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Plant Germplasm Registration Notice@

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

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

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

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

Year	*Grain yield (Kg. ha^{-1})*	*DFF*	*PHT (cm)*	*Panicles/m²*	*Zn (ppm)*
2013	2383 (14)	109 (18)	134 (17)	275 (16)	15.78 (6)
2014 AVT1	2966 (13)	108 (22)	118 (22)	274 (21)	17.16 (6)
2014 IVT	3296 (14)	104 (16)	93 (17)	305 (17)	21.49 (14)
2015 AVT2	3620 (13)	110 (19)	97 (8)	283 (19)	22.4 (18)
2015 AVT1	3505 (13)	111 (18)	95 (18)	264 (18)	22.8 (16)
2015 IVT	2804 (13)	110 (18)	145 (18)	269 (18)	17.5 (15)
2016 AVT2	4005 (14)	106 (23)	94 (24)	283 (22)	23.1 (10)
2016 AVT1	3185 (12)	103 (24)	132 (23)	298 (23)	22.5 (16)
2016 IVT	4017 (9)	107 (22)	142 (22)	275 (22)	18.4 (6)
2017 AVT2	4597 (13)	104 (24)	89 (24)	277 (24)	23.9 (18)
2017 AVT1	3270 (14)	109 (25)	137 (25)	289 (25)	21.4 (16)
2017 IVT	4103 (12)	105 (22)	94 (23)	298 (23)	22.8 (18)
2018 AVT1	4147 (13)	107 (13)	97 (13)	338 (13)	23.9 (12)
2018 IVT	4555 (15)	104 (15)	99 (15)	381 (15)	23.92 (13)
2019 IVT	3671 (20)	99 (20)	96 (20)	309 (20)	21.94 (8)
2020 AVT1	3716 (23)	100 (23)	99 (23)	310 (22)	16.77 (21)
2020 IVT	4041 (17)	87 (17)	92.86 (17)	310 (17)	15.8 (14)
Weighted average	3645.38	104.94	110.07	294.17	20.97

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr2/Lr27/Yr30*, *Sr24/Lr24* and *Sr36/Pm6* were pyramided in the background of HD2833 cultivar through marker assisted backcross approach. Presence of the resistance genes were carried out using molecular markers, *gwm533* (*Sr2*+) (Spielmeyer *et al.*, 2003), *Sr24#12* (*Sr24/Lr24*) (Mago *et al*., 2005) and *stm773-2* (*Sr36/Pm6*) (Tsilo *et al*., 2008), in the pyramided lines. Stable and high yielding line (HW5074) was selected at BC4F7 generation and further evaluated for four seasons in two years. Adult plant reaction of pyramided lines showed resistance to the stem rust, leaf rust and powdery mildew pathotypes prevailing in India. HW5074 is the sister line of HW5073 which is high yielding with good agronomic traits. Using gene pyramids of minor (*Sr2/Lr27/Yr30*) and major resistance genes (*Sr24/Lr24* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment. Genetic stock can diversify the rust resistance genes among the wheat germplasm and provide a vital source for imparting durable rust resistance in wheat.

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

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In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with seedling and adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr24/Lr24*, *Sr26* and *Sr36/Pm6* were pyramided in the background of MACS2496 cultivar through marker assisted backcross approach. Microsatellite markers, *stm773-2* linked to *Sr36* (Tsilo *et al*., 2008), *Sr26#43* (Mago *et al*., 2005) linked to *Sr26* and *Sr24#12* (Mago *et al*., 2005) linked to *Sr24/Lr24* were used to perform marker assisted selection. Stable and high yielding line (HW5068) was selected at BC3F4 generation and further evaluated for four seasons in two years. Seedling and adult plant reaction of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India. Using gene pyramids (*Sr24/Lr24*, *Sr26* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment.

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

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

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Table 1: Trait description of germplasm: IC335971

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

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

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

Reference

Kirigwi FM, M Van Ginkel, G Brown-Guedira, BS Gill, GM Paulsen and AK Fritz (2007) Markers associated with a QTL for grain yield in wheat under drought. *Mol. Breed.* 20: 401-413.

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

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

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

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

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

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

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

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

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Wheat is one of the most widely consumed cereal crops worldwide that provides 20% of dietary calories and protein. In India, wheat is the most important cereal crop after rice with a production of 109 MT during 2020-21. But with the rapidly increasing population, India will need more than 140 million tons of wheat by 2050. Among many factors, intensified agricultural practices and climate change have increased the incidence of pathogens in wheat in the recent years. Stem and leaf rust diseases continually pose threat to wheat production. In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with seedling and adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr24/Lr24*, *Sr26* and *Sr36/Pm6* were pyramided in the background of LOK1 cultivar through marker assisted backcross approach. Microsatellite markers, *stm773-2* linked to *Sr36* (Tsilo *et al*., 2008), *Sr26#43* (Mago *et al*., 2005) linked to *Sr26* and *Sr24#12* (Mago *et al*., 2005) linked to *Sr24/Lr24* were used to perform marker assisted selection. Stable and high yielding line (HW5067) was selected at BC3F4 generation and further evaluated for four seasons in two years. Seedling and adult plant reaction of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India. Using gene pyramids (*Sr24/Lr24*, *Sr26* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

* Coloured check used in trial- Paiyur 2

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

Morpho-agronomic Characteristics

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

Associated Characters and Cultivated Practices

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

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

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

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

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

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

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

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

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

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Vigna stipulacea (Lam.) Kuntze., commonly known as *Minni payaru* is an underutilized legume species and has a great potential to be utilized as food crop. Morphological and molecular characterization of diverse panel of *V. stipulacea conserved in the Indian National Genebank,* was carried out to evaluate and select the best germplasm to be utilize in the breeding program. Significant variation was recorded for the morphological traits. *Euclidean distance using UPGMA method grouped all accessions into two major clusters. Accessions were identified for key agronomic traits* *such early flowering (IC331436, IC251436, IC331437); long peduncle length (IC553564) and more number of seeds per pod (IC553529, IC622865, IC622867, IC553528).* Peduncle length was recorded for the length of the longest peduncle when the first pod changes colour. Accessions IC553564 was identified for long peduncle length (Gore *et al*., 2022). Long peduncles are advantageous in getting the pods above the canopy. This helps in reducing the damage of pods by the pod borer and other insects and is also helpful at the time of harvesting. This trait may be transferred to cultivated *Vigna* for facilitating mechanical harvesting, especially in mungbean, which is highly desirable keeping in view the increasing cost of labour and drudgery involved in manual picking of mature pods.

Reference

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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Cucumber (*Cucumis sativus* L.) is one of the important Cucurbitaceous vegetables consumed throughout the world in salad, cooked and pickle form. Common cucumber varieties have white to greenish flesh and are of low nutritional quality. However, in NE parts of India carotenoid rich cucumber landraces are prevalent and used by the local people as vegetable or in preparation of chutney since a long time. AZMC-1, collected from Aizawl, Mizoram during 2011 is also orange fleshed. AZMC-1 was identified with some unique traits in a segregating form. Desirable plants were selected and maintained through single plant selection for 9 generations. Characterization and evaluation of homozygous families of the germplasm was conducted during 2018-2020. The carotenoid content at physiological maturity stage of this accession was high 54.8 µg/g as compared to 2.53 µg/g in the best check variety Pusa Uday at Delhi conditions (Table 1).

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

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

Table 1: Trait description of AZMC-1

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

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

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

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

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

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

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

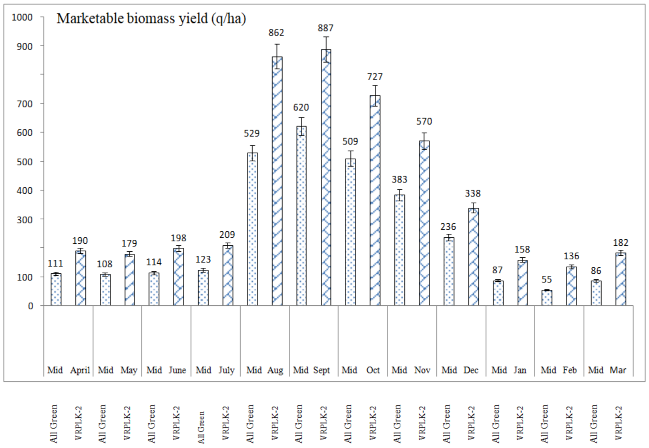

Figure 1: Marketable biomass yield (q/ha) of 'VRPLK-2' and national check 'All Green' (Round the year sowing); (Mean of 2018-19 and 2019-20)

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

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

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

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

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

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

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

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

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

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

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

The genotype DRMR 2017-26 was derived from a cross between NRCHB 101 × DRMR 2269 at ICAR-DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising for thermo tolerance at seedling stage coupled with high seed & oil yield and suitable for early sown conditions. The genotype was tested three years under AICRP-RM plant physiological trials during 2018-19 to 2020-21 at 8 locations (environments) and plant breeding trials during 2018-19 at 9 locations in 2 major mustard growing zones II & III covering Rajasthan, Haryana, Delhi, Jammu, UP and parts of MP and Bihar. Pooled summary over the years and locations indicates that proposed genotype DRMR 2017-26 has less seedling mortality (22.6%), high RWC (73.0%), dry seedling weight (6.3g), SPAD values (chlorophyll), along with high seed & oil yield as compared to heat tolerant (seedling stage) checks PM 25 and JD 6 (Table 1). Proposed genotype DRMR 2017-26 has 8.3 to 10.3% higher oil yield and 7.3 to 9.5% higher seed yield over the checks. This indicates thermo tolerant (at seedling stage) characteristics of DRMR 2017-26 and it can be utilized in breeding programmes for development of high-yielding thermo (heat) tolerant varieties with high seed and oil yield, as it has better yield traits.

Table 1: Pooled summary of physiological parameters (thermo tolerance) and performance for seed & oil yield and contributing traits of proposed genetic stock DRMR 2017-26 and checks under AICRP-RM trials during 2018-19 to 2020-21

Parameters	*No. of locations*	*DRMR 2017-26*	**Check varieties*	
			PM 25	*JD 6*
Seedling mortality (%)	8	22.6	22.6	27.5
Dry weight (g) of 10 seedlings	8	6.3	6.0	4.8
SPAD values (Chlorophyll content)	8	41.6	42.4	40.0
Relative water content (%)	8	73.0	72.2	66.0
Seed yield (kg/ha)	9	2029	1891	1859
Oil yield (kg/ha)	9	834	770	756
1000 Seed weight (g)	9	4.8	4.6	4.4
Oil content (%)	9	41.0	40.7	40.7
Days to maturity	9	121	116	127

* High temperature tolerant (at seedling stage) check genotypes

27. R6 (IC643978; INGR22090), a sesame (*Sesamum* sp.) germplasm with high lignan content (sesamin 61.2 ug/ml; sesamol 15.1 ug/ml); high oil content (52.9% w/w) and tolerance to charcoal rot

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The presence of lignans (sesamin, sesamol) adds pharmaceutical value to the sesame oil. The inter-specific hybrid sesame germplasm, which we developed, is a novel one containing high lignan (sesamin 61.2 ± 1.0 µg/µl, sesamol 15.1 ± 0.6 µg/µl) in its oil (52.9 ± 1.4 % w/w). The Indian high-yielding cultivar of *Sesamum indicum* L. (IC131989 from MP, NBPGR germplasm collection) was the female parent for the hybridization programme (sesamin 20.3 ± 0.8 µg/µl, sesamol 5.3 ± 0.2 µg/µl, oil 54.5 ± 2.3 % w/w). The male parent was wild sesame, *Sesamum mulayanum Nair.* Though the wild is less oil-yielding (36.3 ± 1.4 % w/w), it contains remarkably higher lignan (sesamin 69.0 ± 2.8 µg/µl, sesamol 17.1 ± 0.6 µg/µl) in oil. We performed the hybridization in controlled net house conditions in 2013 in the experimental farm of Bose Institute at Madhyamgram, WB. The breeding method used is pedigree selection. We adopted a combination of seed phenomics and EST-SSR analysis to select the putative hybrids in the F_2 generation. Considering sesamin synthase as a candidate gene, we found a correlation between its expression through qRT-PCR and sesamin content through HPLC analysis (Dutta *et al.,* 2021a).

Besides maintaining the lines at the Bose Institute's experimental farm, we have cultivated this hybrid successfully in the farmers' field of Panskura, West Medinipur of West Bengal, from 2019 to 2024. Similar to *S. mulayanum,* this inter-specific hybrid is tolerant to charcoal rot of sesame seedlings. We have performed a controlled inoculation experiment with *Macrophomina phaseolina*, the causal organism of charcoal rot. *S. mulayanum* showed a high disease tolerance with the lowest disease index score (25%), followed by the recombinant (32%). On the contrary, the cultivated sesame *S. indicum* exhibited a high (92%) disease index score (Dutta *et al.,* 2021b).

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28. EC34372 (EC34372; INGR22091), a soybean (*Glycine max*) germplasm with Anthracnose resistance and early maturity possessing rare alleles for genes of early maturity (*e2, e3, e4* and *e9*)

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Soybean anthracnose disease is caused by *Colletotrichum truncatum* (Schw.) Andrus &W.D. Moore leading to 16-25% yield loss. Central India is a hub for soybean cultivation and farmers prefer early maturing (~90 days) soybean cultivars to adopt soybean-wheat cropping system (Kumawat *et al.,* 2020). Congenial environment for anthracnose disease incidence coincides with the pod filling stage resulting in significant yield loss in susceptible cultivars. Therefore, anthracnose disease is regarded as one of the important and economical soybean diseases in India (Nataraj *et al.,* 2020).

During *Kharif* 2018, a total of 230 soybean germplasm lines have been screened for anthracnose resistance under hot-spot field conditions at ICAR-IISR, Indore. Out of them, genotypes, EC 34372, EC 457254, EC 538828 and Karune were found to be highly resistant while genotypes JS 95-60, Shivalik and IC15089 were found to be highly susceptible. During 2019, genetics of anthracnose resistance in EC 34372 has been carried out under hot-spot field conditions. An F_2 population (EC 34372 (R) × JS 95-60 (S), N=487) along with respective parents were sown in a plot having history of anthracnose disease incidence at ICAR-IISR, Indore. Highly susceptible genotypes viz., JS 95-60, IC 15089 and EC 572136 were sown in regular intervals so as to act as infectors to increase the disease severity and to avoid disease escape. The $\chi^2_{(9:7)}$ test indicated that the mode of inheritance of anthracnose resistance in EC 34372 was through complimentary gene interaction (Nataraj *et al.,* 2020). Resistance disease reaction on EC 34372 was also confirmed during the year 2020 (Annual Report 2020). Furthermore, this genotype is early maturing (88 days) and molecular characterization has been carried out for the traits early maturity and photoperiod response genes which identified high level of genetic variation in tested genes (Kumawat *et al.,* 2020). Out of six genes tested for early maturity and photoperiod response (*E1, E2, E3, E4, E9* and *E10*), four had shown rare alleles (*e2, e3, e4* and *e9*). Therefore, this genotype is a potential and stable resistance donor that can be employed in breeding for early maturity and anthracnose resistance. Also, this genotype can be used to map genes governing resistance for their further transfer in susceptible varieties through marker assisted selection. Details of salient characteristics/chief botanical and morpho-agronomical description of EC34372 have been presented in Table 1.

Table 1: Salient characteristics/chief botanical and morpho-agronomical description of soybean genotype EC34372

S. No.	*Trait*	*Value*	*S. No.*	*Trait*	*Value*
1.	Hypocotyl pigment	Present (Purple)	15.	Early Plant Vigour	Very good
2.	Leaf color	Dark green	16.	Leaf Shape	Pointed ovate
3.	Number of leaflets	3	17.	Stem determination	Determinate
4.	Flower Colour	Purple	18.	Yield/ plant	20.0 g
5.	Pubescence	Present	19.	Pubescence color	Tawny
6.	Pubescence density	Dense	20.	Pubescence density	Normal
7.	Seed Colour	Yellow	21.	Hilum colour	Brown
8.	Plant height	41.0 cm	22.	Days to flower	30
9.	100-seed weight	12.0 g	23.	Days to maturity	88
10.	Cotyledon colour	Green	24.	Seed coat colour	Yellow
11.	Seed Coat Pattern	Uniform	25.	Lodging score	0
12.	Surface lustre	Shiny	26.	Primary branches/plant	3
13.	Pod Colour		27.	No. of nodes / plant	4
14.	Pods/plant	35	28.		

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29. Acc 562 (IC645756; INGR22092), a nutmeg (*Myristica fragrans*) germplasm with monoecious fruits borne in clusters of 2 to 7

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Nutmeg (*Myristica fragrans* Houtt.) is an evergreen, dioecious perennial tree spice that produces two distinctly different spices *viz*. nut and mace from the fruit. The tree is usually dioecious in nature bearing either male or female flowers. Very large variability is seen in the seedling population of this widely cross pollinated crop. Rarely monoecious trees which bear both male and female flowers on the same tree do exists in this population.

During a germplasm survey to Karnataka, 30 seedlings of nutmeg were purchased from the nutmeg plantation maintained by Mr. Poornand Venkatesh Bhat, Shriram Siddhi Estate, Ankola, Karwar, Uttarakand, Karnataka during 2012. The seedlings were germinated in bag during 2012. Twelve seedling of one-year-old were planted in the field in the nutmeg conservatory at ICAR-IISR, Kozhikode in 2013.

It was observed that one of the seedlings, Acc. 562 was precocious in nature and flowered in the second year of planting in 2015. Usually the seedling trees of nutmeg flower after 6 to 7 years of planting making Acc 562 different from other nutmeg trees conserved in the germplasm conservatory at IISR. Acc. 562 is monoecious in nature and both male female and rarely hermaphrodite flowers were seen in the tree and the flowers were borne in clusters. Generally while planting nutmeg male trees also has to be planted in the ratio 1:15 for pollination. As Acc.562 is monoecious in nature, male and female flowers are seen on the same plant there is no need for planting male trees and hence more number of trees can be accommodated per unit area.

The tree is about 6 feet tall during the sixth year and has drooping plagiotropic branches. The tree flowered in the second year of planting and 11 fruits were obtained. The number of fruits increased every year with the growth of the tree. Fruits are borne singly as well as in clusters up to 7. About 400 fruits were obtained in the 6 th year of planting. The fresh fruits weigh about 65 to 75 g, nut 8 -10 g and mace 1.5 to 2 g. The seed is brownish black and medium sized and mace entire.

30. TRA-1 (CIARI-Samridhi) (IC0590905; INGR22093), a noni (*Morinda citrifolia*) germplasm with small fruit (55-60 g), more number of fruits and dwarf stature (1.7-2.5 m)

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Noni (*Morinda citrifolia* L.; Family: Rubiaceae) is a source ingredient in traditional medicine system such as Ayurveda, Chinese, Polynesian, Australian and Nicobari traditional medicinal systems for curing of various ailments including arthritis, colds, diabetes, inflammation and pain. It appears to be 'natural reservoir of bioactives' because more than 200 bioactive compounds have been reported including anthraquinones, flavonoids, polysaccharides, glycosides, iridoids, lignins and triterpenoids (Chan *et al.,* 2006). Almost all parts of Noni plants are useful for medicinal or industrial purpose but fruits are most commonly used for pulp and juice extraction (Singh *et al*., 2012). It is well suited potential crop for tropical coastal and island regions and Noni juice has huge potential as health supplement in national and international markets (West *et al.,* 2018). To explore its commercial potential, it was required to develop genotype(s) which can grow well in open as well as under partial shade condition (in coconut, arecanut plantations) and suitable for high density planting. Its intercropping in existing coconut and arecanut plantations will increase income from same piece of land and fit well with 'zero land 'cultivation.

The Noni genotype 'TRA-1' is developed by selection from local collection for higher juice recovery, small fruits and dwarf statured bush type plants. These are well suited for high density plants at 2.5 x 2.5 m distance as compared to 4.0-5.0 x 4.0-5.0 m for normal growing genotypes. It can tolerate partial shade condition hence, fits well for growing in coconut and areacnut plantations without compromising yield levels. TRA-1 bears fruits year round and maintains around 38.46 % higher yield level than earlier identified genetic stock 'CIARI-1'. The fresh juice recovery from TRA-1 fruits was observed to be 67.72% by standard juice extraction method. Total soluble solids content in juice was 9.5 °Brix which was significantly higher than CARI-1 (5.8 °Brix). It was found to be rich in polyphenol, flavonoid (614.0 mg/100 g), tannin (390.6 mg/100 g), ascorbic acid (93.5 mg/100g) with high DPPH antioxidant activity (82.4 %). The TRA-1 seeds contain 17.60% oil. The GC-MS analysis its seed oil reveled that essential fatty acids i.e. linoleic acid and oleic acid are highest in TRA-1 among the available 33 genotypes.

Hence, the TRA-1 has potential for immediate use for (i) commercial cultivation in open or as intercrop in coconut and arecanut plantations, (ii) tap the nutritive and fatty acids potential in developing better health refreshing products and (iii) also in breeding and genetic studies for fruit size, juice recovery level and phytochemeicals in noni.

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31. ML-2 (IC0594046; INGR22094), a mango (*Mangifera indica*) germplasm with polyembryony and Salt tolerance

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Salt toxicity is a major productivity constraint which limits cultivation of several fruit crops including mango. Development of rootstock tolerant to salinity and sodicity is the only alternative approach to establish the crop in the salt affected soils. The mango rootstock '13-1' is a promising salt tolerant polyembryonic type developed in Israel in 1984. Indian workers have earlier reported the salt tolerance phenomenon in Karukkan and Olour rootstocks but the field level sustenance under high pH and Ec was still a challenge expecting for 13-1.

Mango, being cross pollinated nature exhibits higher heterozygosis in seedling progenies developed from fertilized ovule (monoembryony). Therefore, there is a need to develop true to type polyembryonic rootstocks. Intensive survey in the Andaman and Nicobar Islands after the post tsunami sea water inundations resulted in the collection of 33 accessions among which 15 were polyembryonic. Screening the polyembryonic accessions in pots revealed six accessions possessing moderate to high tolerance to salinity. Further screening six accessions in sodic soils under field conditions for five years resulted in identification of the accessions ML-2 and ML-6 for their salt tolerant trait. The accessions ML-2 and ML-6 showed high tolerance to sodicity exhibiting significantly higher survival rate and plant height and yield than the others used in the study (Table 1).

Furthermore, the study emphasized with the finding that

Table 1: Plant height (cm) of ML-2 in sodic conditions

Accessions	*At planting*	*1st YAP**	*2nd YAP**	*3rdYAP**	*4th YAP*	*5th YAP*
ML-2	31.51	76.00	111.00	164.00	210.00	245.00
ML-3	30.00	33.83	0.00	0.00	0.00	0.00
ML-6	28.00	108.80	125.67	190.00	245.00	270.00
GPL-1	29.83	32.66	0.00	0.00	0.00	0.00
GPL-3	29.00	32.00	0.00	0.00	0.00	0.00
GPL-4	28.00	30.00	0.00	0.00	0.00	0.00
A13-1	29.00	62.67	106.00	130.00	184.00	265.00

the tolerant accessions (ML-2 and ML-6) possessed higher K+ ions accumulating ability in their leaves and meristem tips that caused significant reduction in Na^+/ K^+ ratio (Table 2). Moreover, high proline and much activated antioxidant enzyme activity of the tolerant accessions confirmed the role of antioxidants in imparting tolerance to salt stress. Though 13-1 was observed to explicit sodicity tolerance, the poor fruit set percentage of this cultivar under sub-continent conditions as reported earlier limited its utility in this region. Thus, the accessions ML-2 and ML-6 can be considered as better sodicity tolerant polyembryony rootstocks of mango for the tropics and sub-tropics than 13-1.

The rootstocks ML-2 and ML-6 exhibited the salt tolerant trait along with comparatively higher fruit yield than the standard check 13-1 in the soil of pH ranging from 8.15 to 9.39.

Table 2: Mean soil properties of the CSSRI, experimental field of sodic soil used for screening located at Lucknow, Uttar Pradesh

Soil Depth (cm)	*pH*	*Ec*	*SodiumMeq/l*	*Carbonate Meq/l*	*Bicarbonate Meq/l*	*Ca Meq/l*	*Mg Meq/l*	*SAR*
0-15	9.13 (±0.19)	0.686 (±0.104)	7.38 (±0.79)	4.00 (±0.50)	0.00 (±0.00)	1.50 q(±0.50)	0.00 (±0.00)	8.52 (±0.90)
15-30	9.49 (±0.16)	0.748 (±0.026)	10.47 (±0.72)	3.5 (±0.30)	2.00 (±0.50)	1.00 (±0.20)	0.00 (±0.00)	14.81 (±0.84)
30-60	9.9 (±0.18)	0.834 (±0.029)	11.3 (±0.60)	3.00 (±0.50)	1.00 (±0.50)	1.00 (±0.400)	0.00 (±0.00)	15.98 (±0.98)

Values in the parentheses indicate the standard deviation of the replicates with the mean

32. CHES R-31 (IC642756; INGR22095), a rambutan (*Nephelium lappaceum*) germplasm with yellow colour fruit, greater number of fruits per bunch (15-20 fruits/ Bunch) and medium fruit size.

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Rambutan (*Nephelium lappaceum* var. *lappaceum* L.) is the native of Malaysia and Indonesia and belongs to family of Sapindaceae. The cultivation of Rambutan is spread over all tropical counties. Indonesia and Malaysia contribute more than 95% of total Rambutan production in the world. In India, Rambutan was introduced as a homestead garden in Kerala and slowly it became popular and the area is rapidly increasing in part of Kerala, Karnataka and Tamil Nadu (Tripathi *et al*, 2014; 2020). Rambutan is one of the emerging underutilized fruits with high global demand.

A large collection of rambutan variability was made at Central Horticultural Experiment Station (IIHR), Chettalli, Karnataka during 2001-12. 37 collections of rambutan planted in 2001 were evaluated for growth, flowering and fruiting characters during 2007-12. There was lot of variability in these collections with respect to fruit, fruits size, fruit colour and fruit quality parameters. The growth data reveled that plant height ranged from 2.90 m in CHESR-24 to 6.30 m in CHESR-28. The yield data revealed that highest yield was recorded in CHESR-26 (48.8 Kg.) while CHESR-33 registered the minimum yield of 2.77 Kg. The higher fruit weight recorded in CHESR-27 (44.2 g), whereas, CHESR-156 recorded the lowest fruit weight of 16.5 g. Most these collections were of red colour fruits, only few collections were yellow colour. Among the yellow colour collections, CHESR-31 were found superior than other accessions. The trees of this collection are semi spreading with plant height (5.80 m), Tree Spread (3.49m^2) and Tree volume (35.06m^3) and regular bearer. It is a mid-season variety which flowers in February to April and fruits ripe in October under Chettalli

Table 1: Yield and proximate analysis of Rambutan selection- CHESR-31 (IC642756)

Tree age (years)	*No. of Fruits/ Plant*	*Yield (kg/tree*	*Fruit Weight (g)*	*Fruit Length (cm)*	*Fruit Breadth (cm)*	*Fruit Volume (cc)*	*Pulp Content (%)*	*Peel Content (%)*	*Seed Content (%)*	*TSS (°B)*	*Acidity (%)*	*Vit.- C (mg/100g)*
8	735	17.42	23.70	4.10	3.40	21.40	49.62	43.50	6.88	17.90	0.60	48.60
9	1659	41.31	24.90	4.42	3.15	24.30	52.89	38.51	8.60	18.40	0.48	51.92
10	429	9.93	23.83	4.06	3.14	21.91	51.226	41.03	7.72	17.52	0.56	48.25
11	1700	37.23	21.90	4.50	3.00	22.10	48.40	45.21	6.39	18.10	0.40	49.90
12	1259	21.3	22.9	4.28	3.05	21.7	51.2	41.2	7.6	19.2	0.39	41.2
Average	1156.40	25.44	23.45	4.27	3.15	22.28	50.67	41.89	7.44	18.22	0.49	47.97

(Coorg) conditions. Fruits are yellow in colour. Fruit weight is about 23.45g which is higher than average weight of yellow colour rambutan lines. The aril is white and juicy sweet. Fruit has Total soluble solids content (18.22^{O}Brix), acidity (0.08%) and vitamin C (4797 mg /100 g pulp). ((Tripathi *et al.*, 2014; 2020; Table 1).

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33. VL 360 (IC640694; INGR22096), a white grained finger millet (*Eleusine coracana*) germplasm with early maturity (100 days) trait

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Finger millet grains are in general dark brown in colour due to high levels of tannins and phenolics. The dark colour of grains has been the major hindrance for its acceptability in baking and food industry (Sharathbabu *et al.*, 2008). Sometimes the high amount of tannins and phenolics provide bitter taste to the value added products thereby reducing their consumer acceptability. To overcome this few white grain mutant genotypes were developed but these genotypes were very late in maturity thereby reducing their farmer's acceptability especially in North western Himalayan region (Sood *et al.*, 2019). Early maturity (≤100 days) is one of the most important breeding targets in finger millet breeding as the crop occupies dryland areas where the growth period is mostly limited due to less availability of water for the crop.

VL 360 is an elite early maturing (100 days) finger millet genotype developed from a cross between WR2 (late maturing white seeded genotype) and VL 201 (Early maturing brown seeded released variety) followed by pedigree selection (Anonymous 2010). The major emphasis was to select early maturing white seeded genotype suitable for hills and areas where growth period is limited for the crop due to water stress conditions. This genotype (VL 360) was early in maturity (100 days) among all white seeded genotypes developed across country and evaluated in multi- location trial conducted in six locations in the year 2010 by project coordinating unit (Anonymous 2010). The genotype was again evaluated at Almora location in white seeded finger millet station trial in 2011and found to be earliest in maturity (97 days) among all white genotypes. It is 16 days earlier in maturity than the white parental line WR2 from which it has been derived.

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34. Somatic hybrid (H1* B. j. cv NPJ- 212) (IC645757; INGR22097), an Indian mustard (*Brassica juncea*) germplasm with resistance against *Alternaria brassica*; short height and less duration than its parent

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Alternaria blight is the most devastating disease not only in India but all 53 countries where cultivation of Brassica for oilseeds and vegetables occurs. Alternaria blight is caused by *A. brassicae* in oil seeds and *A. brassicicola* in vegetables. The resistance source for Alternaria blight is unavailable within the cultivated Brassicas. Therefore, the introgression of resistance for this disease from allied genera is the only way to develop resistant germplasm. However, the stability and fertility of the inter-generic hybrids are major concerns. *Sinapis alba* was reported to possess resistance for Alternaria blight, Sclerotinia stem rot (Kumari *et al.*, 2020c), high temperature, With the aim of introgression of the genes responsible for Alternaria blight, *Sclerotinia* stem rot resistance, and high-temperature tolerance, the first stable and fertile somatic hybrid of *B. juncea* and *S. alba* has been developed through PEG mediated protoplast fusion. This allohexaploid Brassica (H1) was registered in the NBPGR genebank with the potential of a high degree of resistance to *brassicae*, *Sclerotinia sclerotiorum*, and thermos tolerance.Kumari and Bhat 2019), However, along with these agronomically important traits, the yield potential was inferior as compared to the cultivated parent (*B. juncea* cv. RLM-198) while the plant height, biomass, and crop duration increased. Therefore, the back crossing was done with the high yielding and short height variety of *B. juncea cv.* NPJ-212 as a pollen donor. Therefore, the pedigree of the genetic stock is (*B. juncea cv.* RLM-198 + *S. alba*) x *B. juncea cv.*NPJ- 212. The BC1F2 progeny of the H1 somatic hybrid has an average height of 198 cm, their leaves attained the lyrate shape. These plants attained 15days early flowering than the BC1F1 progenies obtained after being backcrossed with *juncea* cv. RLM-198and 25 days than the somatic hybrid (H1) while the siliqua attained the length of 3.51cm and13 seeds per silique in comparison to (H1) which 3.11cm siliqua length and approx 7 seeds/ siliquae. However, the seed size is smaller than the H1 allohexaploid Brassica. This genetic stock has revealed 48 chromosomes in their somatic tissues out of them, 36 chromosomes were acquired from *B. juncea* and another 12 chromosomes from *S. alba* proved through genomic *in-situ* hybridization (GISH) probed with fluorescein isothiocyanate (FITC) labeled *S. alba* genome. The meiotic analysis reveals 24 pairs and none of the univalent or multivalent was seen during the study. This genetic stock was screened for the *Alternaria* blight resistance for three consecutive years in three different environments including two off seasons and at the hot-spot for the disease and found resistant over their cultivated parents *B. juncea* (cv. RLM- 198 and NPJ-212) and *S. alba*. Interestingly, the resistance against the *A. brassicae* was revealed by the BC1F2 progeny as similar as shown by the H1 somatic hybrid. Therefore, the subsequent progenies of the BC1 are the valuable genetic stock and have suitable agronomical traits for resistance breeding.

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35. Somatic hybrid (H2*B. j. cv NPJ- 212) (IC645758; INGR22098), an Indian mustard (*Brassica juncea*) germplasm with resistance to *Alternaria brassicae*; higher yield, short height and duration than the H2

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The inter-generic hybridizations were not successful in Brassicas due to pre and post-fertilization barriers. Therefore, somatic hybridization was reported frequently within crop Brassicas and their allied genera with the aim of introgression of several agronomic importance characters (*Kirti et al.,* 1992). Although the fertility of these somatic hybrids and their backcrossed progenies were not recovered due to abnormal Meiosis, but a few workers successfully recovered the back crossed generations and introgressed some agronomical importance traits from wild to cultivated *Brassica* (Singh *et al.,*2021). This allohexaploid Brassica (H2) was registered in the NBPGR gene bank with the potential of a high degree of resistance to *A. Brassicae* and very high-temperature tolerance at the time of seed settings. However, along with these agronomical importance traits the yield potential was inferior as compared to the cultivated parent (*B. juncea cv.* RLM-198). Therefore, we backcrossed the somatic hybrid (H2) with the cultivated variety of *B. juncea* cv.NPJ-212 using as a pollen donor. Thus, the pedigree of the genetic stock is (*B. junceacv.* RLM-198+*S.alba*) x *B. juncea cv.* NPJ- 212. The viability of the recovered seed was found very good (Kumari and Bhat, 2021). The plant height was recorded decreased (176.33cm) while the attained the flowering at the age of 70 days in comparison to somatic hybrids (291.80cm) and 86 days respectively. Similarly, the siliqua beak length also decreased from 1.12 mm in the H2 and 0.87cm in BC1F2. However, the average siliqua length and the number of seeds/siliqua were increased (4.47cm and 16.68) in comparison to the H2 (3.16cm, 6.40). In the same way the crop duration also decreased as compared to H2. These plants carried 48 somatic chromosomes, out of them 36 acquired from the cultivated parent *B. juncea* and another 12 from donor *S. alba*. Interestingly, we have observed the 24 pairs at the meiosis. The first backcrossed generation of the allohexaploid (H2) carries the recombinant mitochondria of *B. juncea* and *S. alba* with chloroplast of the cultivated parent with a high degree of fertility and stability (Kumari and Bhat, 2021). However, these plants showed the same degree of resistance as well as the Allohexaploid (H2) for the *A. brassicae* during the *In-vitro* and *in-vivo* screeningwith a highly virulent strain of *A. Brassicae* for three subsequent years and three different environments including the hotspot conditions to the diseases. The plants attained flowering when the ambient day temperature exceeded

28°C. Therefore, these plants were fit for late sown in mid-November and could attain flowering at the age of ~70 days in February's first week.

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36. DRMR 2018-27 (IC645774; INGR22099), an Indian mustard (*Brassica juncea*) germplasm with high temperature and moisture stress tolerance at seedling stage

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Indian mustard (*Brassica juncea* L.) is an important oilseed crop of India. It is major source of income especially for marginal and small farmers in rainfed areas of 7 states. Under rainfed conditions, early sowing of the crop helps to harvest maximum monsoon rain water. The crop inevitably suffers from moisture stress (drought) during reproductive period when stored water becomes depleted. This leads to a heavy loss of seed yield during severe conditions Germplasm with heat tolerance at seedling stage and a good source of moisture stress tolerance which can be utilized in breeding programmes for development high-yielding thermo and drought-tolerant varieties is the need of the hour. The genotype DRMR 2018-27 was derived from a cross between NRCHB 101 x DRMR 2398 at ICAR-DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising under moisture stress conditions as well as high temperature tolerant (seedling stage) under early sowing. The genotype was tested under AICRP-RM plant physiological trials during 2019-20 and

Table 1: Pooled summary of parameters for thermo (seedling stage) and moisture stress tolerance of proposed genetic stock DRMR 2018-27 and checks in physiological trials for during 2019-20 & 2020-21

Parameter *(A) Thermo tolerance at seedling stage*		*No. of locations*	*DRMR 2018-27*	**Check varieties*	
				PM 25	*JD 6*
Seedling mortality (%)	Controlled condition	7	32.9	39.1	40.4
	Field condition	5	22.9	24.2	24.1
Dry weight of 10 seedlings	Controlled condition (mg)	7	39.4	37.9	32.7
	Field condition (g)	5	5.3	6.4	5.4
SPAD values (Chlorophyll)		4	41.2	44.1	42.9
Relative water content (%)		5	72.0	72.2	65.9
(B) Moisture stress (drought) tolerance				RH 725	RGN 229
Relative water content (Reduction %)		6	13.2	16.9	14.2
SPAD Values (Reduction %)		6	13.4	14.1	9.7
Total Chlorophyll (Reduction %)		3	11.9	20.9	18.9
Carotenoids (Reduction %)		2	2.7	16.2	17.0
Seed yield (Reduction %)		7	26.1	24.3	18.3
1000 seed weight (Reduction %)		6	10.9	16.5	9.3
Drought Susceptibility Index (DSI)		6	1.05	1.05	1.01
Yield Stability Index (YSI)		7	0.74	0.75	0.81
No. of siliquae on main shoot (Reduction %)		5	14.8	10.7	9.6
Seeds/siliqua (Reduction %)		6	11.9	11.7	12.2
Oil content (Reduction %)		4	1.04	2.28	1.32
Biological yield (Reduction %)		7	23.2	24.6	26.0

*Tolerant checks: PM 25 & JD 6 for high temperature (seedling stage) and RH 725 and RGN 229 moisture stress

2020-21 at 4-7 locations (environments) for high temperature tolerance in controlled as well as under field conditions and moisture stress (drought) tolerance. Pooled summary over the years and locations indicates that proposed genotype DRMR 2018-27 has least seedling mortality & higher seedling dry weight (controlled) compared to the heat tolerant checks and maintained higher relative water content (% RWC) & Chlorophyll content (SPAD values) revealed its high thermo tolerance at seedling stage. Similarly, it has maintained higher RWC, chlorophyll content, carotenoids, SPAD values and lesser decline in 1000- seed weight, seeds per siliqua, oil content, biological yield and other morphological traits indicating its moisture stress tolerance characteristics. It shows its tolerance both against moisture stress as well as high temperature at seedling stage (Table 1). Therefore, it will be highly useful in breeding programmes for development of high-yielding thermo and drought tolerant varieties. Genotype DRMR 2018-27 will be a very good addition to existing gene pool in germplasm repository for multiple abiotic stress tolerance as high temperature tolerance at seedling stage is highly required in early sown (September) mustard crop and drought tolerance is very much needed in rainfed crop. Hence, this promising line needs protection through germplasm registration.