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Plant Germplasm Registration Notice[1]

The Plant Germplasm Registration Committee (PGRC) of ICAR held its XXXXVIIth meeting on March 29, 2022 in virtual mode. 128 proposals were received and examined at ICAR-NBPGR out of which 90 proposals complete in all respects and reviewed by experts were considered for registration. 63 proposals with unique/novel features belonging to 26 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. SBTIL121 (IC643999; INGR22001), a rice (*Oryza sativa*) germplasm for sd1gene

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Crosses were attempted using marker- assisted backcross breeding (MABB) approach to introgress two BB resistance genes (*xa13, Xa21*) and one dwarfing gene (*sd1*) from Punjab Basmati 4 (PAU148) into Ranbir Basmati. Genotype namely SBTIL121 identified as “ideal” genotypes, which can be recommended for release and exploited in a resistance breeding program for the region confronting bacterial blight disease alongwith lodging resistance.

Morpho-agronomic characteristics

This genotype is possessing *xa13, Xa21* and *sd1* bacterial blight and lodging resistant genes and good yield potential (40-45 qt/ha). The genotype SBTIL121 is semi-tall type (130-135 cm) and early maturing having 90-95 days for flowering and 125-130 days for maturity. The genotype has 35-40 number of effective tillers alongwith 1000-grain weight of 23 gm.

Associated characters and cultivated practices

The genotype also has good grain quality characteristics of basmati rice. The genotype is having grain length of 7.97 mm with KLAC value of 13.98. It can be grown in on soils suitable for rice cultivation; however, it gives best performance in basmati rice growing areas following under geographical indication (GI). The field should be well prepared for nursery by two to three ploughings and transplanting should be done at 3-4 leaves stage in well ploughed and pudled soils. Apply entire quantity of DAP with 1/3rd of N from Urea at the time of puddling. Fertlizers should be applied @ 30:20:10 NPK kg/ha. Remaining quantity of nitrogen through urea was applied in two equal splits - at tillering stage (30 DAT) and before panicle initiation stage (60 DAT). Apply Butachlor granules 5 G @ 30 kg/ha. Within 24 hours of transplanting. Do not drain the water from the field for one week after application of granules. The seed treatment should be done with fungicide like Thirum/Captan/Carbendazim @ 2.0 g/kg seed before nursery sowing. The optimum nursery sowing time is 1st week of June to 15th of June and transplanting is 1st week of July to 15th of July. The seed rate for nursery sowing is 20-25 kg/ha. If available, about 20 tonnes of organic manures should be incorporated in the soil at the time of land preparation. This genotype has good worth as a donor in future field rice breeding programme towards development of basmati rice varieties with good level of resistance against bacterial blight and in other basic studies.

2. DCMS 9A & DCMS 9B (IC640658 & IC640659; INGR22002), wheat (*Triticum aestivum*) cytoplasmic genetic male sterile line in DBW 17 background with CMS source Chuan 13A alongwith maintainer (B) line

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The proposed genetic stock DCMS 9A was developed using CHUAN 13A based CMS 5A (CHUAN13A/CHUAN13B/4/7*KAUZ/PFAU//VEE#5/3/KAUZ) as female parent in first cross with Indian advanced variety DBW 17 as male parent. DBW 17 was a landmark variety for north western plains zone as well as north eastern plains zone for timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with DBW 17 as recurrent parent in order to

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recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 9A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 9A ranged from 92-104 days with mean of 97 days whereas average plant height was 89 cm with range of 85-95 cm. Compared to this, the maintainer line DCMS 9B showed similar days to heading and plant height which is helpful in synchronised flowering and pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spikelet number per spike, spike length, spike colour, spike shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line DBW 17 (Table 2). The results also indicated more maturity duration in DCMS 9A which is indicative of more grain filling duration leading to better seed development.

It may be concluded that the proposed genetic stock DCMS 9A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS 9A and its maintainer for quantitative traits

Year	*DCMS 9A (CMS- A line)*			*DCMS 9B (DBW 17: B line)*	
	Male sterility(%)	*Days to heading*	*Plant height(cm)*	*Days to heading*	*Plant height (cm)*
2015-16	100	97	85	97	92
2016-17	100	93	85	93	86
2017-18	100	92	91	94	88
2018-19	100	104	95	102	91
Mean	100	97	89	97	89

Table 2: Performance of DCMS 9A and its maintainer DCMS 9B for morphological traits

S. No.	*Traits*	*DCMS 9A*	*DCMS 9B (DBW 17)*
1	Coleoptile Colour	Absent	Absent
2	Growth habit	Semi erect	Semi erect
3	Foliage Colour	Green	Green
4	Spike colour	white	white
5	Spike shape	Tapering	Tapering
6	Awn colour	White	White
7	Grain colour	Amber	Amber
8	Spike length (cm)	10	9
9	Spikelet number	20	20
10	Days to maturity	147	139

3. DCMS 44A & DCMS 44B (IC640660 & IC640661; INGR22003), wheat (*Triticum sativum*) cytoplasmic genetic male sterile line in CBW 38 background with CMS source MTSA 2A

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The proposed genetic stock DCMS 44A was developed using MTSA 2A based CMS 2A (MTSA 2A/8*RAYON) as female parent in first cross with Indian advanced variety CBW 38 as male parent. CBW 38 was released variety for north eastern plains zone for timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with CBW 38 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme (Table 1). The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 44A (Table 2).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 44A was ranged from 994-104 days with mean of 98 days whereas average plant height was 106 cm with range of 101-115 cm. Compared to this, the maintainer line DCMS 44B (CBW 38) showed average days to heading of 99 days and plant height of 110 cm which is in tune to CMS line. This similar heading is helpful in synchronised flowering whereas more height in maintainer line facilitates better pollen movement for maximum seed set.

It may be concluded that the proposed genetic stock DCMS 44A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS 44A and its maintainer DCMS 44B for agro-morphological traits

S. No.	Traits	DCMS 44A	DCMS 44B (CBW 38)
1	Coleoptile Colour	Absent	Absent
2	Growth habit	Semi erect	Semi erect
3	Foliage Colour	Green	Green
4	Spike colour	white	white
5	Spike shape	Tapering	Tapering
6	Awn colour	White	White
7	Grain colour	Amber	Amber
8	Spike length (cm)	10	9
9	Spikelet number	20	20
10	Days to maturity	150	148

Table 2: Performance of DCMS 44A and its maintainer for quantitative traits

Year	DCMS 44A (CMS- A line)			DCMS 44B (CBW 38: B line)	
	Male sterility (%)	Days to heading	Plant height (cm)	Days to heading	Plant height (cm)
2015-16	100	99	102	99	105
2016-17	100	94	101	94	107
2017-18	100	94	115	95	121
2018-19	100	104	104	106	108
Mean	100	98	106	99	110

4. DCMS 35A & DCMS 35B (IC640662 & IC640663; INGR22004), wheat (*Triticum sativu*m) cytoplasmic genetic male sterile line in DBW 55 background with CMS source Chuan 13A

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The proposed genetic stock DCMS 35A was developed using CHUAN 13A based CMS 5A (CHUAN13A/CHUAN13B/4/7*KAUZ/PFAU//VEE#5/3/KAUZ) as female parent in first cross with Indian advanced variety DBW 55 as male parent. DBW 55 was a high yielding elite line evaluated in NIVT 1A meant for north western plains zone as well as north eastern plains zone under timely sown irrigated condition. under timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with DBW 55 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 35A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 35A was ranged from 994-104 days with mean of 98 days whereas average plant height was 96 cm with range of 90-104 cm. Compared to this, the maintainer line DCMS 35B (DBW 55) showed similar days to heading of 98 days with plant height of 98 cm which is in tune to CMS line. These features in DCMS 35A are helpful in synchronised flowering and pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line DBW 55 (Table 2). The results also indicated comparable spikelet number per spike, spike length and maturity period in DCMS 35A as compared to the maintainer line DBW 55. The maturity days was more in the DCMS 35A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

It may be concluded that the proposed genetic stock DCMS 35A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS 35A and its maintainer for quantitative traits

Year	*DCMS 35A (CMS- A line)*			*DCMS 35B (DBW 55: B line)*	
	Male sterility (%)	*Days to heading*	*Plant height (cm)*	*Days to heading*	*Plant height (cm)*
2015-16	100	99	94	99	98
2016-17	100	94	94	94	96
2017-18	100	95	90	97	100
2018-19	100	104	104	103	99
Mean	100	98	96	98	98

Table 2: Performance of DCMS 35A and its maintainer DCMS 35B for morphological traits

S. No.	*Traits*	*DCMS 35A*	*DCMS 35B (DBW 55)*
1	Coleoptile Colour	Absent	Absent
2	Growth habit	Semi erect	Semi erect
3	Foliage Colour	Green	Green
4	Spike colour	White	White
5	Spike shape	Tapering	Tapering
6	Awn colour	White	White
7	Grain colour	Amber	Amber
8	Spike length (cm)	12	11
9	Spikelet number	24	23
10	Days to maturity	148	146

5. DCMS 52A & DCMS 52B (IC640664 & IC640665; INGR22005), a wheat (*Triticum aestivum*) cytoplasmic genetic male sterile line in UP 2338 background with CMS source MTSA 2A

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The proposed genetic stock DCMS 44A was developed using MTSA 2A based CMS 2A (MTSA 2A/8*RAYON) as female parent in first cross with Indian advanced variety UP 2338 as male parent. Variety UP 2338 was released for north western plains zone for timely sown as well as late sown irrigated condition and very popular due to its flexibility in sowing time. After initial cross, 8 generations of backcrosses were made with CBW 38 as recurrent parent in order to recover its agronomic background. The resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 52A (Table 1).

Table 1: Performance of DCMS 52A and its maintainer for quantitative traits

Year	*DCMS 52A (CMS- A line)*			*DCMS 52B (UP 2338: B line)*	
	Male sterility (%)	*Days to heading*	*Plant height (cm)*	*Days to heading*	*Plant height (cm)*
2015-16	100	99	97	99	104
2016-17	100	86	100	86	102
2017-18	100	96	114	99	111
2018-19	100	108	120	111	113
Mean	100	97	108	99	108

Table 2: Performance of DCMS 52A and its maintainer DCMS 52B for agro-morphological traits

S. No.	*Traits*	*DCMS 52A*	*DCMS 52B (UP 2338)*
1	Coleoptile Colour	Absent	Absent
2	Growth habit	Semi erect	Semi erect
3	Foliage Colour	Dark Green	Dark Green
4	Spike colour	White	White
5	Spike shape	Tapering	Tapering
6	Awn colour	White	White
7	Grain colour	Amber	Amber
8	Spike length (cm)	12	11
9	Spikelet number	20	22
10	Days to maturity	149	146

The heading period in DCMS 52A was ranged from 986-108 days with mean of 97 days whereas average plant height was 108 cm with range of 97-120 cm. Compared to this, the maintainer line DCMS 52B (UP 2338) showed average days to heading of 99 days with similar plant height to CMS line.

In addition, few additional agro-morphological traits were observed over these years which showed similar pattern to the parental maintainer line UP 2338 (Table 2). The results indicated comparable spikelet number per spike, spike length and maturity period in DCMS 52A as compared to the maintainer line UP 2338. The maturity days was more in the DCMS 52A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

It may be concluded that the proposed genetic stock DCMS 52A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

6. DWAP 18-12 (IC640668; INGR22006), a wheat (*Triticum aestivum*) germplasm highly tolerant to water stress conditions of warmer areas;low SSI; low yield reduction under stress

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The germplasm line DWAP 1812 was developed from the cross DBW 87/5EGPSN 82//HI 1583 following modified pedigree method. The segregating generations were evaluated at Karnal and 8 shuttle breeding centres in CZ and PZ for target oriented selection. It was evaluated at 10 locations in all four zones *i.e.,* Karnal in NWPZ, Ayodhya in NEPZ, Jabalpur, Junagadh, Vijapur and Bilaspur in CZ and Akola, Niphad and Dharwad in PZ under timely sown irrigated condition and timely sown restricted irrigation condition in replicated trials. The check varieties are the latest commercial cultivars of all the zones for various production conditions. The yield data was analysed location wise to estimate the stress susceptibility index (Fischer & Maurer, 1978) and percent reduction of yield under stress conditions (Choukan *et al.,* 2006). The pooled analysis of SSI and Red (%) indicated wide range of variability among the genotypes in the experiment (Table 1.). In general, the genotypes having SSI <1.0 is considered as stress tolerant genotypes. The proposed genotype DWAP 1812 showed least SSI of 0.15 alongwith least reduction in yield under stress conditions (3.96) which reflects its high tolerance nature to water scarcity conditions (Table 2).

Table 1: Stress susceptibility index

S. No.	*Entry*	*Stress susceptibility index (SSI)*											*Reductionin yield under stress (%)*
		Akola	*Ayodhya*	*Jabalpur*	*Niphad*	*Dharwad*	*Junagadh*	*Powarkheda*	*Vijapur*	*Bilaspur*	*Karnal*	*Pooled*	
1	DWAP 18-12	-0.75	0.91	-22.06	1.07	-0.08	0.79	3.49	0.95	0.96	-0.86	0.15	3.96
2	DBW 110 ©	-0.13	0.66	4.43	1.16	0.80	1.16	4.97	1.13	1.04	-3.62	0.66	17.04
3	DBW 93 ©	1.25	0.59	-24.67	0.79	0.90	0.83	2.68	1.52	1.23	0.53	0.70	18.05
4	HD 2967 ©	-3.13	1.42	-6.52	1.06	1.30	0.89	-1.30	-0.13	1.10	1.06	1.04	26.59
5	HD 2932 ©	1.84	0.59	8.84	0.91	0.98	0.86	0.74	1.00	0.73	1.31	1.12	28.79
6	GW 322 ©	0.84	2.15	3.58	1.01	1.07	1.11	3.46	1.77	1.11	2.65	1.25	31.99
7	MACS 6222 ©	1.57	0.68	1.72	1.09	1.05	1.15	-0.93	0.79	0.89	-0.44	1.28	32.78
8	DBW 222 ©	0.05	2.23	3.61	1.18	1.01	1.43	1.27	1.18	0.77	2.02	1.29	33.05

Table 2: Pooled performance of DWAP 1812 for various traits under water scarce condition

S. No.	*Entry*	*Days to heading*	*Days to maturity*	*Grain filling duration*	*Plant height (cm)*	*Tillers per m row*	*Spike length (cm)*	*Spikelets per spike*	*1000-gr. weight (g)*
1	DWAP 1812	68	115	48	81	86	8	14	39
3	DBW 110 ©	70	116	47	82	79	9	15	41
4	DBW 93 ©	69	114	45	73	87	8	17	35
5	HD 2967 ©	71	114	43	80	112	9	17	37
6	HD 2932 ©	67	116	49	90	85	9	17	39
7	GW 322 ©	67	117	49	80	91	9	17	38
8	MACS 6222 ©	69	115	46	79	85	8	16	38

The genotype DWAP 1812 also showed comparable performance for various agro-morphological traits to all the check varieties. Based on the SSI, and reduction (%), DWAP 1812 can be a promising donor for tolerance to drought/ water scarcity conditions and may be further utilised in wheat improvement programmes.

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7. IC296727 (IC296727; INGR22007), wheat (*Triticum aestivum*) germplasm with High level of grain zinc content (51.3 ppm) and protein content (13.8%)

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Under Consortium Research Project on Agro-biodiversity, one thousand four hundred and eighty-five spring type bread wheat core set germplasm (*Triticum aestivum* L.) comprising Indian as well as exotic lines were evaluated for quality traits based on multi-location grain data form locations *i.e.,* Banaras Hindu University, Varanasi, Punjab Agricultural University, Ludhiana and Agharkar Research Institute, Pune during 2016-17. Sixteen accessions were found to have high protein content and sedimentation value over the locations. Out of these, 12 accessions with moderate thousand grain weight and were nominated for Preliminary Quality Component Wheat Biofortification Nursery during 2019-20 and evaluated for agronomic and quality traits at IIWBR, Karnal. On the basis of initial quality evaluation, two accessions (IC296727 and EC299324) were nominated for Quality Component Wheat Biofortification Nursery under All India Coordinated Research project on Wheat and Barley. These accessions alongwith 50 entries and six checks, DBW187, DDW47, GW322, HS3226, HS490, WB02) were grown at ten locations, Karnal, Hissar, Delhi, Ludhiana, Kanpur, Varanasi, Indore, Vijapur, Pune and Dharwad during the *rabi* season (2020-21). The germplasm accession, IC296727 was found to have highest zinc content (51.3 ppm) among 56 entries tested over the locations and was significantly superior to best check WB-02 which had zinc content 44.34 ppm (Figure 1). This accession had medium maturity, long spike length (~16cm), high grains per spike (~80), high grain protein content (~14%), In addition, it has hectolitre weight (72.4 kg/hl), hardness index (48) and iron content (42 ppm). Considering its superiority for many traits, this accession can be utilized in development of biparental mapping population, genetics study and development of biofortified wheat variety.

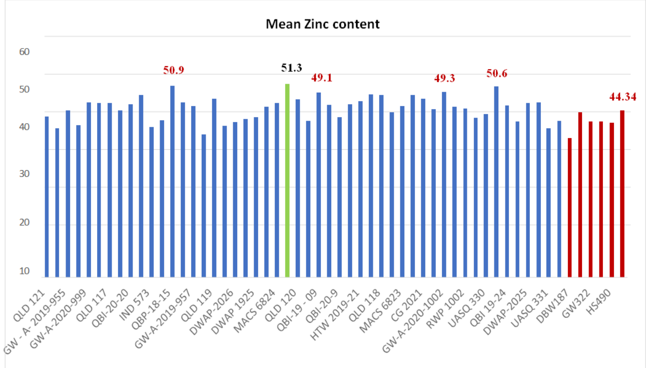

Figure 1: Graphical representation of mean zinc content of wheat genotypes over ten locations

8. IC279317 (IC279317; INGR22008), a wheat (*Triticum sativum*) germplasm for better yield traits and heat stress indices

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Introduction

The temperature on earth is increasing due to global warming and supposed to rise 1 and 3^{0}C by 2025 and 2100, respectively (IPCC). The gradual increase of temperature substantially reduces the productivity of major crops. The effect of high temperature stress is clearly observed in wheat as late planting is very common in India due to intensive cropping system (Agarwal *et al*., 2021). Delayed sowing hastens the seedling emergence, tiller initiation, emergence of flag leaf and spike that shortens the total growth duration of plant (Singh and Pal, 2003). The enhanced wheat production can be achieved only by growing heat tolerant wheat genotypes. To identify the heat tolerant wheat germplasm for hyper-arid regions, a set of 102 germplasm of wheat was collected from National Bureau of Plant Genetic Resources (NBPGR), New Delhi (India) under RKVY project and grown in normal (15 November) as well as in late (15 December) sowing conditions at Instructional farm of Agricultural Research Station, Swami Keshwanand Rajasthan Agricultural University, Bikaner (India).

Morpho-agronomic Characteristics

The diverse germplasm of wheat were tested for four consecutive years (2010-11 to 2013-14) and then in year 2016-17 on various visual, morpho-physiological characters, biochemical traits, stress responsive characters, yield and yield attributes.

Associated characters and cultivated practices

Out of 102 wheat germplasm, a set of eleven germplasm were screened out after three successive years (2010-11 to 2012-13) which was further tested in 2013-14. In 2013-14, three germpalsm were selected as heat tolerant. The experiment was repeated with a set of 11 wheat germplasm in *rabi* season 2016-17 and confirmed the results that three germplasm *viz*., entry no. 26 (IC279317), 43 (IC335971) and 58 (IC336816) were the most suitable heat tolerant wheat germplasm which might be utilized for further breeding programmes to develop heat tolerant wheat varieties. The screened germplasm are multiplied in the *rabi* season 2020-21.

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9. IC336816 (IC336816; INGR22009), a wheat (*Triticum aestivum*) germplasm heat tolerance nature

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Introduction

The temperature on earth is increasing due to global warming and supposed to rise 1 and 3^{0}C by 2025 and 2100, respectively (IPCC). The gradual increase of temperature substantially reduces the productivity of major crops. The effect of high temperature stress is clearly observed in wheat as late planting is very common in India due to intensive cropping system (Agarwal *et al*., 2021). Delayed sowing hastens the seedling emergence, tiller initiation, emergence of flag leaf and spike that shortens the total growth duration of plant (Singh and Pal, 2003). The enhanced wheat production can be achieved only by growing heat tolerant wheat genotypes. To identify the heat tolerant wheat germplasm for hyper-arid regions, a set of 102 germplasm of wheat was collected from National Bureau of Plant Genetic Resources (NBPGR), New Delhi (India) under RKVY project and grown in normal (15 November) as well as in late (15 December) sowing conditions at Instructional farm of Agricultural Research Station, Swami Keshwanand Rajasthan Agricultural University, Bikaner (India).

Morpho-agronomic Characteristics

The diverse germplasm of wheat were tested for four consecutive years (2010-11 to 2013-14) and then in year 2016-17 on various visual, morpho-physiological characters, biochemical traits, stress responsive characters, yield and yield attributes.

Associated characters and cultivated practices

Out of 102 wheat germplasm, a set of eleven germplasm were screened out after three successive years (2010-11 to 2012-13) which was further tested in 2013-14. In 2013-14, three germpalsm were selected as heat tolerant. The experiment was repeated with a set of 11 wheat germplasm in *rabi* season 2016-17 and confirmed the results that three germplasm *viz.,* entry no. 26 (IC279317), 43 (IC335971) and 58 (IC336816) were the most suitable heat tolerant wheat germplasm which might be utilized for further breeding programmes to develop heat tolerant wheat varieties. The screened germplasm are multiplied in the *rabi* season 2020-21.

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10. IC212176 (IC212176; INGR22010), a wheat (*Triticum aestivum*) germplasm Gigas plant with reduced number of tillers (69 Tillers/m row) and long spike (12 cm)

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Plant architecture of wheat plant depends upon the number of tillers. The extent of tillering is governed by number of factors including genetical factors, time of sowing, temperature, and rainfall. Majority of spring wheat varieties produces 8-10 tillers per plant but IC212176 (a local collection from Bhavnagar, Gujarat) is identified as Gigas plant type with 1-2 tillers per plant with long spike length, high number of grains per spike and thick stem. The IC212176 evaluated in NGSN at 31 locations during 2020-21 (Table 1). In NGSN, the average number of tillers per metre in IC212176 was 69 as compared to 81 in IC296729 (INGR 99005) already registered genetic stock for "GIGAS" plant. The check varieties namely Sonalika, HD2967 and HI 8713 recorded a value of 97, 97, and 89 respectively for number of tillers per metre. This genotype also recorded higher number of grains per spike (57 grains per spike) and long spike (12 cm).

Table 1: IC212176 in NGSN 2020-21

S. No.	*Genotype*	*Tillers/ m row*	*Grains/ spike*	*Sp. length (cm)*	*1000-gr. wt. (g)*
1	IC212176	69	57	12	43
2	IC296729 (Already registered genetic stock)	81	48	10.8	44
3	Sonalika (Check)	97	53	9.31	39
4	HD 2967 (Check)	97	53	10.3	39
5	HI 8713 (d) (Check)	89	53	9.17	41
	SD±	10.39	3.84	1.02	3.41

11. QBI19-09 (IC643956; INGR22011), bread wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high grain zinc concentration (48.6 ppm)

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Deficiency of iron leads to reduced hemoglobin and red cells resulting in anemia. Deficiency of Zinc is associated with diarrhea, loss of cognitive function and reduced immunity. The current levels of grain micronutrients in wheat, a staple for Indians, are not sufficient to provide even 50% of the RDA for adults. Therefore, zinc and iron are important nutritional traits to be improved by plant breeding. In this effort, high yielding line QBI19-09 having high grain Zn and Fe concentration was developed at ICAR-IARI. QBP19- 9 was evaluated along with 52 entries and check varieties in nine locations over two years (2019-20 and 2020-21) in the QCWBN conducted by IIWBR, Karnal. This entry recorded higher values of grain zinc and iron and test weight over the Bioforitified variety WB-02 and the checks in the respective zones as shown in Table 1. It also excelled in grain yield over biofortified check WB02 and the yield check GW322 in CZ and PZ during 2020-21 and in CZ during 2019-20. The genotype QBI19-09 was also found resistant, in IPPSN screening by IIWBR Karnal, to stripe rust and leaf rust in all the zones thus making it a valuable resource for high grain Fe and grain Zn concentration.

Table 1: Grain yield, test weight and nutritional quality traits of QBI19-09 along with quality and yield checks

	NWPZ 20-21 (4 LOCATIONS)					*NWPZ 2019-20 (5 LOCATIONS)*				
Genotype	*Grain yield (t/ha)*	*Iron (mg/kg)*	*Zinc (mg/kg)*	*GPC (%)*	*TW (kg/hl)*	*Grain yield (t/ha)*	*Iron (mg/kg)*	*Zinc (mg/kg)*	*GPC (%)*	*TW (kg/hl)*
QBI19-09	64.8	42.6	51.4	13.4	80.4	57.7	40.1	50.9	13	77.5
WB 02	56.2	40.3	44.5	13.9	77.7	54.8	38.3	37.8	12.5	75.8
HD3086 (C)	73.4	38.3	40.6	12.9	78.1	60.9	37.3	35.3	11	78.1
	NEPZ 20-21 (2 LOCATIONS)					*NEPZ 2019-20 (2 LOCATIONS)*				
QBI19-09	46.4	38	49.9	10.9	77.4	26.9	39.4	34	12.3	74.9
WB 02	47	34	38	11.6	75.1	30	38.3	33.1	10.9	78.2
DBW 187 (C)	57.6	32	32.4	10	75.4	34.5	35.5	26.4	11.2	74.9
	CZ 20-21 (2 LOCATIONS)					*CZ 2019-20 (2 LOCATIONS)*				
QBI19-09	52.6	41.9	55.5	13.2	79.8	59.8	38.9	51.4	12.4	80
WB 02	50.9	43.4	53.6	14.6	77.5	63.1	36.7	44.4	12	77.7
GW 322 (C)	51.7	40.2	48.4	11	75.9	50.8	36.3	31.9	10.3	73.9
	PZ 20-21 (1 LOCATION)					*PZ 20-21*				
QBI19-09	37.5	50.1	48.8	13.0	82	-	-	-	-	-
WB 02	29.0	46.7	45.1	15.1	79.5	-	-	-	-	-
GW 322 (C)	36.6	40.1	40.7	11	81	-	-	-	-	-
		All India mean values				*All India mean values*				
QBI19-09	50.325	43.15	51.4	12.625	79.9	41.17	39.47	45.43	12.6	77.5
WB 02	45.775	41.1	45.3	13.8	77.4	40.5	37.77	38.43	11.8	77.2

12. QBI20-20 (IC643957; INGR22012), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm for Low Hardness Index (32) (Soft endosperm); low SDS-Sedimentation value (40.5 mL)

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India is the second largest producer of wheat in the world. It has become more than self-sufficient in wheat production in the last two decades. India has also seen an upsurge in the value based industry. The milling and baking industry of India is rapidly expanding and is valued at ~Rs 69 billion. India has become the third largest producer of biscuits next to USA and China. Ready to make pre-mixes for prodcuts *viz* cake, muffins, pretzels, *etc* all require a specific flour. Grain softness is an important trait that can yield a flour highly suitable for these products. However, all commercially used varieties in India are hard grained. Therefore, genetic improvement to produce soft grained wheat suited for soft textured products has both a domestic and export potential. ICAR-IARI have developed a new strain QBI20-20 for grain softness. This line was evaluated in 2020-21 in 11 locations in Quality Component and Wheat Biofortification Nursery (QCWBN) conducted by IIWBR covering all the four zones. QBI20-20 recorded commercially exploitable value (32) of GHI in all the locations as summarized in Table 1 below. In addition, QBI20-20 also recorded high grain zinc concentration of 45.9 mg/Kg which is similar to biofortified variety WB02. This genotype is also free of rusts as per the IPPSN screening of the AIWBIP 2020-21. Thus with its high grain yield (56.9 q/ha) in NWPZ, lower GHI (30), low sedimentation value (40.4ml) and good amount of grain Fe and Zn make it highly suitable as a donor in soft wheat breeding programme. It also has commercial value as it is free of rusts and can be used by Industry for making bakery products.

Table 1: Summary of Grain yield, grain hardness index, hectoliter weight and nutritional quality of QBI20- 20 along with yield and quality checks in QCBWN of AIWBIP 2020-21

	NWPZ 20-21 (4 Locations)					
	GHI	*SDS-Sed (ml)*	*IRON (mg/Kg)*	*ZINC (mg/Kg)*	*YIELD (t/ha)*	*TW (Kg/hl)*
QBI-20-20	30	41.875	38.5	46.4	56.9	76.3
HD3226	82	60.275	38.3	40.6	73.4	78.1
WB02	76	61.325	40.3	44.5	56.2	77.65
HS490	30	40	36.5	40.7	51.7	74.28
		NEPZ 20-21 (2 Locations)				
QBI-20-20	31	40.15	37.9	41.9	49.7	73.45
DBW 187	74	53.25	32	32.4	57.6	75.4
WB02	81	53.25	34	38	47	75.1
HS490	24	37	33.6	33.9	51.1	73.35
		CZ 20-21 (2 Locations)				
QBI-20-20	36	38.43	43.5	55.6	49.1	76.5
GW 322	89	39.43	40.2	48.4	51.7	75.9
WB02	72	61.3	43.40	53.6	50.9	77.53
HS490	44	40.10	39.8	46.2	46	74.15
		PZ 20-21 (3 Locations)				
QBI-20-20	31	41.3	45.2	42.9	37.8	78.35
GW 322	83	39.2	40.1	40.7	36.6	80.9
WB02	74	66.15	46.7	45.1	29.0	79.45
HS490	40	40.5	40.8	35.6	34.7	76.47
		Mean values (National basis				
QBI-20-20	32	40.4	40.5	45.9	38.925	76.2
WB02	73	61.8	41.7	45.1	38.5	77.5
HS490	35	39.6	37.5	39.5	37.2	74.7

13. DWRBG 2 (IC641989; INGR22013), a barley genotype (*Hordeum vulgare*) germplasm with high hectoliter weight (66.7 kg/hl) coupled with higher protein content 13.0% (dwb) and bold grains (>2.5 mm size)

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DWRBG-2 (tested as BCU 4966) is a two-row hulled barley genotype, selected from 10th EMBSN nursery (entry-29) supplied by ICARDA/CIMMYT. DWRBG-2 has high hectolitre weight of 66.7 kg/hl which is higher than the released malt type varieties (59.3 to 65.4 kg/hl) and the previously registered germplasm DWR 38 (64.0 kg/hl) for this trait. DWRBG-2 has average protein content of 13.0 % (dwb), which is in very desirable range of current specifications by malt industry. Besides these two attributes DWRBG-2 has bold grains ((>2.5 mm size) percentage of more than 96.2% (Table 1). Barley malt is the traditional and key raw material for beer (some speciality whisky also) making besides several malt-based products like energy drinks, confectionary and bakery products. Barley has been the grain of choice for malt making due to certain grain physical and biochemical parameters. The percent use of barley of total barley production is increasing for malting and brewing and the global malt ingredient market is projected to register a CAGR of 7.1% from 2000 to 2025. Test weight or specific weight or Hectolitre weight indicates the density of grains in particular volume at a standardized moisture level and normally reported as kilogram per hectolitre (kg/hl). Test

Table 1: Grain quality traits in DWRBG-2 (tested as BCU-4966) at different locations during 2019-20 and 2020-21

Genotype	*Hisar*	*Karnal*	*Pantnagar*	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	*Mean*
Hectolitre wt (kg/hl)	*2019-20*			*2020-21*						
BCU-4966	61.0	69.8	64.0	63.4	70.9	66.2	69.9	68.4	NA	66.7
DWR 38 (c)*	NT	NT	NT	62.7	63.7	64.8	65.6	65.2	62.0	64.0
DWRUB 52 (c)	60.7	66.7	60.5	61.3	68.7	57.9	70.8	64.5	62.3	63.7
DWRB 101 (c)	60.6	66.5	63.0	59.8	66.3	65.3	70.7	67.7	64.7	65.0
DWRB 123 (c)	57.5	62.6	63.2	60.1	67.0	63.7	69.3	67.3	57.5	63.1
DWRB 92 (c)	56.5	61.3	59.6	57.5	66.0	61.7	67.1	65.1	59.8	61.6
DWRB 91 (c)	62.0	66.9	60.6	58.3	66.4	61.8	69.2	65.1	62.5	63.6
RD 2849 (c)	NT	NT	NT	60.4	69.7	63.8	68.6	65.4	64.3	65.4
DWRB-160 (c)	58.7	62.2	57.5	52.6	62.5	58.5	67.6	63.8	57.4	60.1
DWRB-182 (c)	55.9	62.3	57.7	54.1	59.8	55.6	69.2	63.2	56.1	59.3
DWRB 137 (c)	NT	NT	NT	54.8	63.5	59.5	65.3	61.4	57.2	60.3
Protein content (%)	*2019-20*			*2020-21*						
BCU-4966	13.9	11.4	12.3	13.1	14.0	14.4	14.7	10.5	NA	13.0
DWR 38 (c)	NT	NT	NT	14.2	16.0	13.4	15.0	14.1	15.2	14.7
DWRUB 52 (c)	13.4	10.6	9.8	12.0	11.6	14.5	12.0	9.7	12.5	11.8
DWRB 101 (c)	13.0	11.1	10.2	12.1	11.7	12.8	11.7	9.6	11.1	11.5
DWRB 123 (c)	13.3	10.4	9.8	12.5	12.1	12.6	11.6	9.4	10.1	11.3
DWRB 92 (c)	14.9	11.9	11.5	12.5	14.1	13.5	11.9	10.7	12.7	12.6
DWRB 91 (c)	11.9	11.2	9.5	11.7	12.1	13.4	12.0	10.3	10.3	11.4
RD 2849 (c)	NT	NT	NT	11.6	12.2	11.1	10.4	11.2	9.5	11.0
DWRB-160 (c)	11.6	11.1	9.8	11.8	12.2	12.4	11.3	10.9	10.3	11.3
DWRB-182 (c)	12.8	11.7	11.5	12.2	11.6	14.2	13.2	12.1	10.4	12.2
DWRB 137 (c)	NT	NT	NT	12.8	13.5	12.9	11.2	14.6	10.2	12.5
Bold grain (%)	*2019-20*			*2020-21*						
BCU-4966	98.1	96.0	96.9	89.1	96.9	97.0	98.2	97.5	NA	96.2
DWR 38 (c)	NT	NT	NT	92.4	92.9	95.8	92.9	96.7	94.1	94.1
DWRUB 52 (c)	97.9	76.0	89.0	89.3	81.0	46.5	93.6	75.0	61.0	78.8
DWRB 101 (c)	97.1	79.9	95.7	91.9	87.0	87.5	96.6	73.2	77.9	87.4
DWRB 123 (c)	98.3	81.3	94.5	92.8	91.2	88.5	96.4	88.0	78.8	90.0
DWRB 92 (c)	98.7	89.5	97.4	98.0	98.3	91.3	98.7	98.2	94.7	96.1
DWRB 91 (c)	98.0	85.6	96.2	94.8	97.4	75.6	98.4	96.4	70.5	90.3
RD 2849 (c)	NT	NT	NT	84.5	74.8	79.8	95.1	64.2	79.0	79.6
DWRB-160 (c)	98.7	95.6	99.0	94.9	83.8	85.4	98.4	96.1	92.5	93.8
DWRB-182 (c)	93.2	75.9	68.8	70.6	74.9	63.2	93.3	67.0	73.3	75.6
DWRB 137 (c)	NT	NT	NT	88.9	86.1	82.6	96.0	87.6	83.4	87.4

*Registered stock for the trait

weight depends upon grain weight, shape, size/plumpness and their packing (AACC 55-10, 2000). Test weight is an indirect or crude method to assess the suitability of grains for malting quality. Usually higher test weight grains (> 65 kg/hl) are preferred for malting as the higher test weight normally indicates bigger endosperm and lower husk content. Probability of higher starch content is more in grains with higher values of test weight. There is a positive correlation between hectolitre weight and hot water extract (malt extract) and this trait can serve as good criteria for selection of good malt quality lines in early generation of breeding programme. Thus, DWRBG-2 is a potential genotype which can be used as donor parent for improving the malting quality in barley.

14. QßLM11 (IC644007; INGR22014), a maize (*Zea mays*) germplasm with enhanced beta-carotene (7.46 ppm), lysine and tryptophan (0.298% & 0.080%)

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Introduction

Malnutrition affects growth and development in humans and causes socio-economic losses. Normal maize is deficient in essential amino acids, lysine and tryptophan; and vitamin-A. Crop biofortifcation is a sustainable and economical approach to alleviate micronutrient malnutrition. The present scenario necessitates developing maize genotypes with a combination of QPM and proA so that value-added product reaches poor communities. Buland and PMH1 are the popular maize hybrids released for cultivation in the North-Western Plain Zones of India. Our previous investigation has led to the development of QPM versions *viz*., BulandQ (QLM11 × QLM12) and PMH1Q (QLM13 × QLM14). The present study was thus aimed to (i) pyramid the favorable alleles of crtRB1 and lcyE genes into QPM background using marker-assisted backcross breeding (MABB), (ii) evaluate the nutritional quality of the introgressed lines and reconstituted hybrids, and (iii) assess the agronomic performance and yield potential of the MAS-derived genotypes. The present experiment was conducted at three locations *viz.* (i) Punjab Agricultural University (PAU), Ludhiana, (ii) Regional Research Station (PAU) Gurdaspur and (iii) IARI, New Delhi, India during the years from 2018 to 2019.

QβLM11 inbred line was developed through backcross selection (twicely backcrossed with recurrent female parent) and inbreeding for six generations. Molecular assisted backcross breeding strategy was used for the introgression of opaque-2 (*o2*), β-carotene hydroxylase (*crtRB1*) and Lycopene-Ɛ- cyclase (*lycE*) genes into the elite maize inbred LM11. At the end of six selfing and evaluation, uniform progenies were identified and their selfed seeds were bulked which were multiplied in isolation. This is a late maturing line.

Morpho-agronomic Characteristics

The plant length is tall with medium ear placement. Its tassel is semi-compact with strongly curved and drooping branches. Leaves are long light green and strongly curved and drooping. Cobs are conico-cylinderical and were fully filled with grain & top of the cobs were tightly enclosed with the husk. Grains are yellow orange, flint with caps and are arranged in straight rows on the cob. This improved QβLM11 line with elevated lysine, tryptophan and provitamin A concentration can be used in maize biofortification programs. In addition, on the basis of multilocation trials the introgressed QβLM11 gave 3538.9 kg/hac grain yield which was at par with the original check and beta- carotene content is 7.46 ppm whereas lysine and tryptophan is 0.298% and 0.080%, respectively (Singh *et al*., 2021). This shows that the nutritionally enriched QβLM11 can be used as a potential donor for the development of biofortified maize cultivars in future breeding programmes.

Reference

Singh J, S Sharma, A Kaur, Y Vikal, AK Cheema, BK Bains, N Kaur, GK Gill, PK Malhotra, A Kumar, P Sharma, V Muthusamy, A Kaur, JS Chawla and F Hossain (2021) Marker-assisted pyramiding of lycopene-ε-cyclase, β-carotene hydroxylase1 and opaque2 genes for development of biofortifed maize hybrids. *Sci. Rep*. 11:12642 https://doi.org/10.1038/s41598-021- 92010-8.

15. QßLM12 (IC644008; INGR22015), a maize (*Zea mays*) germplasm with enhanced beta-carotene (7.40 ppm) lysine and tryptophan (0.333% and 0.068%)

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Introduction

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Morpho-agronomic Characteristics

The plant length is tall with medium ear placement. Its tassel is open and lateral branches of tassel are straight. Leaves are short, dark green and straight. Cobs are small & conical in shape and were fully filled with grain & top of the cobs were tightly enclosed with the husk. Grains are bold orange, flint and are arranged in straight rows on the cob. This improved QβLM12 line with elevated lysine, tryptophan and provitamin A concentration can be used in maize biofortification programs. In addition, on the basis of multilocation trials, the introgressed QβLM12 gave 3451.0 Kg/hac grain yield which was at par with the original check and beta-carotene content is 7.40 ppm whereas lysine and tryptophan is 0.333% and 0.068%, respectively (*Singh et al., 2021*). This shows that the nutritionally enriched QβLM12 can be used as a potential donor for the development of biofortified maize cultivars in future breeding programmes.

Reference

Singh J, S Sharma, A Kaur, Y Vikal, AK Cheema, BK Bains, N Kaur, GK Gill, PK Malhotra, A Kumar, P Sharma, V Muthusamy, A Kaur, JS Chawla and F Hossain (2021) Marker-assisted pyramiding of lycopene-ε-cyclase, β-carotene hydroxylase1 and opaque2 genes for development of biofortifed maize hybrids. *Sci. Rep.* 11: 12642 https://doi.org/10.1038/s41598-021- 92010-8.

16. QßLM13 (IC644009; INGR22016), a maize (*Zea mays*) germplasm with enhanced beta-carotene (6.89 ppm) lysine and tryptophan (0.383% & 0.074%)

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Introduction

Malnutrition affects growth and development in humans and causes socio-economic losses. Normal maize is deficient in essential amino acids, lysine and tryptophan; and vitamin-A. Crop biofortifcation is a sustainable and economical approach to alleviate micronutrient malnutrition. The present scenario necessitates developing maize genotypes with a combination of QPM and proA so that value-added product reaches poor communities. Buland and PMH1 are the popular maize hybrids released for cultivation in the North-Western Plain Zones of India. Our previous investigation has led to the development of QPM versions *viz.,* BulandQ (QLM11 × QLM12) and PMH1Q (QLM13 × QLM14). The present study was thus aimed to (i) pyramid the favorable alleles of crtRB1 and lcyE genes into QPM background using marker-assisted backcross breeding (MABB), (ii) evaluate the nutritional quality of the introgressed lines and reconstituted hybrids, and (iii) assess the agronomic performance and yield potential of the MAS-derived genotypes. The present experiment was conducted at three locations *viz.* (i) Punjab Agricultural University (PAU), Ludhiana, (ii) Regional Research Station (PAU) Gurdaspur and (iii) IARI, New Delhi, India during the years from 2018 to 2019. QβLM13 inbred line was developed through backcross selection (twicely backcrossed with recurrent female parent) and inbreeding for six generations. Molecular assisted backcross breeding strategy was used for the introgression of opaque-2 (*o2*), β-carotene hydroxylase (*crtRB1*) and Lycopene-Ɛ- cyclase (*lycE*) genes into the elite maize inbred LM13. At the end of six selfing and evaluation, uniform progenies were identified and their selfed seeds were bulked which were multiplied in isolation. This is a medium maturing line.

Morpho-agronomic Characteristics

The plant length is tall with medium ear placement. Its tassel is dense and lateral branches of tassel are straight. Leaves are long green having straight attitude of blade. Brace roots, anthers and silks have anthocyanin pigmentation. Cobs are conico- cylinderical and were fully filled with grain & top of the cobs were tightly enclosed with the husk. Grains are orange, flint and are arranged in straight rows on the cob. This improved QβLM13 line with elevated lysine, tryptophan and provitamin A concentration can be used in maize biofortification programs. In addition, on the basis of multilocation trials, the introgressed QβLM13 gave 3735.0 kg/ha grain yield which was at par with the original check and beta- carotene content is 6.89 ppm whereas lysine and tryptophan is 0.383% and 0.074%, respectively (Singh *et al.*, 2021). This shows that the nutritionally enriched QβLM13 can be used as a potential donor for the development of biofortified maize cultivars in future breeding programmes.

Reference

Singh J, S Sharma, A Kaur, Y Vikal, AK Cheema, BK Bains, N Kaur, GK Gill, PK Malhotra, A Kumar, P Sharma, V Muthusamy, A Kaur, JS Chawla and F Hossain (2021) Marker-assisted pyramiding of lycopene-ε-cyclase, β-carotene hydroxylase1 and opaque2 genes for development of biofortifed maize hybrids. *Sci. Rep.* 11:12642 https://doi.org/10.1038/s41598-021- 92010-8.

17. QßLM14 (IC644010; INGR22017), a maize (*Zea mays*) germplasm with enhanced beta-carotene (6.12 ppm), lysine and tryptophan (0.336% & 0.079%).

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Introduction

Malnutrition affects growth and development in humans and causes socio-economic losses. Normal maize is deficient in essential amino acids, lysine and tryptophan; and vitamin-A. Crop biofortifcation is a sustainable and economical approach to alleviate micronutrient malnutrition. The present scenario necessitates developing maize genotypes with a combination of QPM and proA so that value-added product reaches poor communities. Buland and PMH1 are the popular maize hybrids released for cultivation in the North-Western Plain Zones of India. Our previous investigation has led to the development of QPM versions viz., BulandQ (QLM11 × QLM12) and PMH1Q (QLM13 × QLM14). The present study was thus aimed to (i) pyramid the favorable alleles of crtRB1 and lcyE genes into QPM background using marker-assisted backcross breeding (MABB), (ii) evaluate the nutritional quality of the introgressed lines and reconstituted hybrids, and (iii) assess the agronomic performance and yield potential of the MAS-derived genotypes. The present experiment was conducted at three locations *viz.* (i) Punjab Agricultural University (PAU), Ludhiana, (ii) Regional Research Station (PAU) Gurdaspur and (iii) IARI, New Delhi, India during the years from 2018 to 2019. QβLM14 inbred line was developed through backcross selection (twicely backcrossed with recurrent female parent) and inbreeding for six generations. Molecular assisted backcross breeding strategy was used for the introgression of opaque-2 (*o2*), β-carotene hydroxylase (*crtRB1*) and Lycopene-Ɛ- cyclase (*lycE*) genes into the elite maize inbred LM14. At the end of six selfing and evaluation, uniform progenies were identified and their selfed seeds were bulked which were multiplied in isolation. This is a late maturing line.

Morpho-agronomic Characteristics

The plant length is tall with medium ear placement. Its tassel is semi-compact and lateral branches of the tassel are curved. Leaves are long green, curved and drooping and the stem is zigzag in nature. Cobs are conico-cylinderical in shape & top of the cobs were not enclosed with the husk. Grains are yellow, flint and are arranged in straight rows on the cob. This improved QβLM14 line with elevated lysine, tryptophan and provitamin A concentration can be used in maize biofortification programs. In addition, on the basis of multilocation trials, the introgressed QβLM14 gave 3648.8 kg/ha grain yield which was at par with the original check and beta-carotene content is 6.12 ppm whereas lysine and tryptophan is 0.336% and 0.079%, respectively (Singh *et al.*, 2021). This shows that the nutritionally enriched QβLM14 can be used as a potential donor for the development of biofortified maize cultivars in future breeding programmes.

Reference

Singh J, S Sharma, A Kaur, Y Vikal, AK Cheema, BK Bains, N Kaur, GK Gill, PK Malhotra, A Kumar, P Sharma, V Muthusamy, A Kaur, JS Chawla and F Hossain (2021) Marker-assisted pyramiding of lycopene-ε-cyclase, β-carotene hydroxylase1 and opaque2 genes for development of biofortifed maize hybrids. *Sci. Rep.* 11:12642 https://doi.org/10.1038/s41598-021- 92010-8.

18. V 601 (IC643993; INGR22018), a maize (*Zea mays*) germplasm liguleless; early maturity; The stock is broadly in the genetic background of elite inbred V 407 (female parent of Vivek Maize Hybrid 53 and CMVL 55); known heterotic affinity of V 407 makes the stock directly usable maize hybrid breeding programmes

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Table 1: Morpho-agronomic characteristics of liguleless stockV601 and its parental lines

	Ligule	*Days to 50% pollen shed*	*Days to 50% silking*	*Plant height (cm)*	*Ear height (cm)*	*Days to 75% brown husk*	*Cob length (cm)*
PDH-3	Absent	49	50	165	90	86	8.4
V407	Present	53	55	135	70	91	15.8
V601	Absent	51	52	170	95	88	17.4

	Cob girth (cm)	*Kernel rows*	*Grains /Row*	*1000-seed wt.*	*Grain type*	*Turcicum leaf blight (1-9)*	*Maydis leaf blight (1-9)*
PDH-3	10.5	12-14	16	160	Yellow Dent	7.0	7.0
V407	14.8	14-16	23	302	Orange Flint	2.0	3.0
V601	13.5	10-12	26	280	Yellow Dent	3.0	3.0

Mutants with defective ligule and auricle development exhibit erect leaf architecture, and such leaf architecture facilitates dense and planting and contributes to higher yields (Duvick 2005). Since indigenous liguleless stocks are not available in Indian public maize breeding programme, liguleless line PDH-3 (EC928978) was obtained from University of Hohenheim, Germany and crossed with normal (liguled) inbred V 407 with the objective of transferring the trait in to locally adapted background. The cross was advanced following pedigree method and in F5 generation, liguleless line V 601 was identified on the basis of its agronomic performance (Table 1). The line V 601 has been developed and is being maintained at ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora (Uttarakhand), India. V 601 is a liguleless line with upright leaves. Its plant height is 170 cm and days to 75% brown husk is 88 (early group) (Table 1). Tassel is medium large and semi-open. Colour of anthers is purple and anthocyanin pigmentation is present in the silk. The cob length and cob girth of V 601 are 17.4 and 13.5 cm, respectively. The grain is yellow dent and test-weight is 280 g. V 601 is moderately resistant to Turcium and Maydis leaf blight.

Liguleless trait can be phenotyped at seedling stage, which makes liguleless genotypes amenable for genetic studies such as gene-editing 'proof-of-concept' demonstration, and haploid induction rate (HIR) assessment of maize haploid inducer lines (Prigge *et al*. 2012). Moreover, since V601 is broadly in the genetic background of elite inbred V 407 (female parent of maize hybrids VMH53 and CMVL 55), it can also be directly used as a parental inbred in maize hybrid breeding programmes.

References

Duvick DN (2005) The contribution of breeding to yield advances in maize (*Zea mays* L.) In: Donald LS (ed) *Advances in Agronomy*. Science Direct:Academic Press. pp 83–145.

Prigge V, X Xu, L Li, R Babu, S Chen, GN Atlin and AE Melchinger (2012) New insights into the genetics of in vivo induction of maternal haploids, the backbone of doubled haploid technology in maize. *Genetics* 190(2): 781-93

19. V 602 (IC643994; INGR22019), a maize (*Zea mays*) germplasm carrying liguleless trait

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The ligular region, which separates leaf blade and sheath, establishes the leaf angle and determines the overall architecture of maize plant. Mutants with defective ligule and auricle development exhibit erect leaf architecture, and such leaf architecture facilitates high density planting and contributes to higher yields (Duvick 2005). A liguleless line V 602 has been developed at ICAR-VPKAS, Almora, from a cross between an elite inbred V 407 and a liguleless donor line PDH-3 (EC928978) obtained from University of Hohenheim, Germany India. The cross was advanced following pedigree method and in F5 generation, liguleless line V 602 was identified on the basis of its agronomic performance.

V 602 is a liguleless line with upright leaves. Its plant height is 165 cm and days to 75% brown husk is 90 (early group) (Table 1). Tassel is medium large and semi-open. Colour of anthers is purple and anthocyanin pigmentation is present in the silk. The cob length and cob girth of V 602 are 15.8 and 13.2 cm, respectively. The grain is yellow with slight dent and test-weight is 265 g. V 602 is moderately resistant to Turcium and Maydis leaf blight.

Owing to the ability of liguleless trait to be phenotyped at seedling stage, liguleless genotypes are useful for genetic studies such as gene-editing 'proof-of-concept' demonstration. Liguleless trait being recessive in nature,

Table 1: Morpho-agronomic characteristics of liguleless stock V602 and its parental lines

	Ligule	*Days to 50% pollen shed*	*Days to 50% silking*	*Plant height (cm)*	*Ear height (cm)*	*Days to 75% brown husk*	*Cob length (cm)*
PDH-3	Absent	49	50	165	90	86	8.4
V407	Present	53	55	135	70	91	15.8
V602	Absent	52	54	185	95	90	15.8
	Cob girth (cm)	Kernel rows	Grains/ Row	1000-seed wt.	Grain type	Turcicum leaf blight (1-9)	Maydis leaf blight (1-9)
PDH-3	10.5	12-14	16	160	Yellow Dent	7.0	7.0
V407	14.8	14-16	23	302	Orange Flint	2.0	3.0
V602	13.2	12-14	26	265	Yellow with Slight Dent	4.0	4.0

liguleless genotypes are also used to assess haploid induction rate (HIR) of maize haploid inducer lines (Prigge*et al.* 2012). V 602 carries the liguleless trait in the genetic background of elite inbred V 407 (female parent of maize hybrids VMH 53 and CMVL 55), which makes it directly useful as a parental inbred in maize hybrid breeding programmes.

References

Duvick DN (2005) The contribution of breeding to yield advances in maize (*Zea mays* L.) In *Advances in Agronomy* (Donald LS ed), pp. 83–145. Science Direct: Academic Press.

Prigge V, X Xu, L Li, R Babu, S Chen, GN Atlin and AE Melchinger (2012) New insights into the genetics of in vivo induction of maternal haploids, the backbone of doubled haploid technology in maize. *Genetics* 190(2): 781-93

20. PML 46 (IC643958; INGR22020), a maize (*Zea mays*) germplasm with tolerance to high density planting, orange colored kernel and medium maturity

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Introduction

The PML 46 is a medium maturing field corn inbred line possessing tolerance to high-density planting under tropical conditions. The PML 46 was developed at ICAR-Indian Agricultural Research Institute, New Delhi (Mukri *et al.* 2020). A pedigree breeding method was followed to derive PML 46 from the field corn hybrid, SAFAL-X12. It is a highly potential germplasm line to develop high-density tolerant cultivars that would enhance productivity through high-density planting.

Morpho-agronomic characteristics

PML 46 has green foliage with semi-droopy leaves. Plant height ranges from 126-140 cm and bears the cob at the middle of the plant (≈75 cm). The average productivity of PML 46 is 2.82 tha-1 under normal/recommended plant density. Under high-density planting, its grain yield potential increases up to 3.80 tha-1 (Table 1). It expressed stable yielding ability across locations and years (Table 2). It has conico-cylendrical cob, and orange, flint kernels.

Table 1: Performance of PML 46 at different plant density

Plant density (plants/ha)	*Plant height (cm)*	*Ear height (cm)*	*Cob length (cm)*	*Grain yield (t/ha)*
66,666	152.5	72.5	14.2	2.82
83,333	162.5	77.5	15	3.06
88,888	175	82.5	12.3	3.8
1,11,111	137.5	67.5	12	3.54

Table 2: Performance of PML 46 at station trials across locations (Delhi and Dharwad) and seasons (2016-2019)

Location/Year	*Plant Population*	*Grain Yield*
2016-17- RRC-Dharwad	83,333 plants/ha	3.83 t/ha
2017- IARI-Delhi	66,666 plants/ha	2.50 t/ha
2017-18-RRC-Dharwad	88,888 plants/ha	4.10 t/ha
2018-IARI-Delhi	66,666 plants/ha	2.60 t/ha
2019-IARI-Delhi	83,333 plants/ha	3.70 t/ha

Associated characters and cultivation practices

PML 46 is resistant to curvularia leaf spot and rust disease and tolerant to lodging. It has field tolerance to stem borer and early water stress. However, to obtain the expected grain yield, PML 46 requires 120 N: 90 P: 60 K per ha. An entire dose of phosphorus, potash, and 20 % nitrogen along with 25 kg-1ha of ZnSO4 should be applied to the soil at sowing and the remaining nitrogen should be given in 4 splits (Dass et al. 2010)

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21. PAUFL 1 (IC643975; INGR22021), a cotton (*Gossypium arboreum*) mutant without Lint, Fuzz and trichomes

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Cotton is the most important source of natural fibre worldwide. Cotton fibre is the extension of ovule epidermal cells and develops in four overlapping stages namely fibre initiation, primary cell wall formation (fibre elongation), secondary cell wall thickening (mainly cellulose deposition), and maturation. Cotton seed fibres are of two types: short (fuzz) and long (lint). In addition to ovule, epidermal outgrowths known as trichomes are also present on almost all aerial plant parts. Here, we report a fibreless (fuzzless and lintless) and trichomeless mutant namely PAUFL 1 of *desi* cotton (*Gossypium arboreum* L.). It was identified as a spontaneous mutant in the plot of *desi* cotton variety LD 327 at PAU Regional Research Station, Faridkot (Punjab). LD 327 was developed from the intra-*arboreum* cross of G 57 × (G 27 × LD 124) following pedigree method and was released for commercial cultivation in the Punjab state during1987. PAUFL 1 is characterized by lack of fuzz and lint fibres on the seed coat and trichomes on other aerial plant parts. Like its wild type parent LD 327, the mutant possesses pigmented (red) plant body, digitate leaves, and variegated (pink and white) petals. PAUFL 1 has consistently maintained its mutant phenotype since its identification in 2003 through 2021. Genetic analysis involving F_2 and backcross populations showed that the fuzzless-lintless-trichomeless phenotype was governed by a single recessive gene (Grover *et al*., 2016).

Monogenic recessive control of fibreless phenotype in *desi* cotton mutants has also been reported by (Rong *et al*. 2005). Tight linkage between fuzzless-lintless- trichomeless traits was observed in the segregating populations derived from PAUFL 1 × wild type *desi* cotton crosses. According to (Arpat *et al*.,2004) and Rong *et al*. (2005), lint fibres and trichomes shared a similar pathway in their early stages of development. Alternatively, they may be under the control of same gene that influences trichome and fibre development (Desai *et al*., 2008). *Desi* cotton mutant PAUFL 1 can be used for the identification of transcriptional regulators and metabolic pathways involved in initiation of cotton fibre and trichomes which has important implications for enhancing cotton fibre yield and quality. In a study involving this mutant, it was shown that a positive correlation existed between trichome density and whitefly population suggesting that lower trichome density favours low incidence of whitefly in cotton (Grover *et al*., 2016).

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22. VR 1141 (IC644006; INGR22022), a finger millet (*Eleusine coracana*) germplasm for banded blight resistance

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Finger millet, VR 1141 is banded blight resistant line developed d by crossing VR 708 with GPU 48 during 2010. through pedigree method of selection. Single plant selections were made from the cross up to five generations and during, 2017 uniform bulk selections were promoted to preliminary yield trial and evaluated with uniform bulks from other crosses. Twenty-four promising lines along with local and national checks for yield; resistant and susceptible check for blast disease resistance were evaluated in Randomized block design with three replications during four consecutive years (*kharif*, 2017 to 2020) at Agricultural Research Station, Viziangaram (lat 18°10′ N, long 83°39′ E and altitude of 74 msl), Andhhra Pradesh which is a hot spot for banded blight disease.

The entry, VR 1141 matures in 124 days and grows to height of 125 cm and it is having more number of fingers per ear (10) with broad finger width (1.2cm). It recorded less incidence of banded blight (3.2% pooled data) among all the 30 entries tested for banded blast resistance. The score for banded blight was significantly lower compared to all the checks during four years of testing. It recorded 49.92%, 74.92% and 88.64% less incidence of finger blast over Resistant check, Local check and susceptible check respectively. It also showed moderate resistance to neck blast (12.4% pooled data) and finger blast (15.8% pooled data). Hence, VR 1141 is unique in terms of banded blight resistance and moreover it is an advanced breeding line which can be directly used for development of high yielding banded blight resistant varieties.

23. VR 1122 (IC0644004; 22023), a finger millet (*Eleusine coracana*) germplasm with finger blast resistance

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Finger millet, VR 1122 is finger blast resistant line developed by crossing VR 708 with GPU 48 during 2010. Pedigree method of breeding was followed. Single plant selections were made from the cross up to five generations and during, 2017 uniform bulk selections were promoted to preliminary yield trial and evaluated with uniform bulks from other crosses. Twenty four promising lines along with local and national checks for yield; resistant and susceptible check for blast disease resistance were evaluated in Randomized block design with three replications during four years (*kharif*, 2017 to 2020) at Agricultural Research Station, Viziangaram (lat 18°10′ N, long 83°39′ E and altitude of 74 msl), Andhhra Pradesh which is a hot spot for blast disease.

VR 1122 belongs to medium maturity (117 days) with medium plant height (118 cm) and more number of productive tillers/plant (4). The entry, VR 1122 was screened along with local variety (VR 847), resistant check (GE 4999) and susceptible check (VR 708) under high disease pressure under field conditions during consecutive four years from 2017 to 2020. It recorded significantly lower score of finger blast over all the checks during all four years of testing. It recorded 66.82%, 85.29% and 96.19% less incidence of finger blast over Resistant check, Local check and Susceptible check respectively. It recorded less incidence of Finger blast (2.1% pooled data) among all the 30 entries tested for finger blast resistance and is considered as resistant to finger blast. It also showed resistance to neck blast (4.6% pooled data) and banded blight (5.6% pooled data). Hence, VR 1122 is unique in terms of finger blast resistance and moreover, it is an advanced breeding line with resistance to neck blast and banded blight as well and can be used directly for development of high yielding blast resistant varieties.

24. SPV 2804 (IC0288432; INGR22024), a sorghum (*Sorghum bicolor*) germplasm with higher Leaf Stem Ratio (0.32) and low HCN content (40.9%)

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Sorghum (*Sorghum bicolor*) is the fourth most important cereal following rice, wheat and maize and staple food in the semi-arid parts of the world. Single cut forage sorghum has importance considering the demand for the fodder from the dairy sector of the country. Good quality fodder must have high leaf: stem ratio. Similarly, HCN is the antinutritional factor present in the sorghum fodder. So low value of HCN is desirable for better fodder quality in forage sorghum. Therefore, identification of the *Kharif* single cut forage sorghum genotype with more leaf: stem ratio and low HCN is if prime importance. Considering this, the *kharif* single cut genotype SPV 2804 which was found superior for both these traits in the National Level trial- Initial Varietal and Hybrid Trial (Single Cut) *Kharif* 2020 conducted by Indian Institute of Millets Research (IIMR), Hyderabad is proposed for registration.

In the National Level trial-Initial Varietal and Hybrid Trial (Single Cut)-*Kharif* 2020, the *Kharif* Single cut forage Sorghum Genotype SPV 2804 contributed by Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) was tested during *Kharif* 2020. Trial consisted of the testing entries along with the checks CSH 40F, CSH 36F, CSV 21F, CSV30F, CSV 35F. The experiments were sown in randomized block design with three replications. The character leaf stem ratio was recorded at 10 locations across the India while the trait HCN content was estimated at four locations across India.

For the character leaf stem ratio, the genotype SPV 2804 ranked first at National level with the value of 0.32 while the checks were with low values i.e. CSH 40F (0.26), CSH 36F (0.29), CSV 21F (0.27), CSV30F (0.29), CSV 35F (0.30). While for the character HCN %, the genotype SPV 2804 recorded lower HCN content at National level with the value of 40.9% while the checks were with high values i.e. CSH 40F (41.3%), CSH 36F (42.5%), CSV 21F (41.9%), and CSV 35F (44.2%).

Thus, it was concluded form the present study that considering the more leaf: stem ratio and low HCN in the genotype SPV 2804, it need to be exploited in breeding for development of genotypes with better fodder quality in single cut forage sorghum as the donor parent in the crossing programme.

25. SPV 2805 (IC643757; INGR22025), a sorghum (*Sorghum bicolor*) germplasm with longer leaves (86.5 cm), greater plant height (276 cm) and more number of leaves per plant (12.9)

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Sorghum (*Sorghum bicolor*) is the fourth most important cereal following rice, wheat and maize and staple food in the semi-arid parts of the world. Single cut forage sorghum has importance considering the demand for the fodder from the dairy sector of the country. Leaf length is one of the important contributing trait in fodder yield. Similarly, higher plant height as well as more number of leaves per plant are also good supporting traits in improving the fodder yield. Therefore, identification of the *Kharif* single cut forage sorghum genotype with more more leaf length along with the supporting traits like higher plant height and more number of leaves per plant is if prime importance. Considering this, the *kharif* single cut genotype SPV 2805 which was found superior for the trait i.e. more leaf length in the National Level trial-Initial Varietal and Hybrid Trial (Single Cut)-*Kharif* 2020 conducted by Indian Institute of Millets Research (IIMR), Hyderabad is proposed for registration.

In the National Level trial-Initial Varietal and Hybrid Trial (Single Cut)-*Kharif* 2020, the *Kharif* Single cut forage Sorghum Genotype SPV 2805 contributed by Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) was tested during *Kharif* 2020. Trial consisted of the testing entries along with the checks CSH 40F, CSH 36F, CSV 21F, CSV30F, CSV 35F. The experiments were sown in randomized block design with three replications. The character leaf length, plant height and number of leaves per plant were recorded at 12 locations across the India.

For the character leaf length, the genotype SPV 2805 ranked first at National level with the value of 86.5 cm. while the checks were with low values *i.e.* CSH 40F (79.9 cm), CSH 36F (82.7 cm), CSV 21F (75.5 cm), CSV30F (79.0 cm), CSV 35F (80.7 cm). While for the character plant height, the genotype SPV 2805 ranked first at National level with the value of 276 cm while the checks were with low values *i.e.* CSH 40F (263 cm), CSH 36F (264 cm), CSV 21F (253 cm), CSV30F (265 cm), CSV 35F (230 cm). Similarly, for the character number of leaves per plant, the genotype SPV 2805 ranked third at National level with the value of 12.9 while the checks were with low values *i.e.* CSH 40F (12.3), CSH 36F (12.7), CSV 21F (12.4), CSV30F (12.8), CSV 35F (12.5).

Thus, it was concluded form the present study that considering the highest leaf length along with the supporting traits like higher plant height and more number of leaves per plant in the genotype SPV 2805, it need to be exploited in breeding for development of genotypes with better fodder yield contributing character in single cut forage sorghum as the donor parent in the crossing programme.

26. SPV 2596 (SM-2288-3) (IC643980; INGR22026), a sorghum (*Sorghum bicolor*) germplasm for high fresh stalk yield and high biomass

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Introduction

Sorghum breeding programs have accomplished the yield gains through use of germplasm from the primary genetic pool, however, overcoming the yield plateau needs introduction of novel variations into the crop gene pool and development of ready-to-use pre- breeding material. Derivatives from incompatible crosses ae reported to produce large de novo variations through genomic shock from the alien. Variations in F2 are advanced through pedigree method and stable lines are used as pre-breeding material.

Associated Characters and Cultivated Practices

The genotype SPV 2596 is a sweet sorghum line with tall plants and thick juicy stalks. It has high fresh stalk yield and high total fresh biomass. Fresh stalk yield and biomass were significantly more than three checks, CSV 19SS, CSV 24SS and CSH 22SS while they were on par with fourth check, SPH 1880. Total sugars were significantly more than two varietal checks CSV 19SS and CSV 24SS and on par with hybrid checks. Brix percentage is very important factor for use of sweet sorghum in the industry and in the present entry it is significantly superior to all. Data was collected in the Initial and Advanced Sweet Sorghum Varietal and Hybrid Trial (AICRP) during *Kharif* 2018 at 10 locations of All India Coordinated Research Project on Sorghum (Table 1). Fresh stalk, biomass and ethanol yield are the important traits for the improvement of sweet sorghum. In terms of plant height, brix % and computed ethanol yields, it was superior to three checks and holds promise as start material for sweet sorghum breeding among the 15 entries tested in AICRP *Kharif* 2018. This genetic stock is a unique material as the cross between Sorghum and Maize has been accomplished for the first time in sorghum crop improvement program.

Table 1: Initial and Advanced Sweet Sorghum Varietal and Hybrid Trial - *Kharif* 2018 All India data across 10 centres

Entry	*Fresh stalk yield (t/ha)*	*All India ranking*	*Total fresh biomass (t/ha)*	*All India ranking*	*Total Sugars (%)*	*All India ranking*	*Brix %*	*All India ranking*	*Plant height cm*	*All India ranking*
SPV 2596	47.5	2	62.8	1	14.3	4	16.8	1	300	2
CSV 19SS (Check1)	39.85	16	54.86	10	13.68	13	15.38	14	280.91	5
CSV 24SS (Check 2)	38.43	18	53.28	15	12.55	19	14.17	19	249.55	19
SPH 1880 (Check 3)	46.23	4	61.42	2	13.68	14	15.60	12	326.21	1
CSH 22SS (Check 4)	42.43	11	53.51	12	13.84	11	15.92	11	284.07	4
General Mean	44.3		56.8		13.67		15.7		272	
CV (%)	17.9		19.52		10.23		11.88		10.32	
SE of Difference	3.65		4.35		0.56		0.59		8.9	
P-Value	0.06		0.04		0.01		0.00		0.00	
CD (5%)	7.3		8.6		1.11		1.16		17.54	
CD (1%)	9.7		11.4		1.47		1.53		23.13	

27. IS 1212-4-1-1 (IC643968; INGR22027), a sorghum (*Sorghum bicolor*) germplasm with high oil content (4.49%); hard seed with bigger germ size

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Oil content in sorghum grains is an important component in determining sorghum as a functional food. Sorghum, with its ability to yield high with low inputs, can be used as an alternative oil source with clinical advantages. Sorghum varieties can be additional sources of edible oil due to the presence of clinically important saturated and high concentration of unsaturated fatty acids. Breeding efforts towards identifying end use specific cultivars are required for increased profitability to the farmers. At IIMR, Hyderabad a set of 256 genotypes including the germplasm lines and released cultivars were evaluated for oil content during 2014-15 and 19 genotypes with high oil content were selected. These 19 were evaluated for oil content and hardness during 2015-16 at IIMR, Hyderabad and at three locations (Gulberga, Solapur and Hyderabad) during 2016-17. These genotypes were planted at three locations, *viz*., Regional Agricultural Research Station, Gulberga; Centre on Rabi sorghum, Solapur and ICAR-Indian Institute of Millets Research (ICAR- IIMR), Hyderabad during *rabi* season of 2016-17.

Data on oil content was recorded for the samples from IIMR during 2015-16 and all the three locations during 2016-17 to study the stability of oil content (Table 1). Oil content ranged from 3.14% to 4.76%. The germplasm line, IS 1212-4-1-1 was found to have high oil content and also better adapted to all test environments with stable mean oil content. IS 1212-4-1-1 is a pure line selection from germplasm line belonging to Kafir-bicolor (KB) race. It is early flowering (flowering in less than 60 days) with semi loose panicle. The grain color is red and the grains are hard with large germ size. Grains of IS 1212 were harder with large germ size. This genotype is a potential candidate while breeding for high oil content with better storability and could be of more value in breeding as they are suitable across environments.

Table 1: Performance of IS 1212 for oil content and seed traits in sorghum during 2015 and 2016

Genotype	*100 grain weight (g)*	*Grain hardness (N)*	*Germ size score*	*Oil Content (%)*					
				2015-16	*2016-17*				
				Hyderabad	*Gulberga*	*Solapur*	*Hyderabad*	*Mean 2016*	*Over all mean*
IS 1212-4-1-1	2.06	8.41	7	4.55	4.41	4.35	4.64	4.46	4.49
M 35-1	3.69	7.32	5	2.79	3.11	3.28	3.28	3.22	3.12
CSV 27	1.91	7.50	5	2.80	3.29	3.41	3.66	3.45	3.29
BJV 74	3.06	7.41	5	2.55	3.09	3.35	3.23	3.22	3.06
Mean	2.57	6.32	4.79	2.97	3.82	3.94	4.07	3.94	3.94
C. V.	18.5	20.7	18	4.53	4.14	3.21	3.18	3.51	
CD 0.05%	1.01	1.89	2	0.23	0.26	0.21	0.21	0.23	

Germ size score 1-9 scale where 1= very small; 3=small; 5= medium; 7= large and 9= very large

28. IS 31714-2-1-1 (IC643969; INGR22028), a sorghum (*Sorghum bicolor*) germplasm or high oil content (4.17%); very bold seed with medium hardness and small germ size

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Grain oil content is an important component in determining sorghum as a functional food. Sorghum, with its ability to yield high with low inputs, can be used as an alternative oil source with clinical advantages, and thus sorghum varieties with high oil content can be additional sources of edible oil due to the presence of clinically important saturated and high concentration of unsaturated fatty acids. At IIMR, Hyderabad a set of 256 genotypes including the germplasm lines and released cultivars were evaluated for oil content during 2014-15 and 19 genotypes with high oil content were selected (Table 1). These 19 were evaluated for oil content and hardness during 2015-16 at IIMR, Hyderabad and at three locations (Gulberga, Solapur and Hyderabad) during post rainy season of 2016-17. Mean oil content across environments ranged from 3.14% to 4.76%. The germplasm line, IS 31714-2-1-1 was found to have oil content significantly more than the check (M 35-1). IS 31714-2-1-1 is a pure line selection from germplasm line belonging to Durra-caudatum (DC) race from Yemen. It has small very compact panicle. The grain color is reddish orange and the grains are medium hard with small germ size. The grains are very bold with 100 grain weight of 4.94 g. It has medium grain hardness and small germ size. This genotype is a potential candidate to breed for high oil content with bold seed. Breeding efforts to identify such end-use specific cultivars are required for increased profitability to the farmers. The information generated and the genotypes identified will help in breeding sorghum with high oil content thus enhancing the demand for sorghum as an industrial crop.

Table 1: Performance of IS 31714 for oil content and seed traits in sorghum during 2015 and 2016

Genotype	*100 grain weight (g)*	*Grain hardness (N)*	*Germ size score*	*Oil Content (%)*					
				2015-16	*2016-17*				
				Hyderabad	*Gulberga*	*Solapur*	*Hyderabad*	*Mean 2016*	*Over all mean*
IS 31714-2-1-1	4.94	4.47	3	4.38	3.93	4.25	4.12	4.10	4.17
M 35-1	3.69	7.32	5	2.79	3.11	3.28	3.28	3.22	3.12
CSV 27	1.91	7.50	5	2.80	3.29	3.41	3.66	3.45	3.29
BJV 74	3.06	7.41	5	2.55	3.09	3.35	3.23	3.22	3.06
Mean	2.57	6.32	4.79	2.97	3.82	3.94	4.07	3.94	3.94
C. V.	18.5	20.7	18		4.14	3.21	3.18	3.51	
CD 0.05%	1.01	1.89	2		0.26	0.21	0.21	0.23	

Germ size score 1-9 scale where 1= very small; 3=small; 5= medium; 7= large and 9= very large

29. SPV 2017 (IC643970; INGR22029), a sorghum (*Sorghum bicolor*) germplasm for high in-vitro true digestibility of dry matter (TDDM/IVDMD), organic matter digestibility (OMD) and Metabolisable energy content (ME); low Acid Detergent Fibre (ADF) and Acid Detergent Lignin (ADL) content

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Common property resources for grazing and land under fodder cultivation are declining in many countries; hence, dependence on crop residues for animal feeding will increase. In developing countries where livestock are reared under mixed-farming systems, crop residues play a significant role in maintenance and production of ruminants. Several newer cultivars of brown midrib sorghum (containing a mutant bmr gene) have been developed through plant breeding and have the potential for early maturity, high grain and forage yields, lower susceptibility to insects and pests and importantly, lower in hydrocyanic acid and lignin contents. Stover cell-wall components such as lignin and structural carbohydrates were shown to be important traits related to stover digestion for quality assessment of stover samples. In vitro gas production kinetics and degradability along with chemical composition can better predict their potential feeding values.

SPV 2017 was developed from a cross between CSV 15 and the bmr germplasm line, IS 21891 during 2007. CSV 15 was released as dual purpose variety for all *kharif* sorghum growing areas in the country and as forage variety for Northern Western zone while IS 21891 is a brown midrib source carrying the gene *bmr 8*. The significance of this brown midrib mutation is that it greatly reduces lignification and cell-wall concentration, increases digestibility and voluntary intake of feed by ruminants. This single-locus mutation signifies the single most rapid and valuable mechanism of genetically modifying nutritional value of forage and dual-purpose sorghum. The SPV 2017 was evaluated in *kharif* 2010 in AICRP on sorghum trials and in 2018 it is evaluated in four rumen-cannulated Murraha buffalo samples where, four stover samples were collected from two field replicates. The four Murraha buffaloes may be considered as four different environments of the study. The SPV 2017 was found superior in stover digestible factor contents in the present analysis and comparison with forage, sweet and grain sorghum cultivars.

The testing of SPV 2017 in AICRP on sorghum IAVHT trials *kharif* 2010, it has been found that SPV 2017 is superior in IVDMD (42.15%) and ME (6.36 mj/kg) and contains lower quantity of ADF (47.60%) and ADL (5.83%) when compared to CSV 23 variety with lower values of IVDMD (38.70%), ME (5.70 mj/kg) and higher values of ADF (49.85%), ADL (6.62%) and in CSV 21F with lower values of IVDMD (38.45%), ME (5.76%) and higher values of ADF (49.85%) and ADL (6.59%). In the study conducted with buffaloes, the stover compositional factors like ADF (31.35% of DM) and ADL (1.67% of DM) contents were lower than other cultivars where, lower lignin values are preferable for good stover quality and the higher TDDM (58.35% after 72h of feeding), OMD (52.24% after 72h of feeding), ME (70.75% after 72h of feeding) where, higher values are preferred for good digestion of stover in animals rumen in SPV 2017 line when compared to other check varieties evaluated. These superior stover digestibility related factors in SPV 2017 line makes it most unique derived line among other cultivated lines. This line will serve as a excellent source to identify the genomic regions related to superior stover quality and also as excellent donor for many favourable traits for the development of single cut forage cultivars.

30. VR 1128 (IC644005; INGR22030), a finger millet (*Eleusine coracana*) germplasm with neck blast resistance

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Finger millet is one of the drought resistant small millet valued for its nutrient content in grains. It is a crop of both food and nutritional security. Blast is a major problem in finger millet crop which can hamper the production upto 70% in severe cases. Hence, finger millet improvement is oriented towards development of blast resistant high yielding varieties. Finger millet, VR 1128 is neck blast resistant line developed by crossing Uduru malligae and GPU 48 during 2010 followed by pedigree method of selection u to F6 generation. It was evaluated with other 23 promising lines along with local and national check for yield; resistant and susceptible check for blast disease resistance in Randomized block design with three replications during consecutive four years (*kharif*, 2017 to 2020) at Agricultural Research Station, Viziangaram (lat 18°10′ N, long 83°39′ E and altitude of 74 msl), Andhhra Pradesh which is a hot spot for blast disease. The proposed entry along with other test entries and two checks were tested under high disease pressure under field conditions during consecutive four years from 2017 to 2020.

The entry, VR 1128 is of late maturity (127 days) with medium plant height (123 cm) and with long ear length (9.4 cm). It recorded significantly lower score of neck blast over all the checks during all four years of testing. It recorded 75.75%, 83.33% NS 96.71% less incidence of neck blast over Resistant check (GE 4999), Local check (VR 847) and Susceptible check (VR 708) respectively. It recorded less incidence of neck blast (2.1% pooled data) among all the 30 entries tested for neck blast resistance and it also recorded resistance to finger blast (9.6% pooled data) and banded blight (4.6% pooled data). Hence, VR 1128 is unique in terms of neck blast resistance and moreover it is an advance breeding line which can be directly used for development of high yielding blast resistant varieties.

31. SPV 2595 (SM-2144-8) (IC643981; INGR22031), a sorghum (*Sorghum bicolor*) germplasm with higher brix and total sugars (14.3%), early maturing (116 days) and early flowering (80 days)

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Introduction

Sweet sorghum is a promising energy crop used for ethanol production. This ethanol can be blend upto 20% in India that demands for higher production and better ethanol yielding genotypes in sweet sorghum. Expansion of genetic base is the key activity for breeding programs to improve the

Table 1: Initial and Advanced Sweet Sorghum Varietal and Hybrid Trial - *Kharif* 2018 All India data across 10 centres

	All India	*All India*	*Ranking*	*All India*	*All India*	*All India*
Entry	*Days to flowering (days)*	*Days to Maturity (days*		*Total Sugars (%)*	*Non Reducing Sugars - Sucrose (%)*	*Brix %*
SPV 2595	80	116	2	14.3	9.99	16.5
CSV 19SS (Check1)	84.76	117.94	7	13.68	9.99	15.38
CSV 24SS (Check 2)	83.73	117.28	5	12.55	9.30	14.17
SPH 1880 (Check 3)	88.42	122.16	17	13.68	9.16	15.6
CSH 22SS (Check 4)	88.06	124.06	19	13.84	9.40	15.92
General Mean	85	119		13.67	9.60	15.7
CV (%)	4.66	4.49		10.23	8.82	11.88
SE of Difference	2	2.04		0.56	0.49	0.59
P-Value	0.00	0.00		0.01	0.87	0.00
CD (5%)	3.94	4.03		1.11	1.03	1.16
CD (1%)	5.2	5.31		1.47	1.41	1.53

traits. Introduction of novel variation is that are not available in the gene pools adds unique opportunity. In these lines we produced and selected one of the de novo variant for sweet sorghum traits. Such agronomically promising novel derivatives from incompatible crosses are reported in rice (Wang *et al.,* 2013, Meng *et al* 2020,). Variations in F_2 are advanced through pedigree method and stable lines are used as pre-breeding material.

Associated Characters and Cultivated Practices

The genotype SPV 2595 is a sweet sorghum line with tall plants and thick juicy stalks. It has high fresh stalk yield and high total fresh biomass. It is an early flowering and early maturing line with more brix than all the checks (Table 1). It has non-reducing sugars 9.99% as high as the best check variety. It showed brix value on par with check, the CSH 22SS (Check 4) and superior significantly compared to all other three checks. Data was collected in the Initial and Advanced Sweet Sorghum Varietal and Hybrid Trial (AICRP) during *Kharif* 2018 at 10 locations of All India Coordinated Research Project on Sorghum. Fresh stalk, biomass and ethanol yield are the important traits for the improvement of sweet sorghum. This genetic stock is a unique material as the cross between Sorghum and Maize has been accomplished for the first time in sorghum crop improvement program.

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32. WWN 55 (IC618375; INGR22032), a finger millet (*Eleusine coracana*) germplasm with bold white grains (3.14 g), longer finger length (12.27 cm) and multi-fingers ear head (10.13 cm)

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A total of 36 white finger millet accessions constituted of 27 landraces and nine released varieties were evaluated for 12 morphological characters including grain yield at Hill Millet Research Station, Waghai; Niger Research Station, Vanarasi under Navsari Agricultural University, Navsari and Hill Millet Research Station, Dahod under Anand Agricultural University at Gujarat, during *Kharif* 2018, 2019 and 2020. The objectives were to assess the genetic potential through the variability, correlation analysis among the quantitative traits. This research was carried out using randomized block design with three replications at each location. The pooled data of all three locations where used to study the genetic potential of white finger millet genotypes. Moderate genotypic and phenotypic coefficient of variation found for the traits *viz,* number of fingers per earhead, number of productive tillers per plant, straw yield per plant, grain yield per plant, finger length, harvest index and main earhead indicating ample scope of variation for these traits, allowing further improvement by selection of these traits. Low value of genotypic coefficient of variation and phenotypic coefficient of variation was found for the traits *viz.,* days to 50% flowering, finger width, days to maturity, plant height and 1000 grain weight indicating low variability for these traits. High heritability estimates were observed for days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, number of fingers per earhead, main earhead length, finger length, 1000 grain weight, grain yield per plant, straw yield per plant and harvest index showing low environmental influence on these traits and presence of additive gene action for these traits. Hence, priority can be given to these traits during selection to get more genetic gains. Genotypes *viz;* WWN 55 followed by GN 5 and GNN-7 were high yielding among all thirty six genotypes of white finger millet so they can be considered for varietal development and release for further selection. Thus, WWN 55 is multifinger (10.13), long finger length (12.27 em), bold grain (3.14 g), multitiller (7.93) white seeded high yielding (11.85 g) promising finger millet genotype with moderately resistance to pest and diseases found during three years of genetic evaluation at three different locations which used as a promising parent in further breeding programme.

33. GPU 28-2081 (IC643979; INGR22033), a finger millet (*Eleusine coracana* ssp. *coracana*) germplasm with longer finger length (10.7 cm)

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Finger millet is largely grown millet next to Pearl millet and Sorghum occupying an area of 1.1 - 1.2 million ha in India. Grains of finger millet are known for its highest level of calcium 300-350 mg/100g which is 20-30 times higher than that of any cereal. GPU28-2081 is a mutant (M_7) line with long fingers derived from induced gamma mutagenesis of GPU 28 variety at ICAR- Indian Institute of Millets Research, Hyderabad. GPU 28 variety were irradiated with gamma rays with doses of 500- 600 Gy. M_1 generation was raised during *kharif*, 2015 and about 2000- 3000 panicles from M_1 populations were harvested separately and were raised in panicle to row progeny in M_2 generation along with parental genotype. Selections were done during M_2 and M_3 generation and 61 selected mutant lines were advanced till M_7 generation. Sixty one promising mutants along their parental genotypes were conducted in replicated field trials in 4 environments: during 2019 and 2020 at Indian Institute of Millets Research, Hyderabad in Telangana, Latitude 17°23′ N, L ongitude 78°40′ E and Altitude of 505 msl) and during 2020 at Agricultural Research Station, Vizianagaram in Andhra Pradesh, Latitude 18°10′ N, Longitude 83°39′ E and Altitude of 74 msl), and AICRP Small Millets Project Coordinating Unit, Bengaluru in Karnataka, Latitude 12°97′ N, Longitude 77°59′ E and Altitude of 920 msl).

The proposed genotype GPU 28-2081 recorded finger length of 10.7 cm (average of four locations) in comparison with its parental variety GPU 28 (7.8 cm) and other check varieties GPU 67 (6.6 cm) and MR 6 (9.9 cm). GPU28-2081 recorded days to 50% flowering of 82.6 days (medium flowering) and recorded 7.4 number of fingers and recorded grain yield of 3.4 t/ha. GPU 28-2081 is unique in terms finger length which is one of the important yield attributing traits and moreover it is an improved breeding line which can be used directly used for grain yield improvement in finger millet.

34. DHBM93-3 (IC643966; INGR22034), a barnyard millet (*Echinochloa frumentacea*) germplasm with glumeless florets and seeds

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Barnyard millet is one of the oldest domesticated crops cultivated in India, Japan, Korea, China and Africa. There are two cultivated species *viz.,* Indian barnyard millet (*Echinochloa frumentacea*) and Japanese barnyard millet (*Echinochloa esculenta*). This crop is mainly cultivated foe both grains and fodder in hilly areas like Uttarakhand and Arunachal Pradesh and plain areas like Tamil Nadu, Andhra Pradesh, Karnataka, Telangana. Nutritionally barnyard millet is rich in dietary fibre content, Iron and Zinc and vitamins.

The recombination breeding is completely lacking in small millets because of the difficulties in doing crosses with tiny flower size and large number of flowers per panicle. The flower opening to remove anthers in emasculation is not a successful way as it leads to drying of the floret. 1000-1200 florets per panicle will open at different time and complete anthesis completes in 7-8 days. The tiny flowers will be covered with two glumes, two lemma and two palea. Lemma and palea are tightly attached and forceful opening damages the ovary and stigma. Anthesis starts from top to bottom but within each receme of the panicle, florets arranged on side of the rachis will open first and middle florets will open later. All these difficulties make the emasculation and pollination work difficult in barnyard millet. The mutant line is having 90% of the florets not covered with glume and covered only with lemma and palea. Lemma and palea are transparent in nature in barnyard millet which makes to see the anther development without opening of the flower. This glumeless character helps the breeder to select florets which are going to open tomorrow and emasculate today or the fully developed anthers can be seen without opening of florets which helps to identify the florets for emasculation. This definitely helps the breeder to go for hand emasculation and pollination in barnyard millet which is otherwise a difficult work in the highly self-pollinated crop like this.

The original variety DHBM93-3 (national check variety) was treated with gamma irradiation at 300 Gy. In M5 generation of a population plants with glumeless were identified and advanced to next generations for improving stability. The glumeless mutant DHBM93-3 (DHBM93-3-8-3-32-43) is having normal plant height of 210 cm with erect growth habit. There is no pigmentation on leaf sheath and glumes like original DHBM93-3. The number of productive tillers produced is 2-4 and the panicle length of 20-22 cm and width of 1.8-2.0 cm. The number of recemes produced is ranging from 36-45 per panicle. The days to flowering is between 70-75 days and days to maturity is between 110-115 days. The average fodder yield of two replications sown in 3m row length of two rows is 2.0-2.5 kg and the grain yield is 1.0-1.2 kg. The panicle shape is compact and the florets are arranged on both sides of rachis.

35. 170-SB-19 (J-2642) (IC643982; INGR22035), a pearl millet (*Pennisetum glaucum*) germplasmwith high Fe content (84 ppm); high Zn content (50 ppm)

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Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is an important coarse grain cereal and forage crop of the arid and semi-arid region of India and several African regions and is grown on 26 million ha in some of the most marginal arid and semi-arid tropical environments of Asia (11 million ha) and Africa (15 million ha), is a major source of dietary energy and nutritional security for a vast population in these regions (Velu *et al.*, 2008). Micronutrient malnutrition has been recognized as vast health issue, affecting over two billion people, mostly women, children and infants worldwide especially in developing countries (WHO 2001 and Berwal *et al.*, 2019). Several approaches, such as medical supplementation, industrial food fortification, dietary diversification and crop bio-fortification have been suggested to address the problem of micronutrient malnutrition. Biofortification refers to the development of crop cultivars with higher level of micronutrients. Bio-fortification of this crop through conventional plant breeding approaches is the cheapest method for achieving this objective. For this it is first and most important thing to have micronutrient dense parental lines, therefore, the present investigation was carried out to identify the micronutrient dense pearl millet parental line to develop bio-fortified pearl millet hybrids.

The proposed parental line tested across 6 locations *viz.*, Mandor, Jaipur, Hisar, New Delhi, Jamanagar and Dhule in zone A and B during kharif 2019 with view to identify the biofortified lines having high Fe and Zn. The trial comprises 22 entries including two checks having high Fe and Zn contributed by different centers of ICAR- AICRP on Pearl millet. In this trial, pearl millet research station, Junagadh Agricultural University, Jamnagar was contributed five entries (J-104, J-2615, 170-SB-19, 171-SB-19 and 172-SB-19). The proposed parental line 170-SB-19 (J-2642) is develop at Pearl Millet Research Station, JAU, Jamnagar and its pedigree is (J-2532 × J-2571)-23-1-1-B- B and designated in the year 2021. Among the all parental lines along with two checks *viz;* PCMHFeB-05 and Dhanshakti analyzed for iron (Fe) content, Zinc (Zn) content, days to flowering, plant height, panicle per plant and agronomic scores. The Fe content ranged from 44 ppm to 136 ppm and Zn content varied from 22 ppm to 63 ppm. On the basis of average value of all the location, six parental lines (170-SB-19, H 19/0002, PCMHFeB-05(C), PCMHFeR17-11, PCMHFeR-17-6 and PCMHFeR-17-7) recorded>85 ppm Fe and >50 ppm Zn in grain. A strong positive correlation was observed between Fe and Zn contents. These results are earlier reported a large variability for grain Fe and Zn content in pearl millet, involving inbred lines, improved open pollinated varieties and germplasm by (Berwal *et al.* 2019 and Velu *et al.,* 2007, 2008). The proposed parental line will be useful for development of biofortified pearl millet hybrids.

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36. EC499760 (EC499760; INGR22036), a lentil (*Lens culinaris*) germplasm with bold seed (7.1-7.83 g)

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Lentil (*Lens culinaris* Medik.) is one of the major cool-season pulse crops worldwide. Its increasing demand as a staple pulse has led to the unlocking of diverse germplasm collections conserved in the genebanks to develop its superior varieties. The Indian National Genebank, housed at the ICAR-National Bureau of Plant Genetic Resources, New Delhi, India, currently has 2,324 accessions comprising 1,796 indigenous and 528 exotic collections. Characterization was conducted to unveil the potential of lentil germplasm by assessing its agro-morphological characteristics and diversity, identifying trait-specific germplasm, and developing a core set. The complete germplasm set was characterized for two years, *i.e.,* 2017–2018 and 2018–2019, and data were recorded on 26 agro-morphological traits. The results revealed significant variations as evident from the mean, range, and coefficient of variations. An unique accession EC499760 was observed with very bold seeds, weighing 7.1–7.83 g of 100 seed weight. The bold seeded expression was validated under field conditions over the years and location.

37. IC241532 (IC241532; INGR22037), a lentil (*Lens culinaris*) germplasm for early flowering (51 days) and maturity (93 days)

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38. IC259504 (IC259504; INGR22038), a wild bean (*Vigna vexillata*) germplasm highly resistant to bruchid

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Genus *Vigna* although a potential grain leguminous group is greatly affected by bruchid infestation in terms of production and post-harvest storage. Moreover, there is dearth of natural and reliable sources of bruchid resistance in cultivated *Vigna*, possibly because of low seed yield owing to a narrow genetic base. Therefore, a diverse sample of 69 black gram germplasm accessions, representing landraces and crop wild relatives (CWR), were assessed for resistance against *Callosobruchus maculatus*. Considerable variation was observed in physical seed traits. Growth parameters like total oviposition, emergence holes, adult emergence (AE), percent seed weight loss (PSWL) and growth index (GI) varied significantly among the accessions. Based on three key traits *viz.* AE, PSWL and GI the accessions were classified into six groups *viz.,* immune (1), resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS). Accessions IC259504 (*V. vexillata*) were immune to bruchid infestation, respectively supported by X-ray radiographic evidence. Correlation heat matrix indicated GI was positively correlated with AE (r= 0.780) and PSWL (r= 0.574). Seed hardness showed a significant negative correlation with AE (r= -0.379). The reported immune accessions could be utilized in various breeding programs for the development of bruchid resistant cultivars in *Vigna* species.

39. IC248326 (IC248326; INGR22039), a wild bean (*Vigna vexillata*) germplasm resistant against *Callosobruchus maculatus*

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Bruchids (Coleoptera: Bruchinae) are serious pests of stored pulses causing up to 100% grain losses under unattended conditions. Among several species, three species *viz., Callosobruchus chinensis* L., *C. maculatus* F., and *C. analis* F., are highly destructive and cosmopolitan in nature. Management of bruchids remained challenging over decades as numerous methods adopted were found ineffective across space and time. In this situation, identifying bruchid resistance in germplasm lines, cultivars or landraces is advocated through HPR studies. Simultaneously, introgression of alien genes from crop wild relatives offers a viable option to diversify and widen the genetic base of legume varieties (Pratap *et al.*, 2020). Identification of resistant wild mungbean (TC1966) against *C. chinensis* opened an array of opportunities to explore wild *Vigna* relatives including cultivated ones for bruchid resistance. Several successful hybridization attempts were made to transfer bruchid resistance genes to the cultivars of interest. Further, studies also identified QTLs responsible for bruchid resistance in wild *Vigna* and their progenies under targeted breeding efforts. However, the studies related to identifying resistance sources from diverse genetic resources in wild *Vigna* species and the attempts to transfer identified genes to cultivated ones still remains limited and therefore warrant additional research.

Considering the above, the study was conducted to screen the wild *Vigna* panel of 42 wild *Vigna* accessions representing thirteen *Vigna* species endemic to India for their relative resistance to three bruchid species (*C. chinensis*, *C. maculatus* and *C. analis*) between 2019-21 at ICAR- IIPR, Kanpur, India. The seeds of *Vigna* accessions were obtained from the Germplasm Bank, Division of Crop Improvement, ICAR- IIPR, Kanpur (India). The qualitative and quantitative seed traits of all the accessions were recorded (following NBPGR minimum descriptors to assess their influence on bruchid infestation and to identify the trait/s responsible for accessions' resistance reaction to bruchids. The accessions were screened against the three bruchid species following a thorough screening method involving 'Free-choice', 'No-choice' and confirmatory 'no-choice', tests (Revanasidda *et al.,* 2021). The accessions were categorized based on per cent seed damage. Based on seed damage, the accession IC248326 of *V. vexillata* was found resistant against *C. maculatus* with 1.1, 4.4 and 1.11 per cent seed damage in free-choice, no- choice and confirmatory no-choice experiments, respectively eventhough the seeds received an average of 1, 1.3 and 2.44 eggs per grain, respectively. Advanced correlation studies indicated that the seed morphological parameters did not influence resistance reaction significantly indicating involvement of certain biochemical components in seed coat and cotyledons. Therefore, this accession can be an invaluable genetic resource for introgression breeding for multiple traits in mungbean and urdbean. Simultaneously, this accession may be deployed in introgression breeding to develop bruchid resistant superior cultivars in *Vigna* crops.

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40. IC331436 (IC331436; INGR22040), a wild bean (*Vigna stipulacea*) germplasm with early flowering (20 days after sowing) and early maturity (49 days after sowing)

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Among various wild and useful *Vigna* species, *Vigna stipulacea* (Lam) Kuntz., is an important one with tremendous potential to be utilized in the Vigna improvement programme. This species is a reservoir of various useful traits *viz*., faster growth, shorter duration and broad resistance to various pests and diseases. The desirable traits can be transferred to the cultivated *Vigna* species. To evaluate and select the best germplasm to be harnessed in the breeding programme, we assessed the genetic diversity of *V. stipulacea* conserved in the Indian National Genebank, based on morphological traits and microsatellite markers. A diverse panel of 94 accessions (acc.) of *V. stipulacea* conserved in the NGB housed at ICAR-NBPGR, New Delhi was grown at ICAR-Indian Institute of Pulses Research (ICAR-IIPR), Kanpur, Uttar Pradesh (26˚27′N latitude, 80˚14′E longitude, 452.4 meter above mean sea level (AMSL) for two consecutive years, *i.e*., during the rainy season (*Kharif*) 2018 and 2019. Significant variation was recorded for the morphological traits studied. Accessions IC331436 was identified for, early flowering. IC331436 was flowered in 20 days after sowing (Gore *et al.,* 2022). Crop duration has a direct impact of fitting a cultivar in a cropping system, and early duration varieties can fit well in short-season windows, thereby offering the opportunities of horizontal increase in area (Pratap *et al*.,2013).

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41. IC251442 (IC251442; INGR22041), a rice bean (*Vigna umbellata*) germplasm highly resistant to *Callosobruchus maculatus* F

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Among 1700 species of bruchids, nearly 20 species cause economic losses to the stored pulses. Among these, three species *viz*., *Callosobruchus chinensis* L., *C. maculatus* F., and *C. analis* F. are considered to be highly destructive and cosmopolitan in nature (Aidbhavi *et al*. 2023). Management of bruchids remained challenging over decades as innumerous methods adopted have been found ineffective across space and time. Host Plant Resistance (HPR), one of the traditional yet most effective methods being adopted for decades. Efforts were made to find resistant sources in various wild legumes, particularly in *Vigna* subgenus *ceratotropics*. Initial identification of bruchid resistance was done in a wild mungbean accession, TC1966, against *C. chinensis*, followed by identification in both cultivated and wild *Vigna* germplasm lines. Hybridization was also attempted between a bruchid susceptible mungbean cultivar VRM (Gg) 1 and a bruchid resistant wild rice bean genotype TNAU Red, revealing a major QTL (qSD05) on chromosome no. 05 responsible for bruchid resistance.

This study focused on screening 42 diverse and endemic *Vigna* accessions three bruchid species (*C.chinensis*, *C. maculatus* and *C. analis*) using improved screening methodology at ICAR- IIPR, Kanpur. The qualitative and quantitative seed traits of all the accessions were recorded following NBPGR minimum descriptors to assess their influence on bruchid infestation and to identify the trait(s) responsible for accessions' resistance reaction. The accessions were categorized based on per cent seed damage (Revanasidda *et al*., 2021b). The accession IC251442 of *V. umbellata* was found highly resistant against *C. maculatus* with 0 per cent seed damage in both first and confirmatory screening experiments. Interestingly, the accession IC251442 of *V. umbellata* has also been reported to be photo-and thermo-period insensitive as well as highly resistant to MYMIV. Therefore, this accession can be an invaluable genetic resource for introgression breeding for multiple traits in mungbean and urdbean. This accession can be characterized by semi-erect growth habit, indeterminate growth pattern and dark green leaves. It has light yellow flowers, smooth, curved and semi flat pods, shiny, beige, oval and large seeds.

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42. IC009634 (IC009634; INGR22042), a rice bean (*Vigna umbellata*) germplasm with bold seeds (100 seed weight 37.44 g)

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Ricebean (*Vigna umbellata* (Thunb.) Ohwi and Ohashi), a multipurpose legume of Fabaceae family mainly grown in *Kharif* season. In the North-eastern hills of India, ricebean is used as a pulse, vegetable, and fodder crop. A total of 2,202 accessions of ricebean collected across the geographical areas of India, which has been conserved in the National Genebank of India at Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR- NBPGR), New Delhi. During routine seed monitoring for seed viability in 2020, one unique accession IC009634 (collected from Sikkim) was noticed for the first time with very bold seeds, weighing 37.44 g of 100 seed weight. To date, we have not found any report in literature with such a stable genotype with high average 100 seed weight in any cultivated ricebean genotype. Hence, to validate the bold seededness IC009634 is grown at two locations *viz;* ICAR-NBPGR, Regional Station, Shimla (31°5 'N and 77°5'E with 1924 amsl) and ICAR-NBPGR, Regional Station Shillong (25°41'N long 91°55'E with 100 amsl during *Kharif* 2020 and 2021. As ricebean is temperate crop, both these growing stations are well suited for getting the desirable expression. The bold seeded expression was validated under field conditions at both the locations during *Kharif* 2020 and 2021(Gore *et al.,* 2022). This accession has the potential to be utilized in the *Vigna* improvement programme.

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43. IPF 2014-16 (IC640783; INGR22043), a pea (*Pisum sativum*) germplasm moderately resistant to rust

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Recognition of stable and durable resistance genotypes of field pea against rust, followed by utilization of these genotypes as donors in a resistance breeding program would be a best strategy for disease management in a trustworthy way. During recent past sincere efforts have been made and numbers of genotypes have been developed with good level of resistance to rust. As mentioned above resistance against this pathogen is partial and influencethe magnitude of environmental and genotype-by-environment interaction was assessed to understand the dynamism of resistance and identification of durable resistant genotypes through multi-location and multi- year evaluation for rust. A panel of 23 promising field pea genotypes was assessed under inoculated conditions for rust disease for two consecutive years at six locations in India. Genotype namely IPF-2014-16 and IPF- 2014-13 identified as “ideal” genotypes, which can be recommended for release and exploited in a resistance breeding program for the region confronting field pea rust.

Morpho-agronomic characteristics

The genotype IPF 2014-16 is tall type (118-130 cm) and leafy type. It has white colour flowers, white & round seed and yellow cotyledon. It flowered and matured in 55-60 days and 105-110 days respectively with 18.0-20.0 gm 100- seed weight. The average yield of the genotype is more than 2.0t/ha.

Associated characters and cultivated practices

This genotype also has powdery mildew resistance and good yield potential (20-22 qt/ha). It can be grown on different type of soil; however, a well-drained soil is essential to achieve good yield potential of this genotype. The field should be well prepared by two to three ploughings. The seed treatment should be done with fungicide like Thirum/ Captan/Carbendazim @ 3.0 g/kg seed + rhizobium culture @ 1 packet/10 kg + Trichoderma @ 4.0 g/kg at 4-5 days before sowing. The optimum sowing time is October 15-Novemebr 15 with 75-80 kg/ha seed rate. If available, about 20 tonnes of organic manures should be incorporated in the soil at the time of land preparation. This should be supplemented with 20-30kg/ha nitrogen as starter dose in basal dressing forms at the time of sowing. The phosphorus and potassium should be applied as a basal dose based on soil test. If soil is deficient in these nutrients, apply 40kg/ha P_2O_5 with 20-30 kg K_2O and 20kg Sulphur per hectare. For Zinc deficiency 0.5 per cent Zinc sulphate +0.25 per cent lime should be applied after the appearance of deficiency symptoms. First irrigation should be given at 45 days and second, if needed, at pod filling stage. This genotype has good worth as a donor in future fieldpea breeding programme towards development of fieldpea varieties with good level of resistance against rust and in other basic studies.

44. IPFD 18-26 (IC640781; INGR22044), a green seeded pea (*Pisum sativum*) germplasm with extra early maturity and resistance to powdery mildew and rust

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The prolonged *kharif* season enforces farmers to undertake field pea under late planting that eventually exposes the crop to terminal high temperature (> 30°C) resulting into increased incidence of powdery mildew, rust and low productivity (Mishra *et al.* 2020). Therefore, to avoid or escape the aforementioned constraints, development of extra early maturing varieties (<100 days maturity) has become mandatory to endorse this crop in these circumstances (Dixit *et al*. 2014; Parihar *et al*.2021). Hence, dedicated breeding efforts were made at ICAR-IIPR, Kanpur, using inter- specific hybridization between *Pisum sativum* L. var. *arvense* (DDR 30, DDR 23) with *Pisum sativum* L. var. *hortense* (VRP 22) and the crosses were synthesized. The superior single plants were selected in different generations as per pedigree methods. On the basis of earliness i.e. days to 50% flowering and days to maturity, superior fixed lines were identified and the most promising lines were further evaluated consecutively for four years *viz*. 2017-18, 2018- 2019, 2019-20 and 2020-21 in post rainy season with available early type released varieties of field pea and vegetable pea. In addition, staggered planting (29/12/18;12/01/19) of the same material was also done during winter 2018-19 to further confirm the earliness. Considering over the years and staggered planting performance, one genotype IPFD 18-26(DDR 23 x VRP 22) was identified as an extra early green seeded genotype, taking < 40 days to achieve 50% flowering and < 100 days to achieve maturity. Hence, IPFD 18-26 can be used as a donor to develop extra early varieties of fieldpea and also for academic studies related to earliness, seed coat colour *etc*. Furthermore, it possesses high degree of resistance to powdery mildew and rust.

Morpho-agronomic characteristics

IPFD 18-26 is a dwarf (45-55 cm) and leafy type with white flowers. The dried seed is round and green in colour with 100-seed weight of 16- 22g. It takes 36-44 days to achieve 50% flowering and maturity period varied between 93- 103 days.

Associated characters and cultivated practices

IPFD 18-26 also demonstrated resistant against powdery mildew and tolerant to rust. This genotype can be cultivated on well drained soil to achieve good yield potential. The field should be well prepared by two to three ploughings. Before 4 to 5 days of sowing, seeds should be treated with fungicide like Thiram/Captan/Carbendazim @ 2.0 g/kg seed, rhizobium culture @ 1 packet/10 kg seed + Trichoderma @ 4.0 g/kg. The sowing should be done betweensecond fortnight of October to first fortnight of November with 100 kg/ha seed rate. At the time of field preparation 40 kg N, 40-60 kg P_2O_5:20-30 kg K_2O: 20 kg S: 15 kg $ZnSO_4$ should be applied. First irrigation should be given at 45 days of sowing and second, if needed, at pod filling stage.

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45. EC564816 (EC564816; INGR22045), a semi-leafless field pea (*Pisum sativum*) germplasm with intact/extended funiculus

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Introduction

Field pea is a minor winter season pulse crop of India and is being mainly cultivated in Uttar Pradesh, Madhya Pradesh, Bihar, Assam and Odisha (Anonymous 2019). Being an admirable source of quality protein, starch, minerals and vitamins, it is widely used as an important component in many food industries (Parihar *et al*. 2016). The crop wild relatives are reservoir of many traits especially in terms of resistance to biotic & abiotic stresses, reduction or loss of dormancy, hard-seeds, seed shattering, toxic compounds in seed coat etc. These set of traits, which are considered as a defensive traits for plant or seed, have been extensively modified during domestication through conscious or unconscious selection/ breeding to meet the requirement of human kind. Like these traits, the intact/extended funiculus is expected to be a defensive/functional trait developed by field pea seed. Generally, field pea seed remains attached to mother plant through funiculus which is the only means of communication between seed and mother plant. When the field pea seed matures, the seed detaches itself from the mother plant from the funiculus, and the mature harvested seed normally does not have funiculus attached to them. However, two accessions (EC 564814 and EC 564816) were found to have the funiculus intactly attached with the mature seed even after harvest during 2017-18. The occurrence of intact funiculus in these accessions was further confirmed during *rabi* season of 2018-19, 2019-20 and 2020-21. During seed development, the funiculus provides anchoring and structural support to a developing embryo; also it makes the nutrients available for embryo (Endo 2012; Chan and Belmonte, 2013). However, the role of intact funiculus after maturity and harvesting is not yet known. The hilar–micropyle region is reported to be an initial point of entry for water in legume seeds (Lamichaney *et al*. 2017). The hilar–micropyle region is covered by the funiculus and when the seed matures, it detaches itself from the funiculus, exposing the hilar– micropyle region. Presence of funiculus in harvested seed as recorded in this investigation may result into slow rate of water imbibitions as intact funiculus could become a physical barrier for entry of water to seed during imbibitions. The investigation suggested that the presence of funiculus in harvested seeds has a significant but negative role in rate of water uptake, as the seeds of both the accessions imbibed more water when funiculus was removed. Such an effect on water uptake, which triggers many physiological metabolisms of dry seed, could have an effect on rate and final germination, dormancy, seed shattering, and cooking time. About 10 million ha area in eastern India is under rice fallow, where initial establishment of the crop is a real challenge due to high initial moisture in the field. Developing field pea varieties with intact funiculus will help in slow uptake of water thus prevents the imbibitional embryo damage due to rapid uptake of water in the standing rice crop and may help in better initial vigour and crop growth. Intact funiculus is not a common trait observed in field pea and may also serve as a morphological marker in seed production programme. Hence, this intact funiculus accessions can be used as donor in field pea breeding program and also for various genetical studies.

Morpho-agronomic characteristics

The genotype (EC564814) is dwarf and leafy type with plant height of about 45-50 cm with purple flower and brown seed. It flowered and matured in 70-75 days and 105-110 days, respectively with 21-22 g of 100-seed weight. The seed recorded an average length, width and thickness of 7.76, 8.32 and 5.79 mm, respectively. Likewise, the genotype (EC564816) is semi-leafless type with plant stature of about 80-90 cm, purple flower and dark brown seed. It flowered and matured in 80-85 days and 115-120 days, respectively with 17-18 g of 100-seed weight. The seed recorded an average length, width and thickness of 6.42, 7.02 and 5.38 mm, respectively.

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46. IPM 526-11 (IC641993; INGR22046), a mung bean (*Vigna radiata*) germplasm highly resistant to yellow mosaic disease caused by mungbean yellow mosaic India virus.

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Among the biotic stresses, yellow mosaic disease (YMD) is the most important factor negatively affecting the productivity of mungbean (Pratap *et al*., 2020; Singh *et al*., 2019; 2020). YMD is caused by at least three begomovirus species (Mungbean yellow mosaic India virus, Mungbean yellow mosaic virus and Horsegram yellow mosaic virus) individually or as mixed infection in the majority of pulse crops including mungbean. The disease is initially characterized by the appearance of yellow and green irregularly shaped areas on the infected leaves of the host plants. The leaf size is gradually reduced, which is followed by complete yellowing and drying. The number of flowers and pods in severely infected plants also become drastically reduced and fewer pods with small and shrivelled seeds are produced in severely affected plants. Furthermore, in severe cases, susceptible mungbean genotypes suffer complete yield loss, which depends upon the stage at which the crop is infected and may vary from 10-100% (Akram *et al.,* 2021).

Host plant resistance (HPR) is advocated as the best strategy to tackle this issue which relies upon the intrinsic capacity of the plant to resist the disease. The plant materials for the study included a diverse panel of 71 elite mungbean lines including 9 cultivars that are currently in the active seed chain and 62 advanced breeding lines including one susceptible check 'DGGV 2'. All the released varieties and advanced breeding lines were developed at ICAR-IIPR between 2002-2016 at ICAR-IIPR, Kanpur following recombination breeding. For this, a series of crosses were attempted between 2002-16 using identified genotypes with the superior agronomic base as the recipients and some elite donors to transfer the lacking trait. All the donors used were resistant to YMD. Each breeding line was subjected to single plant selection at F_2 and subsequent stages thereby leading to the identification of high performing stable lines. The identified lines were then subjected to screening against YMD caused by Mungbean yellow mosaic India virus (MYMIV) continuously for 4 years i.e. 2016-2019 during *Kharif* season. The identity of the YMD-causing virus as MYMIV and its prevalence was ascertained through molecular analysis (Akram *et al.,* 2021).

It was observed that the 71 test genotypes recorded the average disease rating score between 1-4 as against 7.75 in YMD susceptible check/infector row (DGGV2) during all 4 years of testing (2016-2019). DGGV 2 showed high susceptibility to the disease recording a score of 7-9 on a 1-9 scale. This suggested those sufficient sources of inoculums, as well as the vector population, were present during all the crop seasons. Among the test genotypes, 48 exhibited high resistance (1-2 scale) against the disease over the four years of testing. The genotype IPM 526-11 consistently recorded a disease rating score of 1 against YMD and no visible symptoms were observed on the leaves. The plant growth, flowering as well as pod setting were quite normal and the genotype matured in 63-71 days over the years. Therefore, this genotype was identified to be highly promising for resistance against YMD and therefore recognized as a unique material for registration for YMD resistance. This genotype was developed from the cross PDM 139 x SPS 87. Incidentally, both the parents involved in the crossing programme are also resistant to YMD while the genotype PDM 139 is an early maturing variety recommended for cultivation during the Summer season. Owing to its consistently resistant reaction against YMD during the generation advancement stage as well as extensive screening along with other genotypes and the susceptible check, IPM 526-11 has been identified as having a high level of resistance against YMD caused by MYMIV. Therefore, this genotype can be deployed for introgression breeding for transferring resistance against YMD caused by MYMIV and also tested for its agronomic performance and released as a cultivar, if found promising.

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47. DMR-2-0-7 (IC643987; INGR22047), a cauliflower (*Brassica oleracea* var. *botrytis*) germplasm carrying single dominant gene Ppa207 for downy mildew resistance and highly resistant to downy mildew disease

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Cauliflower is an important vegetable crop grown around the world and downy mildew caused by *Hyaloperonospora parasitica* (Pers.:Fr) Fr. Constantinescu and Fatehi is a most devastating disease causing a heavy toll of the crop during November –January months in north Indian plains. The disease occurs during vegetative to curd development stage in mid group of cauliflower. In the absence of host plant resistance, fungicides are being used to control the disease, which are not only proving to be ineffective in controlling this oomycete pathogen, but are becoming cause of health hazards and environmental pollution. Therefore, this line 'DMR-2-0-7' will have tremendous potential in using downy mildew resistance breeding programmes which can go a long way in saving the input cost of farmers, protecting consumers from health hazards and keeping the environment safe. Disease incidence (DI) of the genotype was observed to be 0 to 0.74% under artificial inoculation condition (Table 1). Genetic studies showed that the resistance is governed by a single dominant gene *Ppa*^{207}. The resistant gene *Ppa*^{207} was mapped in 4.8 cM linkage interval on linkage group 2 (C02) of cauliflower, flanked by the markers BoGMS0486 and BoGMS0900 at 3.6 and 1.2 cM, respectively (Saha *et al.,* 2020).

Morpho-agronomic characteristics of downy mildew resistance line DMR 2-0-7

The downy mildew resistant line DMR 2-0-7 was derived from homozygous progeny from a cross of 3-5-1-1 (resistant to downy mildew) × DC-466 (susceptible to downy mildew). The plants are vigorous with dark green leaves which are long having prominent mid-rib and strong puckering on margins. Curds are compact, cream white and medium in size, curd weight is in the range of 600 to 700 g. Curds gets

Table 1: Response of DMR-2-0-7 and commercial cauliflower varieties to downy mildew disease in four different season/environment

Genotype/lines	*DI in Environment 1/ season 1 (a)*	*DI in Environment 2/season 2 (b)*	*DI in Environment 3/season 3 (c)*	*DI in Environment 4/season 4 (d)*	*Disease reaction**
DMR-2-0-7	0.0	0.74	0.0	0.0	Resistant
Pusa Sharad	100	96.29	97.04	100	Highly susceptible

Scoring for downy mildew disease and Disease Incidence (DI) calculation according to Mahajan et al. (1991).

a) Published in peer reviewed journal Euphytica (2020) 216:183https://doi.org/10.1007/s10681-020-02696-6, b) Institute annual report of IARI (2020, Page 36), c) Institute annual report of IARI (2019, page no 26)

ready for harvesting in the month of mid- January. Similar to mid-late group genotypes, the 'DMR 2-0-7' line requires 16-20°C temperature for curd initiation and development. The crop becomes ready to harvest in 70-80 days after transplanting in its normal growing season. Desirable horticultural traits along with single dominant gene *Ppa*^{207} governed downy mildew resistance in mid-group cauliflower genotype DMR 2-0-7 can be explored in downy mildew resistance breeding and hybrid development.

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48. Newar landrace (IC643967; INGR22048), a radish (*Raphanus* sp.) germplasm with high tolerance to irrigation water salinity (ECiw 8-10 dS/m) and soil sodicity (pHs 8.5)

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Introduction

Radish landrace 'Newar' (*Raphanus* sp.), endemic to Jaunpur district of Uttar Pradesh, India, is highly valued for its better keeping long crisp roots, salt tolerance, use in pickling and seed oil extraction. However, changing land use pattern and consumer preferences, and disappearance of the seed network have badly hit its conservation and cultivation (Singh *et al*. 2018).

Morpho-agronomic Characteristics

Based on the DUS descriptors (Srivastava *et al*. 2001), 'Newar' is characterized as a tropical bolting type with mildly pungent, creamy white and crisp roots free from pithiness. It has dark green leaves with purple mid ribs and petioles. It produces light brown bold seeds that maintain viability up to 8 years (Singh *et al*. 2018). The number of leaves (25.0 + 5.0), leaf length (39.5 + 1.0 cm), root length (35.0 + 3.5 cm), root weight (315.0 + 25.0 g) and 1000-seed weight (average 13.5 g) are the distinct morpho-agronomic characteristics (Table 1) of 'Newar' (Singh *et al*. 2020).

Associated Characters and Cultivation Practices

'Newar' displays an exceptionally high salt tolerance in terms of early (4.5 days) and very high (98.5%) seed germination, and high plant vigour at irrigation water salinity (EC_{iw}) of 10.0 dS/m, and maintenance of root fresh weight up to EC_{iw} of

Table 1: Characterization of radish landrace '*Newar*' based on DUS descriptors

S. No.	*Characteristic*	*Stage of observation*	*Remark*
1	Early plant vigour	30 DAS	(7) Good
2	Plant growth habit	Flowering	(6) Elongate branching stem supporting leafs and/or heads
3	Leaf colour	30 DAS	(4) Dark green with purple midribs
4	Leaf length (cm)	MRHS	39.5 + 1.0
5	Leaf width (cm)	MRHS	11.5 + 1.0
6	Leaf margin	MRHS	(1) Crenate
7	Leaf apex shape	MRHS	(4) Oval
8	Leaves per plant	MRHS	25.0 + 5.0
9	Leaf pubescence	MRHS	(7) Abundant
10	Petiole length (cm)	MRHS	7.5 + 1.5
11	Petiole colour	MRHS	(7) Purple
12	Days to 50% root harvest	MRHS	50.0+3.0
13	Crown head habit	MRHS	(1) Erect
14	Crown head colour	MRHS	(1) Light green
15	Crown head diameter (cm)	MRHS	5.0 + 1.5
16	Root length (cm)	MRHS	35.0 + 3.5
17	Root diameter (cm)	MRHS	4.7 + 0.5

18	Root Branching	MRHS	(3) Present
19	Root skin colour	MRHS	(2) Creamy white
20	Root shape	MRHS	(2) Triangular
21	Root tail	MRHS	(1) Acute
22	Root weight (g)	MRHS	315.0 + 25.0
23	Root pithiness	MRHS	(0) Absent
24	Root pungency	MRHS	(3) Mild
25	Root flesh texture	MRHS	(1) Crisp
26	Bolting habit	Flowering	(1) Tropical
27	Inflorescence type	Flowering	(1) Single raceme
28	Days to 50% flowering	Flowering	85.0 + 3.0
29	Flower head size	Flowering	Average number of effective tillers: 8; with flower c diameter of 2.5 cm
30	Seed coat colour	Harvesting	(3) Light brown
31	Weight of pod per plant (g)	Harvesting	240.62
32	Seed weight per plant (g)	Harvesting	60.90
33	1000 seed weight (g)	Harvesting	13.45
34	Biotic stress susceptibility	Throughout crop season	Very low or no visible sign of susceptibility

8.0 dS/m than commercial radish cultivars like 'Pusa Mridula'. The key traits underpinning salt tolerance in 'Newar' include Na^+ exclusion, maintenance of shoot and root K^+ levels and a substantial increase in leaf proline activity. It also maintains root length (35.0 ± 3.5 cm) and fresh root weight (315.0 ± 25.0 g) in sodic soils (pH_s ~8.5, EC_e 1.0 dS/m). It shows very low or no visible signs of susceptibility to insect-pests and diseases. The seeds should be sown in the first fortnight of October on 25 cm high ridges at 2 cm depth, keeping row-to-row and plant-to-plant spacings of 45 cm and 30 cm, respectively.

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49. H-88-78-1 (IC644011; INGR22049), a tomato (*Solanum lycopersicum*) germplasm for multiple resistances (root knot nematode, *Alternaria solani* resistance, ToLCV resistance) and heat tolerance

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Tomato (*Solanum lycopersicum* L.) is a versatile crop cultivated worldwide for its short yield time, culinary importance and health benefits. Biotic stresses caused by pathogens, such as fungi, bacteria, viruses, nematodes etc., cause severe yield penalties leading to significant fluctuations in annual tomato production in India. On the other hand, abiotic stresses especially high temperature limits its production in one or other parts of the country. H-88-78-1 is a unique germplasm with multiple disease resistance and heat tolerance developed and maintained at ICAR-Indian Institute of Vegetable Research Institute, Varanasi. Tomato genotype 'H-88-78-1'was developed through wide hybridization followed by pedigree method of breeding from a cross between Selection-7 × B6013. B6013 is a *Solanum habrochaites* (*Lycopersicon hirsutum* f. *glabratum*) accession.

Under pot conditions at two inoculation rates *viz,* 2000 and 4000 J2/Kg soil of *M. incognita,* tomato genotype 'H-88-78-1' has shown highly resistant to immune reaction. With the help of molecular markers (Mi23 & Pmi), it was confirmed that H-88-78-1 has *Mi1* gene in it (Reddy *et al.,* 2018). Under artificial inoculated conditions, tomato genotype 'H-88-78-1' gave immune reaction to *A. solani* (Singh *et al.,* 2017). The genotype has also shown ToLCD resistance under epiphytotic conditions (Singh *et al* 2015). After 25 days of transplanting H-88-78-1 plants along with heat susceptible

Punjab Chhuhara plants of same age were exposed to high-temperature stress at 42°C by transferring them to a growth chamber. Different molecular, physiological, and biochemical analysis shown that H-88-78-1 has better heat stress profiles in comparison with the susceptible genotype (Karkute *et al.,* 2021).

Tomato line H-88-78-1 is an indeterminate plant with small fruits (average fruit weight 52 g). Fruits have an average locule number of 5 per fruit, pericarp thickness of 0.4 cm and total soluble solids (TSS) of 4.0 Brix. The line H-88-78-1 has slightly flattened shaped fruits with an average fruit length of 3.72 cm and average fruit diameter of 4.62 cm**.**

Mi1 is a well characterized resistance gene. With gene based markers available for *Mi1* gene, H-88-78-1 can be utilized as a parental material in nematode resistance breeding programmes of tomato. The genotypes can be used in ToLCV and early blight resistant breeding programmes. Heat stress is not only major limiting factor for crop productivity but also highly complex character. With proven heat tolerance tomato genotype H-88-78-1 can be used in different basic and applied plant breeding programs to transfer these traits to cultivated varieties.

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50. JS2 (IC643977; INGR22050), an Indian mustard (*Brassica juncea*) germplasm resistant against Sclerotinia sclerotiorum; with mottle seed colour and high male and female fertility

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Introduction

The inter-generic hybridizations were attempted frequently with the aim of transfer of the genetic resistance/ tolerance to the diseases. However, their success was limited due to pre and post-fertilization barriers within the genera. Therefore, somatic hybridizations were used as an alternative approach. The *Sinapis alba* is a Brassica coenospecies which have potential for biotic and abiotic stress tolerance and is frequently used as a potential donor in somatic hybridization against these stresses (Kumari *et al*., 2020a, 2020b). However, the stability of these somatic hybrids was limited to the gene introgression probability to the various traits (Gaikwad *et al*., 1996). Although, very few somatic hybrids of *B. juncea* and *S. alba* were found meiotically stable (Kumari *et al*., 2020c) so far. We have done the PEG mediated protoplast fusion between *B. juncea cv.* RLM-198 and *S. alba* (Gene Bank Accession No. DRMR-2183) as per protocol (Kirti *et al*., 1992) with the aim of the introgression of resistance against *Sclerotinia* stem rot (Kumari *et al.,* 2020c). This genetic stock contains various interesting phenotypes that may be useful for resistance and quality breeding.

Morpho- agronomic characters

Somatic hybrid (JS2) shows intermediate morphological characters of their parents and (JS2) attaining an average 184 cm plant height. While the stems were angular in shape, branched, and covered with dense trichomes, where the leaves were considerably larger, thicker, more cuticular, deeper green in color, had more irregular pinnately lobed with serrate margins, and was more covered with dense trichomes on both the surfaces. The plants attained delayed flowering in comparison to *B. juncea* and along with *S. alba*, The inflorescence of the JS2 had an intermediate pattern of their parents (Kumari *et al*., 2020c). The flower sizes were intermediate relative to the parents' flowers. The stigma was larger than that of the parents with hairy projections on the style, while the stamens of allohexaploids were more prominent than in the parents. The pollen grain viability was found > 91 % with high female fertility remaining as revealed by their seed setting. The siliquae of the allohexaploids were found to be intermediate in size relative to their parents with an increased number of seeds (3–5 seeds/silique) compared to *S. alba*. These allohexaploids produced viable seeds on selfing and backcrossing with B. juncea, which were found to be intermediate in size relative to the parents. However, the 1,000 seeds' weight was recorded as less than their parents.

Associated characteristics and cultivation practices

The *allohexaploid Brassica* JS2 was carried the intermediate seed color of their parents (half yellow and half brown). Interestingly, this is the first instant when half yellow and half brown color seeds were bears after inter-generic protoplast fusion of the two genera which produced different colors seeds. However, these plans were found cytologically stable. The present allohexaploids were found resistant to the *Sclerotinia sclerotiorum* when screened in-vitro and in-vivo for three subsequent years and two locations (Kumari and Singh 2019, Kumari *et al.*,2020c). The plants also showed siliquae shattering resistance during the preliminary study. However, more investigation will be required in this way.

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51. JS1 (IC643976; INGR22051), a yellow seeded Indian mustard (*Brassica juncea*) somatic hybrid resistant against *Sclerotinia sclerotiorum*

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Introduction

A large number of somatic hybridizations have been attempted in oilseed Brassicas with the aim of introgression of genes responsible for many biotic stresses (Henson and Early 1997, Singh *et al.*, 2021). The *S. alba* is a Brassica coenospecies that shows several desirable features such as resistance to biotic diseases, pests and harsh environmental conditions that are unavailable in crop Brassica species (Kumari *et al*. 2020a and 2020b). Therefore, somatic hybridization between *S. alba* (Accession No. DRMR- 2183) and *B. juncea* (RLM-198) through PEG mediated protoplast fusion was attempted. Two symmetric hybrids were recovered from this fusion experiments, out of which one SH (JS_1) had yellow seed colours (Kumari *et al.*, 2020c)

Morpho-agronomic characters

The JS1 plants attained an average plant height of 216 cm. The stems of JS1 were angular, branched, and covered with dense trichomes. The leaf and flower bud margins were similar to *S. alba* with delayed flowering relative to *B. juncea*, where the leaves were considerably larger, thicker, more cuticular, deeper green in color, had more irregular pinnately lobed serrate margins, and was covered with dense trichomes on both surfaces. The inflorescence of JS1 showed an *S. alba*-like condense pattern, the flower sizes were larger in comparison to the parents' flowers. The stigma was larger than that of the parents with hairy projections on the style, while the stamens of allohexaploid were more prominent than in the parents. The pollen grain viability of the allohexaploid (JS1) was recorded between 91 and 93% with female fertility remaining high as revealed by their seed setting. These allohexaploids produced viable seeds on selfing and backcrossing with *B. juncea*, which were found to be intermediate in size relative to the parents. However, the weight of 1,000 seeds of JS1 was higher than their parents (Kumari *et al.*, 2020c).

Associated characteristics and cultivation practices

JS1 is carrying yellow seed color along with high degree of resistance against *Sclerotinia sclerotiorum* causing stem rot, high male and female fertility, and stable over the generation.

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52. EC523368-2 (GMU-7399) (IC643960; INGR22052), a safflower (*Carthamus tinctorius*) germplasm tolerant to safflower aphid (*Uroleucon compositae* Theobald)

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Introduction

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop grown in India during the *rabi* season. Aphid, *Uroleucon compositae* (Theobald) is a serious pest on safflower which can cause upto 100% yield loss in susceptible varieties. Development of resistant cultivars assumes importance to enable environmentally sustainable crop cultivation with less input use by saving the cost of application of pesticides. Identification of sources of resistance to aphid is the pre-requisite to meet this target for which perfection of screening techniques and extensive screening has been carried out in safflower (Srinivas and Mukta *et al.,* 2015). The accession EC523368-2 is a selection from EC523368 received from USDA. The accession was selected based on non/few spiny nature of the outer involucral bracts (OIB) during 2005 at the Germplasm Maintenance Unit of Safflower at IIOR, Hyderabad and was multiplied and maintained as GMU-7399.

Morpho-agronomic characteristics

EC523368-2 (GMU-7399) possesses the following morpho-agronomic characteristics: (i) Non/few spiny nature of the outer involucral bracts (OIB), (ii) yellow disc florets turning orange at faded stage, (iii) medium height with 8-9 branches located on the main stem at 2/3rd height from top (iv) 20-25 capitula of medium size (2.3 cm diameter) and (v) white seeds with 100-seed weight of 3.7 g.

Associated characters and utility

The accession EC523368-2 (GMU-7399) has undergone repeated screening for its reaction to safflower aphid, *Uroleucon compositae* (Theobald) at ICAR- IIOR, Hyderabad. It showed tolerant reaction to *U. compositae* based on the screening parameter, aphid infestation index (A.I.I.) (1.5) while the susceptible check CO-1 showed A.I.I. of 4.9 in 2011-12 (A.I.I. grades range from 1 to 5 with 1 indicating highly tolerant reaction and 4.1-5.0 indicating highly susceptible reaction). A scale based on days to wilt was also developed based on the corresponding A.I.I of entries and days taken to wilt. During 2015-2018, the tolerant reaction of EC523368-2 to aphid was confirmed based on days to wilt after aphid infestation (36-43 days) compared to 19-26 days in the susceptible check CO-1 (Table 1).

Table 1: Tolerance reaction of EC-523368-2 (GMU-7399) against safflower aphid (*Uroleucon compositae* Theobald) at ICAR-IIOR, Hyderabad

Year of screening	*Parameter*	*EC-523368-2 (GMU-7399)*	*Susceptible check: CO-1*
2011-12	Aphid infestation index (A.I.I)	1.5	4.9
2015-16	Days-to-wilt after aphid infestation	36	19
2016-17	Days-to-wilt after aphid infestation	42.1 ±0.8	20.4 ±0.8
2017-18	Days-to-wilt after aphid infestation	43	26

The major mechanism of resistance operating in safflower accession, EC523368-2 (GMU-7399) was tolerance. The accession remained stay green and was found physiologically efficient in tolerating the feeding of aphids (Srinivas *et al.,* 2018). The accession has been utilized in the development of recombinant inbred lines (RILs) through single seed descent method towards mapping of aphid tolerance in safflower based on days to wilt after aphid infestation. A major QTL associated with tolerance to aphid has been detected using SSR markers, which is currently under validation (Jegadeeswaran *et al.,* 2021).

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53. Dedia P-1 (IC643989; INGR22053), a basil (*Ocimum sanctum*) germplasm with unique dark purple leaf colour; maximum essential oil content (0.28 %); maximum eugenol content (60%), ß-caryophyllene (14%) and ß-elemene content (14%).

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Holy basil (*Ocimum sanctum* L.), a sacred medicinal herb is extensively used in Ayurvedic systems of medicine for various ailments from traditional medicinal systems. Medicinally the herb is useful in a variety of diseases in humans and animals. The plants flourish predominantly as herbs or shrub and survive as annuals or perennial plants in habit. The most common uses are in herbal tea, cosmetics, healing remedies, and as a preservative. From *Rama* and *Krishna* variants of holy basils, in the Indian market, *Krishna* (Shyama) tulsi is more preferred by the pharma industries in the form of dry leaf or powder due to being rich in antioxidants.

The Krishna type holy basil, Dedia P-1 is identified for distinctive dark purple leaf colour (RHS Colour chart: Greyed purple group N186 A) of upper part of leaves with greenish colour at a lower side of leaves (RHS colour chart: Yellow-green group 146 A), dark purple inflorescence and branches (Greyed purple group N186 C) colour, while check "CIM-Angana" having a purple colour leaves and inflorescence (RHS Colour chart: purple group N77A). Additionally, It has better essential oil content (0.28 %), maximum eugenol content (60%), β- caryophyllene (14%) and β-elemene (14%) in fresh herbage suitable for industrial use compared to check "Angana" (0.12 % oil content; 12 % β-caryophyllene and 9 % β-elemene) in Tables 1 & 2. Dedia P-1 is collected from the local area of Dediapada, Gujarat and maintained at ICAR-Directorate of Medicinal and Aromatic Plants Research, Boriavi, Anand, Gujarat.

Table 1: Average essential oil content (%) in fresh herbage of Dedia P-1

	2017-18	*2018-19*	*2019-20*	*2020-21*	*2021-22*	*Average (%)*
Dedia P-1	0.31	0.22	0.35	0.25	0.28	0.28
Angana	0.13	0.13	0.08	0.11	0.13	0.12

Table 2: Average chemical compound constitute of Dedia P-1 and CIM-Angna.

Dedia P- 1	*Eugenol content (%)*	*β-caryophyllen (%)*	*β-elemene (%)*
2021	60.62	14.16	13.91
2020	39.15	-	-
2016	78.78	-	-
Average	60	14	14
Angana	*Eugenol content (%)*	*β-caryophyllen (%)*	*β-elemene (%)*
2021	40.42	11.87	8.96
2020	40.65	-	-
2016	39.94	-	-
Average	40	12	9

54. DOB-5 (IC643990; INGR22054), a basil (*Ocimum basilicum*) germplasm with high essential oil content (0.50%) in herbage; linalool (32.13%), ß-elemene (2.53%) and germacrene D (3.32%) contents

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Sweet basil (*Ocimum basilicum* L.) is an important culinary herb and source of aromatic essential oils, which gives it a unique flavor. It has been used as a medicinal as well as aromatic plant for centuries and grown in wild as a perennial herb. Basil is cultivated extensively in India, France, Egypt, Iran, Hungary, Indonesia, Morocco, Greece, and Israel, in various regions with temperate and hot climates. Sweet basils tend to have a higher percentage of methyl chavicol or anethole. Basil is commercially grown for its essential oils containing linalool (20– 40%), methyl chavicol (20–25%), and eugenol (0–12%). It also contains tannins and flavonoids. Sweet basil essential oil is extensively used in food, fragrance, and in traditional medicine for treating cough, colds, and chest congestions, and as a mosquito repellent and pesticide. The genus characterized by great variation among plant morphology, growth habit, inflorescence, leaves, stem colour, oil content as well as essential oil components. Wide morphological diversity including light green leaf colour (R.H.S. Yellow green group 146A) with club type purple inflorescence (R.H.S. Greyed purple group 187A) observed in "DOB-5". Additionally, DOB-5 has a medium plant height (70-90 cm), purple leaf colour of newly developed leaves and mature leaves are light green colour. It has a light green to yellowish stem (R.H.S. Colour chart: Greyed orange group 165A) at full flowering. However, check variety GAB-1 having dark green leaf colour (R.H.S. colour chart: Green group N137A) with club type greenish purple inflorescence (R.H.S. Yellow green group 144A) and it has a dark green grey (R.H.S. Colour chart: Yellow green group 148C) stem colour. Under field condition, DOB-5 had moderate resistance to Anthracnose disease caused by *Colletotrichum* spp. as compared to GAB-1, which is moderately susceptible. The seeds of DOB-5 have a Dark (Jet) black colour, while check having a brownish black colour.

Secondary metabolites characterization is the main criterion for the selection of suitable aromatic varieties for herbal industry. An essential oil-rich chemotype DOB-5 is identified for better essential oil content (0.50 %) in fresh herbage compared to check variety GAB- 1/AOB-5 (0.37 %) in Table 1. Additionally, DOB-5 has better Linalool (32.13%), β-elemene (2.53%) and Germacrene D (3.32%) content. However, check variety GAB-1 has a Linalool, β-elemene, and Germacrene D content about 30.65%, 1.18%, and 1.63%, respectively (Table 2).

Table 1: Oil content (%) data of MLT trials

Particulars	*Year of testing*	*No. of trials*	*Proposed line DOB-05*	*Check variety GAB-1*
Average oil content (%)	2016-17	4	-	0.28
	2017-18	4	0.52	0.42
	2018-19	4	0.55	0.38
	2019-20	4	0.50	0.41
	2020-21	5	0.41	0.36
	Mean		0.50	0.37

Table 2: Chemical profile of DOB-5

Accession	*Linalool*	*β- elemene*	*Germacrene D*
DOB-5 (2017-18)	-	3.12	3.6
DOB-5 (2019-20)	37.44	3.06	2.95
DOB-5 (2020-21)	26.82	1.41	3.41
Average	32.13	2.53	3.32
GAB-1 (2017-18)	-	1.40	1.42
GAB-1 (2019-20)	40.80	1.07	1.31
GAB-1 (2020-21)	20.51	1.09	2.18
Average	30.65	1.18	1.63

55. HD-6 (CIARI-Sampada) (IC590895; INGR22055), a noni (*Morinda citrifolia*) germplasm with big fruit (140-160 g), high pulp recovery; and year round yielder

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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 (McClatchey, 2003). 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. 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. To explore its commercial potential, it was required to develop genotype(s) which can grow well in open with high yield potential and meet the criteria of processing industry.

The HD-6 is developed by selection from local collection for higher pulp recovery, big size fruits and vigorous tree type plants. It has medium tall and sturdy tree type genotype of Noni. Plant canopy spread is 2.0 m and height is around 3.5 m. Trunk diameter of 6 year plants is 20-25 cm with rough bark. Internodal length is small (<8 cm). This is well suited for normal distance planting at 4.0 x 4.0 m in open condition. It is takes around 110-120 days from bud formation to fruit ripening. It performs well in open condition but can be grown in partial shade condition such as in interspaces in coconut and areacnut plantations without compromising yield levels. The HD-6 bears fruits year round and maintains around higher yield level to sustain industrial requirement.

The big size fruits 'HD-6' are good for fresh juice recovery 60.3 % (fresh weight basis). Total soluble solids content in juice was 9.5° Brix which was significantly higher than CIARI-1 (5.8° Brix). It was found to be rich in polyphenol (365.2 g/100 g fw) with high DPPH antioxidant activity (88.83 %) (Singh *et al.,* 2017). The HD-6 seeds contain 16.60% oil which has industrial value. The GC-MS analysis of reveled that seed oil of HD-6 s rich source of essential fatty acids.

The fruits of Noni genotype 'HD-6' are fits well with criteria of processing industry such fruits of medium to big size (125-150 g), medium width and length, obovate to round in shape, depressed fruit base, smooth to partial surface at maturity, thin skin and cream pulp.

Hence, the HD-6 has potential for immediate use for (i) commercial cultivation for pulp and juice industry (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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56. IIHR-4 (IC633777; INGR22056), a tuberose (*Polianthes tuberosa*) germplasm for double type flower compactly arranged on short spike; more number of flowers open at a time (7.10); resistant to root knot nematode (*Meloidogyne incognita*)

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Introduction

Tuberose (*Polianthes tuberosa* L.) is an important bulbous flower crop belongs to the family Asparagaceae, native to Mexico. The flowers of tuberose are valued for its long lasting flowers and sweet fragrance. The genetic stock IIHR-4 was developed through hybridization by crossing Mexican Single x Pearl Double, followed by selection. It was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, India. IIHR-4 is unique for short upright spike, double type flower arranged compactly on spike with shorter internode, more number of flowers open at a time per spike and highly resistant to root knot nematode.

Morpho-agronomic characteristics

IIHR-4 produces shorter spike (62.00 cm) with double florets arranged compactly on spikes with shorter internode and favourable diameter of floret (4.47 cm), number of florets per spike (50.75) and more number of florets (7.10) open at a time (Table 1). The genetic stock IIHR-4 is well suited for cut flower, flower arrangement and garden display.

IIHR-4 was screened for the tolerance/ resistance against root knot nematode *M. incognita* and the results revealed that it was highly resistant under field conditions with least gall index of 1.24. Per cent disease index and host reaction of tuberose genotypes against leaf blight disease caused by *Alternaria* under field conditions were recorded and the results indicated that the breeding line IIHR-4 has better field tolerance to *Alternaria* leaf blight as compared to the other tuberose genotypes evaluated.

Associated characters and cultivation practices

Tuberose prefers tropical climate with the temperature range of 20-35^{0}C. It grows well in loamy to sandy loam soil with the pH of 6.5 to 7.5. Tuberose is sensitive to water logging and hence proper aeration and drainage is necessary. It is a day neutral plant requires vivid sunlight for better flowering. The medium size bulbs of 2.5 cm in diameter are planted on the sides of the ridges with a spacing of 30 x 30 cm at 5.0 cm depth during June-July.

Table 1: Morpho-agronomic description of tuberose genetic stock IIHR-4

S. No.	*Traits*	*Two years pooled data*
1.	Days to spike appearance	154.15
2.	Spike Length (cm)	62.00
3.	Rachis length (cm)	25.59
4.	Number of florets per spike	50.75
5.	Length of floret (cm)	5.22
6.	Diameter of the floret (cm)	4.47
7.	Bud length (cm)	4.98
8.	Single flower weight (g)	3.16
9.	No. of spikes per clump	4.43
10.	Internodal length (cm)	3.45
11.	No. of florets open at a time on spike	7.10
12.	Flower type	Double
13.	Flower bud tinge	Green tinge
14.	Nature of spike	Straight
15.	Type of flower opening	Wide
16.	Reaction to Root knot nematode	Resistant
17.	Reaction to leaf blight disease	Tolerant

57. QNRCB0045/Borchampa (IC250498; INGR22057), a banana (*Musa* spp.) germplasm resistant to *Fusarium oxysporum* f. sp. cubense (Foc) race 1 (VCG 0124)

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Introduction

NRCB Acc. No. 0045 & IC250498 is a short statured variety among the Mysore sub group of AAB genomic group with 1.8 to 2.2 m height. It is commonly found in North Eastern parts of India.

Morpho-agronomic Characteristics

Pseudostem is green, on which black brown blotches appear and slightly ash coated. Leaves are droopy and appearance is dull in nature. Midrib is green in colour on both upper and lower sides but in younger leaves, midrib is pink on both upper and lower sides. Petiole is green, 30-40 cm long and has wide petiolar canal with erect margins. At the edges of the margins, there is a pink line. Base of the petiole clasp the pseudostem with its margins. There are 4-5 hands of fruits in a bunch. Male bud is small, top shaped and is dark purple in colour. Male bracts are dark purple on outer and crimson red on inner surface. There are medium grooves on outer surface with moderate wax coating. Bract tip is gradually pointed without yellow tinges. Bract falls after the flowers fell, before falling, they show both reflex and revolute. Male flowers are cream in colour. Fruits are short and very stout, unusually plumpy fruits with a blunt tip. Bunch weight is around 6-7kgs. Fruits weigh 120 – 130 g, 9 to 10 cm long with 16 to 18 cm circumference at the middle. Pedicel is more than 1 cm long and fruits do not easily drop off from the pedicel. Dark green color fruits change into yellow color upon ripening. Pulp is cream colour, juicy, sweet with aromatic flavor.

Associated Characters and cultivated practices

It is the most fragrant among Mysore sub group. Very short duration with 9-10 months compared to other Mysore members (14 to 15 months).

58. NRCB0197/Poovan (IC250650; INGR22058), a banana (*Musa* spp.) germplasm resistant to *Fusarium oxysporum* f. sp. cubense (Foc) race 1 (VCG 0124)

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Introduction

This genotype NRCB Acc. No 0197 & IC250650 is found in throughout the country. Its tender leaf nature makes this genotype amenable for leaf industry. Fruit is slightly acidic, firm and has typical sour-sweet aroma. Fruits turn to attractive golden yellow upon ripening.

Morpho-agronomic characteristics

Plants are tall and robust with the height of 3.0-3.5m and girth of 60-70cm circumference at the base, Pseudostem is dark green with purplish tinge all along the pseudostem, shiny and there are brown black blotches on either sides of the petiolar base. Leaves are dark green, neither drooping nor erect. Upper side of the leaf is dark green but not shiny. The midrib is green on the dorsal side and pink in colour on lower surface, but the midrib of the tender leaf is pink on both upper and lower surfaces. Leaf length ranges from 2.0-2.25m with 70-75cm width. Petiole is 50 to 60cm length, green in colour and heavily wax coated. Peduncle is dark green in colour and slightly hairy. Bunch is slightly angular in position, cylindrical in shape with 10-12 hands and they are compactly arranged and 15-16 fingers per hand. Medium sized bunch weighing 13-15 kgs, fruit hands are closely packed. Male flower bud is medium sized, purple in colour and ovoid in shape. Male flowers are medium in size and creamish pink in colour. Fruits are dark green in colour, turns towards the peduncle and has bottle necked tip. Fingers are 10-13cm in length and slightly acidic in taste. Fruits turn to attractive golden yellow on ripening. Medium sized bunch, closely packed fruits, good keeping quality and resistant to fruit crackingare the advantages of this variety.

Associated Characters and cultivated practices

Fruits do not easily drop off from the pedicel. Fruit has good keeping quality and resistant to fruit cracking which reduce the post harvest losses. Its tender leaf makes this genotype amenable for leaf industry. Crop duration is 12 to 13 months and suitable for marginal cultivation.

59. NRCB0009/ Borjahaji (IC250462; INGR22059), a banana (*Musa* spp.) germplasm resistant to *Fusarium oxysporum* f.sp. cubense (Foc) race 1 (VCG0124)

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Introduction

This genotype NRCB Acc. No. 0009 & IC250462 belongs to Cavendish sub group. This is semi tall variety with 2.2 to 2.5m height and found in North eastern parts of India. It is highly susceptible to Sigatoka leaf spot diseases. Most of the major banana growing regions of North eastern India are severely infested with Foc race 1.

Morpho-agronomic characteristics

It is a medium statured variety with plant height ranging from 2.0-2.50m and pseudostem girth of 45- 50cm at its base. Pseudostem is green with black brown blotches all along the pseudostem. Leaves are erect, green, dull on both upper and lower surfaces. Peduncle is 30-40cm in length, pubescent in nature and green in colour. Bunch is cylindrical in shape with 10-12 hands of fingers, they are normally packed and fingers turn towards the stalk. Rachis is 50-60cm in length, completely barren and rarely few hands of persistent neutral flowers just above the male bud. Bract scars are very predominant with maximum interspaces. Pendulous in position but it has slight bend at the distal end. Male bud is brown in colour, lanceolate in shape with pointed tip. Male flowers are whitish in colour. Fruits are green in colour, 15- 20cm in length. It has gradual tip. Pulp is creamy with sweet taste. Pedicel is very short with >1cm length.

Associated Characters and cultivated practices

High yield with 20 to 25 kg/bunch, fruits are completely turned towards the peduncle and bunch is cylindrical in shape. Fruits are long measuring 20 cm and the pulp is sweet with good aroma.

60. NRCB0608/William (IC251061; INGR22060), a banana (*Musa* spp.) germplasm with *Fusarium oxysporum* f. sp. cubense Foc race 1 resistance

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Introduction

This genotype NRCB Acc. No. 0608 & IC251061 belongs to AAA genomic group of Cavendish sub group. It is a dwarf statured variety suitable for high density planting. High yielding with 20 to 25 kgs bunches, fruits are completely turned towards the peduncle.

Morpho-agronomic characteristics

Short statured with about 1.8 to 1.9m height. Pseudostem is dull in appearance and has black blotches all along the pseudostem. Light green and has black brown pigments on either sides of the petiole. Leaves are erect, green in colour, dull on both upper and lower surfaces. Peduncle is 35-40cm long, pubescent and has black brown blotches spread all along the length with only one empty node. Bunch is huge and hangs vertically down, truncated cone shaped and slightly pendulous in position. Male bud is light brown in colour, smaller in size with less pointed tip and top shaped. Bracts open 2-3 at a time, have no bract shoulder and they remain persistent. Male flowers are small in size and white in colour. Fruits are light green in colour with gradual tip, 4-5 unequal sides with cream coloured flesh which becomes soggy upon ripening.

Associated Characters and cultivated practices

High yielding with 20 to 25 kg bunches. More suitable for high density system of cultivation.

61. NRCB0050/Karthobiumtham (IC250503; INGR22061), a banana (*Musa* spp.) germplasm with *Fusarium oxysporum* f. sp. cubense Foc race 1 resistance

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Introduction

Karthobiumtham (NRCB Acc. No. 0050 & IC250503), an unique type of ABB genomic group, is distributed in north eastern India. Male bud mutations are often observed (bunch without male bud). Fruits are elongated like Horn plantain. Pulp is sugary with high sugar content with 30-32° Brix.

Morpho-agronomic Characteristics

Normal in stature, pseudostem is green and slightly wax coated, with brown blotches. Leaves are dark green and shiny on upper side and slightly wax coated on lower surface. Petioles are tightly clasped on the pseudostem. Petiole canals are very narrow and the margins are erect. Peduncle is very short, 20-25 cm length and glabrous in nature. Bunch is small, horizontal or slightly angular, 4-5 hands of fruits and loosely packed. Fruits are ashy green, long with 22-24 cm lengths and slightly pointed tip, ashy yellow upon ripening. Male bud is maroon and the male flowers are pink pigmented. Fruit peel is very thick, pulp is cream, very sweet and TSS is up to 32° Brix.

Associated Characters and cultivated practices

Fruit pulp is suitable for making banana figs and wine.

62. MSP/15-26 (IC644002; INGR22062), a potato (*Solanum tuberosum*) clone (*Solanum tuberosum*; 2n=4x=48); possessing yellow flesh colour and high carotenoids in flesh

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Potato has its origin and domestication in Andes Mountains of South America. The introduction of this crop to remaining world was mainly focused on yield and yield attributing traits. Though a potent source of phytonutrients particularly carotenoids coloured flesh potatoes, the commercial exploitation of these health promoting compounds of potatoes have not been emphasized till recently including Indian potato variety breeding mandates. However, increased awareness of health benefits of these plant pigments have interested breeder's to develop coloured varieties including potatoes. Considering this, to get the baseline information of Indian potatoes phytonutrient content status analysis were done and results revealed narrow variations for these compounds (Dalamu *et al*., 2015). However, nutritional profiling of potato germplasm including indigenous varieties depicted presence of significant variations (Dalamu *et al*., 2014, Luthra *et al*., 2018). Thus, development of phytonutrient dense genetic stocks can open new avenues for breeding potatoes with desired functional properties for table purpose as well as for processing.

Carotenoids are fat soluble organic pigments derived from isoprenoids and confer degrees of yellow to orange colour. Cultivated potato (*Solanum tuberosum* L.) contain varying amount of carotenoids in tubers. Potato carotenoids are mainly xanthophylls, and traces of beta-carotene, precursor of vitamin A. Dietary intake of xanthophylls protects from age related macular degeneration while deficiency of vitamin A causes various ailments like xeropthalmia, poor immune system, and infant mortality. Carotenoids concentrations rather than its composition lead to colour variations in potatoes. Worldwide total carotenoids content in white and yellow fleshed potatoes varied from 50 to more than 2000 ug/100g fresh weight (FW).

MSP/15-26 is a promising clonal selection from the segregating progenies of cross Bareilly Red (an indigenous variety × CP 3770) made in year 2014 (Luthra *et al*., 2018). It is late maturing have yield productivity of 35-40 t/ha at 90 days crop duration. Plant is tall. Corolla colour is red-violet. It produces attractive, medium sized 18-20 round red tubers with medium eyes, yellow coloured tuber flesh with red colored vascular ring. It is moderately resistant to late blight, possesses extremely long tuber dormancy (>10 weeks) and have excellent tuber appearance after 75 days of storage. Tubers have good mouth feel/ flavor, floury texture and tuber dry matter content of 20%. Based on average of 4 years analysis, MSP/15-26 on an average possessed high carotenoids (823 ug/100g FW) as compared to parents Barrielly Red (460) and CP3770 (422 ug/100g FW) and distinct yellow flesh colour with red vascular ring.

References

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63. MSP/15-51 (IC644003; INGR22063), a potato (*Solanum tuberosum*) clone with red purple flesh and high ascorbic acid in flesh

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Of late there have been rising trends for natural antioxidants and their health benefits. Epidemiological studies revealed reduction in degenerative ailments with increased consumption of antioxidant rich food. Ascorbic acid is a vitamin that has anti- oxidant properties and enhances mineral absorption particularly iron. Anthocyanins belong to group of naturally occurring pigments that imparts red, blue or purple hues to horticultural and food crops. Anthocyanins have antioxidative properties due to prolific free-radical scavenging activity that helps in mitigating the risk of chronic diseases. Approx. 37 percent of population globally is anaemic due to iron deficiency. The situation is more prevalent in developing nations leading to hidden hunger caused mainly due to insufficient intake of micronutrients like vitamin A, zinc and iron.

Potato (*Solanum tuberosum* L.) holds the position of third most important food crop. This crop has the potential of addressing food security owing to capacity of producing more food per unit area of land. The present potato production scenario depicts more than half of the world's potato crop is produced in developing nations particularly India and China. In addition to good source of energy, potatoes are full of vitamins like ascorbic acid, minerals and proteins of high biological value. Potatoes justifies the concept of biofortified crops owing to good source of ascorbic acid, that itself is antioxidants and also positively correlated with iron bioavailability. In addition potatoes have low levels of anti-nutrients such as phytates and polyphenols that hamper iron availability. Potatoes are in general not considered as good source of anthocyanins however, traditional varieties and /or germplasm with high level of these compounds exists (Dalamu *et al*., 2014). Traditionally, plant breeders including potato have focused on traits like processing quality, yield, and resistance and seldom for nutrient content (Dalamu *et al*., 2015). However, with the projection scenario of rise in per capita demand of potatoes to be reached to 48.50 kg by 2050, there is need of varieties with added advantage of health compounds with yield and other biotic and abiotic stress resistance and/or tolerance.

MSP/15-51 is a clonal selection from the segregating population of cross Bareilly Red × CP 3770 developed in year 2014 (Luthra *et al.* 2018). Plant is tall and corolla colour is white with light purple secondary colour. It is late maturing and have yield productivity of 20-25 t/ha at 90 days crop duration, It produces small (30-32 tubers), purple oblong tubers with medium eyes and red purple flesh. It is moderately resistant to late blight, possesses extremely long tuber dormancy (>10 weeks) and have excellent tuber appearance after 75 days of storage. Tubers have good mouth feel/ flavor, mealy texture and 21 % dry matter content. Based on average of 4 years analysis, MSP/15-51 possessed high ascorbic acid (68 mg/100g FW) in comparison to parents Bareilly Red (56) CP3770 (26) and distinct purple flesh colour and distinct purple flesh.

References

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