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Plant Germplasm Registration Notice*

A total of 121 proposals were received online for consideration of registration of germplasm for unique/superior traits. The member-secretary, Plant Germplasm Registration Committee (PGRC), thoroughly screened the applications, and experts reviewed 65 proposals complete in all respects, which were presented at the 51st PGRC meeting held virtually on November 22, 2023. The PGRC recommended 58 proposals with unique/novel features belonging to 25 crop species for registration. The information on registered germplasm is published for the purpose of disseminating the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes. Descriptions of 29 of the 58 recommended germplasm lines are given below:

1. IL19273 (IC650728; INGR23068), a rice germplasm with tolerance to multiple diseases and drought

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The introgression line 'IL-19273' is a multiple stress-tolerant line in the background of an elite rice (*Oryza sativa* L.) cultivar 'Krishna Hamsa' with multiple disease tolerance and high yield under reproductive-stage drought stress. The multiple stress-tolerant IL-19273 was developed at ICAR-IIRR through marker-assisted forward breeding (MAFB) involving multiple parents (Krishna Hamsa, IRBB 60, Tetep and IR 96321-1447-561-B-1 and selective inter-crossing Hamsa during 2013-2019. In the universal blast nursery (UBN) at ICAR-IIRR, IL-19273 recorded a promising disease susceptibility index (dsi) of 3.0 during *kharif* 2019 and *kharif* 2020 and a significant yield advantage of 261% over the recurrent parent 'Krishna Hamsa' (Badri *et al.*, 2022). It is tolerant to several diseases like sheath blight (dsi-5.0), sheath rot (dsi-4.2), rice tungro disease (RTD) (dsi-4.0), glume discolouration (dsi-4.0), leaf blast (dsi-4.8) and neck blast (dsi-4.8) (ICAR-IRR-AICRPR- Annual Progress Report 2022, Vol 2-Plant Pathology). Based on its promising performance in in-house testing for drought and blast resistance tolerance, it was nominated to the AICRPR rainfed upland (RUL) trial in 2021 and the donor screening nursery (DSN) in 2022. Based on performance across environments and yield stability index (YSi) values, IL-19273 has been identified as a stable genotype with drought tolerance suitable for RUL.

IL-19273 is a semi-dwarf, mid-early duration line with long slender (LS) lustrous creamy grains. It comes to fifty per cent flowering (DFF) in 100 days under irrigated conditions with yield potential of 5750 kg/ha. Each hill bears up to 13-14 tillers with 241-334 panicles per square metre and panicle weight of 413 g/m^2. It has a thousand-grain weight (TW) of 25.6 g, total dry matter of 960 g/m^2 and a harvest index of 47.0%.

IL-19273 recorded a promising index (PI) of 33 and 61 for sheath blight with SI $\leqslant$ 3 and SI $\leqslant$ 5 in 5 and 11 environments out of 16 environments, compared to the PI of 21 and 58, respectively, for the tolerant check 'Tetep'. Similarly, it recorded SI $\leqslant$ 3 and $\leqslant$ 5 at 5 and 13 out of 18 environments for leaf blast, SI of 1 to 3 at Imphal, Mandya and Rajendranagar for neck blast, SI of 3 to 5 at four locations for glume discolouration, SI of 1.0 at Mandya and 5.0 at Coimbatore and Nawagam for sheath rot and SI of 3.0 and 5.0 at Coimbatore and IIRR respectively for RTD (Table 1).

It is suitable for rainfed upland cultivation with high stability for grain yield under drought stress, evident from the multi-location testing of AICRPR-RUL trials during 2021 (ICAR-IRR-AICRPR- Annual Progress Report 2022, Vol 3-Physiology). It recorded a mean grain yield of 694 g/m^2 under reproductive-stage drought stress, which is significantly higher than the recurrent parent (Krishna Hamsa), which yielded only 192 g/m^2 under similar drought stress conditions during *kharif* 2019 (Badri *et al.*, 2022).

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Table 1: Disease reaction of IL-19273 under multi-location testing in AICRPR-2022

	Leaf blast																			
Entry	ALM	CBT	CTK	GNV	GGT	IIRR	IMP	JDP	KJT	LNV	MLN	MND	NLR	NWG	PTB	RCI	REW	UMM	USG	SI
19273	7	6	9	6	5	4	3	7	9	4	3	3	4	5	4	4	5	3	1	4.8
Tetep	5	8	5	4	5	1	3	4	5	3	5	2	3	4	4	6	5	5	3	4.2
HR12	3	6	9	5	5	9	3	8	5	4	5	7	6	8	6	5	4	5	9	6.2
	Neck blast								Glume discolouration											
Entry	ALM	IMP	JDP	MND	NWG	RNR	UMM	SI	CHT	LNV	NVS	NWG	SI							
19273		3	7	1	7	7	4	4.8	3	3	5	5	4.0							
Tetep		3	5	0	3	5	6	3.7	5	5	5	5	5.0							
HR12	5	5	9	9	7	7	3	6.4	3	3	7	5	4.5							
	Sheath blight																			
	ADT	BNK	CHP	CBT	CTK	GNV	IIRR	KUL	LDN	MND	MTU	MSD	MNC	NVS	NDL	PNT	PTB	RPR	TTB	VRN	SI
19273		5	1	3	3	7	7	7	3	3	5	5	3		7	5	7	7	7		5.0
Tetep		5	1	3	3	7	7	7	5	3	5	5	3	3	7	5	7	7	7		5.1
	Sheath Rot								RTD											
	ADT	CBT	MND	NVS	NWG	RPR	RNR	SI	CBT	IIRR	SI									
19273		5	1	7	5	7	0	4.2	3	5	4									
Nidhi									5	3	4									

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2. IRGC 39111 (IC650729; INGR23069), a rice germplasm with strong culm

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IRGC 39111, a tropical japonica accession identified as a strong culm genotype at ICAR-IIRR based on evaluation of morphological traits influencing lodging resistance in rice (*Oryza sativa* L.) *viz.,* plant height, culm diameter and thickness, strength of upper and lower internodes, thickness of stem wall, lignin and cellulose accumulation in the stem wall, and panicle weight and grain number since 2016 (Badri *et al.,* 2020; ICAR-IIRR Annual Report 2020). About 650 germplasm comprising tropical japonica accessions (TJP), indica cultivars and north eastern landraces were evaluated for new plant type traits, including culm traits, in 2016, and a core set was developed; the core set was again evaluated in replicated trials, and agro- morphological and molecular characterization identified IRGC 39111 as a novel strong culm genotype devoid of *scm 2* (Rachana *et al.,* 2019; Rachana *et al.,* 2020). Further, IRGC 39111 was evaluated and used as a donor parent for strong culm traits in the development of a mapping population involving the lodging-susceptible elite cultivar 'Swarna'. It also has high grain number and high panicle weight.

Tiller number (TN) and prostrate tester reading (TR) TN and TR provide a measure of bending stress (BS), while culm diameter is indicative of section modulus (SM). Culm strength is a measure of bending stress at the breaking moment (M) influenced by both section modulus and bending stress. Based on three years of data, IRGC 39111 was found to have M value of 2243 g.f. (Table 1). Molecular characterization of IRGC 39111

Table 1: Component traits of culm strength in rice genotypes

Genotype	Section Modulus (SM)				Bending Stress (BS)				Bending Moment at Breaking Stress (M) gf			
	2016	2017	2019	Mean± SD	2016	2017	2019	Mean± SD	2016	2017	2019	Mean± SD
IRGC 39111	19.69	16.14	9.53	15.12±5.16	179.38	128.93	117.19	141.83±33.04	3532	2081	1117	2243±1216
MTU1010	6.58	7.59	11.77	8.65±2.75	69.75	48.17	43.68	53.87±13.94	459	366	514	446±75
Swarna	4.63	5.75	3.79	4.72±0.98	60.75	43.03	45.71	49.83±9.55	281	247	173	234±55
Swarnadhan	5.77	12.95	7.65	8.79±3.72	58.57	47.06	91.25	65.63±22.92	338	610	698	548±188
BPT 5204	3.73	8.34	5.54	5.87±2.32	45.38	44.75	65.53	51.89±11.82	169	373	363	302±115

using gene-specific markers revealed the absence of *SCM2*, a known gene for strong culm, indicating the possibility of the presence of novel QTL/gene(s) for strong culm. Owing to the higher M values (higher than Habataki) and the absence of known *SCM2*, IRGC 39111 would serve as a potential source for novel QTL/gene(s) for strong culm. We have developed recombinant inbred line (RIL) mapping populations between Swarna and IRGC 39111 for use in QTL mapping studies of culm strength traits.

IRGC 39111 can be grown both in wet and dry seasons. It is a medium duration genotype which comes to fifty percent flowering in 110 days. It is a tall genotype with plant height of 145 cm. It bears up to eight tillers with 6-7 panicles on them which weigh about 8.7 g each. Each panicle has about 420 grains with thousand grain weight of 24.3 g and single plant yield is about 28.16 g. Grain yield on an average is about 880 g/m^2.

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3. IL-19101/19102 (IC650730; INGR23070), a rice germplasm with resistance to gall midge, bacterial blight and blast

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The introgression line 'IL-19101/19102' [RP 6614-101; RP 6614-102] is a multiple biotic stress-resistant line in the background of an elite rice (*Oryza sativa* L.) cultivar 'WGL-14' with resistance to major biotic stresses-gallmidge, bacterial blight and blast (Table 1). It was developed at ICAR-IIRR by selective inter-crossing of WGL14/Improved Samba Mahsuri//WGL 14/RP Bio Patho-1///WGL 14/RP Patho-3//WGL 14/RP 5925-24////WGL 14/RP 5925-23//WGL 14/IR 96321-1447-561-B-1///WGL 14/IR 81896-96-B-B-195//WGL 14/IR 74371-46-1-1-13//////WGL 14/Rathuheenati. It has *Gm8* for gallmidge resistance, *Xa21* for bacterial leaf blight resistance and *Pi54* for blast resistance. In the universal blast nursery (UBN) at ICAR- IIRR, IL-19101/19102 recorded a promising disease susceptibility index (dsi) of 1.0 for blast resistance during *kharif* 2018, *rabi* 2019 and *kharif* 2019, dsi of 1.0 for bacterial blight both under glass house and field conditions using leaf clipping method of inoculation during *kharif* 2018, *rabi* 2019 and *kharif* 2019 and resistance to gallmidge. In the multi-location gallmidge screening (GMS) trial of AICRPR during 2021 and 2022, it was found resistant to gallmidge across the locations (ICAR- IIRR-AICRPR- Annual Progress Report 2022 and

Table 1: Pest and disease reaction of IL-19101/IL-19102 for gallmidge, blast and bacterial blight resistance

Gallmidge screening (GMS trials 2021 and 2022)										
Entry 2021	IIRR	JDP	CHP	CTC	JGT	SKL	WGL	PTB	NLR	
GMS	GH	50DT	50DT	16DAR	50DT	50DT	50DT	50DT	50DT	
	%DP	%DP	%DP	%SS	%DP	%DP	%DP	%DP	%DP	
19102	0	0	0	NT	0	0	5	4.8	20	
Aganni	0	0	0	0	0	10.5	10	9.5	0	
Entry 2022	IIRR	JDP	CHP	ABP	JGT	MTU	PTB	RCI	WGL	GMS NPT
GMS	GH	50DT	50DT	50DT	50DT	50DT	50DT	50DT	52DT	9
	%DP	%DP	%DP	%DP	%DP	%DP	%DP	%DP	%DP	
19102	0	0	NT	60	100	0	0	20	0	5
Aganni	0	0	0	0	100	10	4.8	20	0	5
Entry	2018	2019 (R)	2019 (K)	2018	2019		2018	2019		
	UBN			Bacterial blight screening						
				GH	GH		FS	FS		
19101	1.0	2.0	1.0	1.0	1.0		1.0	1.0		
Tetep	2.0	1.0	2.0							
ISM				2.0	3.0		1.0	1.0		

2023, Vol 2- Entomology).

IL-19101/19102 is a semi-dwarf, medium-duration line with medium slender (MS) grains. It comes to fifty per cent flowering (DFF) in 108 days under irrigated conditions with a yield potential of 5756 kg/ha. Each hill bears up to 10-12 tillers with 191-284 panicles per square metre. It has a thousand-grain weight (TW) of 14.47 g, and single-plant yield of 24 g.

IL-19101/19102 recorded nil damage to gallmidge at Jagdalpur and Sakoli and was promising in five of the nine valid tests in GMS trials of AICRPR during 2021. It recorded nil damage in 5-6 of the nine valid tests in GMS trials of AICRPR during 2022. In UBN, it recorded resistance to blast for three consecutive years and also resistance to bacterial blight both under glasshouse and field screening for three consecutive years. It is suitable for irrigated medium-duration ecology.

JDP-Jagdalpur, CHP-Chiplima, CTC-Cuttack, JGT-Jagitial, SKL-Sakoli, WGL-Warangal, PTB-Pattambi, NLR-Nellore, ABP-Ambikapur, MTU-Maruteru, RCI-Ranchi, UBN-Universal Blast Nursery, GH-Glass House, FS-Field Screening

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4. IET 29834 (IC650767; INGR23071), a rice germplasm with reproductive stage drought tolerance and resistance to blast and bacterial blight

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The genotype IET 29834 (IL-19471) is a multiple stress-tolerant line in the background of an elite rice (*Oryza sativa* L.) cultivar 'Krishna Hamsa' with resistance to blast and bacterial blight and high yield under reproductive-stage drought stress. In the universal blast nursery (UBN) at ICAR-IIRR, IL-19471 recorded a

promising disease susceptibility index (dsi) of 3.0 for blast resistance during *kharif* 2018, *rabi* 2019, *kharif* 2019 and *kharif* 2020 and dsi of 3.0 for bacterial leaf blight both under glass house and field screening in 2018, 2019 and 2020 (Badri *et al.,* 2022). It has *xa5+xa8* for bacterial blight resistance and *Pi9+Pi+Pi20* for blast resistance. The multiple stress-tolerant IL-19471 was developed at ICAR-IIRR through marker-assisted forward breeding (MAFB) from the cross of Krishna Hamsa / IRBB60 // Krishna Hamsa / RP Bio Patho 3///Krishna Hamsa/Tetep during 2013-2019 (Badri *et al.,* 2022). Based on performance across locations and yield stability index (YSI) values, IL-19471 has been identified as a stable genotype with drought tolerance suitable for rainfed upland (RUL) cultivation (ICAR-IRR-AICRPR-Annual Progress Report 2022, Vol 3-Physiology).

IET 29834 is a semi-dwarf (100 cm), medium-duration line (103 days) with long slender (LS) lustrous creamy grains. It has a yield potential of 6000 kg/ha with significant yield superiority over the best check in the eastern zone in 2021 and significant yield advantage over the best check in Odisha in 2021 (ICAR-IIRR AICRPR Progress Report, Vol I 2021) and in Uttar Pradesh in 2022 (ICAR-IIRR AICRPR Progress Report, Vol I 2022). Each hill bears up to 12-14 tillers with 270 panicles per square metre and a panicle weight of 590 g/m^2. It has a thousand-grain weight (TW) of 25.4 g and total dry matter of 1247 g/m^2.

IET 298234 (IL-19101) recorded SES scores of 2.0, 1.0 and 2.0 for blast resistance in *kharif* 2018, *rabi* 2019 and *kharif* 2019, respectively, in UBN at ICAR-IIRR (Table 1). It was screened for BLB resistance both under field and glasshouse conditions artificially in 2018, 2019 and 2020, wherein it recorded SES scores of 1.0 to 3.0 (Table 1) (IIRR Newsletter 2019; Badri *et al.,* 2022). It is suitable for rainfed upland cultivation with high stability for grain yield under drought stress, evident from the multi-location testing of AICRPR-RUL trials during 2021 (ICAR-IRR-AICRPR-Annual Progress Report 2022, Vol 3-Physiology). The least reduction in terms of per cent change in grain yield over the control was recorded by IET 29834 (-26%), while its recurrent parent recorded -37% and the drought-tolerant check recorded -33%. The ranking of genotypes based on drought indices revealed that IET 29834 has a high overall rank and is considered relatively drought tolerant and suitable for rainfed cultivation. The Parametric model for simultaneous selection in yield and stability across locations and YSI values identified IET 29834 as a stable genotype under rainfed conditions (Table 2).

Table 1: Disease reaction in IET 29834 in comparison with checks

Entry	2018 *kharif*	2019 *rabi*	2019 *kharif*	2020 *kharif*	2018 *kharif* (GH)	2019 *kharif* (GH)	2020 *Kharif* (GH)	2018 *kharif* (FS)	2019 *kharif* (FS)	2020 *kharif* (FS)
	UBN - blast screening				BLB screening					
19471	2.0	1.0	2.0	2.0	1.0	3.0	3.0	1.0	1.0	2.0
Tetep	2.0	1.0	2.0	2.0						
ISM					2.0	3.0	2.0	1.0	2.0	1.0

ISM, Improved Samba Mahsuri; UBN, Universal Blast Nursery; GH, Glasshouse; FS, field screening.

Table 2: Drought tolerance indices for IET 29834 in comparison with drought tolerant checks across locations in *kharif* 2022

Entry	DSI	RDI	DTI	GMP	TOL	MP	YI	YSI	DI	SDI	HM	KISTI	K2STI	Overall Rank
IET 29834	25	2	12	5	1	9	1	2	1	25	5	17	4	4
DRR Dhan 44	4	23	10	6	21	4	8	23	11	4	9	4	11	9
Shabhagidhan	22	5	18	14	14	14	9	5	8	22	13	18	15	14

DSI, Drought susceptibility index; RDI, Relative drought index; DTI, Drought tolerance index; GMP, Geometric mean productivity; TOL, Tolerance; MP, Mean production; YI, Yield index; HI, Heat resistance index; YSI, Yield stability index; KIST1, Modified stress tolerance index.

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5. MCM 109 (IC635486; INGR23072), a rice germplasm for salt tolerance

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Soil salinity is a major constraint for rice (*Oryza sativa* L.) productivity in coastal areas. Salt-affected soils of 2501369 ha are in coastal India (Mandal *et al*., 2018). The rice crop is salt sensitive at seedling and reproductive stages, and a threshold electrical conductivity of 3 dS/m is considered as the salinity tolerance (Mohammadi *et al.,* 2013). Agricultural Research Station, Machilipatnam has developed high yielding medium duration salt tolerant rice variety, MCM 109 (IET 24425), by the pedigree method from the cross MTU 2716/BPT 5204 with ICNo635486.

The salt-tolerant culture MCM 109 matures in 130-135 days during *kharif* and can tolerate salinity stress at seedling and reproductive stages (score 3), with a low Na/K ratio of 0.89 compared to the fine-grain salt-sensitive check BPT 5204 (1.51). It is a semi-tall (105 cm) fine-grain culture with 1000-grain weight of 15 g and good cooking quality. It was tested in AICRIP trials during *kharif* 2014, 2015, and 2016 in the coastal saline soils of West Bengal, Odisha, Kerala, Maharashtra, and Andhra Pradesh at EC (5 to 11.95 ds/m), and it has recorded a 17.33% yield advantage over salt-tolerant checks CST7-1 and 31.83% FL 478.

It is moderately tolerant to BPH (score 3), Leaf blast (score 4.9), Brown spot (score 4.2) and possesses favourable alleles for anaerobic germination (*qAG3*), drought (*DTY12.2*), Grain size (*GS3*), and BLB (*Xa21, qXa26, Xa4*).

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6. CRR751-1-12-B-B (IC650731; INGR23073), a rice germplasm with tolerance to reproductive stage drought stress, tolerance to submergence and resistance to blast disease

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The proposed genetic stock, CRR751-1-12-B-B is a near isogenic line (NIL) developed through introgression of QTL for grain yield under reproductive-stage drought stress ($qDTY_{2.2}$) in a popular rice (*Oryza sativa* L.) variety, IR64-Sub1, from the donor IR88287-367-B-B, following marker-assisted backcross breeding. CRR751-1-12-B-B is a medium-duration rice genetic stock with awnless grain, well-exserted panicle, straw-coloured, long, slender grain. It possesses all the attributes of IR 64, such as grain quality and resistance/tolerance to major insect pests and diseases. The stock is tolerant to drought at the reproductive stage and has proved that it can sustain 25-30 days of dry spell during *kharif* season without significant reduction in yield. In addition, it has submergence tolerance and can tolerate flash flooding up to 2 weeks. The proposed genetic stock, CRR751-1-12-B-B, under sequential stresses of submergence followed by drought revealed better

survival, elongation ability, new leaf generation, chlorophyll content and chlorophyll fluorescence traits as indicators of submergence recovery than the recurrent parents, IR64 or IR64Sub1.

In a multilocation trial of AICRIP, the proposed genetic stock showed 96.87% yield superiority over the recurrent parent (RP), IR64 and 63.05% over the yield check variety, MTU1010. Under normal irrigated conditions, this entry was at par in yield with recurrent parent IR64. It has recorded excellent tolerance to 2 weeks of complete submergence under submergence tolerance screening at NRRI, Cuttack. Under submergence, it showed 87.7% survival, which is 10% and 93.5% superior to the survival of RPs IR64-Sub1 and IR64, respectively. This line was evaluated along with RP (IR64), yield check (MTU1010) and sensitive check (Gangavati Ageti) under rainout shelter-managed severe stress conditions as well as under normal conditions in different locations (Jharkhand, Uttar Pradesh, Tamil Nadu, Madhya Pradesh, Chhattisgarh, Andhra Pradesh, Telangana State), and showed 56.08%, 69.47% and 628.85% yield superiority over IR64, MTU1010 and Gangavati Ageti, respectively. The proposed genetic stock, CRR751-1-12-B-B, along with RP, IR64 and other quality checks were analysed for grain quality characteristics as well as other important morphological characters under AICRIP for consecutive years. The proposed genetic stock showed grain quality and morphological traits comparable to the recurrent parent. The data showed the similarity of the proposed genetic stock with its recurrent parent.

The proposed genetic stock, CRR751-1-12-B-B, has undergone foreground selection for $qDTY_{2.2}$ using linked SSR markers RM 279 & RM 236 and for *Sub1* QTL using the InDel marker, 'Sub1BC2' (Singh *et al.,* 2016; Anupam and Mandal *et al.,* 2020). The background genotyping of the proposed stock, CRR751-1-12-B-B, along with selected IR64-Sub1 NILs using a 50K SNP chip showed 97.02% recovery of the recurrent parent genome. CRR751-1-12-B-B also possesses the blast-resistant gene *Pita2* inherited from the recurrent parent IR64. The proposed genetic stock can be a potential donor for the development of climate-resilient varieties with tolerance to these abiotic stresses. As the proposed line has been developed in the elite background, using this line as a donor, the traits of interest can be easily transferred without the risk of linkage drag of undesirable traits.

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7. IET29482 (IC650732; INGR23074), a rice germplasm with high grain Zn and protein content in polished rice grain

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In the studies of Rice (Oryza sativa L.) Biofortification, RP 6211-PR/RIL-Q181 was identified with high grain Zn in polished rice (Suman *et al.*, 2021). It was nominated for the AICRIP Biofortification trial during Kharif-2020. IET 29482 (RP 6211-PR / RIL-Q181) is an inbred line derived from PR116/Ranbir Basmati. It is an early-duration line with 91 days to 50% flowering and possesses a medium bold (MB) grain type (Table 1). It was evaluated in the AICRIP Biofortification trial for three years (during 2020, 2021 and 2022) across the locations (IIRR Progress Report, 2020; 2021 and 2022). The overall mean grain Zn was 28.22 ppm, grain yield was 4185 kg/ha, grain Fe was 2.33 ppm and protein content was 8.08% (Table 2) (IIRR Progress Report, 2020, 2021 and 2022). During the IVT-Biofortification trial (2020), this culture noted 1st rank in Zone-V with 5848 kg/ha grain yield and above the threshold or target grain Zn content of 26.2 ppm in Zone –VII. In the second year of testing, IET 29482 noted polished grain Zn content above the target or threshold value in Zone-II (32.03 ppm), Zone-III (36.84 ppm), Zone-V (34.10 ppm), Zone- VI (28.22 ppm), Zone-VII (29.32 ppm) and overall (31.63 ppm). In 2022, this culture showed high grain Zn content in JYP (29.35 ppm) and PTB (23.78 ppm) locations. It can be used as a potential donor in a breeding program for rice biofortification. Based on its high grain Zn content, this culture is being proposed for registration as a genetic stock.

Table 1: Agro-morphological, yield and grain micronutrient characters of IET 29482 (Based on the AICRIP data)

S. No.	Trait	Value
1	Plant Height (cm)	98-106
2	Tiller Number (Per Hill)	11-13
3	Productive Tiller Number (Per Hill)	11-12
4	Days to 50% Flowering	86-93
5	Panicles per Square meter	279-297
6	Single Plant Yield (grams)	20.63
7	1000 grain weight (grams)	23.79
8	Grain Yield (Kg. ha^{-1})	4185
9	Grain Fe (ppm) in Polished Rice	2.33
10	Grain Zn (ppm) in Polished Rice	28.22
11	Protein (%) in Polished Rice	8.08

Table 2: Data of IET 29482 under AICRIP trials (Biofortification) during 2020, 2021 and 2022

	Fe (ppm)	Zn (ppm)	Protein (%)	Grain Yield (kg/ha)	Days to 50% Flowering	Plant Height (cm)	Panicles/ m^2
2020	2.4 (14)	24.8 (14)	8.58 (8)	4417 (17)	86 (17)	98.87 (17)	288 (17)
2021	2.36 (26)	31.63 (26)	8.49 (10)	4343 (21)	93 (21)	107 (21)	297 (21)
2022	2.02 (6)	21.43 (6)	6.47 (6)	2731 (5)	98 (5)	100 (5)	279 (5)
Weighted mean	2.33	28.22	8.08	4185	91	106	291

Values within the parenthesis indicates number locations tested during AICRIP trials (IIRR Progress Report, 2020, 2021 and 2022).

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8. IET29484 (IC650734; INGR23075), a rice germplasm with high grain Zn content in polished grain

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In the studies of Rice (*Oryza sativa* L.) Biofortification, RP6204-MB/RIL-J159 was identified with high grain Zn in polished rice. It was nominated for the AICRIP Biofortification trial during *Kharif* - 2020. IET 29484 (RP6204-MB/RIL-J159) is an inbred line derived from MTU 1010 × BR 2655 (Rathod *et al.,* 2020, 2021). It is a medium-duration line with 104 days to 50% flowering and possesses a long slender (LS) grain type (Table 1). It was evaluated in the AICRIP Biofortification trial for three years (during 2020, 2021 and 2022) across the locations (IIRR Progress Report, 2022). The overall mean grain Zn was 24.32 ppm in polished rice, grain yield was 3982 kg/ha, grain Fe was 2.36 ppm, and protein content was 7.39% (IIRR Progress Report, 2020, 2021 and 2022). During the IVT-Biofortification trial (2020), this culture showed >24 ppm Zn in polished rice and >4 tonnes grain yield in Zone-VII (26.2 ppm) and overall (24.8 ppm). In addition, it has >5 tonnes yield in Gujarat; >4 tonnes in Uttar Pradesh, Andhra Pradesh, Tamil Nadu and Kerala states. During 2021, this culture noted >24

ppm Zn in Zone-III (30.68 ppm), Z-IV (24.7 ppm), Z-V (27.65 ppm), Z-VII (26.31) and overall (26.37 ppm). It was noted that >4 tonnes of grain yield in Z-II, III and VII. During 2022, this culture showed>4 tonnes of grain yield in Bihar, Uttar Pradesh, Madhya Pradesh, Chhattisgarh, Andhra Pradesh and Tamil Nadu. In addition, this culture showed >24 ppm Zn in Zone-II (27.10 ppm) and Zone-VI (24.70 ppm). It can be used as a potential donor in the breeding program of rice biofortification. Based on its high grain Zn content, this culture is being proposed for registration as a genetic stock.

Table 1: Agro-morphological, yield and grain micronutrient characters of IET 29484 (Based on the AICRIP data)

S. No.	Trait	Value
1	Plant Height (cm)	96-106
2	Tiller Number (Per Hill)	11-13
3	Productive Tiller Number (Per Hill)	11-12
4	Days to 50% Flowering	103-109
5	Panicles per Square meter	292-320
6	Single Plant Yield (grams)	21.58
7	1000 grain weight (grams)	20.36
8	Grain Yield (Kg. ha^{-1})	3982
9	Grain Fe (ppm) in Polished Rice	2.36
10	Grain Zn (ppm) in Polished Rice	24.32
11	Protein (%) in Polished Rice	7.39

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9. RP6257-SJ3 (IC650733; INGR23076), a rice germplasm with high and stable grain yield high nitrogen use efficiency under nitrogen stress

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In the studies of genetic improvement for nitrogen use efficiency (NUE) in rice, RP6257- SJ3 is identified as a promising cultivar under low nitrogen (N) field conditions (without external N application) and 50% of the recommended N (N-50) expressed in terms of grain yield. RP6257-SJ3 was developed from the Sampada × Jaya cross combination. It has 88-90 days to 50% flowering and possesses a medium bold (MB) grain type (Table 1). It was evaluated in the AICRIP plant physiology RNUE trial (Evaluation of Radiation and Nitrogen use-efficient promising rice genotypes) during 2015, 2016, 2017 and 2018 (IIRR Progress Report, 2017, 2018). The overall mean grain yield was noted as 534 g/m^2, 492 g/m^2 and 372 g/m^2 in N-100, N-50 and N-Low treatments. In addition, RP6253-SJ3 has the following significant features:

i). 13.47%, 12.78% and 12.76% yield superiority over Varadhan (Positive check) in the recommended dose of N (N-100), 50% of the recommended dose of N (N-50) and low N treatments during 2017 and 2018.

ii). The per cent reduction in grain yield under N-50 treatment is on par with Varadhan (8.5%).

iii). In the low-N treatment, a 43.5% reduction was observed in RP6257-SJ3, while Varadhan exhibited a 45% reduction in grain yield. RP6257-SJ3 was noted at 1326 g/m and 1232 g/m total dry matter in N-100 and N-50 treatments. The per cent reduction in total dry matter under N-50 treatment is 7.6%, while Varadhan exhibited a 12.3% reduction. In addition, the AMMI biplot analysis of grain yield under Low-N indicates RP6257-SJ3 is the less affected genotype under low nitrogen treatments (Subrahmanyam *et al.,* 2019). Based on the promising performance for high NUE in terms of grain yield, RP6257-SJ3 is being proposed for registration as a genetic stock that can be used as a potential donor in breeding rice for high NUE.

Table 1: Agro-morphological and yield characters of RP6257-SJ3 across N-treatments (N-Low, N-50 and N-100) (Based on the AICRIP data)

1	Plant Height (cm)	104-110	101-105	95-97
2	Productive Tiller Number per Sq.meter	345-380	325-352	238-270
3	Days to 50% Flowering	97-100	93-96	88-90
4	Panicles per Square meter	345-380	292-350	233-268
5	Grain Yield (g/m^2)	534	492	372
6	Total Dry Matter (g/m^2)	1326	1232	985
7	1000 Grain weight (g)	25.5	25.15	25.9
8	Harvest Index (HI)	35-37	36-38	32-33

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10. RP6252-BV/RIL/1689 (IC650735; INGR23077), a rice germplasm with high and stable grain yield under nitrogen stress and under native sodic soil conditions

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In studies of genetic improvement for nitrogen use efficiency (NUE) and abiotic stress tolerances like sodicity in rice (*Oryza sativa* L.), RP6252-BV/RIL/1689 (CNN1) is identified as a promising cultivar under low nitrogen (N) field conditions (without external N application), 50% of the recommended N (N-50), and native sodic conditions (without gypsum amendment; pH 8.5 – 10.0), expressed in terms of grain yield and use efficiency. RP6252-BV/RIL/1689 (CNN1) was developed from BPT5204 × Varadhan. It was evaluated in the AICRIP Soil Science – NUE trial (screening of rice germplasm for Nitrogen use efficiency) during 2019, 2020 and 2021; the Sodicity trial (Screening of germplasm for sodicity and management of sodic soils in RBCS) in 2019 (IIRR Progress Report, 2020; 2021 and 2022). The overall mean grain yield was noted as 4.96 t/ha, 4.07 t/ha and 3.28 t/ha in N-100, N-50 and N-Low treatments (Table 1). In addition, RP6252-BV/RIL/1689 (CNN1) has the following significant features:

i) 5.8% and 12.9% yield superiority over Varadhan (Positive check for NUE) in N-50 and N-100 treatments; On par with N-Low treatment.

ii) Noted promising total nutrient uptake (kg/ha) in comparison with other entries of the trial across the tested locations

iii) Noted higher AE-Agronomical efficiency (kg grain increase/ kg N added) and RE- Recovery efficiency (% of N recovered) in N-50 treatment over N-100 (Table 2). Under native sodic conditions, the mean grain yield and straw yield were 3.35 t/ha and 4.2 t/ha (Table 1). In addition, RP6252-BV/RIL/1689 (CNN1) showed superiority in grain yield (4.4%) and straw yield (10.4%) over CSR23 (tolerant check) under native sodic soils; Noted higher nutrient (NPK) uptake (kg/ha) in comparison with CSR23 across the tested locations under native sodic soils. Based on the promising performance for high NUE and sodicity tolerance, RP6252- BV/RIL/1689 (CNN1) is being proposed for registration as a genetic stock. It can be used as a potential donor in breeding rice for high NUE and sodicity tolerance.

Table 1: Agro-morphological, yield characters of RP6252-BV/RIL/1689 (CNN1) (Based on the AICRIP data)

Trait	Value	Trait	Value
Plant Height (cm)	106-110	Grain Yield (t/ha)	4.96#; 3.35$
Tiller Number/Sq. meter	290-320	Straw Yield (t/ha)	7.10#; 4.20$
Days to 50% Flowering	110-115	Panicles per Square meter	290-307

- N100 treatment; $ - Native Sodic soil; Values within the parenthesis indicates number locations tested during AICRIP trials.

Table 2: Data of RP6252-BV/RIL/1689 (CNN1) under AICRIP trials (Soil science)- NUE trial- 2019, 2020 and 2021

Trait/Treat/Year	Grain yield (t/ha)			Straw yield (t/ha)			Total N uptake (kg/ha)			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)	3.27	4.19	4.99	4.57	5.63	7.00	70.67	92.0	113.3	-	-	-	-	-	-
2020 (N1-6; N2-5; N3-5)	3.61	3.87	4.83	4.61	5.13	6.04	53.58	69.18	90.08	14.00	18.60	46.75	54.00	34.00	42.50
2021 (N1-6; N2-5; N3-5)	3.01	4.04	5.02	4.44	5.41	7.39	44.50	83.50	99.60	30.00	23.30	40.00	39.30	92.70	67.30
Weighted mean	3.28	4.07	4.96	4.54	5.39	6.81	56.25	81.56	101.0	22.00	20.95	43.38	46.65	63.35	54.90

Values within the parenthesis indicates number locations tested during AICRIP trials. 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).

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11. GW 2018-936 (IC642306; INGR23078), a wheat germplasm for high grain Zinc and protein content

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Wheat (*Triticum aestivum* L.) is the second most important crop after rice both in terms of area and production in India. In India during 2020-21, the wheat crop was cultivated in about 31.76 million hectares to produce the all-time highest output of 109.52 million tonnes of wheat with a record average productivity of 34.64 q/ha. (ICAR-IIWBR, 2020). Wheat processing after harvesting markedly decreases grain zinc and micronutrients such as iron, which enhances the chance of zinc deficiency in humans. Hence, there is an urgent challenge and dire need to increase grain zinc content and bioavailability in developing countries. Also, grain protein content assumes significance, as high protein is suitable for bread making and low protein content for biscuit-making. Looking to this need, breeding work for high zinc and protein content started at Wheat Research Station, Vijapur. Considering this aspect, a cross was made using diverse genotypes (LON/2/DUKEM 2//GREEN 38/P 7228) and generation advancement was made using the pedigree selection method. This genotype was developed at Wheat Research Station, S. D. Agricultural University, Vijapur

Table 1: Performance of promising genotype GW 2018-936 during 2019-20 under AICRP mode in Quality Component and Wheat Biofortification Nursery (QCWBN)

Traits	Zone	Genotype	Checks							CD at 10%
		GW 2018-936	UP 2672	MACS 6222	DBW 187	WB 2	HD 3086	GW 322	HS 490	
Zinc content (ppm)	NWPZ	48.8	40.9	39.6	33.7	37.8	35.3	38.2	37.6	4.3
	NEPZ	37.6	32.3	32.3	26.4	33.1	29.6	31.9	31.3	5.7
	CZ	48.7	48.2	44.9	40.0	44.4	42.0	45.9	43.1	3.7
	National	47.1	41.7	40.1	34.4	39.0	36.4	39.5	38.3	2.4
Protein content (%) at12% MB	NWPZ	14.0	12.4	10.7	11.7	12.5	11.0	10.6	11.4	-
	NEPZ	12.3	10.3	10.3	11.2	12.1	10.9	10.7	11.8	-
	CZ	13.9	11.3	11.1	11.7	12.0	10.0	10.3	10.8	-
	PZ	15.7	16.0	13.0	16.2	15.6	15.4	12.2	13.4	-
	Mean	13.9	12.5	11.3	12.7	13.0	11.8	10.9	11.8	-

Note: Grain Zinc content data NWPZ: Delhi, Karnal, Hissar and Ludhiana centers; NEPZ: Kanpur center and CZ: Vijapur and Indore Centers. For Grain Protein content data NWPZ: Delhi, Karnal, Hissar, Ludhiana and Pantnagar centers; NEPZ: Kanpur and Varanasi centers; CZ: Indore and Vijapur and PZ: Dharwad center.

for high zinc and protein content.

GW 2018-936 has a semi-erect growth habit with broad leaves. During the period of testing, it was tested at national level under Quality Component and Wheat Biofortification Nursery (QCWBN) during 2019-20 (ICAR-IIWBR, 2020) across the zones, in which GW 2018-936 found to be superior with 47.1 ppm zinc content and 13.9% protein content over the locations to the check varieties UP 2672 (41.7 ppm) and WB 2 (13.0%) respectively (Table 1)

GW 2018-936 has very broad leaves and flag leaf attitude semi erect type. Grain has a bold, amber colour and oblong shape. Ear is having parallel shape and strong waxiness on the ear and peduncle. It matures within 115 days. A package of practices to be followed as per normal sown irrigated conditions and standard agronomic practices is recommended for the cultivation of this genotype. This genotype is adapted to all parts of the country and resistant to black and brown rust.

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12. TAW186 (IC0648497; INGR23079), a wheat germplasm with drought and heat tolerance

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Wheat (*Triticum aestivum* L.) is sown as winter season crop in most parts of India. Under changing climatic conditions, the larger area under wheat is likely to be exposed to heat stress at seedling and post-anthesis stages, as well as drought stress during crop growth. Wheat improvement program involving crosses with diverse parents to develop high yielding and abiotic stress tolerant genotypes was initiated in the *rabi* 2011-12 at the Nuclear Agriculture & Biotechnology Division of Bhabha Atomic Research Centre, Mumbai. This has resulted in the development of drought- and heat-tolerant genotype, TAW186, with high seed yield

Table 1: Drought sensitivity index, yield performance and yield reduction of TAW186 along with checks in DTSN (2019-20)

		Mean values pooled over six locations		
Genotype	DSI	Yield under drought (g/Plot)	Yield under irrigated (g/plot)	Percent yield reduction
TAW186	0.68	460.75	555.67	13.18
DBW110 (C)	0.81	469.42	589.42	20.36
C-306(C)	0.83	397.58	502.50	20.88
K1317 (C)	0.95	509.50	669.50	23.90
MP3288 (C)	1.36	373.58	565.75	33.97
NI5439 (C)	1.44	385.42	604.00	36.19

DSI, Drought sensitivity index.

Table 2: Heat sensitivity index, Yield performance and yield reduction of TAW186 along with checks in DHTSN (2020-21)

		Mean values pooled over ten locations		
Genotype	HIS	Yield (Timely sown) (g/Plot)	Yield (Late sown) (g/Plot)	Percent yield reduction
TAW186	0.69	780.0	677.0	13.3
C-306(C)	1.62	680.0	468.0	31.1
DBW150(C)	1.18	801.0	619.0	22.7
DDW47(d)(C)	1.11	787.0	618.0	21.4
MP3288(C)	1.35	742.0	550.0	25.9
NI5439 (C)	1.34	803.0	597.0	25.7
WH730(C)	1.35	778.0	577.0	25.9

HSI, Heal sensitivity index.

potential from a cross of HD2733/Dharwad dry//Catbird following the pedigree method of selection.

TAW186, a spring wheat genotype, has a semi-erect growth habit. The genotype is semi dwarf with an average plant height of 86cm and has early maturity of 116 days, with ear heads emerging in 73 days. (AICRP-W&B, 2021a). The ears are tapering, white in colour, with medium density, long awns that are spreading type. Amber coloured grains having an oblong shape, hard texture and are medium bold in size. The grains have round creases with wide germ width. The brush hair is shorter in length with a weak profile.

The genotype TAW186 was evaluated for drought at 15 centres along with five checks namely; DBW110, C306, K1317, MP3288 and NI5439 in the 32nd drought tolerance screening nursery (DTSN) during 2019-20 (AICRP-W&B, 2020). TAW186 was found to be highly drought tolerant with a drought sensitivity index (DSI) of 0.68, and per cent yield reduction was 17.08 (Table 1).

In the following year, 2020-21, the genotype TAW186 was evaluated in the 33rd drought and heat tolerance screening nursery (DHTSN) at 15 centres along with five checks namely; C306, DBW150, DDW47(d), MP3288, NI5439 and WH730 (AICRP-W&B, 2021b). The genotype TAW186 was found to be highly heat tolerant. With a heat sensitivity index (HSI) of 0.69, the per cent yield reduction was 13.3 (Table 2).

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13. TAW185 (IC648496; INGR23080), a wheat germplasm with high thousand-kernel weight

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Wheat (*Triticum aestivum* L.) yields are severely affected under drought stress. Grain yield under moisture-limited conditions is a quantitatively controlled trait, and understanding the contribution of each yield component to maintaining grain yield under drought is most required to develop drought- tolerant genotypes. Thousand-grain weight is one of the main wheat yield components, which is reduced by post-anthesis drought stress. A Wheat improvement programme to develop drought-tolerant genotypes was initiated in the *rabi* 2010-11 at the Nuclear Agriculture & Biotechnology Division of Bhabha Atomic Research Centre, Mumbai. *Triticum aestivum* wheat 185 (TAW185) was developed from a cross of HD2281 and NW1014 using the pedigree selection method. TAW185 is the highest-yielding genotype both under drought and irrigated conditions (AICRP-W&B, 2020) and has the highest thousand-grain weight (AICRP-W&B, 2021).

TAW185, a spring wheat genotype, has a semi-erect growth habit. The genotype is semi-dwarf with an average plant height of 96cm and has early maturity, with ear heads emerging in 75 days (AICRP-W&B, 2021). The ear heads of TAW185 are long and tapering, with a size of 9.86 cm compared to Sonalika (9.31 cm) and HD2967 (10.3 cm). The grains of TAW185 have a soft texture and a bold size. TAW185 maintained the highest grain yield per plot of 555g in comparison to check varieties namely; Sonalika (504 g) and HD2967 (535g) in NGSN, 2020-21 (Table 1).

The genotype TAW185 was evaluated for drought at 15 centres along with five checks, namely, DBW110, C306, K1317, MP3288, and NI5439, in the 32nd drought tolerance screening nursery (DTSN) during 2019-20 (AICRP-W&B, 2020). TAW185 was found to be the highest yielding (538.83 g) under drought stress among 20 genotypes and five checks, with a drought susceptibility index (DSI) of 0.94 and a per cent yield reduction of 23.43. In the following year, 2020-21, the genotype TAW185 was evaluated in the national genetic stock nursery and was found to have the highest thousand-kernel weight of 49.0 g over all 90genotypes and checks; Sonalika (39 g) and HD2967 (39 g) were used in the nursery. The seed yield of TAW 185 is higher than both checks, Sonalika and HD2967, in NGSN, 2020-21.

Table 1: Mean performance of TAW185 for various agronomic traits in NGSN (2020-21)

Traits	Genotype	Checks	
	TAW185	Sonalika	HD2967
Days to heading	75	80	81
Plant height (cm)	96.0	84	92
Tillers per meter row	86	97	97
Grains per spike	51	53	53
1000-grain weight (g)	49.0	39.0	39.0
Spike length (cm)	9.86	9.31	10.3
Grain yield/ plot (g)	555	504	535

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14. TAW41 (IC648495; INGR23081), a wheat germplasm with resistant to spot blotch disease and tolerance to terminal heat

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Wheat (*Triticum aestivum* L.) production is severely affected by a combination of spot blotch (SB) and terminal heat (TH) stress in the eastern Gangetic plains of India (EGP). Spot blotch is caused by *Bipolaris sorokiniana,* and the incidence of infection increases in humid and warm climates. Spot blotch infection resulted in yield loss ranging from 15 to 25% and complete loss of crop under severe disease infection. Genetic resources for resistance against spot blotch are lacking (Kumari *et al*., 2018). Significant improvement in yield can be achieved through the identification of genotypes with a high level of resistance against spot blotch fungus. Induced mutagenesis offers scope to induce genetic variation that could be selected for disease resistance through screening in hotspot locations. A mutation breeding programme to develop mutations for economically important diseases of wheat in popular variety HD2967 using gamma rays was initiated at the Nuclear Agriculture and Biotechnology Division of Bhabha Atomic Research Centre, Mumbai in 2014-15. Mutants developed were evaluated for spot blotch disease at BCKV, West Bengal, in the *rabi* 2018-19, and at the Initial Phytopathological Screening Nursery, ICAR-IIWBR in 2020-21. Further, a set of 29 *Triticum aestivum* wheat (TAW) mutants and a parent, HD2967, along with three checks (HUW234, HUW468 and HUW510) were screened for spot blotch and terminal heat tolerance at the field station of the Institute of Agricultural Sciences of Banaras Hindu University, Varanasi. These mutants were analysed for physiological parameters such as normalised difference vegetation index (NDVI), chlorophyll content (SPAD), and canopy temperature depression (CTD) for evaluating their terminal heat tolerance. NDVI has been used to select genotypes tolerant to the combined stress of spot blotch infection and terminal heat. Besides, extensive expression analysis of pathogenesis-related genes, hormones, cytokinin pathway genes, antioxidant genes and senescence-associated genes showed downregulation of genes promoting senescence (*TaSAG4*, *TaSNAC11)* & upregulation of *w*heat copper binding protein 1 (*WCBP1)* in treatment samples of TAW41. This could be a possible reason for lower AUDPC & higher NDVI, SPAD & CTD of TAW41 at the terminal crop growth stage.

TAW41 is a spot blotch and terminal heat tolerant mutant of the spring wheat variety HD2967. The mutant genotype is semi-dwarf, with an average plant height of 88.7 cm. Mutant TAW41 is late-maturing at 132 days compared to its parent (HD2967) with 120 days and the other three check varieties, namely, HUW234 (123 days), HUW468 (120 days) and HUW510 (122 days). The mutant genotype has bigger spikes of size 11.2 cm compared to 10.4 cm of the parent and the other three check varieties namely HUW234 (8.94 cm), HUW468 (8.70 cm), and HUW510 (9.34 cm). TAW41 has more tillers compared to the parent and other check varieties (Table 1). However, the thousand-grain weight of TAW41 has been found to be compromised due to investment in stress tolerance.

The mutant genotype TAW41 showed significantly lower spot blotch infection compared to HD2967 and other check varieties, namely: HUW 234, HUW 468, and HUW 510 (Table 2). TAW41 had a significantly higher NDVI value, which was 34.2% and 155% higher than

Table 1: Morpho-agronomic traits of mutant TAW41 and checks

Trait	TAW41	HD2967
Days to heading	82	75
Days to maturity	132	120
Plant height (cm)	88.7	82.4
Spike length (cm)	11.2	10.4
Tiller number	12.0	10.0
Thousand kernel weight (g)	26.2	30.6

Table 2: Area under disease progressive curve values for Spot blotch

Genotype	AUDPC (Mean±SE)
TAW41 (Mutant)	354.32±0.23
TAW132 (Mutant)	717.28±0.11
HD2967(Parent)	675.51±0.05
HUW234	750.12±0.06
HUW468	790.74±0.02
HUW510	839.14±0.11
Borlaug 100	689.92±0.04

HD2967 and HUW510. TAW41 maintained significantly higher SPAD values and showed 22.2% and 64.5% more chlorophyll content than HD2967 and HUW510, respectively, under the combined stress of spot blotch and terminal heat. Extensive expression analysis of genes involved in hormone regulation displayed downregulation of senescence-promoting genes *TaSAG4*, *TaSNAC11-4B,* and upregulation of *WCBP1* in treatment samples of TAW41, which could be the probable cause of low AUDPC values (Singh et al., 2022).

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15. HW 3654 (IC650736; INGR23082), a wheat germplasm with one major gene each for stem rust (*Sr36*), leaf rust (*Lr45*) and powdery mildew (*Pm6*) resistance, adult plant rust resistance (*Sr2/Lr27/Sr30*)

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Wheat is one of the most widely consumed cereal crops worldwide, providing 20% of dietary calories and protein. In India, wheat is one of the most important cereal crops after rice, with a production of 112 MT during 2022-23. However, 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. Stem and leaf rust diseases continually pose a threat to wheat production. In recent years, climate change and intensive crop cultivation practices have made powdery mildew a potential threat to wheat production. Deploying resistant cultivars is the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Using a 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. One each major stem rust (*Sr36*), leaf rust (*Lr45*) and powdery mildew (*Pm6*) resistance gene, along with adult plant rust resistance genes (*Sr2/Lr27/Sr30*), were pyramided in the background of the LOK1 cultivar through a marker-assisted backcross approach. Linked molecular markers, *stm773-2* (*Sr36/Pm6*), *G372185* (*Lr45*) (Naik *et al.,* 2015) and *Xgwm533* (*Sr2*+) (Spielmeyer *et al.,* 2003) were used to perform marker-assisted selection. A stable and high-yielding line (HW 3654) was selected at the BC3F6 generation and further evaluated for four seasons in two years. Seedling and adult plant reactions of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India. Using gene pyramids consisting of major (*Sr36/Pm6* and *Lr45*) and minor (*Sr2/Lr27/Sr30*) resistance genes 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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16. HW 3655 (IC650737; INGR23083), a wheat germplasm with one major gene each for stem rust (*Sr36*), leaf rust (*Lr45*) and powdery mildew (*Pm6*) resistance, adult plant rust resistance (*Sr2/Lr27/Sr30*)

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Wheat (*Triticum aestivum L.*) is one of the most widely consumed cereal crops worldwide that provides 20% of dietary calories and protein. In India, wheat is one of the most important cereal crops after rice, with a production of 112 MT during 2022-23. However, 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. Stem and leaf rust diseases continually pose a threat to wheat production. In recent years, climate change and intensive crop cultivation practices have made powdery mildew a potential threat to wheat production. Deploying resistant cultivars is the most economical, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Using a 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. One gene each of major stem rust (*Sr36*), leaf rust (*Lr45*) and powdery mildew (*Pm6*) resistance genes, along with adult plant rust resistance genes (*Sr2/Lr27/Sr30*), were pyramided in the background of MACS 2496 cultivar through a marker-assisted backcross approach. Linked molecular markers, s*tm773-2* (*Sr36/Pm6*) (Tsilo et al., 2008), *G372185* (*Lr45*) (Naik *et al.,* 2015) and *Xgwm533* (*Sr2+*) (Spielmeyer *et al.,* 2003) were used to perform marker-assisted selection. A stable and high-yielding line (HW 3655) was selected at the BC3F6 generation and further evaluated for four seasons in two years. Seedling and adult plant reactions of pyramided lines showed resistance to most of the stem and leaf rust pathotypes prevailing in India. Using gene pyramids consisting of major (*Sr36/Pm6* and *Lr45*) and minor (*Sr2/Lr27/Sr30*) resistance genes that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars more than single gene deployment.

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17. DWRBG15 (IC650738; INGR23084), a barley germplasm with high Protein and high ß-glucan

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Barley is an ancient grain that has been cultivated for thousands of years. Barley is the fourth most important food crop of the world after maize, wheat, and rice (Ghatak *et al.*, 2017; Shabrangy *et al.*, 2021). Owing to its nutritional value, especially being rich in dietary fibre, it is also consumed as a staple food in North and Sub-Saharan Africa (SSA), hilly areas of Central Asia, South-West Asia and Northern Africa. The major barley

production is of hulled type, and to prepare acceptable food products, the hull needs to be removed in the process called pearling. Pearling reduces the contents of insoluble fibre, protein, ash and free lipids, but increases the contents of starch and β-glucan by the removal of outer layers, including the hull (palea and lemma), bran (pericarp, testa) and germ (embryo), which are richer in insoluble fibre, protein, ash and lipids and poorer in starch and β-glucan than the endosperm.

In the coordinated Barley Quality Screening Nursery (2021-22)-3 (Hulless Quality) under AICRP on Wheat and Barley, DWRBG15 (HLR-136; RKS/ASG/UKP-525/) has been found to have a combination of the highest protein content (14.6%) coupled with higher β-glucan (6.0%) content (ICAR- IIWBR, 2022). DWRBG15 (HLR-136; RKS/ASG/UKP-525/) is a six-row hulless barley, a landrace (IC313162) collected from Pangi tehsil of Chamba district in Himachal Pradesh. The genotype was evaluated at six locations (Karnal, Hisar, Ludhiana, Durgapura, Pantnagar and Kanpur) during *rabi* 2021-22 under Coordinated Barley Quality Screening Nursery -3 (Table 1, Table 2). This six-row hulless landrace DWRBG15 (HLR-136; RKS/ASG/UKP-525/) has light purple grains, and spikes bear elevated hood awns.

Barley is an important source of dietary fibre, resistant starch, trace minerals, vitamins, phytoestrogens and antioxidants, which are associated with disease prevention. Barley is one of the richest sources of the soluble fibre β-glucan, a non-starch polysaccharide found primarily in the cell walls of the endosperm and aleurone layer of the grain. The health benefits of β-glucan are the most extensively reported of all fibres. The use of plant-based protein is a significant trend in the healthy food sector. Barley, like all plant-based proteins, can be combined with other protein sources in order to yield a product that is considered a "complete" protein. The hulless landrace DWRBG15 (HLR- 136; RKS/ASG/UKP-525/) was identified to possess both traits i.e., reasonably good protein and β-glucan and can serve as a unique source of these traits for the food barley improvement programme of the country.

Table 1: Grain protein content (%db) in DWRBG15 (HLR-136; RKS/ASG/UKP-525/) at different locations during 2021-22

Genotype	Row Type	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Mean
HLR-136	6	17.7	15.1	13.6	12.2	14.3	17.9	14.6
Karan-16 (C)	6	16.5	10.4	11.1	10.3	NA*	10.8	10.7
NDB-943 (C)	6	17.3	12.1	11.7	11.3	11.3	12.5	11.8
PL891 (C)	2	14.7	11.1	10.0	12.4	12.8	11.7	11.6

*Not available

Table 2: Grain β-glucan content (%db) in DWRBG15 (HLR-136; RKS/ASG/UKP-525/) at different locations during 2021-22

Genotype	Row Type	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Mean
HLR-136	6	5.6	5.6	6.1	6.3	7.1	5.3	6.0
Karan-16 (C)	6	5.2	5.2	6.3	5.5	NA	4.5	5.3
NDB-943 (C)	6	5.6	5.1	5.9	5.8	5.6	4.5	5.4
PL891 (C)	2	5.8	5.2	6.3	6.2	6.5	5.1	5.9

*Not available

for hulless quality (BQSN- 3) of AICRP Wheat and Barley (copies enclosed). The quality analysis of the multi-location samples was done at the quality lab of ICAR-Indian Institute of Wheat and Barley Research, Karnal, for nutritional quality traits of grains. The genotype has the highest protein content (14.6% on a dry weight basis) as compared to the best check NDB-943 (11.8% on a dry weight basis) and good β-glucan (6.0% on a dry weight basis), which was comparable to PL-891 (β-glucan of 5.9% on a dry weight basis), a two- row variety

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18. DWRBG16 (IC650739; INGR23085), a barley germplasm with high ß-glucan

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Around 3.7% of total barley (*Hordeum vulgare* L.) production is used as a human food annually worldwide, but in some countries like Morocco, Ethiopia, and Eretria, barley use as food is high, up to 60% of total production. The use of barley as a calorie food source for human consumption is mainly confined to marginal areas with problematic soils and scanty rainfall. Recent research regarding dietary composition in barley has renewed interest in its end-use, confirming the health benefits of barley in human diets through more soluble dietary fibre, beta glucan content, and higher amylase activity than other food cereals.

In the coordinated Barley Quality Screening Nursery (2021-22)-3 (Hulless Quality), DWRBG16 (HLR-240; NKG/49/) has been found to have high β-glucan (6.1% on a dry-weight basis). DWRBG16 (HLR-240; NKG/49/) is a six-row hulless barley landrace (IC82717), collected from Chango village in Pooh tehsil of Kinnaur district in Himachal Pradesh. This landrace was evaluated at six locations (Karnal, Hisar, Ludhiana, Durgapura, Pantnagar and Kanpur) during the *rabi* 2021-22 season under the coordinated Barley Quality Screening Nursery -3 for hulless quality (BQSN-3) of AICRP on Wheat and Barley (ICAR-IIWBR, 2022). The quality analysis of the multi-location samples was done at the Quality Lab of ICAR-Indian Institute of Wheat and Barley Research, Karnal, for nutritional and physical grain-quality traits. The proposed genotype DWRBG16 (HLR-240; NKG/49/) has higher β-glucan (6.1% on a dry weight basis) content compared to the best check PL-891 (5.9% on a dry weight basis), a two-row variety (Table 1). In addition to its special attributes, this landrace has also good protein content (12.0% on a dry weight basis), and 1000-grain weight (34.0 g).

The research carried out during the last three decades has unequivocally shown the health benefits of consuming barley on a regular basis. Barley consumption can prevent several diseases, especially cardiovascular disease, diabetes, colon cancer and hypertension. Among cereal grains, barley has the highest functional value, especially because of its higher content of soluble fibres called β-glucan and several other phytochemicals. For food purposes, the naked or hulless barley grains are preferred because of better texture and palatability of end products. Furthermore, removal of the husk in hulled barley requires extra effort for pearling and also leads to loss of nutrients from the outer layer of the grain. For breeding improved hulless barley genotypes with superior nutraceutical values, the sources need to be identified. The identified germplasm line DWRBG16 (HLR-240; NKG/49/) is a landrace having high grain β-glucan, an important contributor to the health-benefiting value of food barley, and may serve as an important donor for food barley improvement programme.

Table 1: Grain β-glucan content (%db) in DWRBG16 (HLR-240; NKG/49/) at different locations during 2021-22

Genotype	Row Type	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Mean
HLR-240 (NKG/49/)	6	6.3	6.1	6.1	6.4	6.6	5.2	6.1
Karan-16 (C)	6	5.2	5.2	6.3	5.5	-	4.5	5.3
NDB-943 (C)	6	5.6	5.1	5.9	5.8	5.6	4.5	5.4
PL-891 (C)	2	5.8	5.2	6.3	6.2	6.5	5.1	5.9

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19. DWRBG19 (IC650740; INGR23086), a barley germplasm with low grain ß-glucan content

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Barley (*Hordeum vulgare* L.) is one of the major crops in India, and approximately 30% of its produce is used for malting purposes. β-glucan content is an important criterion to determine the malt quality of barley, and less than 4% is an acceptable value desirable for malting purposes. DWRBG19 (tested as RMB2103) is a two-row hulled barley genotype derived from a backcross DWRB101*2/SLOOPSAWL3167 and further advanced through pedigree selection as a part of a plant breeding approach. DWRBG19 was evaluated in the Barley Quality Screening Nursery in AICRIP trials during 2021-22 along with checks at five locations and, as expected, gave the lowest score of grain β- glucan percentage, which is a rarely found level in two-row hulled barley in an elite genetic background. DWRBG19 has shown the lowest level of grain β- glucan content (3.7% dwb), which is lower than Indian malt varieties (⩾ 4.5% dwb) released so far and DWR 37 (4.6% dwb), the previously registered genetic stock for this trait. This unique lowest level of grain β- glucan is very much desirable for the malt industry and is not yet reported or registered to date in Indian barley germplasm. DWRBG19 is the outcome of the institute barley breeding programme and can serve as a potential candidate genotype across AICWBIP for introgression of malt quality trait in barley.

Average values for agro-morphological traits were observed as 50% flowering in 97 days and maturity in 147 days. Plant height was measured at 114 cm, and foliage colour was green. The other traits analysed for the genotype are 1000-grain weight (51.1 g), protein content (10.9%) and starch content (62.9).

DWRBG19 (RMB2103) has shown the lowest level (3.7% dwb) of grain β- glucan as compared to β-glucan score (⩾ 4.5% dwb) in Indian malt barley varieties released, including the latest variety DWRB182 (4.5% dwb) and registered stock DWR37 (4.6% dwb) (Table 1). DWRBG19 is the first-ever barley genotype developed in the country to enhance the commercially utilitarian trait malting quality (low β-glucan score) in barley.

Table 1: β-glucan (% dwb) in grains of different genotypes from different locations in BQSN 2021-22

Code	Genotype	Durgapura	Karnal	Hisar	Kanpur	Ludhiana	Pantnagar	Mean
MB-1	RMB2101	4.6	5.9	4.5	5.2	5.7	5.4	5.2
MB-2	RMB2102	4.3	4.5	4.6	4.3	5.6	5.4	4.8
MB-3	RMB2103	3.7	3.9	3.2	3.5	4.1	4.0	3.7
MB-4	RMB2104	3.9	4.8	4.0	4.3	4.1	3.8	4.1
MB-5	DWR37©	4.3	4.5	4.5	4.3	4.4	5.4	4.6
MB-6	DWR39©*	NA	NA	NA	NA	NA	NA	NA
	Average	4.2	4.7	4.2	4.3	4.8	4.8	

*Not analyzed because of observation of a few off-type plants in the field

20. IC138110-Sel (IC650741; INGR23087), a barley germplasm for early heading and early maturity

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Barley (*Hordeum vulgare* L.) is an important feed and fodder crop; besides, it provides essential raw material for the malting and brewing industries. About 44% of the area under barley cultivation is rain-fed in India;

hence, breeding for early maturity is the main breeding target. Therefore, identification of promising trait-specific accessions through evaluation of germplasm collections is a pre-requisite to diversify the parental material for sustained and continued increase in yield and quality of this crop. In this context, 6778 accessions of barley germplasm from the National Genebank (NGB), ICAR-NBPGR, New Delhi were characterized for agro-morphological traits and trait-specific accessions were validated during the years 2016-21. *S*ix-rowed barley *a*ccession IC138110 showed early heading (53 days) and early maturity (113 days), which is significantly superior compared to the check variety (BH902) for heading (89 days) and maturity (130.40 days) based on evaluation data in five consecutive years (*Rabi* 2016-17 to *Rabi* 2020-21) (Table 1). In addition, this genotype exhibited a dwarf plant habit with an average plant height of 72.35 cm compared to check variety BH902 (110.04 cm). Early types are essential in most barley-producing areas in India as rain-fed barley production needs early maturing varieties to escape drought and terminal heat in late March and early April. Besides this, the short duration and fast-growing genotypes of barley perfectly fit the major cropping system cereal-legume (for food and feed) in dryland areas of arid/semi-arid zones. Dwarf plant height is highly desirable as barley is a lodging-prone crop. This genotype can be utilized in barley breeding programs for developing improved varieties with earliness and dwarf plant stature.

Table 1: Year wise data of days to heading and days to attain physiological maturity in barley accession IC138110

Year	Days to heading		Days to physiological maturity	
	IC138110	BH902 (Check var.)	IC138110	BH902 (Check var.)
2016-17	51	87	111	127
2017-18	49	89	110	129
2018-19	55	88	114	135
2019-20	57	89	114	129
2020-21	54	92	116	132
Mean	53.2**	89	113**	130.40

**indicates significantly superior at $P_{0.001}$.

21. IC113045-Sel (IC650742; INGR23088), a barley germplasm for drought tolerance at seedling and adult plant stage

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IC113045 was evaluated along with other barley (*Hordeum vulgare* L.) genebank accessions during the year 2016-17 and was found to have desirable traits for drought tolerance such as early spike emergence, leaf rolling, and early maturity. A set of 214 selected accessions, including IC113045, was evaluated in hydroponics under controlled conditions in PEG-6000 (0.295 MPa at 25°C) in the year 2017-18. Accession IC113045 maintained better root system architecture and root biomass, as indicated by a low Stress Susceptibility Index (SSI) for root length (0.37) and root surface area (0.23) under PEG stress. The same set of 214 accessions was then evaluated for drought stress in field conditions during *Rabi* 2017-18. The SSI for grain yield showed that IC113045 had an SSI value of 0.10, while the check varieties BH902 (high-yielding check) and RD2624, RD2660 (NWPZ: Rainfed timely sown check) had SSI values of 0.86, 0.56, and 0.89, respectively (Manju *et al.*, 2023).

Based on laboratory and field evaluation, allelic variation of the candidate gene, *Hordeum vulgare aleurone 1* (*HVA1*), and its promoter sequence was studied in a selected subset of four drought-tolerant accessions (including IC113045) and four susceptible accessions in the year 2018-19. Indigenous drought-tolerant accessions IC113045 and IC582699 were found

to have an insertion of a 14 bp sequence in the promoter region, leading to the gain of an additional *cis* regulatory element ARRIAT. Further, four selected accessions (drought-tolerant IC113045, IC582699 and drought-susceptible IC542206, EC578822) were evaluated again in hydroponics under PEG treatment for validation as well as gene expression in the year 2019-20. The total root surface area in tolerant accession IC113045 was significantly higher (10.20 cm^2) than in the susceptible accessions (IC542206 and EC578822), which showed a greater reduction in total root surface area (6.11 and 8.12 cm^2, respectively), thereby indicating better root surface area as an important drought-adaptive mechanism under water stress. Accession IC113045 was able to maintain higher RWC (77.40%), while the susceptible accessions showed comparatively lower RWC of 68.32% (IC542206) and 66.36% (EC578822) in response to PEG stress. The membrane stability index was also significantly higher (82.8%) in IC113045, compared to a low of 57.56% and 62.2% in susceptible accessions IC542206 and EC578822, respectively. In addition, IC113045 had also more chlorophyll content and survival rate (74.58%) compared to 52.52% (IC542206) and 60.33% (EC578822) in susceptible accessions. A significant increase (more than 10-fold at 48 h post-treatment) was recorded in the transcript abundance of *HVA1* in the accession IC113045 in comparison to susceptible accessions. Moreover, IC113045 also displayed early maturity, which is an advantageous trait to escape drought stress. It had been earlier registered (INGR19055) for extra dwarf plant average stature, having a height of 44.39 cm coupled with early maturity in 117 days (Kaur *et al.,* 2022).

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22. J-2648 (IC650743; INGR23089), a pearl millet germplasm with high Fe and Zn content

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Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an essential food for more than 90 million people in the world's semi-arid tropics, where droughts and low soil fertility cause crop failures. It is an important nutrient-rich grain cereal grown on 26 mha by millions of farmers in arid regions of the world. It is the sixth most important and widely grown cereal crop in the world and is the fourth in India after rice, wheat and maize, with an annual cultivated area of 8 million ha (Yadav and Rai, 2013). Micronutrient malnutrition has been recognized as a vast health issue, affecting over two billion people, mostly women, children and infants worldwide, especially in developing countries. Several approaches, such as medical supplementation, industrial food fortification, dietary diversification and crop bio-fortification, have been suggested to address the problem of micronutrient malnutrition. Biofortification refers to the development of crop cultivars with higher levels of micronutrients. Bio-fortification of this crop through conventional plant breeding approaches is the cheapest method for achieving this objective. For this, it is the first and most important thing to have micronutrient dense parental lines, therefore, the present investigation was carried out to identify the micronutrient-dense pearl millet parental line to develop biofortified pearl millet hybrids.

We are proposing pearl millet restorer line 298-SB-21, designated in the year 2022 as a J-2648 for registration as a pearl millet breeding line with high grain iron (Fe) and zinc (Zn) content (Table 1). It is unique because it is rich in iron and zinc, with 95 ppm and 53 ppm in the grain, respectively. The proposed line was tested in the CRP Biofortification Parental Line Trial (CRPB PLT) under the CRP Biofortification Project, ICAR-AICRP on Pearl Millet across 6 locations of the country *viz*., Mandor, Jaipur, Hisar, New Delhi, Jamanagar and Dhule, in zones A and B during *kharif* 2021, with a view to identify the biofortified lines having high Fe and Zn. The trial comprises 24 entries

Table 1: Mean data of proposed genotype grain iron and zinc content across different locations along with checks

Entry Name	Mandor		Jaipur		Hisar		New Delhi		Jamnagar		Dhule		Mean	
	Fe	Zn	Fe	Zn	Fe	Zn	Fe	Zn	Fe	Zn	Fe	Zn	Fe	Zn
J-2648 (298-SB-21)	92	44	84	55	128	58	96	63	103	64	67	33	95	53
Dhanshakti (C)	74	33	68	51	169	106	110	52	94	53	66	33	97	55
ICMB 98222 (C)	59	32	65	52	111	79	112	61	90	51	63	30	83	51

Source: Anonymous (2021).

contributed by different ICAR-AICRP on Pearl millet centres along with two checks, ICMB 98222 and Dhanshakti, having high Fe and Zn. The proposed breeding line J-2648 (298-SB-21) was developed at Pearl Millet Research Station, JAU, Jamnagar. The J-2648 (298-SB-21) recorded iron (Fe) content of 95 ppm and the highest zinc (Zn) content of 53 ppm among the test entries (Anonymous, 2021).

The morpho-agronomic characters of proposed line J 2648 (298-SB-21) were revealed as days to 50% flowering (60 days), plant height (171 cm), panicles per plant (1.9), head length 21 cm), head diameter (3.0), seed set (80%) and agronomic score (3.1). The proposed line will be useful for development of biofortified pearl millet hybrids.

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23. J-2571 (IC650744; INGR23090), a pearl millet germplasm for resistant to downy mildew, high grain Iron and zinc content

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Pearl millet [*Pennisetum glaucum* (L.) R. Br.], a crop of international importance, is indigenous to areas in North Africa. It is cultivated in dry regions of arid and semi-arid tropics where no other cereal can be successfully grown. Pearl millet, which accounts for about two-thirds of millet production in India, is grown in the drier areas of the country, mainly in the states of Rajasthan, Maharashtra, Gujarat, Uttar Pradesh, and Haryana. It occupies an area of 6.93 million ha with an average production of 8.61 million tons and productivity of 1243 kg/ha (Directorate of Millets Development, 2020). The causative agent of downy mildew is *Sclerospora graminicola* (Sacc.) Schroet., originally described from Europe (Schroeter, 1979). Pearl millet downy mildew is distributed worldwide and is one of the most important diseases causing losses up to 60% of grain yield.

The proposed genotype, designated J-2571 in the year 2012, was developed at Pearl Millet Research Station, Junagadh Agricultural University, Jamnagar. The proposed genotype J-2571 was tested in the Pearl Millet Downy Mildew Virulence Nursery (PMDMVN) experiment under a collaborative research project of ICAR-AICRP on PM and ICRISAT across 11 locations of the country *viz.,* Aurangabad, Anand, Coimbatore, Dhule, Gwalior, Hisar, Mandor (Jodhpur), Jamnagar, Mysuru and Patancheru, in zones A and B during *kharif* 2021, with a view to downy mildew resistant source identification (Table 1). The proposed genotype was also tested in the CRP Biofortification Parental Line Trial (CRPB PLT) under the CRP Biofortification Project, ICAR-AICRP on Pearl Millet across 6 locations during *kharif* 2017 and 5 locations during *kharif* 2018 of the country *viz.,* Mandor, Jaipur, Hisar, New Delhi, Jamnagar and

Table 1: Downy mildew reaction of proposed genotype across different locations along with checks

S.No.	Trait Description	Proposed line J-2571 (N=11)	Downy mildew susceptible line 7042S (c) (N=11)
1	DM incidence (%) at 30 DAS	0.7 (0.0-2.3)	51.7 (0.0-84.2)
2	DM incidence (%) at 60 DAS	1.1 (0.0-3.4)	64.0 (2.0-100.0)

Table 2: Mean data of on grain iron and zinc content across different locations

SN	Trait Description	J-2571		ICMB 98222 (c)		Dhanshakti (c)	
		2017 (N=6)	2018 (N=5)	2017 (N=6)	2018 (N=5)	2017 (N=6)	2018 (N=5)
1	Fe content (ppm)	81(40-107)	81 (35-106)	78 (36-117)	75 (35-86)	83 (43-123)	93 (52-115)
2	Zn content (ppm)	48 (30-75)	51 (35-60)	53 (41-83)	47 (35-58)	55 (37-97)	57 (45-69)
3	Agronomic score (AS)	3.7 (3.3-4.3)	3.4 (3.0-3.8)	2.4 (1.3-3.8)	3.1 (2.2-4.7)	3.1 (2.5-3.7)	3.5 (2.8-4.7)
4	Days to 50% flowering	54 (51-57)	53 (48-60)	53 (50-60)	49 (45-57)	51 (46-55)	48 (42-56)
5	Plant height (cm.)	130 (107-148)	146 (123-175)	140 (112-180)	162 (142-181)	176 (131-233)	184 (162-200)
6	Panicle/plant	1.2 (1.2-1.7)	2.4 (1.0-3.2)	1.4 (1.1-1.8)	2.1 (1.3-2.8)	1.7 (1.3-2.1)	2.2 (1.0-3.3)

(N= No. of locations)

Dhule, in zones A and B with a view to identifying the biofortified lines having high Fe and Zn. The J-2571 was recorded with 81 ppm grain iron (Fe) content in both tested years, whereas zinc content was 48 ppm in 2017 and 51 ppm in 2018, which was higher or comparable to both checks, ICMB 98222 and Dhanshkti (Table 2). The morpho- agronomic characters of the proposed line J-2571 were as days to 50% flowering (54 and 53 days), plant height (130 and 146 cm), panicles per plant (1.2 and 2.4) and agronomic score (3.7 and 3.4) during 2017 and 2018, respectively. So, we are proposing this J-2571 genotype as a biofortified and downy mildew resistance source for further pearl millet breeding studies and development of a biofortified, downy mildew-resistance hybrid.

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24. IPU99-43 (IC650745; INGR23091), a urd bean germplasm with high seed iron concentration

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Pulses are an important source of protein, dietary fibres, folates, micronutrients and many other nutrients or phytochemicals, including resistant starch, pre-biotics. Urdbean [*Vigna mungo* (L.) Hepper] is a popular *Vigna* pulse crop in India. Besides India, many countries in Southeast Asia grow and consume urdbean as a vegetarian source of protein. Due to the recent surge in demand for gluten-free products as well as alternative sources of animal protein, many countries, including the United States of America, Russia and the European Union introducing and testing many pulse crops as food sources. India is the largest producer as well as consumer of urdbean. It produces about 3.36 million tonnes of urdbean annually from about 4.83 million hectares of area with an average productivity of 696 kg per hectare (Project Coordinator's Report, 2019). Identification of sources for high concentrations of Fe and Zn is an important area of research in urdbean crop improvement programs. The experimental genotypes included 83 urdbean genotypes, including 3 checks (IPU94-1, IPU02-43, Shekhar-2). This set of genotypes comprised 20 varieties or advanced breeding lines and 60 germplasm lines. The seeds were obtained from the urdbean breeding program of ICAR-IIPR, Kanpur. In the present study, 83 urdbean genotypes of diverse origin were tested for Fe and Zn concentrations at two locations. Data obtained were subjected to variance analysis, where genotype effects were found significant for both traits at both locations. The mean value of iron concentration was 117 mg/kg, and it ranged from 19-235 mg/kg in the first location (loc1). In the second location (loc2), the mean value of Fe concentration was 91 mg/kg, and it varied between 16-255 mg/kg. The mean value of zinc concentration was 44 mg/kg, and it ranged from 5-134 mg/kg in loc1. In loc2, the mean value of Zn concentration was 29 mg/kg, and it varied between 12-59 mg/kg. The combined analysis of variance 'Genotype', 'Location' and 'Genotype' (G) × 'Location'(E) interaction effects were significant for both traits. In GGEBiplot analysis identified the best

genotypes for Fe and Zn concentration based on mean value and stability over locations. The most stable urdbean genotypes with high Fe concentration were PU 31 (159 mg/kg) and IPU 99-43 (162 mg/kg). In the case of Zn concentrations, genotypes BGP 28 (58 mg/kg) and HPU 120 (54 mg/kg) had high Zn concentration as well as comparatively higher stability.

25. HPU120S (IC650746; INGR23092), an urd bean germplasm with high seed zinc concentration

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Pulses are an important source of protein, dietary fibres, folates, micronutrients and many other nutrients or phytochemicals, including resistant starch, pre-biotics. Urdbean [*Vigna mungo* (L.) Hepper] is a popular *Vigna* pulse crop in India. Besides India, many countries in Southeast Asia grow and consume urdbean as a vegetarian source of protein. Due to the recent surge in demand for gluten-free products as well as alternative sources of animal protein, many countries, including the United States of America, Russia and the European Union, are introducing and testing many pulse crops as food sources. India is the largest producer as well as consumer of urdbean. It produces about 3.36 million tonnes of urdbean annually from about 4.83 million hectares of area with an average productivity of 696 kg per hectare (Project Coordinator's Report, 2019). Identification of sources for high concentrations of Fe and Zn is an important area of research in urdbean crop improvement programs. The experimental genotypes included 83 urdbean genotypes, including 3 checks (IPU94-1, IPU02-43, Shekhar-2). This set of genotypes comprised 20 varieties or advanced breeding lines and 60 germplasm lines. The seeds were obtained from the urdbean breeding program of ICAR-IIPR, Kanpur. In the present study, 83 urdbean genotypes of diverse origin were tested for Fe and Zn concentrations over two locations. Data obtained were subjected to variance analysis, where genotype effects were found significant for both traits over both locations. The mean value of iron concentration was 117 mg/kg, and it ranged from 19-235 mg/kg in the first location (loc1). In the second location (loc2), the mean value of Fe concentration was 91 mg/kg, and it varied between 16-255 mg/kg. The mean value of zinc concentration was 44 mg/kg, and it ranged from 5-134 mg/kg in loc1. In loc2, the mean value of Zn concentration was 29 mg/kg, and it varied between 12-59 mg/kg. In the combined analysis of variance, 'Genotype', 'Location' and 'Genotype' (G) × 'Location'(E) interaction effects were significant for both traits. In GGEBiplot analysis identified the best genotypes for Fe and Zn concentration based on mean value and stability over locations. The most stable urdbean genotypes with high Fe concentration were PU 31(159 mg/kg) and IPU 99-43 (162 mg/kg). In the case of Zn concentration, genotypes BGP 28 (58 mg/kg) and HPU 120 (54 mg/kg) had high Zn concentration as well as comparatively higher stability.

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26. L4717-NM (IC650748; INGR23093), a lentil mutant germplasm with seed-coat color anomalies

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A unique lentil (*Lens culinaris* Medik.) genotype L4717-NM, a natural mutant identified from an Indian variety L4717, gives brown, black, and spotted seed-coat-coloured seeds in a single plant, generation after

generation, with varying frequencies. Generally, the seed coat in any self-pollinated (homozygous) plant should display only one seed coat colour. Wilson and Hudson *et al.,* (1978) reported the expression of black, mottled, and bicoloured seed coats only in early generations (F2 and F3) from a cross derived from black × beige parents. However, we found such seed-coat expression in a fixed genotype (F9 onwards), generation after generation, without any specific pattern. (Fruwirth 1917) reported such a phenomenon in a lentil genotype 'Puy' after rounds of selfing and selection. Early generation (F1) seed coat mottling was reported in pulses like *Phaseolus vulgaris*, and in *Vigna sinensis* (L.) Savie × Hassk (Harland 1919). Such a type of anomalous seed coat colour in the cases of mottled beans and spotted peas was termed pseudo-mutation.

Based on the results, we presume the presence of some hyperactive transposable element or some epigenetic factors regulating the seed coat colour (anthocyanin pathway) in the studied genotype. The presence of environmental factors like temperature or photoperiod regulating the seed coat colour can be ruled out, as even two adjacent pods have shown both brown and black seed coat colour. The parental genotype of L4717-NM came to IARI, New Delhi, as a nursery from ICARDA, Lebanon in the year 2011-12. The anomalous seed-coat colour expression in the identified genotype on a single-plant (pod-to-pod) basis was studied from 2017-18 to 2022-2023. All the morphological features of L4717-NM and L4717 are exactly the same. Lentil is a naturally highly self-pollinated crop having cleistogamous flowers and with <0.8% natural cross-pollination; thus, the possibility of intra-genic recombination for generations is negligible.

Molecular analysis was also done for L4717 and L4717-NM (brown, black, and spotted seeds) using 54 SSR primers, which showed a monomorphic banding pattern. L4717-NM is an early-maturing (100-102 days) and small-seeded (100-seed weight: 2.14 g) genotype. The seed-coat is grey, black and mottled coloured while the cotyledons are red coloured. The optimum temperature for seed germination is about 22±2°C, while spacing of 30 cm × 10 cm is optimum when planted in rows. Due to its normal plant habit, prolific branching and first flowering node not before the 5th node. Standard cultivation practices can be adopted to raise a healthy crop.

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27. ILWLS 118 (IC650747; INGR23094), a lentil germplasm for early flowering and early maturity

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Lentil (*Lens culinaris* Medik.) is a cool-season crop, which is mostly grown under residual soil moisture conditions. Therefore, it invariably encounters terminal moisture and heat stresses. As a result, it leads to forced maturity and lower yield. This forced maturity can increase in coming years due to climate change and also due to delayed sowing after the late harvesting of rice. Consequently, in India, about 11.7 million ha of rice area currently remains fallow due to the late harvesting of rice (Subbarao *et al.,* 2001). These situations leave a window of 100-110 days for growing lentil in rice fallow areas (Kumar *et al.,* 2018). Thus, early maturing cultivars with the highest yield potential fitting well within this time are required. These early maturing cultivars will enhance lentil cultivation in rice fallow areas by escaping forced maturity (Kumar *et al.,* 2018). Thus, the timing of flowering in lentil can have an important role in the development of suitable plant types, including early maturing cultivars that can adapt under changing environmental conditions.

Therefore, lentil breeders are continuously making efforts toward the identification of diverse source germplasm lines for earliness to broaden the genetic base. A selection from accession ILWL-118 belonging to the wild species *Lens orientalis* flowered within 30 days, podded in 37 days and matured in 62 days in pot conditions (Kumar, 2015). This genotype is designated ILWLS 118 or IPLWS 118, which was further evaluated over two locations (ICAR-IIPR, Kanpur and RS-IIPR, Dharwad, Karnataka) and two years (2014-15 and 2015-

16) along with released cultivars under field conditions. This genotype flowered at the Kanpur location for 37-38 days (average 37.5 days) and 37-42 days (average 39.5 days) at Dharwad over two years (Kumar *et al.,* 2018). Further validation of this genotype during Rabi-season 2021- 22 showed flowering in 39 days. This genotype matures normally in 80-92 days. Other agro-morphological characteristics of ILWLS 118 are medium-size green leaves, medium seed size (2.6 g/100 seeds), medium plant height (27-29 cm), and orange seed cotyledon colour. Thus, identified early flowering genotype from wild species would be useful for widening the genetic base of the cultivated gene pool and also for developing early-maturing cultivars in lentil. Currently, it is utilized as a donor for earliness in the AICRP crossing program for developing early maturing cultivars for rice fallow areas.

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28. PSL-17 (IC643972; INGR23095), a lentil germplasm with high salt tolerance

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The lentil (*Lens culinaris* Medik.) crop is mainly grown in dry and SAT of the Indian-sub-continent as well as in the Middle East. Excessive salts in soil affect the growth of the lentil by disturbing the water and nutritional balance of crop plants. Earlier studies have indicated that the lentil crop is sensitive to salt stress. Significant genetic variation for salinity tolerance prevails among the genotypes of lentil (Singh *et al.,* 2017). So, identification of the salt-tolerant genotypes/genetic stock can be an appropriate approach for minimizing yield losses under salt stress conditions and for future breeding programmes. PSL-17 is a salt-tolerant line which has been developed from a cross between L-4076 × PSL-11 using the single seed descent method.

PSL-17 produces normal green foliage with erect and profuse branching. The plants are tall with normal green leaf colour. The seeds are bold (macrosperma) with dotted green testa. The cotyledon colour is green. This line matures, on average, in 125 days and takes 79 days to flower. Its average 100-seed weight is 2.7 g under salinity/sodicity stress conditions (AICRP on MULLaRP, IIPR, Kanpur, 2020-21).

Line PSL-17 along with two national salinity checks PDL-1, PSL-9 (salt tolerant) were evaluated under ALL India Co-ordinated Research on MULLaRP, Indian Institute of Pulses Research, Kanpur (U.P.) at 6 locations *i.e.* Central Soil Salinity Research Institute, Karnal (Haryana), Narendra Dev University of Agriculture and Technology, Kumar Ganj (Ayodhyaya), Krishi Vigyan Kendra, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (Uttar Pradesh), Krishi Vigyan Kendra, Sri Karan Narendra Agriculture University, Jobner (Rajasthan), Central Arid Zone Research Institute, RRS Pali, (Rajasthan) and Issapur farm of National Bureau of Plant Genetic Resources, New Delhi under salt stress condition during 2020-21. PSL-17 recorded a seed yield of 1063.0 kg/ha, which was higher than the salinity checks PSL-9 (1020 kg/ha) and PDL-1 (930.0 kg/ha) under salt stress conditions (AICRP report on MULLaRP 2020-21). PSL-17 also revealed higher seedling survivability, seedling growth and lower salt stress symptoms under salinity stress conditions (120 mM NaCl).

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29. PMR-1 (IC650749; INGR23096), a mung bean germplasm with resistance to MYMIV infection under north Indian conditions

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Yellow mosaic disease (YMD) is the most important production constraint of mungbean [*Vigna radiata* (L.) R. Wilczek] and other grain legumes in the Indian subcontinent. In India, the disease was first reported on mungbean during the 1950s at the Indian Agricultural Research Institute (IARI), New Delhi. Based on the severity of infection, the yield loss may vary between 10 and 100%. YMD is caused by whitefly-transmitted begomoviruses, *i.e.* Mungbean yellow mosaic India virus (MYMIV) under North Indian conditions. Due to the non- availability of diverse resistant sources to YMD, most of the commercially available cultivars were derived from a few resistant sources, which has resulted in a narrow genetic base, especially for YMD resistance. Further, almost all the reportedly resistant cultivars are known to lose their YMD resistance in due course of time. The PMR-1 (a selection from KM- 14-44) and Pusa Vishal (susceptible control) were screened for MYMIV infection under open-field conditions at IARI, New Delhi, which is the hotspot for MYMIV. PMR-1 showed complete field resistance to YMD during 2015-16 under field conditions and was subsequently reconfirmed for its resistance in fields during 2016-17, 2017-18 and 2018- 2019. However, Pusa Vishal was found susceptible to MYMIV infection.

In addition, the PMR-1 and Pusa Vishal were also grown in the partially controlled glasshouse conditions and were infected using the viruliferous whiteflies (collected from the infected mungbean plants grown at IARI, New Delhi fields). Briefly, five healthy whiteflies maintained on *Nicotiana tabacum* were allowed to feed on the virus source plant mentioned earlier for 24 h to acquire the virus and were released to individual PMR-1 plants (a total of10 plants were inoculated, each with 5 whiteflies) with an inoculation access period of 24 h. After killing the whiteflies with a systemic insecticide, the inoculated plants were maintained in cages to monitor the symptoms. The infection was confirmed through (i) the appearance of the YMD symptom and also by (ii) MYMIV and MYMV CP gene-specific PCR amplification and sequencing of the product.

A YMD-resistant mungbean genotype, PMR-1, a selection from KM-14-44, was found resistant to MYMIV infection when tested under field and also under controlled conditions (using viruliferous whiteflies). RNA-Seq analysis revealed that resistance to MYMIV in mungbean (PMR-1) is regulated by a complex gene network, which begins with the production of general PAMPs, then activation of various signalling cascades like kinases, jasmonic acid (JA) and brassinosteroid (BR), and finally the expression of specific genes (like PR proteins, virus resistance and R-gene proteins) leading to a resistance response.

The MYMIV-resistant genotype PMR-1 is an ideal material for the mapping of YMD resistance QTLs using a mapping population (RILs) derived by crossing PMR-1 and any other susceptible parent. This genotype can also be used for crossing with other MYMIV-resistant genotypes for allelic studies and for the transfer of MYMIV resistance to other mega varieties (now susceptible to MYMIV). In addition, PMR-1 can be used for various genomic studies (GBS, QTL-Seq, RNA-Seq, *etc.*) for the identification of loci governing MYMIV resistance in mungbean.

PMR-1 is a small-seeded (100-seed weight: 3.3 g) and late-maturing genotype (90-100 days) in *kharif* under North Indian conditions. The seed-coat colour is bright green, and the leaflet margin is lobed. The optimum temperature for seed germination is about 30±2°C, while spacing of 30 cm × 10 cm is optimum when planted in rows. Standard cultivation practices can be adopted to raise a healthy crop.