	17.68

σ^2g = Genotypic variance, σ^2p = Phenotypic variance, GCV = Genotypic coefficient of variance, PCV = Phenotypic coefficient of variance, $h^2_{(b)}$ = Heritability (Broad sense), GA = Genetic advance, GAM = Genetic advance as per cent mean.

Table 4: Phenotypic (above diagonal) and genotypic (below diagonal) correlation among various characters in mung bean

Character	*DFF*	*DM*	*PH*	*PBPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*BYPP*	*HI*	*GYPP*
DFF	1.000	0.405**	0.067	-0.026	0.124	-0.175	-0.011	-0.16	-0.364**	0.0494	-0.067
DM	0.544**	1.000	0.168*	-0.038	0.323	-0.144	-0.061	-0.026	-0.27**	0.196*	0.103
PH	-0.004	0.190*	1.000	-0.002	0.038	0.348**	0.005	-0.437**	-0.196*	0.406**	-0.051
PBPP	-0.075	-0.074	-0.009	1.000	0.209**	0.126	0.243**	0.077	0.164*	-0.021	0.290**
NPPP	0.198*	0.386**	0.051	0.270**	1.000	-0.0118	0.162*	-0.112	0.013	0.040	0.629**
PL	-0.246**	-0.13	-0.457**	0.153	0.050	1.000	0.248**	0.347**	0.054	-0.064	0.053
NSPP	0.016	0.048	0.046	0.364**	0.162*	0.308**	1.000	-0.135	-0.019	0.091	0.171*
100-SW	-0.233*	-0.026	-0.505**	0.078	-0.128	0.648**	-0.157	1.000	0.297**	-0.107	0.108
BYPP	-0.424**	-0.295**	-0.231**	0.248**	-0.015	0.07	-0.044	0.460**	1.000	0.012	0.287**
HI	0.040	0.328**	0.65**	-0.064	0.070	-0.040	0.114	-0.162*	0.038	1.000	-0.031
GYPP	-0.068	0.128	-0.085	0.296**	0.694**	0.057	0.171*	0.112	0.428**	-0.063	1.000

**Significant at 1% level

*Significant at 5% level

DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP - Primary branches per plant (No.), NPPP - Pods per plant (No.), PL - Pod length (cm), NSPP - Number of seeds per pod (No.), 100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%).

give a clear picture of the extent of genetic advances for selection. Johnson *et al.*, (1955) also suggested that high heritability coupled with high genetic advance could be helpful in establishing a close relationship between genotype and phenotype.

In the present study, results revealed that the high heritability (bs) was observed for plant height (0.89) followed by pods per plant (0.82) and seeds per pod (0.81), indicating the less influence of environment on these characters (Table 3). These findings confirm the studies of Suresh *et al.* (2010) and Siddique *et al.* (2006). The heritability is not sufficient to select the best individual. However, heritability associated with genetic advance is more reliable as compared to only heritability. The high genetic advance as a percent of the mean was recorded for primary branches per plant (20.37) and biological yield per plant (11.38). Tabasum *et al.* (2010) and Yaqoob *et al.,* 2010. High heritability coupled with high genetic advance as a percent of the mean indicated the presence of additive genes for better selection plant height, pods per plant, seed yield per plant, primary branches per plant, 100-seed weight and biological yield per plant. Moderate to high heritability and low genetic advance were recorded for primary branches per plant, days to 50% flowering, seeds per pod and 100-seed weight,

Table 5: Estimates of direct (bold values) and indirect effects at genotypic level between yield and its components in mung bean

Characters	*DFF*	*DM*	*PH*	*PBPP*	*NCPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*PC*	*BYPP*	*HI*	*Correlation with SY*
DFF	-0.163	0.195	-0.001	0.016	-0.143	0.196	0.068	0.006	-0.030	-0.006	-0.240	-0.020	-0.068
DM	-0.089	0.359	0.028	0.016	-0.265	0.383	0.036	-0.017	-0.003	0.013	-0.167	-0.164	0.128
PH	0.007	0.068	0.146	0.002	0.020	0.051	0.127	0.017	-0.065	0.004	-0.131	-0.325	-0.085
PBPP	0.012	-0.027	0.013	-0.214	0.028	0.267	-0.043	0.132	0.009	-0.041	0.140	0.040	0.296**
NPPP	-0.032	0.138	0.007	-0.058	-0.380	0.992	0.014	0.059	-0.017	0.017	-0.009	-0.035	0.654**
PL	0.040	-0.047	-0.066	-0.033	0.103	-0.049	-0.278	0.112	0.083	0.019	0.153	0.021	0.057
NSPP	-0.003	-0.017	0.007	-0.078	-0.014	0.161	-0.086	0.363	-0.020	-0.009	-0.025	-0.107	0.171*
100-SW	0.004	-0.009	-0.073	-0.105	0.087	-0.127	-0.180	-0.057	0.129	-0.020	0.260	0.081	0.112
BYPP	0.069	-0.106	-0.034	-0.053	0.049	-0.015	-0.075	0.016	0.059	0.003	0.566	-0.019	0.428**
HI	-0.007	0.118	0.094	0.014	0.028	0.069	0.011	0.077	-0.020	0.032	0.021	-0.501	-0.063

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP - Primary branches per plant (No.), NCPP - Clusters per plant (No.), NPPP - Pods per plant (No.), PL - Pod length (cm), NSPP - Number of seeds per pod (No.), 100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%), PC - Protein content (%)

Table 6: Estimates of direct (bold values) and indirect effects at phenotypic level between yield and its components in mung bean

Characters	*DFF*	*DM*	*PH*	*PBPP*	*NCPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*PC*	*BYPP*	*HI*	*Correlation with SY*
DFF	-0.064	-0.017	-0.003	-0.003	0.021	0.070	0.016	0.001	-0.029	0.000	-0.071	-0.002	-0.067
DM	-0.026	-0.043	0.007	0.005	-0.040	0.183	0.013	-0.003	-0.005	0.001	-0.053	-0.006	0.103
PH	0.004	0.007	0.041	0.000	-0.005	0.022	0.031	0.000	-0.079	0.000	-0.380	-0.012	-0.051
PBPP	0.002	0.002	0.000	0.132	-0.004	0.118	0.011	-0.010	0.014	-0.005	0.032	0.001	0.290*
NPPP	-0.008	-0.014	0.002	0.028	0.065	0.565	0.001	0.007	0.020	0.002	0.003	-0.001	0.629**
PL	0.011	-0.047	-0.066	0.033	0.103	-0.049	-0.278	0.112	0.083	0.018	0.153	0.021	0.053
NSPP	-0.003	-0.017	0.007	-0.078	-0.014	0.161	-0.085	0.363	-0.020	-0.009	-0.025	-0.107	0.171**
100-SW	0.010	0.001	-0.018	-0.010	-0.015	-0.063	-0.049	-0.005	0.180	-0.002	0.058	0.003	0.108
BYPP	0.023	0.012	-0.008	0.022	-0.002	0.007	-0.014	-0.001	0.005	-0.001	0.195	0.000	0.287*
HI	-0.064	-0.017	-0.003	-0.003	0.021	0.070	0.016	0.001	-0.029	0.000	-0.071	-0.002	-0.031

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP - Primary branches per plant (No.), NPPP - Pods per plant (No.), PL - Pod length (cm), NSPP - Number of seeds per pod (No.), 100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%), PC - Protein content (%).

showing non-additive gene action and selection may not be effective. These findings confirm the studies of Yaqoob *et al.,* (2010) and Rahim *et al.* (2010).

Correlation Studies

Yield is a complex polygenic trait that has a large number of other contributing component traits. Correlation analysis reveals the information on the relationship of dependent variable yield with its independent variables, thus, an association of various traits would determine their relative significance to improve yield.

In the present study, the correlation coefficient on genotypic and phenotypic levels between yield and its component traits has been worked out and the results revealed that there is a strong inherent association between the various traits (Table 4). Seed yield per plant exhibited a highly significant and positive phenotypic correlation with number of seeds per pod. Thus, the number of pods per plant, primary branches per plant, and biological yield per plant emerged as a significant and strong association with seed yield per plant, while days to 50% flowering and harvest index were negatively associated with seed yield. At the

genotypic level, the correlation coefficient (Table 4) for these traits was the same in direction but higher in magnitude with seed yield, indicating that these traits could be helpful for the improvement of seed yield/plant through improving these traits. Similar results were reported by Rahim *et al.* (2010), Suresh *et al.* (2013) and Pushpa Reni *et al.* (2013).

Among other traits, days to 50% flowering exhibited positive and significant genotypic correlation with days to maturity, number of pods per plant and positive and non-significant correlation with harvest index. It showed a negative and significant correlation with 100-seed weight, pod length and biological yield per plant. The high association of days to 50% flowering with these important yield components revealed that the selection of early flowering genotypes would lead to simultaneous improvement in yield. These results are in agreement with the findings of Khaimichho *et al.* (2014), Patel *et al.* (2014) and Titumeer *et al.* (2014). Primary branches per plant were positively and significantly associated with the number of pods per plant, number of seeds per pod and biological yield per plant, while seeds per pod showed a positive and significant correlation with primary branches per plant, number of pods per plant, pod length and seed yield per plant (Shivade *et al.* 2011; Ahmad *et al.* 2014).

Path Coefficient Analysis

The correlation values decide only the nature and degree of association existing between the two characters. However, this may not give a true picture and this might affect the true association of component characters, both in magnitude and direction. Hence it is necessary to partition the correlation coefficient into direct and indirect effects of yield components on seed yield, which provides a better index for selection.

The estimate of direct effects revealed that the number of pods per plant depicted maximum positive direct effects on seed yield at phenotypic as well as genotypic levels, respectively, followed by biological yield per plant, number of seeds per plant, days to maturity, plant height and 100 seed weight (Tables 5 & 6). Thus, these traits emerged as the most important direct yield component. So, these results clearly indicated the improvement in seed yield in mung bean, and major emphasis should be given to these traits. The findings are in accordance with the findings of Raselmiah *et al.* (2016), Rathor *et al.* (2015), Gadakh *et al.* (2013), Prasanna *et al.* (2013) and Tabasum *et al.* (2010).

Biological yield per plant showed maximum positive indirect effect *via* days to 50% flowering while it exhibited maximum negative indirect effect via pod length both at phenotypic and genotypic levels. These results are in contrast with the earlier reports of Tabasum *et al.* (2010) and Singh *et al.* (2009), who found maximum negative indirect contribution *via.*, days to 50% flowering.

Conclusion

The present results confirmed that geographical background plays an important role in creating variations among the morphological traits and thus, these traits can be considered as favorable attributes for improvement through various breeding programs.

Acknowledgments

The authors are highly thankful to SKUAST-Kashmir (J&K) for providing the financial support to carry out this research work. Further, the authors do not have any conflict of interest for publication of this paper.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.13

Indian Journal of Plant Genetic Resources

RESEARCH ARTICLE

Evaluation of Grass Pea (*Lathyrus sativus* L.) Landraces for Genetic Variability and Character Association for Growth, Yield and Quality Attributes

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Abstract

To study the genetic variability and character association for yield and quality traits of seeds and forage of grass peas, a field experiment was conducted during Rabi 2021–22 using local collections from Assam. Significantly, wider variability was observed for important traits such as days to maturity (111.6–130.67), green forage yield (41.27–20.67 g/plant), seed yield (3.09–5.67 g/plant), β-N-oxalyl-L-α, β-diaminopropionic acid (β-ODAP) and protein content in seeds (0.08–0.44% and 23.6–28.8%) and forage (0.07–0.37% and 13.3–20.1%), respectively. High heritability (>60%) and high genetic advance (>20%) were observed for leaf width, green forage yield, dry matter yield, crude protein content in leaves, and β-ODAP content in leaf and seed. β-ODAP content in leaf and seed has exhibited a negative correlation with green and dry forage yield/plant, number of primary branches, and seed weight. Therefore, genotypes with low β-ODAP content in forage and seeds can be developed through selection.

Keywords: Correlation, Landrace, Grass pea, β-ODAP, Genetic variability, Path.

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Received: 16/09/2023 **Revised:** 21/06/2024

Accepted: 20/08/2024

How to cite this article: Dutta N, SB Neog, PK Barua and VK Verma (2024) Evaluation of Grass Pea (*Lathyrus sativus* L.) Landraces for Genetic Variability and Character Association for Growth, Yield and Quality Attributes. *Indian J. Plant Genet. Resour.* 37(3): 502-512.
DOI: 10.61949/0976-1926.2024.v37i03.13

Introduction

Grass pea (*Lathyrus sativus* L.) is an important cool-season multipurpose legume crop cultivated mainly for its seeds and green fodder. It belongs to the family Fabaceae and the subfamily Faboideae with 2n = 14 diploid chromosomes. It is widely cultivated in India, Bangladesh, Nepal, Pakistan, and Ethiopia. The major grass pea or *khesari* cultivating states in India are Chhattisgarh, Madhya Pradesh, Uttar Pradesh, Bihar, Orissa, West Bengal and Maharashtra (Mahata *et al*., 2018). Grass pea is considered a drought-tolerant, hardy crop that has the ability to grow in low-rainfall areas and in land with poor soil fertility (Palmer *et al*., 1989). It is resistant to various pests and diseases in comparison to other legumes (Yan *et al*., 2006). Grass pea can be used as a soil ameliorant due to its symbiotic nitrogen fixation (108–125 kg nitrogen ha^{-1}) with a mean value of 116 kg ha^{-1} (Peoples *et al*., 2008). Grass pea also fits well in the rice-based utera cropping system as it is adaptable to the heavy soil left after harvesting rice. The high proteinaceous tender leaves of grass pea cut at 50% flowering stage are good feed for domestic animals, whereas its seeds are used for human consumption as dal after splitting it or as pakoda prepared from its ground flour. Therefore, grass pea has immense potential to be utilized as a dual-purpose crop in low-input farming conditions.

Grass pea is a very nutritious crop as it contains 362.3 Kcal of energy per 100 g seed, 2.7% fat, 31.6% protein, 1.1% crude fiber, 51.8% nitrogen-free extract, and 2.2% ash content in its seeds (Rahman *et al*., 1974). Besides having a higher crude protein

content (24–31%), it has a good amino acid profile to provide balanced nutrition to impoverished people (Hanbury *et al*., 2000). In spite of having so many advantages, the use of this crop is limited due to the presence of a neurotoxin, viz., β-N-oxalyl-L-α, β-diaminopropionic acid (β-ODAP) in different parts of the plant, including a higher content in seeds (Prakash *et al*., 1977; Jiao *et al*., 2006). β-ODAP is considered the causative factor for a neurodegenerative disorder called 'Neurolathyrism' in humans and animals that causes spastic paralysis and muscle atrophy of the lower limbs (Rao *et al*., 1964). The content of β-ODAP in grass pea germplasm varies from 0.02 to 2.59% (Kumar *et al*., 2011). Grass pea seeds containing less than 0.2% β-ODAP are deemed safe for ingestion by humans (Abd El-Moneim *et al*., 1999).

Low productivity and the presence of the neurotoxin β-ODAP are two major constraints for the cultivation of grass peas. In northeastern India, it is grown traditionally by the farmers using the local landraces, and there is no commercial cultivar that is higher in yield, suitable for livestock as well as pulse production, and low in neurotoxin content. Therefore, the development of grass pea varieties low in neurotoxin content, high green fodder, and high seed yield has become the main focus of plant breeders in the grass pea improvement program. The prospect of crop improvement in a particular crop species depends on the presence of genetic variability, as the effectiveness of the selection depends on the genetic base of the population. Among the multivariate analyses, the PCA has been found effective in identifying traits with high variability; correlations reveal the strength of the relationship between various yields and their components. Keeping the above facts in view, the present investigation was undertaken to study the genetic variability and character association with respect to growth, yield, and quality attributes among the local landraces of the grass pea.

Materials and Methods

Plant Materials

A total of 16 genotypes, including local checks (Prateek and Madhuri) of grass peas were collected from different parts of Assam for the evaluation trials. Prateek is a low β-ODAP containing grass pea variety with high-yielding ability, which is often used as a check-in grass pea germplasm evaluation programme in India. On the other hand, Madhuri is a high-yielding variety recommended for Assam, but it has a high concentration of β-ODAP (0.2%).

Crop Evaluation

The experiment was conducted in a randomized block design (RBD) with three replications at the Instructional cum Research Farm, Assam Agricultural University, Jorhat, during Rabi 2021-22 (26.046 ^{0}N latitude and 94.016 ^{0}E longitude with an altitude of 86.6 m above mean sea level). The seeds of each variety were sown in plots of 3×3 m^2 area by maintaining a spacing of 25 cm between rows and 15 cm between plants. The recommended package of practices was followed during crop production. The observations were recorded on five randomly selected plants from each replication for the following quantitative traits: days to 50% flowering, days to maturity, plant height (cm), number of leaves/plant, number of primary branches/plant, number of secondary branches/plant, leaf length (cm), leaf width (cm), green forage yield (g/plant), dry matter yield (g/plant), pods/ plant, number of effective pods/ plant, pod length (cm), pod width (cm), number of seeds per pod, seed yield (g/plant), 100 seed weight (g).

Biochemical Analyses

The quality parameters, viz., β-ODAP and protein contents, were analyzed for both leaves and seeds. The β-ODAP content was estimated by following the spectrophotometric method as described by Rao (1978). Total nitrogen was estimated using the modified Kjeldahl method described by Scales and Harrison (1920). The nitrogen percentage was then multiplied by 6.25 to get the crude protein percentage.

Statistical Analyses

The mean data from each replication was used for further statistical analysis using the package "variability" of software R Studio version 4.3.1. The genetic parameters, viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, and genetic advance (GA), were estimated using the methodology as described by Burton and Devane (1953). The genotypic and phenotypic correlation coefficients for the traits were estimated as per the method of Al-Jibouri *et al*. (1958). Further, the path analysis was done following the procedure of Dewey and Lu (1959).

Results and Discussion

Genetic Variability for Growth, Yield and Quality Traits

The results of the present study have revealed the presence of substantial variation among the genotypes for all the traits except pod length and pod width (Table 1). Similar findings were also noticed by other researchers in grass pea (Singh and Roy, 2013; Jeberson *et al*., 2018; and Mahapatra *et al*., 2020; Tripathi *et al*., 2021). The poor variability for pod characters like length and width may be due to the narrow genetic base of the population. Abate *et al*., (2018) and Arslan *et al*., (2021) also observed non-significant variations for these traits.

Out of 21 traits, 19 were found to be significant and showed a considerable range of variation by the genotypes in their mean performances (Table 2). The green forage yield per plant varied from 11.27 to 20.67 g. The green forage yield of seven genotypes was observed to be above the

Table 1: Analysis of variance of grass pea genotypes for various quantitative characters

Source of variation	DF	Mean squares																			
		Days to 50% flowering	Days to maturity	Plant height (cm)	Leaves/ plant	Primary branches / plant	Secondary branches/ plant	Leaf length (cm)	Leaf width (cm)	Green forage yield (g/ plant)	Dry matter yield (g/ plant)	Pods/ plant	Effective pods/ plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Seed yield (g/ plant)	100 seed weight (g)	Leaf β-ODAP %	Seed β-ODAP %	Leaf crude protein %	Seed crude protein %
Replications	2	0.270	10.940	4.020	0.180	0.020	0.020	0.140	0.000	0.340	0.110	0.530	1.080	0.080	0.010	0.006	0.018	0.17	0.000	0.000	0.040	0.060
Genotypes	15	88.550**	59.330**	16. 350*	147. 160**	0.610**	2.300**	0.700**	0.010**	19. 180**	2.350**	45. 930**	34.370**	0.040	0.010	0.210*	1. 210**	0.45*	0.025**	0.039**	14. 740**	7.610**
Error	30	2.410	5.650	7.830	19.890	0.200	0.760	0.100	0.000	1.410	0.390	12.790	9.800	0.030	0.005	0.090	0.380	0.19	0.000	0.000	0.055	0.040
C.V %		1.68	1.87	5.58	8.06	14.61	8.28	6.02	7.00	7.54	18.45	14.87	15.56	NS	NS	6.54	16.95	8.80	2.45	1.42	1.41	0.73

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

Table 2: Mean performance of grass pea genotypes for various quantitative traits

Name of the genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Leaves/ plant	Primary branches	Secondary branches	Leaf length (cm)	Leaf width (cm)	Green forage yield (g/plant)	Dry matter yield (g/plant)	Leaf crude protein (%)	Leaf β-ODAP %	Pods/ plant	Effective pods/ plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Grain yield (g/plant)	100 seed weight (g)	Seed crude protein (%)	Seed β-ODAP (%)
JCL-21-N-4	93.67	128.00	52.91	52.60	3.33	10.13	5.38	0.61	16.93	3.40	19.95	0.097	27.47	24.07	3.43	1.14	4.73	4.34	5.32	28.18	0.176
JCL-21-N-3	92.67	130.00	50.82	62.03	3.27	11.33	5.32	0.60	15.60	3.30	18.67	0.228	35.53	30.20	3.41	1.08	4.60	5.67	4.87	27.59	0.291
JCL-21-N-2	94.00	129.67	50.05	56.33	3.00	10.93	5.38	0.56	15.33	3.93	15.40	0.190	29.13	23.13	3.69	1.16	4.67	3.96	4.80	25.02	0.208
JCL-21-N-1	92.33	128.00	53.59	65.20	3.67	11.47	5.09	0.57	20.67	6.07	19.19	0.071	27.80	23.87	3.44	1.09	4.73	4.51	5.44	27.71	0.095
JCL-21-N-6	94.33	129.00	52.75	63.47	3.00	11.00	5.09	0.58	13.33	2.80	16.98	0.349	26.07	21.40	3.39	1.15	4.87	3.42	4.95	26.48	0.417
JCL-21-N-5	93.33	130.33	51.65	52.07	3.40	12.27	4.76	0.54	18.00	3.53	16.10	0.195	27.27	22.33	3.31	1.11	4.53	4.05	4.61	25.38	0.236
JCL-21-M-6	93.33	126.67	45.43	44.53	2.07	9.93	5.05	0.48	12.80	2.53	15.23	0.259	25.27	20.67	3.30	1.14	4.47	3.63	4.73	24.85	0.373
JCL-21-M-5	95.00	128.33	51.39	44.20	2.27	9.20	5.03	0.48	11.27	2.27	13.30	0.303	23.80	20.47	3.25	1.11	4.33	3.61	4.83	23.92	0.394
JCL-19-M-1	90.67	124.33	48.03	52.27	3.07	10.53	4.44	0.41	17.50	3.33	18.49	0.084	22.93	20.40	3.48	1.07	4.33	3.95	5.12	27.07	0.109
JCL-19-M-2	92.67	127.00	51.08	48.20	3.33	10.40	5.69	0.47	13.13	2.70	13.48	0.241	18.27	15.07	3.27	1.09	4.33	3.30	4.58	24.50	0.274
JCL-10-3	94.00	129.00	48.55	49.73	2.80	9.93	5.61	0.64	13.07	3.40	20.13	0.371	26.73	21.73	3.53	1.17	4.33	3.52	4.75	28.82	0.441
JCL-10-2	94.00	130.67	49.10	52.13	2.60	9.80	4.67	0.63	15.00	2.80	17.15	0.250	24.00	17.60	3.51	1.17	4.40	3.87	5.09	26.83	0.328
JCL-10-4	92.67	128.00	51.66	63.87	3.67	9.87	5.63	0.59	18.20	4.33	16.63	0.151	20.53	19.60	3.45	1.15	4.13	3.09	4.64	26.08	0.170
JCL-10-1	93.67	127.33	50.41	54.87	2.73	11.80	6.05	0.47	17.03	3.07	16.16	0.202	22.67	18.00	3.42	1.08	4.60	3.16	4.77	25.67	0.254
Madhuri	94.00	126.00	46.78	61.33	3.13	9.60	5.44	0.52	15.27	3.60	15.11	0.181	27.33	23.40	3.36	1.13	4.47	4.31	4.70	24.33	0.200
Prateek	72.00	111.67	47.62	62.87	3.07	9.87	6.24	0.67	17.97	3.23	13.71	0.075	27.07	22.73	3.47	1.30	3.80	4.05	6.08	23.63	0.080
Mean	92.02	127.13	50.11	55.36	3.03	10.50	5.30	0.55	15.69	3.39	16.60	0.203	25.74	21.54	3.42	1.13	4.46	3.90	4.96	26.00	0.250
SE (m)	0.89	1.37	1.62	2.57	0.25	0.50	0.18	0.02	0.68	0.36	0.13	0.003	2.06	1.81	0.09	0.04	0.17	0.36	0.25	0.11	0.002
CD (5%)	2.70	4.14	4.87	7.76	0.77	1.51	0.56	0.07	2.06	1.09	0.41	0.009	6.22	5.45	NS	NS	0.51	1.08	0.76	0.33	0.006

average (>15.69 g/plant) of all the genotypes. The highest green forage yield was found in JCL-21-N-1 with 15.02% more yield than Prateek and 35.36% more yield than Madhuri. JCL-10-4 followed it with 1.28% more yield than Prateek and 19.19% more yield than that of Madhuri in the present study. The variation in dry matter yield/plant was from 2.27 g to 6.07 g. The range of seed yield/plant and 100 seed weight was 3.09 to 5.67 g and 4.61 to 6.08 g, respectively. Among the 16 genotypes, the seed yield of eight genotypes was above average (>3.90 g/plant). Out of them, the highest seed yield was recorded from JCL-21-N-3 followed by JCL-21-N-1. The seed yield of genotype JCL-21-N-3 was 40 and 31.55% higher over the check Prateek and Madhuri, respectively. On the other hand, the yield of the second-best genotype JCL-21-N-1 was 11.36% higher than Prateek and 4.64% higher than Madhuri's. JCL-21-N-1 was the only genotype to perform well for both fodder and seed yield. Comparatively, higher seed yield and seed weight were observed by Tadesse and Bekele (2003) in Ethiopian landraces of the grass pea.

Days to maturity varied from 111.67 to 130.67 days. Prateek was observed to be the earliest among all the genotypes to reach 50% flowering as well as pod maturity stage. Among the landraces, JCL-19-M-1 was the early genotype with 124.33 days to maturity.

For quality traits, among the genotypes, high variation was observed for β-ODAP content in leaves (0.071–0.371%) and seeds (0.080–0.441%). A similar range of β-ODAP concentration in seed was also observed by Parihar *et al*. (2006) and Hanbury *et al.* (2000). Since the critical limit of β-ODAP level in grass pea grains for human consumption is 0.2%, we always choose genotypes with low (<0.2%) β-ODAP content (Abd El-Moneim *et al*., 1999; Yan *et al*., 2006). Among the genotypes under study, the concentration of β-ODAP in leaves was found to be below average (<0.203%) in nine genotypes. The lowest β-ODAP content in leaves was observed in JCL-21-N-1 followed by Prateek, JCL-19-M-1 and JCL-21-N-4. However, only JCL-21-N-1 had 5.63% lower β-ODAP content as compared to check variety Prateek (0.075%). Thus, these superior genotypes could be considered a good source for grass pea improvement for fodder purposes.

The β-ODAP content in seed was below average (<0.250%) in nine genotypes, but no genotype was observed with seed β-ODAP content less than the check variety Prateek (0.080%). However, four genotypes had seed β-ODAP content less than that of the local check variety Madhuri (0.200%). They were JCL-21-N-1, JCL-19-M-1, JCL-10-4 and JCL-21-N-4 with 52.5, 45.5, 15 and 12% less β-ODAP concentration, respectively, than that of Madhuri. These four genotypes were found safe for human consumption as they contain less than 0.2% β-ODAP and can be considered to promote commercial production.

Similarly, a wide range of variability was also observed for crude protein content in leaves (13.30–20.12%) and seeds (23.62–28.82%). The crude protein content in leaves was found to be above average (>16.60%) in eight genotypes. It was highest in the genotype JCL-10-3, followed by JCL-21-N-4 and JCL-21-N-1. The genotype JCL-10-3 had 46.82% more protein content in its leaf than that of Prateek and 33.22% more than that of Madhuri. In seed also, the crude protein content was above average (>26.00%) in eight genotypes, with the maximum protein content in JCL-10-3 followed by JCL-21-N-4 and JCL-21-N-1. The genotype JCL-10-3 had 21.96% more seed protein content than that of Prateek and 18.45% more than that of Madhuri. In contrast to our germplasm, Rajendran *et al*. (2019) observed the highest range of seed protein content (28.82–27.2%) in the set of germplasm from the ICARDA and β-ODAP content in seeds from the sets of germplasm from Ethiopia (0.32–0.47%) and Pakistan (0.38–0.53%). Moreover, genotype JCL-21-N-1, possessing good fodder and seed-yielding ability also had a high amount of crude protein content and low neurotoxin content in its leaves and seeds. This promising genotype could be a good source for future grass pea improvement programs.

The estimates of genetic parameters are presented in Table 3. Among the characters studied, β-ODAP content in leaf, followed by β-ODAP content in seed and dry matter yield/plant exhibited higher GCV and PCV. It will offer a good scope of selection for these three characters. High GCV and PCV for β-ODAP content were also reported by Sharma *et al*. (2001) and Bhosle *et al*. (2008). Lyngdoh (2018) reported high GCV and PCV for β-ODAP content and dry matter yield/plant. The high magnitude of PCV was observed for seed yield/plant, number of pods/plant, and effective pods/plant, though GCV for these characters was found to be moderate, and there was a large difference between PCV and GCV, indicating a higher effect of environment on these characters. A moderate level of GCV and PCV was observed for leaves per plant, primary branches/plant, green forage yield/plant, leaf width, and leaf crude protein, which suggests the possibility of further improvement out of the variability for these traits. Low GCV and PCV were observed for days to 50% flowering, days to maturity, plant height, leaf width, seeds per pod, and crude protein content in the seed, which was in congruence with the findings of Bhosle *et al*. (2008), Parihar *et al*. (2015), Basaran *et al*. (2013), Jeberson *et al*. (2018) and Ranjithkumar *et al*. (2020). However, secondary branches per plant, leaf length, and 100 seed weight showed low GCV with moderate PCV.

Heritability (broad sense) estimates give information on the degree of genetic determination out of the total variation observed for a character (Singh, 2002). High heritability was recorded for β-ODAP content in leaf and seed, crude protein content in leaf and seed, days to 50% flowering, green forage yield per plant, leaf width, days to maturity, number of leaves /plant, leaf length, and dry matter yield/plant. Similar findings for β-ODAP content,

Table 3: Genetic variability parameters for growth, yield and quality traits in grass pea genotypes

Traits	*Range*	*Mean ± SEM*	*GCV (%)*	*PCV (%)*	h^2_{bs}	*GA (% of mean)*
Days to 50% flowering (DAS)	72.0-95.0	92.02 ± 0.89	5.82	6.06	92.28	11.52
Days to maturity (DAS)	111.67-130.67	127.13 ± 1.37	3.33	3.82	76.01	5.98
Plant height (cm)	45.43-53.59	50.11 ± 1.62	3.36	6.52	26.63	3.58
Leaves per plant	44.20-65.20	55.36 ± 2.57	11.77	14.26	68.08	20.00
Primary branches	2.07-3.67	3.03 ± 0.25	12.26	19.07	41.32	16.23
Secondary branches	9.20-12.27	10.50 ± 0.50	6.81	10.72	40.32	8.91
Green forage yield (g/plant)	11.27-20.67	15.69 ± 0.68	15.51	17.25	80.87	28.73
Dry matter yield (g/plant)	2.27-6.07	3.39 ± 0.36	23.77	30.09	62.40	38.68
Leaf length (cm)	4.44-6.24	5.30 ± 0.18	8.40	10.34	66.08	14.07
Leaf width (cm)	0.41-0.67	0.55 ± 0.02	12.68	14.49	76.63	22.87
Pods per plant	18.27-35.53	25.74 ± 2.06	13.82	20.30	46.35	19.38
No. of effective pods per plant	15.07-30.20	21.54 ± 1.81	14.22	21.08	45.52	19.77
No of seeds per pod	3.80-4.87	4.46 ± 0.17	4.44	7.90	31.56	5.14
Seed yield (g/plant)	3.09-5.67	3.90 ± 0.36	14.34	22.21	41.70	19.07
100 seed weight (g)	4.61-6.08	4.96 ± 0.25	5.98	10.63	31.58	6.92
Leaf β-ODAP%	0.071-0.371	0.203 ± 0.003	45.75	45.82	99.71	94.11
Seed β-ODAP%	0.080-0.441	0.253 ± 0.002	45.31	45.33	99.90	93.29
Leaf Crude protein%	13.30-20.12	16.60 ± 0.13	13.32	13.40	98.89	27.29
Seed Crude protein%	23.62-28.82	26.00 ± 0.11	6.11	6.15	98.59	12.49

green forage yield, and dry matter yield were reported by Pandey *et al.* (1997) in grass peas and Kumar *et al.* (2002) in cowpeas. This suggests that there is a low influence of the environment on the phenotypic expression of these characters. The moderate heritability was exhibited by primary branches per plant, secondary branches per plant, number of pods per plant, number of effective pods per plant, number of seeds per pod, seed yield per plant, and 100 seed weight, whereas plant height showed low heritability. Mahapatra *et al.* (2020) reported high heritability for days to 50% flowering and days to maturity, while moderate heritability was reported for branches per plant and 100 seed weight. A similar finding for days to maturity and seeds per pod was also reported by Jeberson *et al.* (2018). Moderate heritability for primary and secondary branches per plant and low heritability for plant height were in agreement with Ranjithkumar *et al.* (2020).

The studies of heritability and genetic advance can decipher the mode of gene action involved in controlling the traits. Johnson *et al.* (1955) reported that estimates of heritability along with genetic gain would be more rewarding than heritability alone in predicting the resulting effect of selection to identify the best individual. In the present study, high heritability coupled with high genetic advance was recorded for β-ODAP content in leaf and seed, crude protein content in leaf, green forage yield/plant, dry matter yield/plant, and leaf width. This indicated a significant contribution of additive gene action to the

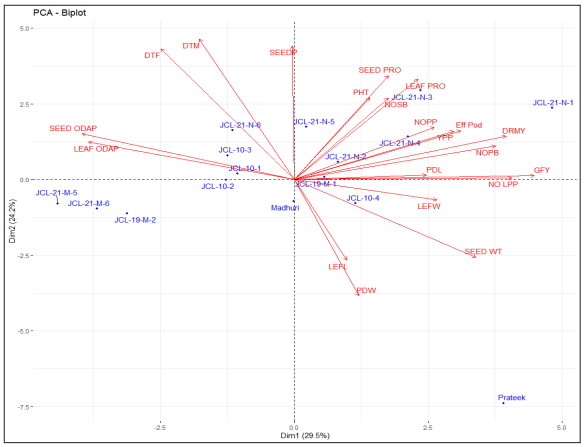

Figure 1: Principal component analysis (PCA) biplot representing the distribution of genotypes and their interrelationship with quantitative traits (PC1 and PC2)

expression of these traits, thus providing a good opportunity for the selection of these traits. Similar findings were also reported by Pandey *et al.* (1997) and Lyngdoh (2018) for β-ODAP content, green forage yield, and dry matter yield in grass peas. High heritability coupled with moderate genetic advance was observed for leaves/plants, days to 50% flowering, and leaf length. Besides that, moderate heritability coupled with moderate genetic advance was observed for the number of primary branches/plant, pods per plant, effective pods/plant, seed yield/plant, and crude protein content in seed. These results indicated the

involvement of both additive and dominant gene action in controlling the expression of these traits. Further, days to maturity, number of secondary branches/plant, seeds per pod, and 100 seed weight exhibited high to moderate heritability coupled with low genetic advance, suggesting that the expression of these traits was preponderantly under the influence of non-additive gene action. The high to moderate heritability observed for these traits was an indication of high environmental influence, due to which simple selection would not be effective. In addition, low heritability as well as low genetic advance was observed for plant height, which indicates the predominance of non-additive gene action for the trait plant height. As suggested by Singh and Narayanan (1993), selection would not be effective for the traits controlled by non-additive gene action; rather, heterosis breeding for such traits would be useful. Similar findings for days to maturity, days to 50% flowering, primary branches/plant, seed yield/plant, number of seeds/pod, 100 seed weight, and plant height were also reported by other researchers (Wutletaw and Endashaw, 2003; Abate *et al*., 2018; Jeberson *et al*., 2018; Mahapatra *et al*., 2020; and Ranjithkumar *et al*., 2020).

Principal Component Analysis

PCA is one of the most widely used methods of multivariate analysis to analyze the genetic variability in a given population. PCA is a measure of how important an impact a certain trait has in explaining total variability, and each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated (Sanni *et al*., 2012). In the present study, the first five principal components exhibited eigenvalues >1.00 and contributed to 81.98% cumulative variance among the traits studied (Table 4). According to various reports, the first three components (PC1, PC2 and PC3) and associated traits are the most reliable to explain the variation present in the population. In the present study, the first three PC contributed 66.90% of the total variations. Similar findings have also been observed by Tripathi *et al*., (2021) in grass pea.

The first principal component (PC1) showed 29.53% of the total variability. The higher absolute values in the principal components indicate a higher contribution of traits towards the divergence. Among the traits green forage yield (0.85), number of leaves (0.77), dry matter yield (0.75), number of primary branches (0.71), 100 seed weight (0.64), number of effective pods (0.59) and seed yield/plant (0.57) have contributed maximum and positive to the genetic divergence in PC1, while the characters seed β-ODAP content (-0.75) and leaf β-ODAP content (-0.73) exhibited the maximum negative contribution to the first principal component. The second component (PC2) contributed 24.22% to the total variance. The major characters contributing to the second component include days to maturity (0.88), number of seeds/plant (0.84), days to flowering (0.83), seed crude protein content (0.65), leaf crude protein content (0.63), plant height (0.51) and number of secondary branches/plant (0.51). Principal component 3 (PC3) exhibited 13.15% of the total variance. The characters, viz., number of pods/plant (0.66), leaf width (0.61), number of effective pods/plant (0.53), seed β-ODAP content (0.50) and leaf β-ODAP content (0.47) showed the maximum positive contribution to the genetic variance of PC3.

The biplot diagram (Figure 1) for principal components represents the distribution and diversity for both traits and genotypes. The PCA biplots differentiated the genotypes by traits. Genotypes that are closer to the origin and closer to each other are said to have more similarity, while genotypes that are apart from each other are more divergent. PC1 differentiated the genotypes for days to flowering, maturity, and β-ODAP contents in leaves and seeds. The divergent parents from the biplot can be selected for the further improvement program, like Prateek for seed weight and JCL-21-N-1 for growth and yield attributes with low β-ODAP content.

Correlation and Path Analysis

Yield is a complex trait and dependent on many other quantitative related traits. The interrelationship among yield and its component traits can be determined through correlation analysis. On the other hand, path coefficient analysis helps in partitioning the correlation coefficients into direct and indirect effects, which enables the identification of the cause of the association of yield attributes with yield. Two separate correlation and path analyses were performed to study the relationship between green forage yield as well as seed yield and its attributes.

Correlation and Path Coefficient Analysis for Green Forage Yield with its Component Characters

Green forage yield/plant was positively correlated with leaves/plant, number of primary branches/plant, number of secondary branches/plant, and dry matter yield/plant at both genotypic and phenotypic levels (Table 5). A considerable amount of phenotypic correlation was observed between green forage yield/plant and crude protein content in leaves. Selection of promising genotypes for these traits would result in an improvement in green forage yield/plant. Similar findings were also reported by Mihailovic *et al*. (2013) and Lyngdoh (2018). On the other hand, β-ODAP content in leaves was found to be negatively correlated with green forage yield/plant at genotypic as well as phenotypic levels. This suggested that improvement in green forage yield would also result in the development of genotypes with low neurotoxin content in their leaves. For the selection of genotypes, a negative correlation of β-ODAP content in leaves with any other character is considered useful. In this study, a significant negative correlation of

Table 4: Principal component analysis in grass pea for growth, yield and quality traits

Traits	*PC1*	*PC2*	*PC3*	*PC4*	*PC5*
Days to 50% flowering (DAS)	-0.47	0.83	-0.11	0.09	-0.04
Days to maturity (DAS)	-0.34	0.88	-0.00	0.15	0.04
Primary branches	0.71	0.21	-0.40	0.17	0.24
Secondary branches	0.33	0.51	-0.29	-0.14	0.31
Leaves per plant	0.77	0.01	-0.02	0.13	0.36
Plant height (cm)	0.27	0.51	-0.28	0.29	0.41
Green forage yield (g/plant)	0.85	0.02	-0.43	0.02	-0.11
Dry matter yield (g/plant)	0.75	0.27	-0.29	0.17	-0.03
Leaf length (cm)	0.19	-0.51	0.04	0.28	0.51
Leaf width (cm)	0.51	-0.13	0.61	0.46	0.19
Number of pods per plant	0.50	0.33	0.66	-0.40	0.15
Number of effective pods per plant	0.59	0.31	0.53	-0.43	0.14
Pod length (cm)	0.47	0.03	0.27	0.42	-0.30
Pod width (cm)	0.23	-0.73	0.47	0.31	0.07
Number of seeds per pod	-0.01	0.84	0.03	-0.07	0.15
Seed yield per plant (g)	0.57	0.30	0.40	-0.58	-0.02
100 seed weight (g)	0.64	-0.49	0.19	-0.02	-0.20
Leaf β-ODAP (%) content	-0.73	0.24	0.47	0.24	0.28
Seed β-ODAP (%) content	-0.75	0.29	0.50	0.18	0.18
Leaf Crude protein (%) content	0.44	0.63	0.23	0.29	-0.41
Seed Crude protein (%) content	0.33	0.65	0.24	0.38	-0.37
Eigenvalue	6.20	5.09	2.76	1.78	1.39
Variance (%)	29.53	24.22	13.15	8.48	6.60
Cumulative variance (%)	29.53	53.75	66.90	75.38	81.98

Table 5: Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation between green forage yield and its component traits

	D50%F	*DM*	*PH*	*Leaves/pl.*	*PB*	*SB*	*LL*	*LW*	*Leaf β-ODAP*	*Leaf CP*	*DMY*	*GFY*
D50% F		1.000**	0.458	-0.338	-0.146	0.167	-0.490	-0.392	0.476	0.288	-0.024	-0.344
DM	0.858**		0.599*	-0.289	0.018	0.401	-0.548*	-0.215	0.498*	0.385	0.026	-0.271
PH	0.149	0.266		0.349	0.755**	0.851**	-0.150	0.184	-0.092	0.398	0.533*	0.404*
Leaves/pl.	-0.281	-0.126	0.244		0.878**	0.454	0.286	0.521*	-0.423	0.241	0.730**	0.694**
PB	-0.074	-0.035	0.425**	0.444**		0.566*	0.191	0.345	-0.656**	0.396	0.878**	0.943**
SB	0.114	0.149	0.166	0.093	0.265		-0.018	-0.140	-0.173	0.323	0.471**	0.624**
LL	-0.439**	-0.357*	0.034	0.274	0.097	-0.141		0.302	-0.085	-0.287	-0.010	0.043
LW	-0.323*	-0.061	0.118	0.369**	0.135	-0.108	0.325*		0.018	0.310	0.254	0.163
Leaf β-ODAP	0.460**	0.435**	-0.046	-0.359*	-0.421**	-0.123	-0.065	0.025		-0.098	-0.618*	-0.870**
Leaf CP	0.281	0.330*	0.181	0.175	0.242	0.186	-0.232	0.268	-0.095		0.481	0.359
DMY	-0.023	0.084	0.258	0.488**	0.526**	0.226	0.070	0.189	-0.480**	0.370**		0.913**
GFY	-0.330	-0.200	0.179	0.501**	0.454**	0.324*	0.101	0.202	-0.781**	0.327*	0.573**	

*Significant at 5% probability level, **Significant at 1% probability level

D50%F= Days to 50% flowering
DM = Days to maturity
PH = plant height (cm)
Leaf CP = Crude protein content in leaf (%)
Leaves/pl. = number of leaves per plant
PB = Primary branches per plant
SB = Secondary branches per plant
DMY = Dry matter yield per plant (g)
LL = Leaf length (cm)
LW = Leaf width (cm)
Leaf β-ODAP = β-ODAP content in leaf (%)
GFY = Green forage yield per plant (g)

leaf β-ODAP content with dry matter yield per plant and primary branches/plant was observed at the genotypic and phenotypic levels. Basaran *et al.* (2013) have also reported a significantly negative correlation of β-ODAP content with yield and yield attributes of grass peas and mentioned that this may help to develop a variety higher in yield with low β-ODAP content.

As shown in Table 6, the maximum positive direct effect on green forage yield/plant was exhibited by plant height, followed by dry matter yield/plant, crude protein content in leaves, and number of leaves/plant. Out of these, only dry matter yield and number of leaves per plant showed a significant and positive correlation with green forage yield per plant. Thus, direct selection for these two traits would be helpful in enhancing green forage yield. The direct contribution of plant height and number of leaves/plants to green forage yield was also reported by Singh and Roy (2013). The positive direct effect of leaf β-ODAP content on green forage yield was nullified by the high negative indirect effect of leaf β-ODAP *via* days to maturity and dry matter yield/plant, which ultimately resulted in the negative correlation between leaf β-ODAP and green forage yield/plant. The number of primary and secondary branches/plants showed a negative direct effect on green forage yield/plant. The positive correlation between these two traits and green forage yield was due to high positive indirect effects *via* plant height and dry matter yield/plant. The residual value was 0.043 which indicated that only a small proportion of the variation in green forage yield was contributed by some unknown variables not included in this study.

Correlation and Path Coefficient Analysis for Seed Yield with its Component Characters

Among the traits, a strong positive correlation for seed yield was observed with the number of pods/plants and the number of effective pods/plants at both phenotypic and genotypic levels (Table 7). Therefore, the selection of promising genotypes for these two traits would simultaneously improve the seed yield/plant. These findings also concurred with those of other researchers (Mahapatra *et al*., 2020; Jeberson *et al*., 2018; and Ranjithkumar *et al*., 2020). The characters that showed a significant negative correlation with seed β-ODAP content were primary branches/plant, green forage yield/plant, and 100 seed weight. The significant negative correlation between seed β-ODAP content and 100 seed weight was earlier reported by Quader (1985) and Das and Kundagrami (2002). On the other hand, β-ODAP content in seeds had a significant and positive correlation with days to 50% flowering and maturity, which was also reported by Talukdar (2009). These findings suggest that selection for early flowering and early maturity, along with the enhancement of primary branches/plant, seed size, and green forage yield, would pave the way for the development of low neurotoxin-containing varieties. Crude protein content in seeds showed a significant and positive correlation with the number of seeds per pod. Thus, protein content in seeds would increase with the increase in the number of seeds/pod.

The direct and indirect effects of different yield attributes on seed yield are presented in Table 8. The characteristics that exhibited a positive direct effect on seed yield/plant were the number of seeds/pod, number of effective pods/plant, number of primary and secondary branches/plant, and crude protein content in the seed. However, only the number of effective pods/plants had a significant positive association with seed yield/plant. Therefore, direct selection for a high number of effective pods/plants would pave the way to a high seed yield/plant. Similar findings were reported by Ranjithkumar *et al*. (2020) and Mahapatra *et al*. (2020). A positive indirect effect nullified the negative direct effect of pods/plant on seed yield via the number of effective pods/plant and the number of seeds/pods, which

Table 6: Direct (diagonal) and indirect effects of component characters on green forage yield per plant at genotypic level

	D50%F	*DM*	*PH*	*Leaves/pl.*	*PB*	*SB*	*LL*	*LW*	*Leaf β-ODAP*	*Leaf CP*	*DMY*	*r with GFY*
D50%F	0.1171	-2.3039	0.8962	-0.0432	0.0431	-0.0988	0.2065	0.3741	0.3111	0.1711	-0.0174	-0.3440
DM	0.1171	-2.3041	1.1705	-0.0369	-0.0053	-0.2377	0.2461	0.2057	0.3252	0.2288	0.0193	-0.2713
PH	0.0537	-1.3789	1.9559	0.0446	-0.2227	-0.5043	0.0632	-0.1754	-0.0601	0.2369	0.3912	0.4041
Leaves/pl.	-0.0396	0.6665	0.6828	0.1276	-0.2587	-0.2689	-0.1205	-0.4965	-0.2779	0.1431	0.5357	0.6938
PB	-0.0171	-0.0410	1.4775	0.1121	-0.2947	-0.3354	-0.0806	-0.3294	-0.4286	0.2357	0.6444	0.9428
SB	0.0195	-0.9242	1.6642	0.0579	-0.1668	-0.5927	0.0074	0.1341	-0.1129	0.1919	0.3457	0.6241
LL	-0.0574	1.3461	-0.2936	0.0365	-0.0564	0.0104	-0.4212	-0.2884	-0.0554	-0.1707	-0.0073	0.0427
LW	-0.0460	0.4978	0.3603	0.0666	-0.1019	0.0835	-0.1276	-0.9523	0.0121	0.1842	0.1868	0.1633
Leaf β-ODAP	0.0558	-1.1472	-0.1801	-0.0543	0.1935	0.1025	0.0357	-0.0176	0.6530	-0.0584	-0.4532	-0.8704
Leaf CP	0.0337	-0.8866	0.7792	0.0307	-0.1168	-0.1912	0.1209	-0.2949	-0.0641	0.5947	0.3530	0.3586
DMY	-0.0028	-0.0607	1.0427	0.0932	-0.2588	-0.2792	0.0042	-0.2424	-0.4033	0.2861	0.7339	0.9128

Residual = 0.043

Table 7: Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation between seed yield and its component traits

	D50%F	*DM*	*PH*	*PB*	*SB*	*GFY*	*Pods/pl.*	*Eff. pods*	*SPP*	*100SW*	*Seed β-ODAP*	*Seed CP*	*SY*
D50%F		1.000**	0.458	-0.146	0.167	-0.344	-0.086	-0.109	0.926**	-1.058**	0.512*	0.346	-0.116
DM	0.858**		0.599*	0.018	0.401	-0.271	0.053	-0.007	0.908**	-1.052**	0.525*	0.464	-0.032
PH	0.149	0.266		0.755**	0.851**	0.404	0.061	0.123	0.666**	-0.035	-0.093	0.480	0.121
PB	-0.074	-0.035	0.425**		0.566*	0.943**	0.044	0.310	0.260	0.208	-0.761**	0.354	0.408
SB	0.114	0.149	0.166	0.265		0.624**	0.251	0.179	0.859**	-0.069	0.213	0.279	0.314
GFY	-0.330*	-0.200	0.179	0.454**	0.324*		0.207	0.310	-0.111	0.611*	-0.884**	0.247	0.372
Pods/pl.	-0.046	0.110	-0.007	0.139	0.328*	0.062		1.060**	0.672**	0.337	-0.023	0.363	0.984**
Eff. pods	-0.090	0.028	0.078	0.214	0.261	0.178	0.834**		0.511*	0.356	-0.197	0.379	0.927**
SPP	0.493**	0.527**	0.370**	-0.062	0.288	0.049	0.100	0.086		-0.684**	0.319	0.550*	0.439
100SW	-0.547**	-0.437**	0.021	0.072	-0.151	0.315*	0.146	0.164	-0.053		-0.696**	0.048	0.375
Seed β-ODAP	0.493**	0.461**	-0.054	-0.496**	-0.144	-0.797**	-0.013	-0.135	0.178	-0.392**		0.082	-0.331
Seed CP	0.333**	0.393**	0.230	0.213	0.180	0.216	0.219	0.235	0.317*	0.051	0.081		0.358
SY	-0.089	0.081	0.009	0.158	0.152	0.186	0.737**	0.805**	0.088	0.245	-0.214	0.210	

*Significant at 5% probability level, **Significant at 1% probability level
Pods/pl. = number of pods per plant Eff. Pods = number of effective pods per plant SPP= number of seeds per pod
100SW= 100 seed weight (g) Seed β-ODAP = β-ODAP content in seed (%) SY = Seed yield per plant (g)
Seed CP = Crude protein content in seed (%)

Table 8: Direct (diagonal) and indirect effects of component traits on seed yield per plant at genotypic level

	DTF	*DM*	*PH*	*PB*	*SB*	*GFY*	*Pods/pl.*	*Eff. pods*	*SPP*	*100SW*	*Seed β-ODAP*	*Seed CP*	*r with SY*
DTF	0.0117	-0.8783	-0.1759	-0.0633	0.0292	0.1467	0.0172	-0.0749	0.6930	0.1680	-0.0830	0.0933	-0.1163
DM	0.0117	-0.8784	-0.2297	0.0077	0.0704	0.1157	-0.0107	-0.0049	0.6792	0.1670	-0.0851	0.1251	-0.0320
PH	0.0054	-0.5257	-0.3838	0.3272	0.1492	-0.1723	-0.0123	0.0850	0.4982	0.0056	0.0151	0.1295	0.1210
PB	-0.0017	-0.0156	-0.2900	0.4331	0.0993	-0.4019	-0.0088	0.2133	0.1945	-0.0330	0.1233	0.0955	0.4079
SB	0.0020	-0.3523	-0.3266	0.2451	0.1754	-0.2661	-0.0502	0.1235	0.6428	0.0109	0.0345	0.0752	0.3142
GFY	-0.0040	0.2383	-0.1551	0.4083	0.1095	-0.4263	-0.0414	0.2135	-0.0833	-0.0971	0.1433	0.0665	0.3722
Pods/pl.	-0.0010	-0.0467	-0.0235	0.0190	0.0439	-0.0881	-0.2004	0.7303	0.5027	-0.0534	0.0037	0.0979	0.9842
Eff. pods	-0.0013	0.0062	-0.0474	0.1341	0.0315	-0.1322	-0.2125	0.6889	0.3824	-0.0566	0.0319	0.1023	0.9273
SPP	0.0108	-0.7974	-0.2556	0.1126	0.1507	0.0474	-0.1347	0.3521	0.7482	0.1087	-0.0518	0.1483	0.4393
100SW	-0.0124	0.9237	0.0135	0.0901	-0.0120	-0.2606	-0.0675	0.2455	-0.5120	-0.1588	0.1128	0.0131	0.3754
Seed β-ODAP	0.0060	-0.4612	0.0357	-0.3293	-0.0373	0.3767	0.0045	-0.1353	0.2391	0.1105	-0.1621	0.0221	-0.3307
Seed CP	0.0040	-0.4078	-0.1843	0.1535	0.0489	-0.1052	-0.0728	0.2613	0.4114	-0.0077	-0.0133	0.2696	0.3577

Residual = 0.086

resulted in a positive correlation between pods/plant and seed yield. Days to maturity, plant height, green forage yield per plant, 100 seed weight, and β-ODAP content in seed showed a negative direct effect on seed yield. Similar findings were reported by Kour and Agarwal (2016) and Jeberson *et al.* (2018). The residual value was 0.086, which signified that a small proportion of the variation in seed yield was due to some unknown variables that were not included in this study.

Conclusion

Among the genotypes, except pod length and width, ample variation has been observed for fodder, seed yield, and quality attributing traits, which suggests the scope for developing improved varieties of grass pea. Among the genotypes, JCL-21-N-1 exhibiting high fodder and seed yield along with low β-ODAP content, could be used as a dual-purpose grass pea variety for Assam. High GCV and PCV were observed for β-ODAP content in leaf and seed and

dry matter yield per plant. High heritability coupled with high genetic advance was recorded for β-ODAP content in leaf and seed, crude protein content in leaf, green forage yield per plant, dry matter yield per plant, and leaf width. Selection based on these traits would be effective in bringing improvement in the studied grass pea genotypes. The principal component analyses have shown wider variations and can be used to identify the parameters contributing to variability and the selection of suitable genotypes for selection and crop improvement. Among the characters studied, β-ODAP content in leaves, number of leaves per plant, and dry matter yield per plant were highly heritable and had exhibited a strong direct effect on green forage yield, with a significant correlation indicating the importance of these characteristics for improving green forage yield. In the case of seed yield components, the number of effective pods per plant had moderate heritability, high positive direct and indirect effects on seed yield, and a significant positive correlation. Therefore, selection for these traits would be effective for improving seed yield.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.14

Indian Journal of Plant Genetic Resources

SHORT COMMUNICATION

Assessment of Genetic Divergence for Bean Traits in *Coffea arabica* Germplasm

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Abstract

About 68 *Coffea arabica* accessions are being maintained in the germplasm bank at Coffee Research Sub Station in North Kodagu, Karnataka, India. Evaluation of these accessions for bean parameters indicated a wide variability for "A" grade bean percentage (9–82.9%) and bean density (15.08–25.96 g).

Keywords: Arabica, Bean traits, Coffee, Germplasm.

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Received: 14/03/2024 **Revised:** 12/06/2024

Accepted: 01/07/2024

How to cite this article: Gopinandhan TN and BR Shivalingu (2024) Assessment of Genetic Divergence for Bean Traits in *Coffea arabica* Germplasm. *Indian J. Plant Genet. Resour.* 37(3): 513-517. **DOI:** 10.61949/0976-1926.2024.v37i03.14

Introduction

Coffee is one of the most consumed beverages worldwide, with about three billion cups consumed every day. The genus *Coffea* encompasses more than one hundred species (Mishra *et al.,* 2014). Nonetheless, only two species *viz*., *Coffea arabica* (arabica) and *Coffea canephora* (robusta), are cultivated on a commercial scale. All coffee species are diploid (2n = 22) and self-incompatible except *C. arabica,* which is a natural allo-tetraploid self-compatible species (2n = 44). In the world market, arabica coffee is preferred over robusta coffee because of its superior bean characteristics and beverage quality. The arabica coffee grown all over the world is derived from either typica or bourbon genetic base, which has resulted in low genetic diversity among the cultivated arabicas (Van der Vossen, 1985). Coffee quality is mainly assessed on bean traits (size, shape, color, density and occurrence of defective beans) and sensorial attributes (acidity, aroma, taste and body). Within the same variety, bigger bean size fetches better price and thus coffee variety having a higher percentage of "A" grade beans is preferable. Arabica coffee is one of the world's most valuable agricultural commodities and its economic value is determined to a larger extent by bean characteristics and liquor qualities. However, selection for these traits is constrained by the low genetic variability of arabica coffee. Genetic improvement of bean quality can be successful if knowledge of the variability pattern present is available before embarking on exploitation by breeding. Screening of arabica accessions available in the germplasm bank is one way of identifying the variability for bean parameters. In light of the increasing demand for high-quality coffee with superior bean and beverage characteristics, there is a need to evaluate the arabica accessions available in the germplasm bank, as most of the

Table 1: List of arabica accessions used in the study

Code	*Accession number*	*Accession name*	*Source*	*Code*	*Accession number*	*Accession name*	*Source*
AG 1	S.1463	Typica	Guatemala	AG 35	S.1584	Dalecha	Portugal
AG 2	S.1464	Bourbon	Guatemala	AG 36	S.1699	Mbirizi de Mulungo	Portugal
AG 3	S.1465	Pache	Guatemala	AG 37	S.1726	Candina Marca	Portugal
AG 4	S.1467	Sumatra	Guatemala	AG 38	S.2126	S6 Cioccie (113/1)	Portugal
AG 5	S.1468	Surinam	Guatemala	AG 39	S.2127	S6 Cioccie (113/2)	Portugal
AG 6	S.1469	San Ramon	Guatemala	AG 40	S.2128	S4Agaro (110/5)	Portugal
AG 7	S.1470	Blue Mountain	Guatemala	AG 41	S.2129	S4Agaro (110/2)	Portugal
AG 8	S.1471	Padang	Guatemala	AG 42	S.1483	Kents KP423	Tanzania
AG 9	S.1472	Phillippinian	Guatemala	AG 43	S.1586	K7 Ruiru	Tanzania
AG 10	S.1473	Gudaluope	Guatemala	AG 44	S.1741	Barbuk Sudan	Tanzania
AG 11	S.1495	Tafarikela	Ethiopia	AG 45	S.1742	Margogype	Tanzania
AG 12	S.1497	S12 Kaffa	Ethiopia	AG 46	S.1743	Giesha	Tanzania
AG 13	S.1768	Murta	Ethiopia	AG 47	S.1648	Costa Rica	France
AG 14	S.1782	Badabuna Gimma Kaffa	Ethiopia	AG 48	S.1652	Macenta	France
AG 15	S.1783	Babaca Kaffa	Ethiopia	AG 49	S.1653	Togokouma	France
AG 16	S.1784	Misan Taferikala	Ethiopia	AG 50	S.1655	Makablou	France
AG 17	S.1785	Ainamba Kaffa	Ethiopia	AG 51	S.1659	Kouti	France
AG 18	S.1587	Rume Sudan	Kenya	AG 52	S.1660	Kenya	France
AG 19	S.1590	Dalle Mixed	Kenya	AG 53	S.1661	Nkourgam	France
AG 20	S.1591	Dalle Melavalle	Kenya	AG 54	S.1662	Foumbon	France
AG 21	S.1593	Gimma galla sidamo	Kenya	AG 55	S.1663	Reunion	France
AG 22	S.1502	Bourbon Mayagese	Congo	AG 56	S.1664	Nicaragua	France
AG 23	S.1504	Mysore	Congo	AG 57	S.1667	Mazeron	France
AG 24	S.1690	C.arabica-Green tip	Congo	AG 58	S.1490	Bourbon Amarelho	USDA
AG 25	S.1691	Las Palmas	Congo	AG 59	S.1491	Bourbon Vermelho	USDA
AG 26	S.1692	Barbarina	Congo	AG 60	S.1492	Caturra Amarelho	USDA
AG 27	S.1693	Coorg	Congo	AG 61	S.1494	Munda Novo	USDA
AG 28	S.1694	Puerto Rico	Congo	AG 62	S.1734	Martinigue	Ceylon
AG 29	S.1695	Antiqua	Congo	AG 63	S.1735	Dernum	Ceylon
AG 30	S.1696	Granza Bloomy	Congo	AG 64	S.1576	S26 Enneria	FAO
AG 31	S.1697	Tumbadir	Congo	AG 65	S.1656	Salvadur	Guinea
AG 32	S.1698	Local Bronze De Mulungu	Congo	AG 66	S.1700	COF297	East Africa
AG 33	S.1582	S16 Wollamo	Portugal	AG 67	S.1737	Madagascar	Middleton
AG 34	S.1583	S17 Yergalam	Portugal	AG 68	S.1905	SL34 Ruiru	Burma

accessions are yet to be characterized for bean traits. Thus, the objective of the study was to examine the variability for bean traits of the arabica accessions available in the germplasm bank. The most promising accessions identified from this screening exercise can be exploited as a potential genetic stock for developing arabica plants with superior bean traits.

About 68 *Coffea arabica* accessions having a designated identity were used for the current study. These arabica accessions are part of exotic gene bank introduced from different parts of the world, including the wild Ethiopian landraces collected during an FAO-sponsored expedition to Ethiopia in 1964 (Narasimmaswamy, 1965), were introduced to coffee research sub-station at Kodagu district (Karnataka)

Table 2: Genetic divergence in 68 *Coffea arabica* accessions for bean traits

Code	*"A" grade bean (%) **	*Besan density (g)***	*Code*	*"A" grade bean (%)**	*Besan density (g)***
AG 1	55.8 ± 1.13	17.03 ± 0.20	AG 35	48.4 ± 1.84	20.33 ± 0.25
AG 2	59.3 ± 1.41	17.22 ± 0.27	AG 36	9.00 ± 1.70	16.81 ± 0.28
AG 3	57.1 ± 1.48	16.89 ± 0.22	AG 37	61.4 ± 2.19	17.95 ± 0.20
AG 4	38.9 ± 1.34	15.89 ± 0.30	AG 38	40.0 ± 3.04	19.62 ± 0.29
AG 5	49.0 ± 1.48	17.39 ± 0.23	AG 39	41.0 ± 1.77	18.47 ± 0.34
AG 6	50.0 ± 1.98	19.05 ± 0.21	AG 40	57.1 ± 1.27	21.61 ± 0.14
AG 7	67.6 ± 1.63	17.97 ± 0.12	AG 41	36.6 ± 2.47	18.39 ± 0.29
AG 8	64.3 ± 1.06	17.00 ± 0.18	AG 42	51.6 ± 3.18	17.93 ± 0.13
AG 9	65.0 ± 0.78	16.68 ± 0.37	AG 43	69.0 ± 1.63	17.37 ± 0.33
AG 10	45.0 ± 1.13	17.20 ± 0.25	AG 44	34.3 ± 1.56	17.79 ± 0.17
AG 11	12.3 ± 1.27	16.13 ± 0.23	AG 45	25.6 ± 2.33	15.80 ± 0.23
AG 12	61.3 ± 2.12	20.51 ± 0.23	AG 46	40.5 ± 2.26	17.44 ± 0.31
AG 13	31.5 ± 1.84	15.70 ± 0.13	AG 47	52.4 ± 1.70	17.45 ± 0.20
AG 14	73.5 ± 1.56	25.96 ± 0.27	AG 48	35.0 ± 1.98	18.50 ± 0.11
AG 15	36.4 ± 1.63	17.76 ± 0.39	AG 49	62.0 ± 2.05	19.73 ± 0.23
AG 16	22.4 ± 1.41	19.11 ± 0.37	AG 50	39.7 ± 2.19	16.72 ± 0.21
AG 17	40.2 ± 1.84	16.99 ± 0.27	AG 51	54.3 ± 2.05	17.76 ± 0.23
AG 18	12.3 ± 1.98	15.08 ± 0.14	AG 52	60.1 ± 3.11	17.00 ± 0.09
AG 19	20.3 ± 1.77	15.87 ± 0.13	AG 53	43.3 ± 2.83	18.58 ± 0.22
AG 20	31.6 ± 1.56	16.84 ± 0.21	AG 54	47.5 ± 2.40	18.11 ± 0.10
AG 21	31.7 ± 1.34	17.77 ± 0.35	AG 55	45.4 ± 1.70	19.45 ± 0.21
AG 22	55.6 ± 1.77	19.65 ± 0.37	AG 56	61.7 ± 2.26	17.05 ± 0.10
AG 23	56.8 ± 1.84	18.53 ± 0.31	AG 57	60.1 ± 2.40	18.62 ± 0.18
AG 24	33.0 ± 2.12	17.63 ± 0.24	AG 58	47.1 ± 1.84	17.63 ± 0.15
AG 25	67.8 ± 1.77	18.80 ± 0.18	AG 59	53.8 ± 2.33	18.00 ± 0.20
AG 26	38.0 ± 1.34	17.70 ± 0.27	AG 60	64.6 ± 2.47	18.16 ± 0.20
AG 27	72.2 ± 1.34	18.62 ± 0.15	AG 61	49.9 ± 2.90	16.27 ± 0.20
AG 28	67.3 ± 1.70	18.79 ± 0.19	AG 62	82.9 ± 2.83	19.16 ± 0.18
AG 29	18.0 ± 2.19	16.93 ± 0.20	AG 63	72.0 ± 2.97	18.72 ± 0.15
AG 30	48.6 ± 1.70	19.14 ± 0.14	AG 64	43.2 ± 1.77	18.26 ± 0.22
AG 31	55.5 ± 1.70	16.68 ± 0.13	AG 65	48.6 ± 1.13	16.15 ± 0.14
AG 32	43.7 ± 1.70	17.42 ± 0.18	AG 66	38.0 ± 2.26	16.43 ± 0.26
AG 33	57.7 ± 1.77	18.25 ± 0.15	AG 67	49.6 ± 2.12	18.49 ± 0.14
AG 34	19.6 ± 1.91	17.63 ± 0.16	AG 68	51.6 ± 2.62	19.40 ± 0.20
CD (5%)				3.6	0.25

Values are average of two harvest seasons; **- Values are average of two harvest seasons with three determinations per harvest season.

in 1967. These arabica accessions are being maintained following the recommended agronomic practices (Table 1).

The handpicked ripe fruits from all the plants in each arabica accession were pooled and 12 kg of fruits were processed by wet method. In the wet method, the fruits are pulped to remove the outer skin. Each fruit usually yields two beans, which are covered by a thin layer of mucilage, mostly consisting of sugars and pectin. The mucilage is removed using an aqua-washer machine and the resulting coffee beans are soaked in water for about 6 hours to

remove the residual mucilage clinging to the coffee bean. Then, the coffee samples are sun-dried until the moisture level in the coffee samples reaches 10%. The moisture content in the coffee bean samples was determined by a Sinar moisture analyzer (Sinar Technology, AP 6060 model England). The coffee thus processed is called parchment coffee. The parchment coffee samples were de-husked using peeler-cum-polisher machine (Marshall-Fowler Group, PP7/ LS-407 model UK) to obtain the bulk coffee bean sample. The bulk coffee bean samples were winnowed to remove all extraneous matters, weighed and then subjected to size grading.

The bulk coffee bean samples were size-graded using a standard screen (McKinnon Co., Aberdeen, Scotland). The "A" grade beans were separated using screen number 17 (6.65 mm size). The peaberries and imperfect beans present in the "A" grade bean were manually removed. The total weight of the "A" grade bean was measured using a sensitive analytical balance (Precisa 320 XB model, Switzerland). The percentages of "A" grade bean was calculated following the standard formula (total quantity of "A" grade bean (g)/ total quantity of bulk coffee bean sample (g) x 100). To measure the density of coffee beans, one hundred numbers of perfectly shaped "A" grade beans were weighed using a sensitive electronic analytical balance (Precisa 320 XB model, Switzerland) in triplicates. The data were subjected to analysis of variance according to the least significant difference test to indicate statistically significant differences between the arabica accessions following the Agress package (version 3.01 data entry module and version 7.01 ANOVA package).

The mean data on "A" grade bean percentage and 100 "A" grade bean weight (density) recorded in 68 arabica accessions during two consecutive seasons were presented in Table 2. Among the 68 arabica accessions evaluated, significantly (p = 0.05) highest "A" grade beans (82.9%) were recorded in Martinique accession from Ceylon (S.1734) followed by 73.5% in Badabuna Gimma Kaffa accession from Ethiopia (S.1782), 72.2% in Coorg accession from Congo (S.1693) and 72% in Dernum accession from Ceylon (S.1595). The lowest "A" grade percentage (9%) was recorded in Mberizi de Mulungo's accession from Portugal (S.1699). About 30 out of 68 accessions recorded over 50% of "A" grade percentage ranging from 50% (S.1469-San Ramon accession from Guatemala) to 82.9% (S.1734-Martinique accession from Ceylon). The range of "A" grade bean percentage recorded in the present study (9–82.9%) was in good agreement with the previous report (Das *et al*., 2021).

Of the 68 arabica accessions examined, significantly (p = 0.05) highest bean density (25.96 g) was registered in Badabuna Gimma Kaffa accession from Ethiopia (S.1782) followed by 21.61 g (S.2128 - Agaro 110/5 accession from Portugal), 20.51 g (S.1497- S12 Kaffa accession from Ethiopia) and 20.33 g (S.1584 – Delecha accession from Portugal). The lowest bean density (15.08 g) was recorded in Rume Sudan accession from Kenya (S.881). The bean density recorded in the current study ranged from 15.08 to 25.96 g with an overall average of 17.96 g and the results differed from the previous reports, which ranged from 13.12 to 19.13 g with an average of 15.2 g (Yonas *et al.,* 2014), 14.99 to 17.07 g with a mean of 16.27 g (Fabrício, 2016), 7.74 to 24.21 g with an average of 17.1 g (Gizachew and Hussein, 2017), 16 to 22 g (Lison, *et al.,* 2020) and 17.63 to 19.8 g (Das *et al*., 2021).

The success of a new arabica variety depends on bean traits and cup quality. The results of the present study indicated that the Badabuna Gimma Kaffa accession from Ethiopia recorded superior bean traits. As reported by Santaram (2005), the cup quality of most of the Ethiopian accessions scores a fair average quality (FAQ) rating and this prompts that Badabuna Gimma Kaffa seems to be a prospective donor for developing arabica plant with superior bean traits. However, it is proposed to evaluate the genetic variance of 68 arabica accessions for cup quality as a future line of work.

Acknowledgment

The authors are grateful to Central Coffee Research Institute, Coffee Research Station, Chikkamagaluru district and Coffee Research Sub Station, Chettalli, Kodagu district in Karnataka, for the infrastructure and facilities provided during the course of the investigation.

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P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2024.v37i03.15

Indian Journal of Plant Genetic Resources

SHORT COMMUNICATION

Genetic Evaluation of Different Genotypes of Cabbage (*Brassica oleracea* var. *capitata* L.) under Natural Farming Condition in Hill region

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Abstract

The present investigation was carried out to identify the potential genotypes of cabbage for growing under natural farming conditions. About 14 genotypes, including check, were evaluated in a randomized complete block design with three replications during *Rabi*, 2018-19. Analysis of variance for all the traits showed the presence of sufficient variability in the germplasm as revealed by significant differences for all the characters excluding marketable heads per plot. Based upon overall performance, the genotype KGAT-III (123.95 q/ha) gave maximum marketable head yield. However, it was statistically at par with four other genotypes *viz.,* GA-P (118.94 q/ha), M-GA-P (115.52 q/ha), DPCH-112 (108.52 q/ha) and DPCbH-1 (108.08 q/ha) and check variety Pusa Mukta (101.47 q/ha) under natural farming conditions. High PCV estimates were recorded for marketable head yield per plot. High heritability coupled with high genetic advance was observed for net head weight.

Keywords: Cabbage, Genetic advance, Heritability, Natural farming, Variability.

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Received: 16/06/2022 **Revised:** 27/06/2024

Accepted: 28/06/2024

How to cite this article: Chauhan S, S Chadha and S Sharma (2024) Genetic Evaluation of Different Genotypes of Cabbage (*Brassica oleracea* var. *capitata* L.) under Natural Farming Condition in Hill region. *Indian J. Plant Genet. Resour.* 37(3): 518-521. **DOI:** 10.61949/0976-1926.2024.v37i03.15

Introduction

Cabbage (*Brassica oleracea* var. *capitata* L. and chromosome no. 2n=2x=18), a member of family Brassicaceae, is one of the most important cole-group vegetable crops. It is originated from *B. oleracea* var. *oleracea* L. (syn. *B. oleracea* var. *sylvestris* L.), commonly known as wild cabbage, cliff cabbage or colewort through mutation, human selection and adaptation. Off-late the concept of natural farming is becoming popular for raising vegetable crops without the use of synthetic fertilizers and pesticides. The farming system, as proposed by *Padam Shri* Sh. Subhash Palekar is zero budget natural farming (ZBNF), which was recently also made popular as Subhash Palekar natural farming (SPNF). The farmers have observed improvements in yield, soil conservation, seed diversity, quality of produce, household food autonomy, income and health. They experienced a reduction in farm expenses and on dependence on the borrowed money, which is one of the major problems faced by Indian farmers. Scientific validation of different techniques as suggested by Sh. Subhash Palekar is required at the university level for further adoption and promotion of SPNF. Therefore, in view of producing safe, healthy and quality food present study was carried out to identify the potential genotypes for marketable head yield and other horticultural traits under natural farming conditions (SPNF).

The present investigation was carried out at the experimental farm, Department of Organic Agriculture and Natural Farming,

CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh., during *Rabi,* 2018-19. The experiment was laid out in randomized complete block design (RCBD) with three replications. Observations were recorded on five randomly selected plants for characters, namely plant spread (cm), number of non-wrapper leaves, gross head weight (g), net weight head (g), polar diameter (cm), equatorial diameter (cm), head shape index, days to harvest, head compactness (g/cm^3), marketable heads per plot, marketable head yield per plot (kg) and TSS (^{0}Brix). The data were statistically analyzed as per the methods given by Panse and Sukhatme (1984). The phenotypic and genotypic coefficients of variation were estimated as suggested by Burton and De Vane (1953). Heritability in a broad sense (h^{2bs}) and expected genetic advance were calculated by Burton and De Vane (1953) and Johnson *et al*., (1955). The statistical analysis for each trait was carried out for each observed character under study using MS Excel and OPSTAT (developed by CCS Haryana Agricultural University, Hisar, India).

Analysis of variance for the experimental data revealed that mean squares were highly significant for all the studied traits indicating sufficient variability except marketable heads per plot (Table 1). Maximum gross head weight was observed in the genotype Tinnu (740 g) and was statistically significant with the genotype M-GA-P (701.67 g). The genotype GA-(P) (438 g) exhibited the maximum net head weight, followed by the genotype M-GA-(P) (428 g). Meena *et al*., (2009) and Thakur and Vidyasagar (2016) revealed significant differences for net head weight. The genotype GA-(P) (1.04) had a maximum head shape index and was statistically significant with eight other genotypes, including check. The genotype KGAT-III (41.62 g/cm^3) exhibited maximum head compactness, followed by the genotype M-GA(P) (39.44 g/cm^3). These results are closely related to the findings of Thakur and Thakur (2002a) and Atter (2004). The highest marketable yield per plot was observed in KGAT-III (4.47 kg). The range for TSS varied from [7.57(^{0}Brix)] in GA-(P) to [8.90(^{0}Brix)] in KTCBHR-35 (Table 2). A high phenotypic coefficient of variation (PCV) was observed only for the marketable head yield per plot (23.24%). Moderate PCV estimates were exhibited for the net weight (18.66%), head compactness (16.96%), gross weight (15.53%), number of non-wrapper leaves (14.93%) and plant spread (13.19%). Moderate GCV estimates were recorded for marketable head yield per plot (18.08%), net weight (16.60%), gross weight (12.69%), head compactness (10.12%) and number of non-wrapper leaves (10.04%). High heritability estimates were exhibited by net head weight (79.15%), gross head weight (66.84%) and marketable head yield per plot (60.49%). A high estimate for the genetic advance was obtained only for net weight (30.43%). However, moderate estimates were obtained for marketable head yield per plot (28.96%), gross weight (21.38%), number of non-wrapper leaves (13.92%) and head compactness (12.44%). High PCV estimates were observed only for the trait marketable head yield per plot (Table 3). Thus, from the present investigation, it may be concluded that the trait viz., net head weight and marketable head yield per plot can be improved by doing effective selection in the early generations for further crop improvement.

Table 1: Analysis of variance for agronomic/horticultural and quality traits in cabbage

S. No.	*Sources of variations traits*	*Replications 2*	*Genotypes 13*	*Error 26*
1	Plant spread (cm)	15.436	28.450*	13.413
2	No. of non-wrapper leaves	5.672	4.486*	1.290
3	Gross weight (g)	5792.667	20,975.22388*	2951.179
4	Net weight (g)	2,616.500	10,959.342*	884.628
5	Polar diameter (cm)	0.164	1.283*	0.360
6	Equatorial diameter (cm)	0.121	0.580*	0.258
7	Head shape index	0.000	0.005*	0.002
8	Days to harvest	165.452	242.996*	104.299
9	Head compactness (g/cm^3)	64.456	56.7328*	21.342
10	Marketable heads per plot	5.643	1.108	0.745
11	TSS (◦Brix)	0.032	0.375*	0.076
12	Marketable head yield per plot (kg)	1.479	1.408*	0.252

Significant at 5% level of significance

Table 2: Mean performance of genotypes for agronomic/horticultural and quality traits in cabbage

Genotype	Plant spread (cm)	No. of non-wrapper leaves	Gross weight (g)	Net head weight (g)	Polar diameter (cm)	Equatorial diameter (cm)	Head shape index	Days to harvest	Head compactness	Marketable heads per plot	Marketable head yield per plot (kg)	Marketable head yield (q/ha)	TSS
M-GA(P)	30.54	10.74	701.67	428.00	10.26	10.30	1.00	138.67	39.44	9.67	4.16	115.52	8.17
KTCBH-R35	30.04	7.94	410.00	230.00	8.41	9.44	0.90	127.34	32.45	9.34	2.16	59.81	8.90
DPCH-112	25.54	8.27	646.00	404.00	9.75	10.70	0.92	139.34	38.08	9.67	3.91	108.52	8.47
DPCb-131	33.21	10.87	596.00	322.00	10.17	10.32	0.99	144.67	30.48	9.67	3.13	86.83	8.34
KGAT-II	34.23	10.80	628.00	358.67	10.01	10.06	1.00	139.34	35.58	10.00	3.59	99.72	8.70
KGAT-III	33.22	10.67	620.67	404.34	9.86	10.09	0.98	150.00	41.62	11.00	4.47	123.95	8.27
Glory-7	33.50	11.07	486.34	261.34	9.53	9.46	1.01	151.34	31.43	9.34	2.45	68.04	7.84
I-4-4	34.36	10.00	646.00	342.67	10.40	10.30	1.02	138.00	30.95	9.67	3.29	91.37	8.10
S-Glory-1	33.78	10.14	646.67	371.67	9.78	10.36	0.95	146.67	36.43	9.00	3.35	92.92	8.20
DPCbH-1	30.69	10.34	598.67	363.34	10.08	10.55	0.96	132.34	33.42	10.67	3.90	108.08	7.80
DPCb-1101	32.19	12.54	639.00	333.34	9.45	9.74	0.98	141.34	38.00	9.00	3.00	83.33	8.47
GA(P)	31.35	10.34	600.67	438.00	11.28	10.90	1.04	140.00	32.07	9.67	4.27	118.39	7.57
Pusa Mukta	33.73	8.87	547.00	339.67	10.68	10.52	1.00	120.34	28.80	10.67	3.66	101.47	8.20
TINNU	39.47	11.34	740.00	290.00	10.08	10.54	0.96	152.00	26.56	9.67	2.80	77.57	8.07
Grand mean	32.56	10.28	607.62	349.07	9.97	10.23	0.97	140.[-010	33.95	9.79	3.43		8.22
SE(d)±	2.99	0.92	44.35	24.28	0.49	0.41	0.03	8.33	3.77	0.70	0.40		0.22
CD(5%)	6.14	1.90	91.19	49.92	1.00	0.85	0.06	17.14	7.75	------	0.84		0.46
CV(%)	11.24	11.05	8.94	8.52	6.01	4.96	4.03	7.28	13.61	8.82	14.61		3.34
Range	25.54-39.47	7.94-12.54	419.00-740.00	230-438	8.41-11.28	9.44-10.9	0.90-1.04	120.34-150	26.56-41.62	9.00-11.00	2.16-4.47	59.81-123.95	7.57-8.90

Table 3: Estimates of PCV, GCV, heritability and genetic advance for marketable yield and other traits in cabbage

S. No.	*Traits*	*PCV (%)*	*GCV (%)*	*h^2bs (%)*	*GA as percentage of mean*
1	Plant spread (cm)	13.185(M)	6.877(L)	27.203(L)	7.389(L)
2	No. of non-wrapper leaves	14.934(M)	10.044(M)	45.235(M)	13.916(M)
3	Gross weight (g)	15.525(M)	12.693(M)	66.838(H)	21.376(M)
4	Net weight (g)	18.660(M)	16.601(M)	79.150(H)	30.425(H)
5	Polar diameter (cm)	8.191(L)	5.558(L)	46.052(M)	7.77(L)
6	Equatorial diameter (cm)	5.908(L)	3.206(L)	29.452(L)	3.584(L)
7	Head shape index	5.346(L)	3.347(L)	39.189(M)	4.316(L)
8	Days to harvest	8.758(L)	4.853(L)	30.713(M)	5.541(L)
9	Head compactness (g/$cm^{3)}$	16.958(M)	10.118(M)	35.597(M)	12.435(M)
10	Marketable heads per plot	9.511(L)	3.553(L)	13.953(L)	2.734(L)
11	TSS (brix)	5.096(L)	3.841(L)	56.807(M)	5.963(L)
12	Marketable head yield per plot (kg)	23.244(H)	18.078(M)	60.489(H)	28.964(M)

PCV = Phenotypic coffecient of variation {Low (L): <10%, Moderate (M): 10-20%, High (H): >20%}
GCV = Genotypic coffecient of variation {Low (L): <10%, Moderate (M): 10-20%, High (H): >20%}
h^2bs = Heritability (broad sense) {Low (L): <30%, Moderate (M): 30-60%, High (H): >60%}
GA = Genetic advance {Low (L): <10%, Moderate (M): 10-30%, High (H): >30%

Acknowledgment

The authors are thankful to the Department of Organic Agriculture and Natural Farming Chaudhary Sarwan Kumar Himachal Pradesh Agriculture University, Palampur, Himachal Pradesh (176062), for providing the necessary research facilities.

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Indian J. Plant Genet. Resour. 37(3): 522-551 (2024)

Plant Germplasm Registration Notice[@]

60 proposals for consideration of registration of germplasm for unique/superior traits were received online and examined by member-secretary, Plant Germplasm Registration Committee. 42 proposals complete in all respects were got reviewed by the experts and were presented in XXXXVIII[th] meeting of the Plant Germplasm Registration Committee of ICAR held in virtual mode on July 08, 2022. 36 proposals with unique/novel features belonging to 21 species were finally recommended for registration. The information on registered germplasm is published with the purpose to disseminate the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes.

1. Chittimuthyalu (IC426273; INGR22064), a short grain aromatic rice (*Oryza sativa*) germplasm with high Zn concentration (>24 ppm) in polished grain

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"Chittimuthyalu" is a well-known landrace of Telangana region. The word "Chittimuthyalu" means "small pearl" (Chitti-small, Muthyalu-pearl) which might have been given based on the physical appearance of the grain to the naked eye. Apart from this unique grain type, it is also popular for its aroma among the local rice farmers and consumers. Recently, it was also found to be rich in Zn content (> 24 ppm) in polished rice at ICAR-Indian Institute of Rice Research (Babu *et al.,* 2020). The native Chittimuthyalu was collected as a part of program for evaluation of farmer varieties and landraces for their high grain micronutrient. During the preliminary field trials for characterization of agro-morphological traits and yield, Chittimuthyalu has shown a lot of segregation and heterozygosity. Panicle to

Table 1: AICRPR data of grain yield, grain Zn content of Chittimuthyalu from 2013 to 2020 across the locations

Year	*Grain yield (Kg. ha^{-1})*	*DFF*	*PHT (cm)*	*Panicles/m^2*	*Zn (ppm)*
2013	2383 (14)	109 (18)	134 (17)	275 (16)	15.78 (6)
2014 AVT1	2966 (13)	108 (22)	118 (22)	274 (21)	17.16 (6)
2014 IVT	3296 (14)	104 (16)	93 (17)	305 (17)	21.49 (14)
2015 AVT2	3620 (13)	110 (19)	97 (8)	283 (19)	22.4 (18)
2015 AVT1	3505 (13)	111 (18)	95 (18)	264 (18)	22.8 (16)
2015 IVT	2804 (13)	110 (18)	145 (18)	269 (18)	17.5 (15)
2016 AVT2	4005 (14)	106 (23)	94 (24)	283 (22)	23.1 (10)
2016 AVT1	3185 (12)	103 (24)	132 (23)	298 (23)	22.5 (16)
2016 IVT	4017 (9)	107 (22)	142 (22)	275 (22)	18.4 (6)
2017 AVT2	4597 (13)	104 (24)	89 (24)	277 (24)	23.9 (18)
2017 AVT1	3270 (14)	109 (25)	137 (25)	289 (25)	21.4 (16)
2017 IVT	4103 (12)	105 (22)	94 (23)	298 (23)	22.8 (18)
2018 AVT1	4147 (13)	107 (13)	97 (13)	338 (13)	23.9 (12)
2018 IVT	4555 (15)	104 (15)	99 (15)	381 (15)	23.92 (13)
2019 IVT	3671 (20)	99 (20)	96 (20)	309 (20)	21.94 (8)
2020 AVT1	3716 (23)	100 (23)	99 (23)	310 (22)	16.77 (21)
2020 IVT	4041 (17)	87 (17)	92.86 (17)	310 (17)	15.8 (14)
Weighted average	3645.38	104.94	110.07	294.17	20.97

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Acknowledgement is due to ***Mr. Arup Das,*** *Young Professional, for providing technical assistance in compilation.*

row purification over years lead to the identification of a stable accession with consistent Zn content (23.92 ppm) in polished rice over most of the popular rice varieties across multiple seasons. Based on its high grain Zn content, Chittimuthyalu was also included as a micronutrient check (national check) from the inception of AICRIP Biofortification trial (*Kharif*-2013).

The weighted average (2013 to 2020) grain yield was 3645 kg/ha, and grain Zn content was 23.92 ppm in polished rice in AICRIP Bio-fortification trials (Table 1). It is a widely preferred donor in rice biofortification programs and contributed for many promising RILs for high grain Zn in various genetic backgrounds (Sanjeeva Rao *et al.,* 2020). The identified genetic stock, Chittimuthyalu (IC426273; INGR22064) possess grain Zn (>24 ppm) content in polished rice, unique aroma and aromatic short grain type.

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2. RP6338-9 (IC643971; INGR22065), a rice (*Oryza sativa*) germplasm with high stable yield and increased coefficient of non-photochemical quenching (qN) trait under high temperature stress

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In the context of developing genetic resources for high-temperature tolerance, KMR-3 Rwas introgressed with a heat tolerance QTL (*qHTSF4.1*) through marker assisted backcross breeding. Nagina22 is a potential donor for heat tolerance and was exploited in current study. Based on in-house experiments, RP6338-9, a stable backcross (BC_2F_6) introgression line was identified as promising for grain yield under high-temperature stress. It is an early duration restorer line with 87 days to 50% flowering and medium bold grain type. Further, it was nominated to high-temperature stress MLT, AICRPR-Plant Physiology during 2020-2021 at five locations *viz.,* Hyderabad (IIRR), Pantnagar, Pattambi, Rewa and Titabar. High-temperature stress was imposed by poly cover tent method. An increase in canopy temperature (>5ºC) over the ambient conditions was noticed inside the poly cover tent. RP6338-9 yielded 430 g/m^2 under high-temperature stress and 678 g/m^2 under control. It also exhibits grain yield superiority over the parents under ambient and high-temperature conditions. RP6338-9 has 26% and 65% yield advantage over KMR-3R; 109% and 116% yield advantage over Nagina22 under ambient and high-temperature stress respectively. In addition, RP6338-9 showed only 36% grain yield reduction which is comparatively less than that of Nagina 22, while the recurrent parent exhibited 51% yield reduction under high-temperature stress. The stability variance and stability

Table 1: Agro-morphological and yield characters of RP6338-9, KMR-3R and Nagina22

Trait	*RP6338-9*		*KMR-3R*		*Nagina22*	
	Control	*HT*	*Control*	*HT*	*Control*	*HT*
Plant Height (cm)[a]	120.3	120.3	106.1	107	104.2	108.8
Days to 50% Flowering [a]	88	87	93	92	72	71
Grain yield (g/m^2) [a]	678	430	538	260	324	199
Total Dry Matter (g) [a]	1562	1353	1550	1412	660	930
1000 grain weight (g) [a]	21.4	22.1	17.9	16.8	17.1	18.5
Maximum efficiency of PSII photochemistry (Fv/Fm)[b]	0.81	0.80	0.82	0.79	0.81	0.78
Electron transport rate (ETR) [b]	28.03	25.37	22.26	23.16	22.23	24.5
Coefficient of photochemical quenching (qP) [b]	0.63	0.54	0.51	0.53	0.55	0.58
Coefficient of non-photochemical quenching (qN) [b]	0.27	0.32	0.34	0.32	0.41	0.36

a- (Based on the data from AICRPR trials across locations); b- (Based on the data collected at IIRR location). HT – High-temperature stress. Control – Ambient temperature.

rating also determine the relative heat tolerance of RP 6338-9. The Coefficient of non-photochemical quenching (qN) is a significant fluorescence trait and an increase in this trait values under stress was observed in RP6338-9 (15.8%) suggesting tolerance to high-temperature (Table 1). In addition, RP6338-9 noted promising for grain quality under high-temperature stress (Jaldhani *et al.,* 2021). The identified genetic stock RP6338-9 (IC0643971; INGR22065) with *Rf3, Rf4* and *qHTSF4.1* is a potential rice restorer with high-temperature tolerance. It can be used as a potential donor in heterosis breeding program.

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3. Bindli (AC33015) (IC642852; INGR22066), a rice (*Oryza sativa*) germplasm with low phytic acid (0.83g/100g) and high zinc content in unpolished grain (59.1 mg/kg)

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Rice is an important source of essential nutrients like zinc (Zn) and iron (Fe) and their deficiencies are major health threats worldwide which need to be tackled on priority. Unfortunately, rice does not supply these micronutrients adequately as these are present in limited quantity in the outer layer of grain (bran); the processing of rice further decreases their content significantly. Phytic acid (PA), (myo-inositol 1, 2, 3, 4, 5, 6, hexakisphosphate) is the primary phosphorus (P) storing molecule in plants. In cereals, PA bound P accounts for around 75% of seed total P, while inorganic acid P accounts for approximately 5% (Lott *et al.,* 1995). Phytic acid is a strong chelating agent that binds essential minerals like calcium, magnesium, Fe, and Zn. Phytic acid present in rice is reported to interfere with the absorption of Fe and Zn, thereby reducing their bio-availability. When a mineral binds to PA, it becomes insoluble, precipitates and is not absorbed in non-ruminant intestines, including human. This process thus contributes to mineral shortages in person or may even inhibit gastrointestinal absorption of high mineral content meals when consumed alongside high phytate rice. Micronutrient malnutrition, particularly, Zn deficiency affects 49% of the world population that accounts for three-four billion people while over two billion people suffer from Fe deficiency worldwide. Phytic acid also has the potential to bind charged amino acid residues of proteins, with the concomitant reduction of protein availability. In view of the anti-nutritional effects of phytic acid, genotype with low phytic acid (LPA) would be a better way to increase the bioavailability of the minerals to counter malnutrition. We discovered a natural rice variation of PA with a 30-35 percent reduction in PA when compared to other genotypes. The genotype AC33015 (Bindli) contains LPA content (0.83g/100g) and higher Zn content (59.1 mg/kg) in rice grain. The PA and Zn content were constant over the year as reported by Kumar *et al.,* (2019). Due to LPA content, it also showed higher bioavailability of Zn (12.51 mg/kg)). Thus, this landrace would be a potential donor for grain quality improvement and can enrich the nutritional composition against malnutrition in rice. The AC32579 (Bindli) was collected from Muzaffarnagar, Uttar Pradesh. The plant is short height (95cm), 7-9 tillers, 18.5-22cm panicle length, 60-80 number of grains per panicle, test weight is 20.84 g, grain length is 8-9mm, grain breadth is 2.9-3.1mm, awned grain, purple apiculus, white colour grain, maturity duration of 110-115 days and 15-18g of grain yield per plant. Apart from low PA and high Zn traits, it also contains high protein (10-11%) and intermediate amylose content (20%). Amylose content is considered to be the single most important characteristic for predicting rice cooking and processing behaviours. Most consumers prefer rice with intermediate AC ranged between 20-25%. This genotype also has added advantage of aroma. Bindli shows high hulling percentage of 76%, milling percentage of 66%, head rice recovery percentage of >55 with less chalkiness percentage of ~20%. The chemical properties (alkali spreading value, gel consistency) were excellent with the best cooking quality (appearance, cohesiveness, tenderness on touching, tenderness on chewing, taste, elongation).

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4. RP6252-BV/RIL/1705 (IC645776; INGR22067), a rice (*Oryza sativa*) germplasm with High Nitrogen Use Efficiency (NUE), Physiological Efficiency (PE) and Recovery Efficiency (RE) under N-50 input

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In the studies of genetic improvement for nitrogen use efficiency (NUE) in rice, RP6252-BV/RIL/1705 was identified as promising culture under low nitrogen (N) field condition (without external N application) and 50% of the recommended N (N-50) expressed in terms of grain yield and use efficiency. It was developed from BPT5204/ Vardhan cross. It is a medium duration line with 110-113 days to 50% flowering and possess medium bold (MB) grain type (Table 1). It was evaluated in AICRPR Soil science-NUE trial (screening of rice germplasm for nitrogen use efficiency) during 2019, 2020 and 202.. The overall mean grain yield was noted as 5.03 t. ha^{-1}, 4.27 t. ha^{-1}, 3.51 t. ha^{-1} in N-100, N-50 and N-Low treatments (Table 2). In addition, it has the following significant features: i) 4% and 5% yield superiority over Vardhan (Positive check-Srikanth et al., 2016) in recommended dose of N (N-100) and N-Low treatments. ii) Noted promising total nutrient uptake (Kg ha^{-1}) in comparison with other entries of the trial across the tested locations and iii) Noted higher PE- Physiological efficiency (kg grain increase/ kg N uptake) and RE- Recovery efficiency (% of N recovered) in N-50 treatment over N-100 (Table 2). The identified genetic stock RP6252-BV/RIL/1705 (IC645776; INGR22067) possess high NUE and can be used as a potential donor in breeding rice for high NUE.

References

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Table 1: Agro-morphological, yield and grain micronutrient characters of RP6252-BV/RIL/1705 (CNN5) in N-100 treatment (based on the AICRPR data)

Trait	*Value*	*Trait*	*Value*
Plant Height (cm)	105-108	Grain Yield (t ha^{-1})	5.03
Tiller Number/Sq. meter	331-335	Straw Yield (t ha^{-1})	7.10
Days to 50% Flowering	110-113	Single plant yield (grams)	17.28
Panicles per Square meter	292-305	1000 Grain weight (grams)	23.2

Table 2: Data of RP6252-BV/RIL/1705 under AICRPR trials (Soil science) during 2019, 2020 and 2021

Trait/ Treat/ Year	*Grain yield (t ha^{-1})*			*Straw yield (t ha^{-1})*			*Total nutrient (N) uptake (Kg ha^{-1})*			*AE*		*PE*		*RE*	
	N1	*N2*	*N3*	*N1*	*N2*	*N3*	*N1*	*N2*	*N3*	*N2*	*N3*	*N2*	*N3*	*N2*	*N3*
2019 (N1-9; N2-9; N3-9)	3.42	4.49	5.14	4.74	6.16	7.24	75.89	100.89	115.89	-	-	-	-	-	-
2020 (N1-6; N2-5; N3-5)	3.79	3.98	4.98	4.95	5.20	6.55	61.08	69.95	91.20	17.80	23.20	63.50	59.00	40.80	49.00
2021 (N1-6; N2-5; N3-5)	3.37	4.15	4.87	4.71	6.04	7.38	50.25	82.00	100.40	25.70	22.00	37.00	40.30	75.00	58.30
Weighted mean	3.51	4.27	5.03	4.79	5.87	7.1	62.41	84.28	102.5	21.75	22.6	50.25	49.65	57.9	53.65

Values within the parenthesis indicates number locations tested during AICRPR trials. (IIRR Progress Report, Vol 3, 2019, 2020 and 2021). N1- Low N; N2-50% of Recommended N; N3-N100 Kg/ha. AE- Agronomic efficiency (kg grain increase/kg N added); PE- Physiological efficiency (kg grain increase/ kg N uptake); RE- Recovery efficiency (% of N recovered).

5. HW5074 (IC640677; INGR22068), a wheat (*Triticum aestivum*) germplasm with pyramided chromosomal segments containing *Sr2/Lr27/Yr30, Sr24/Lr24* and *Sr36/Pm6* exhibiting resistance to the prevailing stem rust, leaf rust and powdery mildew pathotypes

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In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Most of the rust resistance genes are all stage resistance (ASR)/ major gene and therefore succumb to new variants of the respective pathogen soon after their deployment, whereas adult plant resistance (APR)/minor genes have small to intermediate effects when present alone. High and durable rust resistance can be achieved by combining the ASR and APR genes together.

Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr2/Lr27/Yr30, Sr24/Lr24* and *Sr36/Pm6* were pyramided in the background of HD2833 cultivar through marker assisted backcross approach. Presence of the resistance genes were carried out using molecular markers, *gwm533* (*Sr2*+) (Spielmeyer *et al.,* 2003), *Sr24#12* (*Sr24/Lr24*) (Mago *et al*., 2005) and s*tm773-2* (*Sr36/Pm6*) (Tsilo *et al*., 2008), in the pyramided lines. Stable and high yielding line (HW5074) was selected at BC4F7 generation and further evaluated for four seasons in two years. Adult plant reaction of pyramided lines showed resistance to the stem rust, leaf rust and powdery mildew pathotypes prevailing in India. HW5074 is the sister line of HW5073 which is high yielding with good agronomic traits. Using gene pyramids of minor (*Sr2/Lr27/Yr30*) and major resistance genes (*Sr24/Lr24* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment. Genetic stock can diversify the rust resistance genes among the wheat germplasm and provide a vital source for imparting durable rust resistance in wheat.

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6. HW5068 (IC645768; INGR22069), a wheat (*Triticum aestivum*) germplasm with pyramided chromosomal segments containing *Sr24/Lr24, Sr26* and *Sr36/Pm6* exhibiting resistance to the prevailing stem rust, leaf rust and powdery mildew pathotypes of India

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In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Using conventional selection system, it is difficult to select

two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with seedling and adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr24/Lr24*, *Sr26* and *Sr36/Pm6* were pyramided in the background of MACS2496 cultivar through marker assisted backcross approach. Microsatellite markers, s*tm773-2* linked to *Sr36* (Tsilo *et al*., 2008), *Sr26#43* (Mago *et al*., 2005) linked to *Sr26* and *Sr24#12* (Mago *et al*., 2005) linked to *Sr24/Lr24* were used to perform marker assisted selection. Stable and high yielding line (HW5068) was selected at BC3F4 generation and further evaluated for four seasons in two years. Seedling and adult plant reaction of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India. Using gene pyramids (*Sr24/Lr24*, *Sr26* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment.

References

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7. IC335971 (IC335971; INGR22070), a wheat (*Triticum aestivum*) germplasm with high heat tolerance index (1.13)

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Terminal heat stress hastens the seedling emergence, tiller initiation, emergence of flag leaf and spike in wheat that shortens the total growth duration of plant (Singh and Pal, *et al*., 2003). The enhanced wheat production can be achieved only by using elite heat tolerant germplasm but the identification & confirmation of traits related to heat tolerance in germplasm material are still lacking. A diverse set of 102 wheat germplasm was tested for four years (2011-12 to 2013-14 & 2016-17) under normal & late sown conditions to identify heat tolerant wheat germplasm. In this investigation IC335971 showed lower days to anthesis (70.34 days), transpiration rate (4.65 m mol $m^{-2}s^{-1}$) & heat susceptibility index (0.91) but higher membrane stability index (30.05), photosynthetic rate (15.35 µ mol $m^{-2}s^{-1}$), economic yield (2.32 g $plant^{-1}$), percentage increment in economic yield by Raj 4083 (11.86 %) and heat tolerance index (1.13) as compared to another germplasm (Table 1). Based on these traits IC335971 was found the most suited wheat germplasm for hyper-arid regions may be utilized for further breeding programs to develop heat tolerant hybrids. The identified traits for heat tolerance might be used in future to confirm the thermos tolerance in other plants.

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Table 1: Trait description of germplasm: IC335971

Character	*2011-12*	*2012-13*	*2013-14*	*2016-17*	*Average*
Days to anthesis	72.00	68.67	70.67	70.00	70.34
Photosynthetic rate (µ mol $m^{-2}s^{-1}$)	15.93	16.82	14.91	13.73	15.35
Transpiration rate (m mol $m^{-2}s^{-1}$)	5.80	4.69	4.42	3.70	4.65
Membrane stability index	28.58	28.51	34.55	28.55	30.05
Economic yield (EY, g $plant^{-1}$)	2.32	2.49	2.50	1.95	2.32
Heat susceptibility Index	0.88	0.86	0.99	0.90	0.91
Heat tolerance Index	1.74	0.96	1.07	0.74	1.13
% increment in EY by Raj 4083	12.08	15.81	11.61	7.14	11.66

8. DTW119 (IC645762; INGR22071), a wheat (*Triticum aestivum*) germplasm with low heat stability index (0.79)

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The genotype DTW119 (RIL119) was developed from the cross Dharwar Dry/DPW621-50 at ICAR- Indian Institute of Wheat & Barley Research (ICAR-IIWBR), Karnal. The parental line DPW621-50 is high yielding genotype released for timely sown irrigated conditions of the NWPZ whereas Dharwar Dry is reported as drought tolerant Indian genotype (Kirigwi *et al.,* 2007). The parental adaptability to endure in the stress condition has been combined in wheat genotype DTW119. The promising genotype DTW119 was screened under in 33rd Drought and Heat Tolerance Screening nursery (DHTSN) of AICRP on Wheat & Barley, under late sown and rainfed condition during 2020-21 crop seasons. The nursery was conducted across ten locations (Dharwad, Prabhani, Indore, Durgapura, CSSRI (Karnal), IIWBR (Karnal), Ludhiana, Pusa and Sabour. The nursery comprised of 49 genotypes including 8 checks (C306, DBW110, DBW150, DDW47 (d), MP3288, K3717, NI5439 and WH730). Data on agro-morphological and yield associated traits were recorded. Phenotypic data such as, days to heading, days to maturity, plant height, grain yield, grain number per spike and thousand grain weight (TGW) were also recorded. Based on the pooled data, it was found that DTW119 showed lesser percentage yield reduction (15.2%) as compared to all the checks under late sown condition. DTW119 (0.79) was found to be superior with lowest Heat Susceptibility Index (HSI) in pooled analysis across centres as compared to check varieties *viz.,* C 306 (1.62), DBW 150 (1.18), DDW49 (d) (1.24), MP3288 (1.35), NI5439 (1.34), WH730 (1.35) (Tables 1 and 2).

Reference

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Table 1: Pooled analysis of HSI and agro-morphological traits of DHTSN genotypes during crop season 2020-21

Trait/component	*Test genotype*	*Checks*					
	DTW119	*WH730*	*DBW150*	*NI5439*	*MP3288*	*C306*	*DDW47(d)*
Days to heading	68	68	69	71	74	75	76
Days to maturity	112	111	111	113	115	117	115
Thousand grain weight (g)	39	37	37	37	40	39	38
Plant height (cm)	82	85	92	100	88	111	85
Grain number per spike	46	45	49	45	39	44	49
HSI	0.79	1.35	1.18	1.34	1.38	1.62	1.11
% Yield reduction	15.2	25.9	22.7	25.7	25.9	31.1	21.4

Source: 2020-21, DHTSN (AICRP-W&B programme)

Based on the pooled data across locations and years, genotype DTW119 showed lowest HSI (0.42) and DSI (-0.25) as compared to all the checks used (Table 2). The identified donor can be used as potential donor for heat stress in wheat with adaptability to water stress condition also.

Table 2: Pooled analysis of Heat and Drought Susceptibility Index of genotypes

Genotype	*2019-20*	*2020-21*			*Pooled*	*2019-20*	*2020-21*		*Pooled*
	KNL	*KNL*	*NBPGR*	*IARI*	*HSI*	*KNL*	*KNL*	*NBPGR*	*DSI*
	HSI					*DSI*			
DTW-119	1.72	-1.26	0.76	0.47	0.42	0.82	0.57	-2.14	-0.25
AKAW3717 ©	5.25	1.91	-0.09	1.27	2.09	-1.47	0.69	0.41	-0.12
WH 730 ©	2.22	1.31	0.57	1.29	1.35	-1.83	0.87	-0.23	-0.40
DBW 150 ©	5.19	0.21	-2.27	1.31	1.11	3.43	0.51	-0.40	1.18
DHTW 60 ©	0.84	0.36	1.53	1.42	1.04	1.08	1.01	-0.34	0.58
AKW2862-1©	3.80	1.22	1.96	1.32	2.08	0.60	1.15	-0.84	0.30
HTW11(c)	2.34	0.83	1.35	1.57	1.52	-0.22	1.16	2.21	1.05

KNL-(ICAR-IIWBR, Karnal), NBPGR-National Bureau of Plant Genetic Resources, New Delhi, IARI-Indian Agricultural Research Institute, New Delhi)

9. HW5067 (IC645769; INGR22072), a wheat (*Triticum aestivum*) germplasm with three stem rust (*Sr24, Sr26* & *Sr36*), one leaf rust (*Lr24*) and one powdery mildew (*Pm6*) resistance genes possesses resistance to the prevailing stem rust, leaf rust and powdery mildew pathotypes of India

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Wheat is one of the most widely consumed cereal crops worldwide that provides 20% of dietary calories and protein. In India, wheat is the most important cereal crop after rice with a production of 109 MT during 2020-21. But with the rapidly increasing population, India will need more than 140 million tons of wheat by 2050. Among many factors, intensified agricultural practices and climate change have increased the incidence of pathogens in wheat in the recent years. Stem and leaf rust diseases continually pose threat to wheat production. In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with seedling and adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr24/Lr24*, *Sr26* and *Sr36/Pm6* were pyramided in the background of LOK1 cultivar through marker assisted backcross approach. Microsatellite markers, s*tm773-2* linked to *Sr36* (Tsilo *et al*., 2008), *Sr26#43* (Mago *et al*., 2005) linked to *Sr26* and *Sr24#12* (Mago *et al*., 2005) linked to *Sr24/Lr24* were used to perform marker assisted selection. Stable and high yielding line (HW5067) was selected at BC3F4 generation and further evaluated for four seasons in two years. Seedling and adult plant reaction of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India. Using gene pyramids (*Sr24/Lr24*, *Sr26* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment.

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Tsilo TJ, Y Jin and JA Anderson (2008) Diagnostic microsatellite markers for the detection of stem rust resistance gene *Sr36* in diverse genetic backgrounds of wheat. *Crop Sci.* 48: 253-261.

10. IC73591 (IC73591; INGR22073), a wheat (*Triticum aestivum*) germplasm with resistance to leaf rust

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It is projected that India will require approximately 109 million tons of wheat in 2020. But this aim will be challenging to achieve given the numerous biotic stressors, including wheat blast and rust (leaf, stem, and stripe), which are becoming more prevalent as a result of climate change. *Puccinia triticina* Eriks, formerly known as *Puccinia recondita* f. sp. *tritici*, is thought to be a major cause of leaf rust in practically every region of the world where wheat is produced, and a considerable yield loss results from it. Leaf rust, often known as brown rust, can reduce yield by 15% to 60% on average (McIntosh, 1998).

A comprehensive germplasm evaluation study of wheat accessions conserved in the National Genebank, India was conducted to identify sources of leaf rust. Field

testing for leaf rust resistance was carried out at 10 different locations Pantnagar (Uttarakhand), Ludhiana (Punjab), Karnal (Haryana), Varanasi (Uttar Pradesh), Kumarganj (Uttar Pradesh), Vijapur (Gujarat), Powarkheda (Madhya Pradesh), Pune (Maharashtra), Dharwad (Karnataka) and Wellington (Tamil Nadu) for two years followed by molecular screening to detect the presence of APR genes in Indian wheat germplasm. 190 wheat germplasm lines which were selected from 6319 accessions based on *Ltn* disease screening and average coefficient of infection. Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance. Molecular analysis of 190 selected germplasm lines was done to identify different combinations of APR genes imparting resistance to leaf rust. 49 accessions were identified which were carrying either two or three APR genes were evaluated for yield stability across four different locations in India *viz*., Pantnagar, Varanasi, Powarkheda and Pune, using additive main effects and multiplicative interaction (AMMI) model. Among identified 49 germplasm lines, IC73591 which is a collection from Bhowali, Nainital has shown resistance to leaf rust pathotypes prevalent in Indian condition [Highest Score (HS) = 0; Average coefficient of Infection (ACI) = 0.0], also showed the presence of leaf rust resistance genes, *Lr34*+ (*Lr34/Yr18/Sr57/Pm38*), *Lr46*+ (*Lr46/Yr29/Sr58/Pm39*) and *Lr67*+ (*Lr67/Yr46/Sr55/Pm46/Ltn3*) and yield stability in above said four different locations may be considered promising multiple disease resistant germplasm and could be included in breeding program as parents for developing new durable multiple rust resistant cultivars.

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11. DWRBG7 (IC645765; INGR22074), a barley (*Hordeum vulgare*) germplasm with high 1000 grain weight (43.2 g) and high bold grains percentage (76.7) in six rowed hull less type

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The present day six-row hulless barley genotypes suffer from very low proportion of bold grains and lower thousand grain weight, leading to lower flour recovery. The identified genotype DWRBG7 has higher bold grain percentage coupled with higher thousand grain weight and high beta glucan percentage.

DWRBG7 was derived from a cross DL456/IEBON17 and subjected to pedigree selection of breeding approach.

Table 1: Bold grain (%) in DWRBG7 at different locations during 2020-21

Genotype	*Durgapura*	*Pantnagar*	*Kanpur*	*Hisar*	*Karnal*	*Ludhiana*	*Average*
DWRBG-7 (DWRFB40)	92.7	82.9	76.8	61.1	82.2	64.7	76.7
Dolma ©	25.9	13.8	7.1	3.8	13.4	19.6	13.9
NDB943©	31.5	NA	36.0	38.2	26.5	21.6	30.8
Karan16 ©	33.5	32.8	18.9	19.4	7.9	19.4	22.0
BHS352 ©	20.0	3.5	6.5	2.0	8.6	2.9	7.2
Geetanjali ©	39.3	16.8	26.9	6.9	29.8	11.5	21.9
HBL276 ©	34.8	13.6	13.4	5.5	24.7	14.7	17.8

Table 2: 1000-grain weight (g) in DWRBG7 at different locations during 2020-21

Genotype	*Durgapura*	*Pantnagar*	*Kanpur*	*Hisar*	*Karnal*	*Ludhiana*	*Average*
DWRBG-7 (DWRFB40)	49.7	43.2	42.5	39.4	45.2	39.0	43.2
Dolma ©	32.1	26.4	28.7	23.1	31.3	26.1	28.0
NDB943©	37.5	NA	30.8	30.2	32.4	27.7	31.7
Karan16 ©	38.2	31.2	30.1	26.9	29.5	25.9	30.3
BHS352 ©	34.3	28.2	28.9	24.5	32.0	22.8	28.5
Geetanjali ©	35.7	30.5	34.7	25.6	32.5	23.8	30.5
HBL276 ©	36.1	32.1	29.7	28.4	34.6	26.0	31.1

Subsequently, it was tested with released huskless cultivars/ checks at six locations in the AICRP Barley Quality Screening Nursery for quality traits during 2020-21. DWRBG7(tested as DWRFB 40) showed higher bold grain percentage (76.7) and thousand grain weight (43.2 g) Tables 1 & 2*)* as compared to all tested hulless genotypes/checks. In addition, this genotype had a good combination of the promising quality traits such as hectolitre weight (72.9 kg/hl), starch content (63.3%), and ß-glucan content (6.0% db)

DWRBG7 was also evaluated in a set of 24 advanced breeding lines along with three local checks for agro-morphological traits in barley station trials at ICAR-IIWBR, Seed and Research Farm, Hisar during 2018-19 and 2019-20. The agro-morphological traits based on two years recordings in station trials indicate average values for tillers/meter (86), days to heading (88 days), maturity (129 days) and plant height (101 cm). The spike length (8.9 cm) is medium with 64 grains/spike.

12. DWRBG 8 (IC645770; INGR22075), a hulless barley (*Hordeum vulgare*) germplasm with combination of high grain beta glucan (7.0 %) and protein (16.6 %) content

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Barley (*Hordeum vulgare* L) is one of the earliest domesticated crops and used to be the part of staple food in ancient times since Neolithic period. In Rigvedic period "Yava" (barley) was the only cultivated crop (Roy 2009). Barley consumption can prevent several diseases, especially cardiovascular, diabetes, colon cancer and hypertension. Among cereal grains, barley has the highest functional value especially because of higher content of soluble fibres called β- glucans and several other phytochemicals. For food purposes, the naked or hulless barley grains are preferred because of better textural and palatability of end products. Further the removal of husk in hulled barley requires extra efforts for pearling and lead to the loss of nutrients from outer layer of grain. For breeding improved hulless barley genotypes with superior nutraceutical values, the sources need to be identified. The germplasm BCU 8028 is a landrace collected from Leh & Ladakh region of India, having higher grain beta glucan content along with the higher crude protein value. Both

Table 1: Grain beta glucan content (%db) in DWRBG-8 (BCU 8028) at different locations during 2020-21*

Genotype	*Karnal 18**	*Karnal 19**	*Hisar 21*	*Karnal 21*	*Ludhiana 21*	*Durgapura 21*	*Kanpur 21*	*Pantnagar 21*	*Average*
BCU 8028	7.3	6.5	6.9	7.6	6.4	7.0	6.2	7.9	7.0
Dolma (c)	6.5	6.5	6.6	6.1	6.3	7.7	6.2	5.7	6.5
NDB 943 (c)	5.8	5.6	5.2	5.7	5.2	6.7	5.1	NA	5.6
Karan 16 (c)	5.3	4.9	5.3	5.5	5.3	6.3	6.0	5.4	5.5
BHS 352 (c)	6.6	6.5	7.2	8.1	8.0	7.6	7.1	8.0	7.4
Geetanjali (c)	5.3	5.6	5.9	5.8	3.8	6.2	3.9	5.7	5.3
HBL 276 (c)	6.0	6.7	6.6	7.8	6.6	6.7	6.1	6.5	6.6
PL 891 (c)	NA	NA	6.3	5.7	6.3	6.8	5.2	5.9	6.0

* Karnal 18 & 19= ICAR-IIWBR Karnal 2017-18 & 2018-19 data and rest are 2020-21 data.

Table 2: Grain protein (%db) in DWRBG-8 (BCU 8028) at different locations during 2020-21*

Genotype	*Karnal 18**	*Karnal 19**	*Hisar 21*	*Karnal 21*	*Ludhiana 21*	*Durgapura 21*	*Kanpur 21*	*Pantnagar 21*	*Average*
BCU 8028	11.1	14.4	16.4	18.7	15.6	NA	20.4	19.8	16.6
Dolma (c)	10.2	14.5	14.2	17.4	12.8	16.2	15.6	16.9	14.7
NDB 943 (c)	10.9	13.5	14.5	NA	12.4	15.3	13.9	16.3	13.8
Karan 16 (c)	10.0	12.1	12.2	13.7	11.9	14.3	13.8	14.7	12.8
BHS 352 (c)	10.3	12.8	13.8	16.3	11.8	14.6	14.4	15.4	13.7
Geetanjali(c)	9.7	14.9	14.4	14.0	10.6	NA	13.5	18.2	13.6
HBL 276 (c)	11.1	14.3	13.0	11.5	11.8	15.4	12.9	16.4	13.3
PL 891 (c)	NA	NA	14.1	15.0	13.9	15.4	16.2	15.2	15.0

*Karnal 18 & 19 = ICAR-IIWBR Karnal 2017-18 & 2018-19 data and rest are 2020-21 data.

these traits are very important contributors to the health and nutrition benefitting value of food barley and may serve as important donor for food barley improvement programme.

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13. IIMR FxM-7 (FXV 645) (IC643959; INGR22076), a foxtail millet (*Setaria italica*) germplasm with early duration, multiple disease resistance and thick and compact inflorescence

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Foxtail millet [*Setaria italica* (L.) P. Beauv.] is one of the oldest of the small millets cultivated in the world. It is good as food for human consumption, feed for poultry and cage birds, and fodder for cattle. Due to high drought tolerance, foxtail millet was once an indispensable crop of vast rainfed areas in semi-arid regions in India. Now it is cultivated on a limited area in Andhra Pradesh, Karnataka, Telangana, Tamil Nadu, Maharashtra, Rajasthan and north eastern states.

IIMR FxM-7 (FXV 645) is a foxtail millet selection with early duration, multiple disease resistance and thick and compact inflorescence. from ISe 1593 with significantly early flowering (44 days) and early maturity (77 days), with high grain yield (1897 kg/ha) and per day productivity. It has thick and compact inflorescence with thick stem and less tillering (Table 1). The early flowering and maturity can help in avoiding terminal moisture stress in locations where rainy season withdraws early. Also in regions where foxtail millet followed by pulses cropping pattern is followed, this helps in early sowing of second crop thus ensuring better germination and crop stand. The low tillering habit with thick stem is a useful trait for mechanical harvesting. IIMR FxM-7 (FXV 645) has recorded multiple disease resistance (Table 1). Thus, it can be used as donor parent for incorporating earliness and disease resistance in recombination breeding to combine high yield, short duration and multiple disease resistance.

Table 1: Grain yield and related traits, disease and insect incidence in IIMR FxM-7 (FXV 645) vs. Checks

S. No.	*Entry*	*Genotype*	*Grain yield (kg/ha)*	*Days to flowering*	*Days to maturity*	*No. of Prod. tillers/plant*	*Per day productivity (kg/ha/day)*	*Brown spot (G)*	*Rust (G)*	*Leaf blast (G)*
1	FXV615	SiA 3159	2023	52	86	3	23.52	3.24	2.33	2.86
2	FXV625	SiA 3303	1968	49	82	3	24.00	3.46	3.89	3.28
3	FXV626	SiA 4200	2075	54	88	3	23.58	3.84	2.44	2.99
4	FXV628	GPUF 4	2093	50	84	3	24.92	3.58	5.00	4.62
5	FXV632	IIMR FxM-5	1755	47	80	3	21.94	3.53	5.22	4.96
6	FXV637	GPUF 15	1876	51	85	3	22.07	3.87	4.67	4.41
7	FXV640	SiA 4210	1956	54	87	3	22.48	3.62	4.44	3.93
8	FXV641	SiA 4213	1971	53	86	3	22.92	3.36	4.67	4.14
9	FXV642	TNSi 379	1858	53	87	3	21.36	3.73	4.22	3.84
10	FXV643	TNSi 380	2045	52	87	3	23.51	2.67	4.22	4.20
11	FXV644	IIMR FxM-6	2015	51	84	3	23.99	3.24	4.22	4.15
12	FXV645	IIMR FxM-7	1897	44	77	2	24.64	1.96	1.78	2.83
13	Check 1	DHFt109-3	1941	52	86	3	22.57	3.64	3.22	3.36
14	Check 2	SiA3156	1997	51	85	3	23.49	4.13	4.67	4.39
	CD (5%)		240	3	3	0		2.11	3.05	2.17

14. LMV 533 (IC483093; INGR22077), a little millet (*Panicum sumatrense*) germplasm with early flowering (50-52 days) and early maturity (83-85 days) and grain and fodder yield advantage

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Little millet is indigenous to India with an area about 2.3 lakh hectare, known for high grain iron content and other superior nutritional parameters. LMV 533 is early flowering and early maturing little millet entry tested in AICRP All India trials during *kharif* 2019 and *kharif* 2020. LMV 533 is a pureline selection from GPmr 6 germplasm line. The line was tested with four checks varieties JK 8 (early maturing), DHLM36-3 (medium maturing), BL 6 (medium maturing) and OLM 203 (late maturing). The entry was tested in a total of 35 locations for days to 50% flowering and for days to maturity. The entry LMV 533 showed consistent performance with average days to 50% flowering of 48-50 days and days to maturity of 80-83 days across locations and years and on-a-par performance with early maturing check variety JK8. LMV 533 recorded grain yield of 1370 kg/ha in comparison with similar maturing check JK which recorded 1316 kg/ha. Similarly, LMV 533 recorded fodder yield of 4808 kg/ha in comparison with similar maturing check which recorded 4593 kg/ha. For both grain and fodder yield, LMV 533 showed superiority of 4-5% over the similar maturing check JK 8.

LMV 533 recorded plant height of (105-110 cm) recorded 5-6 number of productive tillers per plant with the similar maturing check JK 8. LMV 533 can serve as an important genetic stock for breeding improved varieties for early flowering, early maturing coupled with high grain yield.

15. SPV 2625 (IC643961; INGR22078), a yellow grained sorghum sorghum (*Sorghum bicolor*) germplasm with short height (171.4 cm) and early maturity (110.3 days)

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Yellow-grains of sorghum is a valued commodity in the regions of Telangana, Andhra Pradesh and adjoining areas of Karnataka. It is known to contain higher amounts of tannin (Hahn and Rooney 1985, Dykes and Rooney, 2006). The local germplasm of yellow grain sorghum is tall, medium to long in duration and susceptible to foliar diseases. Hence they are prone to lodging and infested by diseases and pests under erratic monsoon in *kharif* season. Therefore, short duration, dwarf varieties are beneficial for farmers. Dwarf plant type is also desirable to enhance the ease of mechanized harvesting. The notified yellow-grain variety PYPS 2 was used as donor of the yellow grain colour, which was also taller. The donor for short duration, high grain yield and dwarfness was parental line C43, male parent of sorghum hybrid CSH 16. Pedigree breeding method was followed at the Indian Institute of Millets Research, Hyderabad, and

Table 1: Performance of SPV 2625 AICRP on Sorghum Speciality Trials across during *kharif* 2018 (4 locations) and *kharif* 2019 (4 locations)

	Plant height (cm)			*Days to 50% flowering*			*Days to maturity*		
Yellow-grain genotypes	*Kharif 2018*	*Kharif 2019*	*Mean*	*Kharif 2018*	*Kharif 2019*	*Mean*	*Kharif 2018*	*Kharif 2019*	*Mean*
SPV2613	230.7	270.6	250.6	68.5	65.8	67.2	114.4	111.2	112.8
SPV2614	255.2	270.4	262.8	70.3	65.4	67.8	115.6	110.8	113.2
SPV2617	266.6	306.9	286.8	90.7	78.1	84.4	138.4	125.7	132.0
SPV2620	247.2	254.4	250.8	68.1	69.9	69.0	112.8	115.8	114.3
SPV2625	157.8	185.0	171.4	67.0	61.8	64.4	111.8	108.8	110.3
SPV2626	234.2	266.5	250.3	67.5	64.3	65.9	114.7	109.5	112.1
SPV2628	266.8	269.5	268.1	75.7	74.2	74.9	119.6	119.3	119.4
Paiyur 2*	240.1	267.0	253.5	76.6	71.3	73.91	125.2	116.8	121.0
CD at 5%	31.4	52.4		8.0	5.7		10.2	7.3	

* Coloured check used in trial- Paiyur 2

selections were done in segregating generations with selfing. The selection SPV 2625, after selection upto F_7 generations was found promising for earliness, yellow grain colour and dwarf plant stature. This was further multiplied and tested in AICRP sorghum multi-locational trials during *kharif* seasons of the years 2018 and 2019 (Table 1).

Morpho-agronomic Characteristics

The yellow-grained sorghum genetic stock SPV 2625 is early to mature – matures in 110.3 days; it is 11 days earlier to check and 2 days earlier to other genetic stock. In multilocation trials, SPV 2625 was the earliest to flower (64.4 days) and maturity (110.3 days) which was 1.5 to 2 days earlier than next best yellow entry SPV 2626 and 10 days earlier than coloured grain check Paiyur 2. The genetic stock SPV 2625 was dwarfer (171.4 cm height) and uniform in height which makes it non-lodging. Its height was similar to CSV 17, the dwarf white-grained variety.

Associated Characters and Cultivated Practices

SPV 2625 is *kharif* adapted, suitable for cultivation in Telangana, Andhra Pradesh and adjoining areas of Karnataka. It is moderately resistant to pests and diseases and useful to escape from grain mold due to end of the season rains.

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16. HPKM191 (IC643992; INGR22079), a horse gram (*Macrotyloma uniflorum*) germplasm with very early maturity (84 days) and Semidwarf trait (67 cm)

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Horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] (2n=20) is a lesser known but an important pulse crop, being cultivated in the diverse climatic conditions of the world. It is considered to be the most tolerant to biotic and abiotic stresses. Despite the presence of many significant properties in the species, the area and production could not be increased due to its poor plant architecture. The present plant type possesses many wild characteristics such as indeterminate and twining growth habit, photosensitivity, late flowering and asynchronous maturity, resulted into unsuitability for modern farming system. All the efforts in the past to improve the existing plant structure could not bear any results mainly due to non-availability of desirable traits in the Indian germplasm. Therefore, desirable mutations were induced with different doses of gamma radiation in two well adapted promising lines of horsegram namely HPKC 2 and VLG 1 at Department of Crop Improvement, CSK Himachal Pradesh Agricultural University, Palampur. Desirable mutants were selected from segregating material in M2 population. Line HPKM 191 is a mutant developed after gamma radiation treatment @ 250 Gy to a local line HPKC 2. The plant type of this mutant is with medium height which gives its appearance as a semi-dwarf look but not a busy type. The reduced leaf angle to stem compared to parent, gives this line an additional benefit in the form of increased photosynthetic efficiency. It matures early and synchronously and has an erect growth habit. Having a medium plant height, the plants belong to the semi dwarf category. The other distinguishable characteristics of this line are small, yellowish-green leaves and very early flowering. HPKM 191 takes 35-42 days to flower and 82-84 days to mature.

The other important characteristics of this line are given in the following Table 1.

Table 1: Agronomically characterisation of HPKM-191 (Horsegram genotype)

S. No.	*Plant traits*	*L-191 (2008-2009) (mean values)*
	Morpho-physiological traits	
1	Leaf area index	2.68
2	Leaf area (cm^2)	6.96
3	Branch angle (degree)	32.12
4	Leaf angle (degree)	43.66
5	Number of Nodules/plants	21.37
	Structural and phenological traits	
1	Days to 50% flowering	42.12
2	Days to 75% maturity	84.55
3	Plant height (cm)	67.00
4	First pod height (cm)	7.56
	Seed yield traits	
1	Pods/plant	83.45
2	Seeds/pod	5.96
3	Pods/cluster	3.94
4	100-seed weight (g)	3.22
5	Grain yield/plant	8.46

17. IC553521 (IC553521; INGR22080), a wild bean (*Vigna stipulacea* (Lam.) Kuntze.) germplasm with high protein content (24.6%)

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The nutritional composition plays a crucial role in food acceptability and food preferences as it is directly linked to consumers' health and well-being. *Vigna stipulacea* (Lam.) Kuntze, known locally as *Minni payaru*, is being utilized in the southern part of India, mainly in Tamil Nadu, for animal feeding, manure production, and in traditional dishes like *Idli* and *Vada* (Gore *et al.,* 2020). However, *V. stipulacea* remains as an under-researched legume with no reports available on the variability of minerals like., iron (Fe), zinc (Zn) and calcium (Ca) concentration and protein content in its grains. In a study, 99 accessions of *V. stipulacea* were tested for Fe, Zn and Ca concentration and protein content over two locations, *viz*., ICAR-Indian Institute of Pulses Research (IIPR), Kanpur (Loc1) and ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi (Loc2). Total protein was estimated as per the AOAC official method. Combined analysis of variance (ANOVA) for each parameter (Fe, Zn, Ca, and protein) was performed to elucidate the significant effects of genotype, environment and genotype-environment interaction (G x E) that revealed significant effects of genotype for all the traits over both locations. The genetic advance was estimated. Finally, the stability of the tested genotypes over the locations was enumerated and portrayed graphically by deploying GGE biplot analysis. GGE biplot showed that for grain protein concentration IC553521 was the most "ideal type with highest protein content (24.8%) (Gore *et al.,* 2021). Based on the desirability index, Loc1 (Kanpur) was identified as ideal for Fe, Zn and Ca concentration and for grain protein content Loc2 (New Delhi) was the ideal type. A significant positive correlation was observed between Zn and protein concentrations, while a negative association was found between phytate and protein concentrations across the locations. This study identified valuable donor genotype and expanded our understanding of developing biofortified *Vigna* cultivars. Promoting the domestication of this nutrient-rich, semi-domesticated, underutilized species will support sustainable agriculture and help alleviate hidden hunger.

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18. IC553564 (IC553564; INGR22081), a wild bean (*Vigna stipulacea* (Lam.) Kuntze) germplasm with long peduncle length (63 cm)

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Vigna stipulacea (Lam.) Kuntze., commonly known as *Minni payaru* is an underutilized legume species and has a great potential to be utilized as food crop. Morphological and molecular characterization of diverse panel of *V. stipulacea conserved in the Indian National Genebank,* was carried out to evaluate and select the best germplasm to be utilize in the breeding program. Significant variation was recorded for the morphological traits. *Euclidean distance using UPGMA method grouped all accessions into two major clusters. Accessions were identified for key agronomic traits*

such early flowering (IC331436, IC251436, IC331437); long peduncle length (IC553564) and more number of seeds per pod (IC553529, IC622865, IC622867, IC553528). Peduncle length was recorded for the length of the longest peduncle when the first pod changes colour. Accessions IC553564 was identified for long peduncle length (Gore *et al*., 2022). Long peduncles are advantageous in getting the pods above the canopy. This helps in reducing the damage of pods by the pod borer and other insects and is also helpful at the time of harvesting. This trait may be transferred to cultivated *Vigna* for facilitating mechanical harvesting, especially in mungbean, which is highly desirable keeping in view the increasing cost of labour and drudgery involved in manual picking of mature pods.

Reference

Gore PG, V Gupta, R Singh, K Tripathi, R Kumar, G Kumari, M Latha, HK Dikshit, Kamala V, A Pandey, N Singh, KV Bhat, RM Nair and A Pratap (2022) Insights into the genetic diversity of an underutilized Indian legume, *Vigna stipulacea* (Lam.) Kuntze., using morphological traits and microsatellite markers. *PLoS ONE* 17(1): e0262634..

19. ACC. 1666 (IC645764; INGR22082), an onion (*Allium cepa*) germplasm for water logging tolerance resulting in lower yield reduction (16.9%)

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Onion is highly prone to waterlogging, especially during the *kharif* season, reducing yields by 50–70%. Hence, identifying tolerant genotypes with adaptive traits are crucial for flood-prone areas. To identify waterlogging-tolerant onion genotypes, ICAR-Directorate of Onion and Garlic Research, Pune conducted pot and field experiments where 100 genotypes including Accession 1666 (selection from Accession 1473; IC594035) were screened under artificially created water-logging conditions. In the pot experiment, 45-day-old onion plants were waterlogged for 10 days with water 3 cm above the soil. Identified genotypes were field-tested for waterlogging tolerance over four years (2018-2021) at ICAR-DOGR. Waterlogging was induced 45-65 days post-transplantation using flood and sprinkler irrigation, following ICAR-DOGR practices.

Of the 100 genotypes screened, Accession 1666 showed 100% survival and complete recovery after waterlogging stress. This genotype showed a 36.2% bulb size reduction compared to control plants and maintained a higher number of leaves, leaf length, and an improved root-shoot ratio, along with less leaf area reduction under waterlogged conditions. Accession 1666 produced larger bulbs than sensitive genotypes and showed a 38.5% yield reduction under waterlogged conditions compared to well-watered conditions during 2018 and 2019 (Gedam *et al.,* 2022). Notably, it achieved 2.27 times higher bulb yield (16.0 t/ha) compared to susceptible checks (4.9 t/ha) under waterlogged conditions (Table 1). Further large-plot evaluations during the monsoon seasons of 2020 and 2021 at ICAR-DOGR, India, confirmed these findings, with Accession 1666 showing only a 16.9% yield reduction under waterlogged conditions compared to well-watered conditions. This genotype exhibited a higher membrane stability index, lower chlorophyll reduction under waterlogging stress, and higher pyruvic acid and antioxidants. Waterlogging tolerance in Accession 1666 was confirmed through transcriptome sequencing studies using waterlogging tolerant and sensitive onion genotypes (Gedam *et al.,* 2023).

References

Gedam PA, DV Shirsat, A Thangasamy, S Ghosh, SJ Gawande, V Mahajan, AJ Gupta and Major Singh (2022) Screening of onion (*Allium cepa* L.) genotypes for waterlogging tolerance. *Front. Plant Sci.* 12: https://doi.org/10.3389/fpls.2021.727262

Table 1: Traits description of Accession 1666: IC No. 594035 (INGR22082)

Parameters	*Acc. 1666*		*Susceptible genotype 1*		*Susceptible genotype 2*	
	Control	*Stress*	*Control*	*Stress*	*Control*	*Stress*
Survival (%)	100	100	100	100	100	100
Recovery (%)	-	100	-	60	-	47
% change in bulb wt.	-	36.2	-	89.4	-	94.4
Plant height (cm)	53.7	50.0	53.3	48.6	51.2	44.6
Leaf area (cm^2)	24.4	22.3	30.9	20.6	25.9	19.5
TSS (%)	13.7	12.8	14.8	12.4	15.0	12.8
Bulb yield (t/ha)	25.1	16.0	20.7	4.9	22.0	4.8

Gedam, PA, K Khandagale, D Shirsat, A Thangasamy, O Kulkarni, A Kulkarni, SS Patil, VT Barvkar, V Mahajan, AJ Gupta and KP Bhagat (2023) Elucidating the molecular responses to waterlogging stress in onion (*Allium cepa* L.) leaf by comparative transcriptome profiling. *Front. Plant Sci.* 14: https://doi.org/10.3389/fpls.2023.1150909.

20. Accession 1656 (IC645763; INGR22083), an onion (*Allium cepa*) germplasm with high drought tolerance efficiency (92.95%)

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Onions are particularly vulnerable to climatic extremes like drought due to their shallow root system. Frequent droughts have caused about a 30% reduction in onion production. To address this issue, developing drought-tolerant onion varieties with adaptive traits is crucial for improving productivity in drought-prone regions. Four hundred ten onion genotypes, including Accession 1656 selected from Accession 1218 (IC No. 571949), were evaluated for drought tolerance by artificially imposing stress through irrigation withholding. Field evaluations of Accession 1656 during 2017-18 and 2018-19 showed better plant height and higher leaf area compared to controls under drought conditions. This genotype exhibited improved physiological and biochemical traits, including higher chlorophyll concentration (6.97 mg/g FW), relative water content (74.57%), membrane stability index (75.86%), and drought tolerance efficiency (92.95%) (Table 1). Additionally, Accession 1656 showed increased TSS, antioxidant activity, total phenol, and pyruvic acid concentrations under drought stress, with only a 7.05% yield reduction compared to well-watered conditions (Gedam *et al.,* 2021). Plant Phenomics study revealed that Accession 1656 showed better performance by maintaining water status and higher water consumption under drought stress, unlike most genotypes that reduced their transpiration rate. Drought tolerance was further validated through RNA Seq analysis, revealing significant differential gene expression in Accession 1656 compared to the drought-sensitive genotype 1627. Specifically, 1189 genes were up-regulated and 1180 down-regulated in Accession 1656, while 872 genes were up-regulated and 1292 down-regulated in 1627. Differential expression was observed in genes related to transcription factors, cytochrome P-450, membrane transporters, flavonoids, and carbohydrate metabolism, confirming the drought tolerance potential of Accession 1656 (Ghodke *et al*., 2020).

References

Gedam PA, A Thangasamy, DV Shirsat, Bhagat KP, Sourav Ghosh, OA Sogam, AJ Gupta, V Mahajan, PS Soumia, NS Vanita, YP Khade, SJ Gawande, PS Hanjagi, R Shiv Ramakrishnan and M Singh (2021) Screening of onion (*Allium cepa* L.) genotypes for drought tolerance using physiological and yield based indices using multivariate analysis. *Front. Plant Sci*. 12: https://doi.org/10.3389/fpls.2021.600371

Ghodke PH, K Khandagale, A Thangasamy, A Kulkarni, N Narwade, DV Shirsat, P Randive, P Roylawar, I Singh, SJ Gawande, V Mahajan, A Solanke, and M Singh (2020) Comparative transcriptome analyses in contrasting onion (*Allium cepa* L.) genotypes for drought stress. *PLoS One.* 15(8):e0237457

Table 1: Traits description of Accession 1656: IC No. 571949

Parameters	*Acc. 1656*		*Sensitive check 1*		*Sensitive check 2*	
	Control	*Drought*	*Control*	*Drought*	*Control*	*Drought*
Leaf area (cm^2)	46.15	39.72	37.84	32.20	45.55	24.74
Chlorophyll (mg/g FW)	8.98	6.97	8.11	3.10	7.86	1.96
Yield (t/ha)	40.49	37.79	38.00	7.61	39.44	7.11
Yield reduction (%)	-	7.05	-	80.04	-	83.1
Drought tolerance efficiency (%)	-	92.95	-	19.96	-	16.89

21. VL In. 31-1A (CMS Female) & VL In. 31-1B (Maintainer) (IC645760 & IC645761; INGR22084), an onion (*Allium cepa*) germplasm with long day/intermediate day length

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Production of hybrid onions became possible with the discovery of male sterile cytoplasm in the onion cultivar 'Italian red' which is conditioned by the sterility inducing cytoplasm (S) and the single nuclear restorer gene in its recessive condition (ms/ms) (Jones and Clarke, 1943). In the CMS-S system, male sterile lines are propagated by crossing with the maintainers possessing N cytoplasm with homozygous recessive alleles at the Ms locus (Jones and Davis, 1944). Development of VL In. 31-1A (Smsms-Female) & VL In. 31-1B (Nmsms-Maintainer) is shown in Table 1.

PCR based markers, 5' cob-based marker amplified 180- bp fragment in N cytoplasm whereas in S cytoplasm amplification of two fragments (180 and 414bp) was used. Another PCR based marker of OPT, linked to the restorer of fertility (Ms) locus (Bang *et al.,* 2011) was used to distinguish fertility restorer (Ms) locus. Fertility/sterility of plants were validated by acetocarmine staining of the pollens and correlated with observations made using molecular markers. Only 7 plants happened to be completely male sterile and single maintainer plant was identified in VL Piaz 3. This is the first example of deploying DNA markers for identification and purification of male sterility and hybrid development in long/ intermediate day length onion in Indian population.

Reference

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Jones HA and G Davis (1944) Inbreeding and heterosis and their relation to the development of new varieties of onions. USDA *Tech. Bull.* 874: 1-28.

Bang H, DY Cho, KS Yoo, MK Yoon, BS Patil and S Kim (2011) Development of simple PCR- based markers linked to the Ms locus, a restorer-of-fertility gene in onion (*Allium cepa* L.). *Euphytica* 179: 439- 449.

Table 1: Development of VL In. 31-1A (Smsms-Female) & VL In. 31-1B (Nmsms-Maintainer)

Segregating population of In. 13 ms/ In. 43 (VLP-3)	*Activities*
During Rabi 2008-11	Crossing between sterile and fertile plants present in the segregating population and maintained
Rabi 2011-12	MAS was practiced and 7 sterile plants (Smsms) and one maintainer (Nmsms) was selected in the population and these 7 plants were maintained with single maintainer plant and single maintainer plant was maintained by selfing.
Rabi 2012-13	Bulb production of sterile (Smsm) and maintainer (Nmsms) plants
Rabi 2013-14	Morphologically simillar palnts were selected in sterile and maintainer population and maintained as mentioned above
Rabi 2014-15	Bulb production of morphologically simillar selected plants of Smsm and Nmsms plants
Rabi 2015-16	Morphologically simillar palnts were selected in sterile and maintainer population and maintained as mentioned above
Rabi 2016-17	Bulb production of morphologically simillar selected plants of Smsm and Nmsms plants
Rabi 2017-18	Morphologically simillar palnts were selected in sterile and maintainer population and maintained as mentioned above

Selected sterile line designated as VL In. 31-1A & maintainer line as VL In. 31-1B

22. ADM/VV-1/ AZMC-1 (IC645771; INGR22085), a cucumber (*Cucumis sativus*) germplasm with high carotenoid content (54.8 µg/g in mature fruits; 8.12 µg/g in tender fruits) and Orange flesh colour

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Cucumber (*Cucumis sativus* L.) is one of the important Cucurbitaceous vegetables consumed throughout the world in salad, cooked and pickle form. Common cucumber varieties have white to greenish flesh and are of low nutritional quality. However, in NE parts of India carotenoid rich cucumber landraces are prevalent and used by the local people as vegetable or in preparation of chutney since a long time. AZMC-1, collected from Aizawl, Mizoram during 2011

is also orange fleshed. AZMC-1 was identified with some unique traits in a segregating form. Desirable plants were selected and maintained through single plant selection for 9 generations. Characterization and evaluation of homozygous families of the germplasm was conducted during 2018-2020. The carotenoid content at physiological maturity stage of this accession was high 54.8 µg/g as compared to 2.53 µg/g in the best check variety Pusa Uday at Delhi conditions (Table 1).

Previously, IC420405 has been registered for high carotenoid content (reg no. INGR18029). However, AZMC-1 has more carotenoid content even at commercial harvest stage (8.12 µg /g) than INGR 18029 (6.07 µg /g) as well as check variety Pusa Uday (2.54 µg /g)

Hence, this line could be directly utilized or could be utilized in breeding programme to develop carotene rich cucumber which in turn will play a significant role in meeting global nutritional security. Since cucumber is cheap and easily available round the year, it can help in reducing vitamin A deficiency in the nutritionally vulnerable group of our population.

Table 1: Trait description of AZMC-1

S. No.	*Trait*	*AZMC-1*	*Check variety (Pusa Uday)*
1.	Vine length (cm)	3.23	2.35
2.	Days to flowering	75	45
3.	Response to day length and temperature	Short day and low temperature for flowering	Day neutral
4.	Node number at which first pistillate flower appear	13.14	8.5
5.	Fruit length (cm)	19.49	13.87
6.	Fruit shape	Oblong	Oblong
7.	Fruit length (cm)	29.78	21.45
8.	Fruit diameter (cm)	6.46	9.54
9.	Seedcavity length (cm)	27.23	19.34
10.	Seedcavity breadth (cm)	5.21	8.24
11.	Fruit weight (g)	469	567
12.	Fruit skin colour (market stage)	Cream	Creamish green
13.	Fruit skin colour (mature stage)	Orange yellow	Brown netted
14.	Tubercle colour	Black	Black
15.	Flesh colour (marketable stage)	Creamish green	Green
16.	Flesh colour (mature stage)	Dark orange	Off white
17.	TSS (^{0} B)	4.4	4.2
18.	Ash (% dw)	9.21	9.13
19.	Total sugar (%)	2.98	1.73
20.	Ascorbic acid (µg/g)	97.8	78.8
21.	Total carotenoid in immature tender fruits (µg/g)	8.12	2.54
22.	Total carotenoid in mature fruits (µg/g)	54.8	2.53

23. VRPLK-2 (IC632944; INGR22086), a spinach (*Beta vulgaris* var. bengalensis) germplasm with delayed bolting habit (16-33 days), faster plant growth (15.4% higher biomass production per cutting) and heat tolerance at 43^{0}C

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Spinach beet or palak [*Beta vulgaris* L. ssp. *vulgaris* var. *cicla* or *Beta vulgaris* L. ssp. *vulgaris* (Cicla Group)] is also known as beet leaf, desi palak or Indian spinach. Spinach beet is an important & nutritious leafy vegetable which provides nature's best nutrition supplement; packed with minerals, vitamins, antioxidants and fibre which are vital components of a healthy & balanced diet to human. Production of spinach beet is constrained by various abiotic factors during off-season such as high temperature, long-day and rainfall, especially in North Indian plains. Once bolting is initiated in spinach beet grown for the tender leaves, it loses its economic value, becoming bitter and hard. The usages of

Table 1: Agronomical and yield traits of 'VRPLK-2' and national check 'All Green' during different seasons (Mean of 2018-19 and 2019-20)

Sowing month	*Variety*	*Marketable biomass*		*Number of cutting*	*Total cropping period (days)*	*Biomass production per cutting(q/ha)*
		Yield (q/ha)	*Increase inyield (%)*			
March to July	All Green	108	-	1.9	53	57
sowing		(86-123)		(1.5-2.0)	(47-61)	(54-62)
(Summer/ rainy	VRPLK-2	192	78.3	2.9	70	66
season crop)		(179-209)	(65.5-112.3)	(2.5-3.0)	(65-76)	(60-73)
August to	All Green	510	-	5.3	101	97
November sowing		(383-620)		(3.5-6.5)	(68-132)	(81-109)
(Autumn/ winter	VRPLK-2	762	49.4	6.3	123	122
season crop)		(570-887)	(42.6-62.9)	(4.5-7.5)	(82-165)	(115-127)
December to	All Green	126	-	1.3	41	94
February sowing		(55-236)		(1-2)	(33-53)	(55-118)
(Spring season crop)	VRPLK-2	211 (136-338)	91.2 (43.1-148.8)	2.3 (2-3)	54 (46-63)	90 (68-113)
Mean of 12	All Green	247	-	2.9	66	78
months sowing		(55-620)				
	VRPLK-2	386	-	3.9	83	90
		(136-887)				
	Overall increase	56.5%	-	34.5%	25.8%	15.4%
		(42.6-148.8%)				

bolting tolerant (delayed bolting habit) and heat tolerant genotypes could be a good choice for round-the-year production of spinach beet.

The ICAR-IIVR, Varanasi, UP has developed a superior genotype of spinach beet i.e. 'VRPLK-2' (IC632944) named as Kashi Baramasi through mass selection from open population of locally collected material (Singh and Singh, 2021) having attractive, smooth and succulent lush-green leaves with entire margin; faster & luxuriant plant growth (produces 15.4% higher biomass per cutting during round the year cropping seasons); delayed bolting habit by 16-33 days (favours 1-2 more number of cuttings during year round sowing); heat tolerance (tolerates average monthly temperature maxima of 39-43 °C during April to June); wider adaptability (suitable for round-the-year sowing i.e. winter, spring, summer, rainy and autumn seasons); and longer cropping period (25.8% higher). The marketable biomass yield potential of VRPLK-2 (Table 1 and Figure 1) is very high i.e. 570-887 q/ha (43-63% higher than national check variety i.e. 'All Green') during August to November sowing (Autumn/Winter crop), 136- 338 q/ha (43-149% higher than national check variety i.e. 'All Green') during December to February sowing (Spring crop); and 179-209 q/ha (65-112% higher than national check variety i.e. 'All Green') during March to July sowing (Summer/Rainy crop). In conclusion, the higher biomass yield potential, delayed-bolting habit, heat tolerance, faster plant growth, more number of cutting, longer cropping period and wider adaptability to different growing conditions/seasons for genotype VRPLK-2 make it a unique genotype whose genetic potential could be utilized in breeding programmes to widen the genetic variability towards delayed bolting habit, heat tolerance and to increase the genotypic adaptability in varied climates.

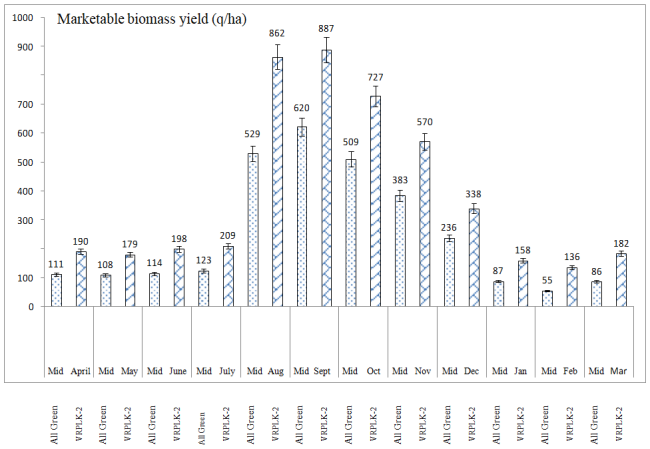

Figure 1: Marketable biomass yield (q/ha) of 'VRPLK-2' and national check 'All Green' (Round the year sowing); (Mean of 2018-19 and 2019-20)

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24. VRPE-29 (IC642307; INGR22087), an extra early pea (*Pisum sativum* subsp. hortense) germplasm with synchronous maturity suitable for mechanical harvesting and multiple cropping

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Early maturing peas are most preferred by the farmers/ consumers owing to their high economic return and quality. VRPE-29 (IC0642307) has been developed through pedigree selection (PM-5 × Ageta). VRPE-29 is a determinate (height 60cm) and an extra early (DTF≤32 days) genotype of vegetable peas that bears 10-12, slightly curved, dark green pods of 8-8.5cm long, pod width of 1.5cm, pod weight of 8-9.5g, 100-green seed weight of 54g, shelling percentage of 50% and yield potential of 90-100 q/ha (Table 1). For green pods, crop is over within 60-65 days with its suitability for single picking due to synchronous maturity of the crop. Seeds are dimpled in shape, remain green on seed maturity with 1000-seed weight of 243g (dry). Due to earliness, it also escapes the major pea disease like powdery mildew and rust. It can also easily fit in to various cropping sequences (where gap between two main crops is between 2-3 months), and especially suitable for rice-wheat cropping sequence of the Indo-Gangetic region.

Table 1: DUS characterization of VRPE-29 **(**IC0642307) as per the guidelines provided by Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA) Government of India

S. No.	*DUS type of assessment*	*DUS Characteristics*	*VRPE-29 (IC0642307)*
1.	VS	Stem: Anthocyanin colouration	Absent
2.	VG	Foliage: colour	Dark Green
3.	VG	Foliage: waxy bloom	Present
4.	VG	Leaf: leaflets	Present
5.	VS	Leaf: axil colour	Green
6.	VG	Stipule: rabbit eared stipules	Present
7.	VG	Stipule: type	Normal
8.	VG	Flower: opening (days)	Extra Early
9.	VG	Flower: standard petal colour	White
10.	VS	Pod: number/axil	Double (mostly)
11.	VG	Pod: curvature	Medium
12.	VS	Pod: shape of distal part	Pointed
13.	VG	Pod: intensity of green colour	Green
14.	MS	Plant: height	Short (≤60cm)
15.	VG	Seed: shape	Dimpled
16.	VG	Seed: surface	Curved
17.	VG	Seed: cotyledon colour	Green
18.	MG	Seed: weight of 1000-seed	243g (dry seeds)
19.	VG	Seed: testa mottling	Absent
20.	VG	Seed: parchment	Absent

MG: Measurement by a single observation of a group of plants or parts of plants
MS: Measurement of a number of individual plants or parts of plants
VG: Visual assessment by a single observation of a group of plants or parts of plants
VS: Visual assessment by observation of individual plants or parts of plants
* Intensity of color measured by Royal Horticultural Society Color Charts (1804)

25. VRCAR-252 (A-line) & Kashi Krishna (B-line) (IC623130 & IC642961; INGR22088), black carrot (*Daucus carota*) germplasm with better heterotic potential for root yield, high anthocyanin (278 mg/100 g FW) & phenolics (323 mg GAE/100 g FW) content and greater antioxidative ability (FRAP value of 47 µmol TE/g FW)

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The cultivated carrot (*Daucus carota* subsp. *sativus*), on the basis of presence of root pigments, is broadly classified into two groups *i.e.* Carotenoid group (Orange, Red and Yellow carrot) and anthocyanin/purple group (Black and Rainbow carrot); and have commercial significance globally. Black carrot is very much suitable for healthy salad; preparations of sweets, fresh & fermented juice and purple tea; and pharmaceutical & nutraceutical uses as protective food supplements, healthy food colorants & cosmetics. The role of cytoplasmic male sterility (CMS) in development & cost-effective seed-multiplication of F_1 hybrids is well known. VRCAR-252 (A-Line, IC642961), a petaloid-CMS line was developed by crossing naturally occurring CMS plant in an open-pollinated population having orangish-red coloured root with a black carrot variety Kashi Krishna (VRCAR-126). CMS line VRCAR-252 (A-Line, IC642961) is very uniform to its maintainer Kashi Krishna (B-Line or Maintainer Line, IC623130) for leaf & root morphology (BC_5F_1 stage & onwards), and have better heterotic potential for root yield, uniformity and anthocynins content.

The qualitative traits of CMS line VRCAR-252 and its maintainer Kashi Krishna are uniform such as black coloured root & core, purplish-green coloured leaf, purple coloured petiole, root shape of Danvers type (Tapering), bears purplish-white flowers in umbel and ready to seed harvest in about 4.5 months after transplanting of stecklings. Moreover, the quantitative traits (pooled values for 2019-20 & 2020-21) of CMS line VRCAR-252 and its maintainer Kashi Krishna was statistically at par for gross plant weight (165.3 & 160.4 g, respectively), root length (23.9 & 23.4 cm, respectively), root weight (115.6 & 108.7 g, respectively), shoulder diameter (4.57 & 4.35 cm, respectively), root yield potential (276 & 265 q/ha), days to 50% flowering (62.4 & 55.2 day, respectively), plant height at flowering (125.6 & 128.5 cm, respectively), anthocyanins content (278 & 282 mg/100 g FW, respectively), phenolics content (323 & 311 mg GAE/100 g FW, respectively) and flavonoids content (143 & 140 mg CE/100 g FW, respectively); having better anthocyanin yield potential (67 & 69 kg/ha, respectively); and greater anti-oxidative ability (FRAP value of 47 & 44 µmol TE/g FW, respectively).

In conclusion, hybrid breeding by utilizing black coloured CMS line VRCAR-252 would be very effective in harnessing heterotic potential and thereby increasing the root yield, uniformity for root morphology & maturity, anthocyanins content (colour intensity), anti-oxidative ability, and cost- effective commercial hybrid seed production of carrot.

26. DRMR 2017-26 (IC645773; INGR22089), an Indian mustard (*Brassica juncea*) germplasm with high temperature tolerance at seedling stage coupled with high seed and oil yield (41%)

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Indian mustard (*Brassica juncea*) is an important oilseed crop grown in tropical and subtropical regions as a winter crop. An optimum temperature around 25°C is required for proper germination and seedling establishment in mustard crop. However, due to changing climatic conditions the temperatures during last many years crossed this limit in major mustard areas and soil temperature reaches up to 40-42°C affecting germination and plant stand in the field. This prevents early sowing, generally on conserved moistures recommended in many areas. Therefore, it is highly needed to have germplasm lines with heat tolerance at seedling stage and will be utilized in breeding programmes.

The genotype DRMR 2017-26 was derived from a cross between NRCHB 101 × DRMR 2269 at ICAR-DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising for thermo tolerance at seedling stage coupled with high seed & oil yield and suitable for early sown conditions. The genotype was tested three years under AICRP-RM plant physiological trials during 2018-19 to 2020-21 at 8 locations (environments) and plant breeding trials during 2018-19 at 9 locations in 2 major mustard

growing zones II & III covering Rajasthan, Haryana, Delhi, Jammu, UP and parts of MP and Bihar. Pooled summary over the years and locations indicates that proposed genotype DRMR 2017-26 has less seedling mortality (22.6%), high RWC (73.0%), dry seedling weight (6.3g), SPAD values (chlorophyll), along with high seed & oil yield as compared to heat tolerant (seedling stage) checks PM 25 and JD 6 (Table 1). Proposed genotype DRMR 2017-26 has 8.3 to 10.3% higher oil yield and 7.3 to 9.5% higher seed yield over the checks. This indicates thermo tolerant (at seedling stage) characteristics of DRMR 2017-26 and it can be utilized in breeding programmes for development of high-yielding thermo (heat) tolerant varieties with high seed and oil yield, as it has better yield traits.

Table 1: Pooled summary of physiological parameters (thermo tolerance) and performance for seed & oil yield and contributing traits of proposed genetic stock DRMR 2017-26 and checks under AICRP-RM trials during 2018-19 to 2020-21

Parameters	*No. of locations*	*DRMR 2017-26*	**Check varieties*	
			PM 25	*JD 6*
Seedling mortality (%)	8	22.6	22.6	27.5
Dry weight (g) of 10 seedlings	8	6.3	6.0	4.8
SPAD values (Chlorophyll content)	8	41.6	42.4	40.0
Relative water content (%)	8	73.0	72.2	66.0
Seed yield (kg/ha)	9	2029	1891	1859
Oil yield (kg/ha)	9	834	770	756
1000 Seed weight (g)	9	4.8	4.6	4.4
Oil content (%)	9	41.0	40.7	40.7
Days to maturity	9	121	116	127

* High temperature tolerant (at seedling stage) check genotypes

27. R6 (IC643978; INGR22090), a sesame (*Sesamum* sp.) germplasm with high lignan content (sesamin 61.2 ug/ml; sesamol 15.1 ug/ml); high oil content (52.9% w/w) and tolerance to charcoal rot

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The presence of lignans (sesamin, sesamol) adds pharmaceutical value to the sesame oil. The inter-specific hybrid sesame germplasm, which we developed, is a novel one containing high lignan (sesamin 61.2 ± 1.0 µg/µl, sesamol 15.1 ± 0.6 µg/µl) in its oil (52.9 ± 1.4 % w/w). The Indian high-yielding cultivar of *Sesamum indicum* L. (IC131989 from MP, NBPGR germplasm collection) was the female parent for the hybridization programme (sesamin 20.3 ± 0.8 µg/µl, sesamol 5.3 ± 0.2 µg/µl, oil 54.5 ± 2.3 % w/w). The male parent was wild sesame, *Sesamum mulayanum Nair*. Though the wild is less oil-yielding (36.3 ± 1.4 % w/w), it contains remarkably higher lignan (sesamin 69.0 ± 2.8 µg/µl, sesamol 17.1 ± 0.6 µg/µl) in oil. We performed the hybridization in controlled net house conditions in 2013 in the experimental farm of Bose Institute at Madhyamgram, WB. The breeding method used is pedigree selection. We adopted a combination of seed phenomics and EST-SSR analysis to select the putative hybrids in the F_2 generation. Considering sesamin synthase as a candidate gene, we found a correlation between its expression through qRT-PCR and sesamin content through HPLC analysis (Dutta *et al.,* 2021a).

Besides maintaining the lines at the Bose Institute's experimental farm, we have cultivated this hybrid successfully in the farmers' field of Panskura, West Medinipur of West Bengal, from 2019 to 2024. Similar to *S. mulayanum,* this inter-specific hybrid is tolerant to charcoal rot of sesame seedlings. We have performed a controlled inoculation experiment with *Macrophomina phaseolina*, the causal organism of charcoal rot. *S. mulayanum* showed a high disease tolerance with the lowest disease index score (25%), followed by the recombinant (32%). On the contrary, the cultivated sesame *S. indicum* exhibited a high (92%) disease index score (Dutta *et al.,* 2021b).

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28. EC34372 (EC34372; INGR22091), a soybean (*Glycine max*) germplasm with Anthracnose resistance and early maturity possessing rare alleles for genes of early maturity (*e2, e3, e4* and *e9*)

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Soybean anthracnose disease is caused by *Colletotrichum truncatum* (Schw.) Andrus &W.D. Moore leading to 16-25% yield loss. Central India is a hub for soybean cultivation and farmers prefer early maturing (~90 days) soybean cultivars to adopt soybean-wheat cropping system (Kumawat *et al.,* 2020). Congenial environment for anthracnose disease incidence coincides with the pod filling stage resulting in significant yield loss in susceptible cultivars. Therefore, anthracnose disease is regarded as one of the important and economical soybean diseases in India (Nataraj *et al.,* 2020).

During *Kharif* 2018, a total of 230 soybean germplasm lines have been screened for anthracnose resistance under hot-spot field conditions at ICAR-IISR, Indore. Out of them, genotypes, EC 34372, EC 457254, EC 538828 and Karune were found to be highly resistant while genotypes JS 95-60, Shivalik and IC15089 were found to be highly susceptible. During 2019, genetics of anthracnose resistance in EC 34372 has been carried out under hot-spot field conditions. An F_2 population (EC 34372 (R) × JS 95-60 (S), N=487) along with respective parents were sown in a plot having history of anthracnose disease incidence at ICAR-IISR, Indore. Highly susceptible genotypes viz., JS 95-60, IC 15089 and EC 572136 were sown in regular intervals so as to act as infectors to increase the disease severity and to avoid disease escape. The $\chi^2_{(9:7)}$ test indicated that the mode of inheritance of anthracnose resistance in EC 34372 was through complimentary gene interaction (Nataraj *et al.,* 2020). Resistance disease reaction on EC 34372 was also confirmed during the year 2020 (Annual Report 2020). Furthermore, this genotype is early maturing (88 days) and molecular characterization has been carried out for the traits early maturity and photoperiod response genes which identified high level of genetic variation in tested genes (Kumawat *et al.,* 2020). Out of six genes tested for early maturity and photoperiod response (*E1, E2, E3, E4, E9* and *E10*), four had shown rare alleles (*e2, e3, e4* and *e9*). Therefore, this genotype is a potential and stable resistance donor that can be employed in breeding for early maturity and anthracnose resistance. Also, this genotype can be used to map genes governing resistance for their further transfer in susceptible varieties through marker assisted selection. Details of salient characteristics/chief botanical and morpho-agronomical description of EC34372 have been presented in Table 1.

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Table 1: Salient characteristics/chief botanical and morpho-agronomical description of soybean genotype EC34372

S. No.	*Trait*	*Value*	*S. No.*	*Trait*	*Value*
1.	Hypocotyl pigment	Present (Purple)	15.	Early Plant Vigour	Very good
2.	Leaf color	Dark green	16.	Leaf Shape	Pointed ovate
3.	Number of leaflets	3	17.	Stem determination	Determinate
4.	Flower Colour	Purple	18.	Yield/ plant	20.0 g
5.	Pubescence	Present	19.	Pubescence color	Tawny
6.	Pubescence density	Dense	20.	Pubescence density	Normal
7.	Seed Colour	Yellow	21.	Hilum colour	Brown
8.	Plant height	41.0 cm	22.	Days to flower	30
9.	100-seed weight	12.0 g	23.	Days to maturity	88
10.	Cotyledon colour	Green	24.	Seed coat colour	Yellow
11.	Seed Coat Pattern	Uniform	25.	Lodging score	0
12.	Surface lustre	Shiny	26.	Primary branches/plant	3
13.	Pod Colour		27.	No. of nodes / plant	4
14.	Pods/plant	35	28.		

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29. Acc 562 (IC645756; INGR22092), a nutmeg (*Myristica fragrans*) germplasm with monoecious fruits borne in clusters of 2 to 7

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Nutmeg (*Myristica fragrans* Houtt.) is an evergreen, dioecious perennial tree spice that produces two distinctly different spices *viz*. nut and mace from the fruit. The tree is usually dioecious in nature bearing either male or female flowers. Very large variability is seen in the seedling population of this widely cross pollinated crop. Rarely monoecious trees which bear both male and female flowers on the same tree do exists in this population.

During a germplasm survey to Karnataka, 30 seedlings of nutmeg were purchased from the nutmeg plantation maintained by Mr. Poornand Venkatesh Bhat, Shriram Siddhi Estate, Ankola, Karwar, Uttarakand, Karnataka during 2012. The seedlings were germinated in bag during 2012. Twelve seedling of one-year-old were planted in the field in the nutmeg conservatory at ICAR-IISR, Kozhikode in 2013.

It was observed that one of the seedlings, Acc. 562 was precocious in nature and flowered in the second year of planting in 2015. Usually the seedling trees of nutmeg flower after 6 to 7 years of planting making Acc 562 different from other nutmeg trees conserved in the germplasm conservatory at IISR. Acc. 562 is monoecious in nature and both male female and rarely hermaphrodite flowers were seen in the tree and the flowers were borne in clusters. Generally while planting nutmeg male trees also has to be planted in the ratio 1:15 for pollination. As Acc.562 is monoecious in nature, male and female flowers are seen on the same plant there is no need for planting male trees and hence more number of trees can be accommodated per unit area.

The tree is about 6 feet tall during the sixth year and has drooping plagiotropic branches. The tree flowered in the second year of planting and 11 fruits were obtained. The number of fruits increased every year with the growth of the tree. Fruits are borne singly as well as in clusters up to 7. About 400 fruits were obtained in the 6 th year of planting. The fresh fruits weigh about 65 to 75 g, nut 8 -10 g and mace 1.5 to 2 g. The seed is brownish black and medium sized and mace entire.

30. TRA-1 (CIARI-Samridhi) (IC0590905; INGR22093), a noni (*Morinda citrifolia*) germplasm with small fruit (55-60 g), more number of fruits and dwarf stature (1.7-2.5 m)

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Noni (*Morinda citrifolia* L.; Family: Rubiaceae) is a source ingredient in traditional medicine system such as Ayurveda, Chinese, Polynesian, Australian and Nicobari traditional medicinal systems for curing of various ailments including arthritis, colds, diabetes, inflammation and pain. It appears to be 'natural reservoir of bioactives' because more than 200 bioactive compounds have been reported including anthraquinones, flavonoids, polysaccharides, glycosides, iridoids, lignins and triterpenoids (Chan *et al*., 2006). Almost all parts of Noni plants are useful for medicinal or industrial purpose but fruits are most commonly used for pulp and juice extraction (Singh *et al*., 2012). It is well suited potential crop for tropical coastal and island regions and Noni juice has huge potential as health supplement in national and international markets (West *et al.,* 2018). To explore its commercial potential, it was required to develop genotype(s) which can grow well in open as well as under partial shade condition (in coconut, arecanut plantations) and suitable for high density planting. Its intercropping in existing coconut and arecanut plantations will increase

income from same piece of land and fit well with 'zero land 'cultivation.

The Noni genotype 'TRA-1' is developed by selection from local collection for higher juice recovery, small fruits and dwarf statured bush type plants. These are well suited for high density plants at 2.5 x 2.5 m distance as compared to 4.0-5.0 x 4.0-5.0 m for normal growing genotypes. It can tolerate partial shade condition hence, fits well for growing in coconut and areacnut plantations without compromising yield levels. TRA-1 bears fruits year round and maintains around 38.46 % higher yield level than earlier identified genetic stock 'CIARI-1'. The fresh juice recovery from TRA-1 fruits was observed to be 67.72% by standard juice extraction method. Total soluble solids content in juice was 9.5 °Brix which was significantly higher than CARI-1 (5.8 °Brix). It was found to be rich in polyphenol, flavonoid (614.0 mg/100 g), tannin (390.6 mg/100 g), ascorbic acid (93.5 mg/100g) with high DPPH antioxidant activity (82.4 %). The TRA-1 seeds contain 17.60% oil. The GC-MS analysis its seed oil reveled that essential fatty acids i.e. linoleic acid and oleic acid are highest in TRA-1 among the available 33 genotypes.

Hence, the TRA-1 has potential for immediate use for (i) commercial cultivation in open or as intercrop in coconut and arecanut plantations, (ii) tap the nutritive and fatty acids potential in developing better health refreshing products and (iii) also in breeding and genetic studies for fruit size, juice recovery level and phytochemeicals in noni.

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31. ML-2 (IC0594046; INGR22094), a mango (*Mangifera indica*) germplasm with polyembryony and Salt tolerance

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Salt toxicity is a major productivity constraint which limits cultivation of several fruit crops including mango. Development of rootstock tolerant to salinity and sodicity is the only alternative approach to establish the crop in the salt affected soils. The mango rootstock '13-1' is a promising salt tolerant polyembryonic type developed in Israel in 1984. Indian workers have earlier reported the salt tolerance phenomenon in Karukkan and Olour rootstocks but the field level sustenance under high pH and Ec was still a challenge expecting for 13-1.

Mango, being cross pollinated nature exhibits higher heterozygosis in seedling progenies developed from fertilized ovule (monoembryony). Therefore, there is a need to develop true to type polyembryonic rootstocks. Intensive survey in the Andaman and Nicobar Islands after the post tsunami sea water inundations resulted in the collection of 33 accessions among which 15 were polyembryonic. Screening the polyembryonic accessions in pots revealed six accessions possessing moderate to high tolerance to salinity. Further screening six accessions in sodic soils under field conditions for five years resulted in identification of the accessions ML-2 and ML-6 for their salt tolerant trait. The accessions ML-2 and ML-6 showed high tolerance to sodicity exhibiting significantly higher survival rate and plant height and yield than the others used in the study (Table 1).

Furthermore, the study emphasized with the finding that

Table 1: Plant height (cm) of ML-2 in sodic conditions

Accessions	*At planting*	*1st YAP**	*2nd YAP**	*3rdYAP**	*4th YAP*	*5th YAP*
ML-2	31.51	76.00	111.00	164.00	210.00	245.00
ML-3	30.00	33.83	0.00	0.00	0.00	0.00
ML-6	28.00	108.80	125.67	190.00	245.00	270.00
GPL-1	29.83	32.66	0.00	0.00	0.00	0.00
GPL-3	29.00	32.00	0.00	0.00	0.00	0.00
GPL-4	28.00	30.00	0.00	0.00	0.00	0.00
A13-1	29.00	62.67	106.00	130.00	184.00	265.00

the tolerant accessions (ML-2 and ML-6) possessed higher K+ ions accumulating ability in their leaves and meristem tips that caused significant reduction in Na^+/ K^+ ratio (Table 2). Moreover, high proline and much activated antioxidant enzyme activity of the tolerant accessions confirmed the role of antioxidants in imparting tolerance to salt stress. Though 13-1 was observed to explicit sodicity tolerance, the poor fruit set percentage of this cultivar under sub-continent conditions as reported earlier limited its utility in this region. Thus, the accessions ML-2 and ML-6 can be considered as better sodicity tolerant polyembryony rootstocks of mango for the tropics and sub-tropics than 13-1.

The rootstocks ML-2 and ML-6 exhibited the salt tolerant trait along with comparatively higher fruit yield than the standard check 13-1 in the soil of pH ranging from 8.15 to 9.39.

Table 2: Mean soil properties of the CSSRI, experimental field of sodic soil used for screening located at Lucknow, Uttar Pradesh

Soil Depth (cm)	*pH*	*Ec*	*SodiumMeq/l*	*Carbonate Meq/l*	*Bicarbonate Meq/l*	*Ca Meq/l*	*Mg Meq/l*	*SAR*
0-15	9.13 (±0.19)	0.686 (±0.104)	7.38 (±0.79)	4.00 (±0.50)	0.00 (±0.00)	1.50 q(±0.50)	0.00 (±0.00)	8.52 (±0.90)
15-30	9.49 (±0.16)	0.748 (±0.026)	10.47 (±0.72)	3.5 (±0.30)	2.00 (±0.50)	1.00 (±0.20)	0.00 (±0.00)	14.81 (±0.84)
30-60	9.9 (±0.18)	0.834 (±0.029)	11.3 (±0.60)	3.00 (±0.50)	1.00 (±0.50)	1.00 (±0.400)	0.00 (±0.00)	15.98 (±0.98)

Values in the parentheses indicate the standard deviation of the replicates with the mean

32. CHES R-31 (IC642756; INGR22095), a rambutan (*Nephelium lappaceum*) germplasm with yellow colour fruit, greater number of fruits per bunch (15-20 fruits/ Bunch) and medium fruit size.

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Rambutan (*Nephelium lappaceum* var. *lappaceum* L.) is the native of Malaysia and Indonesia and belongs to family of Sapindaceae. The cultivation of Rambutan is spread over all tropical counties. Indonesia and Malaysia contribute more than 95% of total Rambutan production in the world. In India, Rambutan was introduced as a homestead garden in Kerala and slowly it became popular and the area is rapidly increasing in part of Kerala, Karnataka and Tamil Nadu (Tripathi *et al*, 2014; 2020). Rambutan is one of the emerging underutilized fruits with high global demand.

A large collection of rambutan variability was made at Central Horticultural Experiment Station (IIHR), Chettalli, Karnataka during 2001-12. 37 collections of rambutan planted in 2001 were evaluated for growth, flowering and fruiting characters during 2007-12. There was lot of variability in these collections with respect to fruit, fruits size, fruit colour and fruit quality parameters. The growth data reveled that plant height ranged from 2.90 m in CHESR-24 to 6.30 m in CHESR-28. The yield data revealed that highest yield was recorded in CHESR-26 (48.8 Kg.) while CHESR-33 registered the minimum yield of 2.77 Kg. The higher fruit weight recorded in CHESR-27 (44.2 g), whereas, CHESR-156 recorded the lowest fruit weight of 16.5 g. Most these collections were of red colour fruits, only few collections were yellow colour. Among the yellow colour collections, CHESR-31 were found superior than other accessions. The trees of this collection are semi spreading with plant height (5.80 m), Tree Spread (3.49m^2) and Tree volume (35.06m^3) and regular bearer. It is a mid-season variety which flowers in February to April and fruits ripe in October under Chettalli

Table 1: Yield and proximate analysis of Rambutan selection- CHESR-31 (IC642756)

Tree age (years)	*No. of Fruits/ Plant*	*Yield (kg/tree*	*Fruit Weight (g)*	*Fruit Length (cm)*	*Fruit Breadth (cm)*	*Fruit Volume (cc)*	*Pulp Content (%)*	*Peel Content (%)*	*Seed Content (%)*	*TSS (°B)*	*Acidity (%)*	*Vit.- C (mg/100g)*
8	735	17.42	23.70	4.10	3.40	21.40	49.62	43.50	6.88	17.90	0.60	48.60
9	1659	41.31	24.90	4.42	3.15	24.30	52.89	38.51	8.60	18.40	0.48	51.92
10	429	9.93	23.83	4.06	3.14	21.91	51.226	41.03	7.72	17.52	0.56	48.25
11	1700	37.23	21.90	4.50	3.00	22.10	48.40	45.21	6.39	18.10	0.40	49.90
12	1259	21.3	22.9	4.28	3.05	21.7	51.2	41.2	7.6	19.2	0.39	41.2
Average	1156.40	25.44	23.45	4.27	3.15	22.28	50.67	41.89	7.44	18.22	0.49	47.97

(Coorg) conditions. Fruits are yellow in colour. Fruit weight is about 23.45g which is higher than average weight of yellow colour rambutan lines. The aril is white and juicy sweet. Fruit has Total soluble solids content (18.22^{O}Brix), acidity (0.08%) and vitamin C (4797 mg /100 g pulp). ((Tripathi *et al*., 2014; 2020; Table 1).

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33. VL 360 (IC640694; INGR22096), a white grained finger millet (*Eleusine coracana*) germplasm with early maturity (100 days) trait

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Finger millet grains are in general dark brown in colour due to high levels of tannins and phenolics. The dark colour of grains has been the major hindrance for its acceptability in baking and food industry (Sharathbabu *et al*., 2008). Sometimes the high amount of tannins and phenolics provide bitter taste to the value added products thereby reducing their consumer acceptability. To overcome this few white grain mutant genotypes were developed but these genotypes were very late in maturity thereby reducing their farmer's acceptability especially in North western Himalayan region (Sood *et al*., 2019). Early maturity (≤100 days) is one of the most important breeding targets in finger millet breeding as the crop occupies dryland areas where the growth period is mostly limited due to less availability of water for the crop.

VL 360 is an elite early maturing (100 days) finger millet genotype developed from a cross between WR2 (late maturing white seeded genotype) and VL 201 (Early maturing brown seeded released variety) followed by pedigree selection (Anonymous 2010). The major emphasis was to select early maturing white seeded genotype suitable for hills and areas where growth period is limited for the crop due to water stress conditions. This genotype (VL 360) was early in maturity (100 days) among all white seeded genotypes developed across country and evaluated in multi- location trial conducted in six locations in the year 2010 by project coordinating unit (Anonymous 2010). The genotype was again evaluated at Almora location in white seeded finger millet station trial in 2011and found to be earliest in maturity (97 days) among all white genotypes. It is 16 days earlier in maturity than the white parental line WR2 from which it has been derived.

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34. Somatic hybrid (H1* B. j. cv NPJ- 212) (IC645757; INGR22097), an Indian mustard (*Brassica juncea*) germplasm with resistance against *Alternaria brassica*; short height and less duration than its parent

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Alternaria blight is the most devastating disease not only in India but all 53 countries where cultivation of Brassica for oilseeds and vegetables occurs. Alternaria blight is caused by *A. brassicae* in oil seeds and *A. brassicicola* in vegetables. The resistance source for Alternaria blight is unavailable within the cultivated Brassicas. Therefore, the introgression of resistance for this disease from allied genera is the only way to develop resistant germplasm. However, the stability and fertility of the inter-generic hybrids are major concerns. *Sinapis alba* was reported to possess resistance for Alternaria blight, Sclerotinia stem rot (Kumari *et al*., 2020c), high temperature, With the aim of introgression of the genes responsible for Alternaria blight, *Sclerotinia* stem rot resistance, and high-temperature tolerance, the first stable and fertile somatic hybrid of *B. juncea* and *S. alba* has been developed through PEG mediated protoplast fusion. This allohexaploid Brassica (H1) was registered in the NBPGR genebank with the potential of a high degree of

resistance to *brassicae*, *Sclerotinia sclerotiorum*, and thermos tolerance.Kumari and Bhat 2019), However, along with these agronomically important traits, the yield potential was inferior as compared to the cultivated parent (*B. juncea* cv. RLM-198) while the plant height, biomass, and crop duration increased. Therefore, the back crossing was done with the high yielding and short height variety of *B. juncea cv.* NPJ-212 as a pollen donor. Therefore, the pedigree of the genetic stock is (*B. juncea cv.* RLM-198 + *S. alba*) x *B. juncea cv.*NPJ- 212. The BC1F2 progeny of the H1 somatic hybrid has an average height of 198 cm, their leaves attained the lyrate shape. These plants attained 15days early flowering than the BC1F1 progenies obtained after being backcrossed with *juncea* cv. RLM-198and 25 days than the somatic hybrid (H1) while the siliqua attained the length of 3.51cm and13 seeds per silique in comparison to (H1) which 3.11cm siliqua length and approx 7 seeds/ siliquae. However, the seed size is smaller than the H1 allohexaploid Brassica. This genetic stock has revealed 48 chromosomes in their somatic tissues out of them, 36 chromosomes were acquired from *B. juncea* and another 12 chromosomes from *S. alba* proved through genomic *in-situ* hybridization (GISH) probed with fluorescein isothiocyanate (FITC) labeled *S. alba* genome. The meiotic analysis reveals 24 pairs and none of the univalent or multivalent was seen during the study. This genetic stock was screened for the *Alternaria* blight resistance for three consecutive years in three different environments including two off seasons and at the hot-spot for the disease and found resistant over their cultivated parents *B. juncea* (cv. RLM- 198 and NPJ-212) and *S. alba*. Interestingly, the resistance against the *A. brassicae* was revealed by the BC1F2 progeny as similar as shown by the H1 somatic hybrid. Therefore, the subsequent progenies of the BC1 are the valuable genetic stock and have suitable agronomical traits for resistance breeding.

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35. Somatic hybrid (H2*B. j. cv NPJ- 212) (IC645758; INGR22098), an Indian mustard (*Brassica juncea*) germplasm with resistance to *Alternaria brassicae*; higher yield, short height and duration than the H2

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The inter-generic hybridizations were not successful in Brassicas due to pre and post-fertilization barriers. Therefore, somatic hybridization was reported frequently within crop Brassicas and their allied genera with the aim of introgression of several agronomic importance characters (*Kirti et al.,* 1992). Although the fertility of these somatic hybrids and their backcrossed progenies were not recovered due to abnormal Meiosis, but a few workers successfully recovered the back crossed generations and introgressed some agronomical importance traits from wild to cultivated *Brassica* (Singh *et al.,*2021). This allohexaploid Brassica (H2) was registered in the NBPGR gene bank with the potential of a high degree of resistance to *A. Brassicae* and very high-temperature tolerance at the time of seed settings. However, along with these agronomical importance traits the yield potential was inferior as compared to the cultivated parent (*B. juncea cv.* RLM-198). Therefore, we backcrossed the somatic hybrid (H2) with the cultivated variety of *B. juncea* cv.NPJ-212 using as a pollen donor. Thus, the pedigree of the genetic stock is (*B. junceacv.* RLM-198+*S.alba*) x *B. juncea cv.* NPJ- 212. The viability of the recovered seed was found very good (Kumari and Bhat, 2021). The plant height was recorded decreased (176.33cm) while the attained the flowering at the age of 70 days in comparison to somatic hybrids (291.80cm) and 86 days respectively. Similarly, the siliqua beak length also decreased from 1.12 mm in the H2 and 0.87cm in BC1F2. However, the average siliqua length and the number of seeds/siliqua were increased (4.47cm and 16.68) in comparison to the H2 (3.16cm, 6.40). In the same way the crop duration also decreased as compared to H2. These plants carried 48 somatic chromosomes, out of them 36 acquired from the cultivated parent *B. juncea* and another 12 from donor *S. alba*. Interestingly, we have observed the 24 pairs at the meiosis. The first backcrossed generation of the allohexaploid (H2) carries the recombinant mitochondria of *B. juncea* and *S. alba* with chloroplast of the cultivated parent with a high degree of fertility and stability (Kumari and Bhat, 2021). However, these plants showed the same degree of resistance as well as the Allohexaploid (H2) for the *A. brassicae* during the *In-vitro* and *in-vivo* screeningwith a highly virulent strain of *A. Brassicae* for three subsequent years and three different environments including the hotspot conditions to the diseases. The plants attained flowering when the ambient day temperature exceeded

28°C. Therefore, these plants were fit for late sown in mid-November and could attain flowering at the age of ~70 days in February's first week.

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36. DRMR 2018-27 (IC645774; INGR22099), an Indian mustard (*Brassica juncea*) germplasm with high temperature and moisture stress tolerance at seedling stage

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Indian mustard (*Brassica juncea* L.) is an important oilseed crop of India. It is major source of income especially for marginal and small farmers in rainfed areas of 7 states. Under rainfed conditions, early sowing of the crop helps to harvest maximum monsoon rain water. The crop inevitably suffers from moisture stress (drought) during reproductive period when stored water becomes depleted. This leads to a heavy loss of seed yield during severe conditions Germplasm with heat tolerance at seedling stage and a good source of moisture stress tolerance which can be utilized in breeding programmes for development high-yielding thermo and drought-tolerant varieties is the need of the hour. The genotype DRMR 2018-27 was derived from a cross between NRCHB 101 x DRMR 2398 at ICAR-DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising under moisture stress conditions as well as high temperature tolerant (seedling stage) under early sowing. The genotype was tested under AICRP-RM plant physiological trials during 2019-20 and

Table 1: Pooled summary of parameters for thermo (seedling stage) and moisture stress tolerance of proposed genetic stock DRMR 2018-27 and checks in physiological trials for during 2019-20 & 2020-21

Parameter		*No. of locations*	*DRMR 2018-27*	**Check varieties*	
(A) Thermo tolerance at seedling stage				*PM 25*	*JD 6*
Seedling mortality (%)	Controlled condition	7	32.9	39.1	40.4
	Field condition	5	22.9	24.2	24.1
Dry weight of 10 seedlings	Controlled condition (mg)	7	39.4	37.9	32.7
	Field condition (g)	5	5.3	6.4	5.4
SPAD values (Chlorophyll)		4	41.2	44.1	42.9
Relative water content (%)		5	72.0	72.2	65.9
(B) Moisture stress (drought) tolerance				RH 725	RGN 229
Relative water content (Reduction %)		6	13.2	16.9	14.2
SPAD Values (Reduction %)		6	13.4	14.1	9.7
Total Chlorophyll (Reduction %)		3	11.9	20.9	18.9
Carotenoids (Reduction %)		2	2.7	16.2	17.0
Seed yield (Reduction %)		7	26.1	24.3	18.3
1000 seed weight (Reduction %)		6	10.9	16.5	9.3
Drought Susceptibility Index (DSI)		6	1.05	1.05	1.01
Yield Stability Index (YSI)		7	0.74	0.75	0.81
No. of siliquae on main shoot (Reduction %)		5	14.8	10.7	9.6
Seeds/siliqua (Reduction %)		6	11.9	11.7	12.2
Oil content (Reduction %)		4	1.04	2.28	1.32
Biological yield (Reduction %)		7	23.2	24.6	26.0

*Tolerant checks: PM 25 & JD 6 for high temperature (seedling stage) and RH 725 and RGN 229 moisture stress

2020-21 at 4-7 locations (environments) for high temperature tolerance in controlled as well as under field conditions and moisture stress (drought) tolerance. Pooled summary over the years and locations indicates that proposed genotype DRMR 2018-27 has least seedling mortality & higher seedling dry weight (controlled) compared to the heat tolerant checks and maintained higher relative water content (% RWC) & Chlorophyll content (SPAD values) revealed its high thermo tolerance at seedling stage. Similarly, it has maintained higher RWC, chlorophyll content, carotenoids, SPAD values and lesser decline in 1000- seed weight, seeds per siliqua, oil content, biological yield and other morphological traits indicating its moisture stress tolerance characteristics. It shows its tolerance both against moisture stress as well as high temperature at seedling stage (Table 1). Therefore, it will be highly useful in breeding programmes for development of high-yielding thermo and drought tolerant varieties. Genotype DRMR 2018-27 will be a very good addition to existing gene pool in germplasm repository for multiple abiotic stress tolerance as high temperature tolerance at seedling stage is highly required in early sown (September) mustard crop and drought tolerance is very much needed in rainfed crop. Hence, this promising line needs protection through germplasm registration.

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- Wither LA and F Engelmann (1998) In vitro conservation of plant genetic resources. In: A Altman (ed) *Agricultural Biotechnology*. Marcell Deker Inc., New York, pp 57-58.
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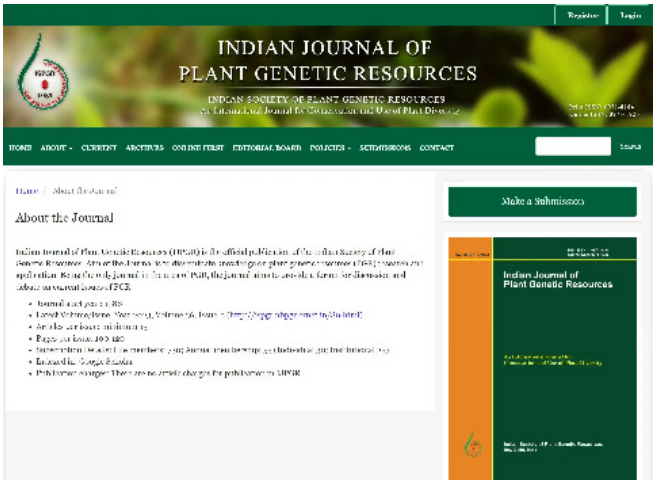

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Indian Journal of
Plant Genetic Resources

Print ISSN: 0971-8184
Online ISSN: 0976-1926
Vol. 37 No. 3 2024

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Published by the *General Secretary*, Indian Society of Plant Genetics Resources, NBPGR Campus, New Delhi-110012 and
Printed by *MRI Publication Pvt Ltd.*, Lucknow, Uttar Pradesh. Email ID: info@mripub.com