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Plant Germplasm Registration Notice*

A total of 180 proposals were received online for the consideration of registration of germplasm for unique/superior traits. The applications were thoroughly screened by the member-secretary, Plant Germplasm Registration Committee (PGRC) and 94 proposals complete in all respects were reviewed by the experts and were presented in the 50th meeting of the PGRC held in virtual mode on June 12, 2023. 67 proposals with unique/novel features belonging to 29 species were recommended for registration by PGRC. The information on registered germplasm is published with the purpose to disseminate the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes. Description of the 34 out of the 67 germplasm lines registered after recommendation by PGRC is given below:

1. Meghalaya Lakang (IC648583; INGR23001), a rice germplasm with combined resistance to leaf blast and neck blast

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Among the biotic stresses, blast is one of the most devastating diseases in rice which infects most of the plant parts and leads to cause huge economic losses in term of yield and quality. Identification and development of resistant genotype/sources for blast diseases is most sustainable strategies and widely adopted by the rice breeders to tackle this disease. Rice landraces and its wild relatives which are distributed in North East India are the most potential and unexplored/unexploited sources for tolerance/resistant against the major biotic and abiotic stresses of rice that can be utilized in rice breeding programme for development of resistant varieties. Meghalaya Lakang is a unique landrace adapted to the specific ecology of North Eastern India. This landrace was collected through an exploration trip by scientists of ICAR RC Manipur Centre. After its collection, the germplasm line was purified, maintained and characterized at ICAR RC Manipur Centre, Lamphelpat, Imphal (Table 1). The line was constantly screened for two seasons under Uniform blast nursery (UBN) and natural epiphytic conditions (Two season at ICAR RC Manipur Centre Lamphelpat)

Table 1: Characteristics of Meghalaya Lakang

Plant type	**Tall (125-130 cm)**
Habitat	Cultivated, annual
Days to 50% flowering	95 days
Days to maturity	140-145 days (Late)
Effective tillers	6-8
Grain type	Medium bold/Short bold
Yield per ha	1.8t/ha
Adaptation	Specific environment of Meghalaya and other parts of the North East Hill region
Unique characterizes	Highly resistant to leaf and neck blast, possesses novel gene(s)/ QTL(s)

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and recorded complete resistance to blast. It exhibited combined resistance to leaf blast (score 2 on SES scale) and neck blast (score 1 on SES scale). It was subjected to gene profiling using well known 12 major blast resistance gene (*Pitp, Pi33, Pi54, Pib, Pi20, Pi38, Pita2, Pi1, Piz, Pi9, Pizt* and *Pi40*) and intriguing, they didn't habour any functional allele/positive alleles of the 12 blast resistance genes (Bangale *et al.,* 2017). These revealed that this germplasm contains some unique and novel gene (s)/QTL (s) for blast resistance leaf and neck blast.

Reference

Bangale U, V Balija, PS Kumar, SJS Devi, VP Bhadana, P Senguttuvel, S Kumar, SK Sharma, PK Sharma, MS Prasad and MS Madhav (2017) Diverse rice landraces of north-east India enables the identification of novel genetic resources for Magnaporthe resistance. *Front. Plant Sci.* 08: 01-13.

2. RP6253-MV2 (IC648978; INGR23002), a rice germplasm with high nitrogen use efficiency (NUE) under N-Low and N-50 input

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In the studies of genetic improvement for nitrogen use efficiency (NUE) in rice (*Oryza sativa*), RP6253-MV2 is identified as 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. RP6253-MV2 was developed from the Varadhan × MTU1010 cross combination. It has 88-90 days to 50% flowering and possesses long bold (LB) 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 2015-18 (IIRR Progress Report, 2018). The overall mean grain yield was noted as 557 kg/m^2, 510 kg/m^2, 398 kg/m^2 in N-100, N-50 and N-Low treatments. In addition, RP6253-MV2 has the following significant features: i). 17%, 16% and 21% yield superiority over Varadhan (Positive check) in the recommended dose of N (N-100), 50% of the recommended dose of N (N50) 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. iii). In low N treatment, 40% reduction was observed in RP6253-MV2, while Varadhan exhibited 45% reduction in grain yield. RP6253-MV2 was noted at 1445 kg/m^2, 1295 kg/m^2 total dry matter in N-100 and N-50 treatments. The per cent reduction in total dry matter under N-50 treatment is 11%, which is on par with Varadhan. In addition, the AMMI biplot analysis of grain yield under Low-N indicates RP6253-MV2 is the least affected genotype upon low nitrogen treatments (Subrahmanyam *et al.,* 2019). RP6253-MV2, therefore, can be used as a potential donor in breeding rice (*Oryza sativa* L.) for high NUE.

References

Progress Report (2017) Vol.3, Crop Production (Agronomy, Soil Science and Plant Physiology), Indian Institute of Rice Research (2018) All India Coordinated Rice Improvement Programme (ICAR). www.icar-iirr.org

Subrahmanyam D, P Raghuveer Rao, CN Neeraja and SR Voleti (2019) Research Highlights of NICRA on Rice (2011-2019), Technical Bulletin No. 107/2019. ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad-500030, Telangana, 71 p.

3. MSM-3 (IC648592; INGR23003), a rice germplasm with increased root length and root volume and better seedling vigour index

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Considering the importance of well-developed root systems for plant growth and yield, a total of 10,500 BPT-5204 seeds were treated with EMS and developed a Samba Mahsuri mutant population in collaboration with CSIR-CCMB. After several series of screening of the mutant population against deep root system and high seed vigour index, a mutant line (TI- 3) was identified, which has higher root length (cm), volume (cm^3), root dry weight (g) as compared to BPT 5204, CR Dhan 201 and MAS 946-1 under aerobic conditions. TI-3 also recorded a higher seedling vigour index as calculated considering the seedling length (SVI-I) and dry weight (SVI-II) (Addanki *et al*., 2018). The selection of TI-3 was done in M2 generation and advanced to M8 through panicle to row method to check the inheritance & stability of the trait. TI-3 showed higher root length (cm) and volume (cm^3), and root dry weight. In addition to these, the line also showed a higher seedling vigour index (SVI- I & II) than wild type (BPT 5204) measured at 14 and 21 days after germination (IIRR, Newsletter-2020). Owing to the above superior traits, the line TI-3 can be deployed in aerobic rice (*Oryza sativa* L.) breeding programs (Table 1). Genotyping of TI-3 was also carried out with 51 SSR markers. Genotypic data revealed that TI-3 had a genetic similarity of 94.12% with that of wild type (BPT 5204).

References

Addanki KR, D Balakrishnan, YV Rao, S Malathi, M Sukumar, B Kavitha and N Sarla (2018) Swarna × *Oryza nivara* introgression lines: A resource for seedling vigour traits in rice. *Plant Genet. Resour.* 17(1): 1-12.

IIRR Newsletter (2020) Vol: 18(2): April- June.

Table 1. Meteorological data from different locations used in the study

S.No	Characteristics	Aerobic	Irrigated	BPT5204 (Irrigated)
1	Days to 50% flowering	99	106	119
2	Number of panicles (No.)	15	16	16
3	Panicle length (cm)	22.6	23.0	18.4
4	Yield/plant (g)	29.4	32.8	22.5
5	Grains per panicle (No.)	210.6	318.7	190
6	Root length (cm)	36.6	33.4	27.52
7	Shoot dry weight (g)	31.8	27.1	19.4
8	Root dry weight (g)	15.7	12.7	6.14
9	Total dry weight (g)	47.5	59.8	25.51
10	Grain type	Medium Bold	Medium Bold	Medium slender

4. Black Gora (IC640862; INGR23004), a rice germplasm with tolerance to submergence with high anaerobic germination potential

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Black gora (IC640862) rice (*Oryza sativa* L.) is an early maturing upland *aus* landrace collected from Jharkhand (Roy *et al.,* 2021a). It has been characterized to possess a high level of tolerance to major abiotic stresses like drought, submergence (at both germination and seedling stages), and low-phosphorus conditions in multilocation/ season experiments. In addition, it is also resistant to blast disease. IC640862 showed a tolerant reaction (SES = 3-5) to vegetative-stage drought stress (Roy *et al.,* 2021b). Under osmotic stress induced by 1% and 2% Mannitol, it showed superior tolerance response in terms of lesser reduction (20-25%) in root and shoot biomass and lengths. It maintains a higher chlorophyll content under osmotic stress. Screening with DTY (grain yield under drought) QTL-linked markers indicated the possible presence of *qDTY2.2* in this accession. IC640862 showed, on average, 65% survival rate in multilocation trials. It possesses the *SUB1A-1* gene and follows a 'quiescence' strategy for survival under submergence similar to FR13A. Under germination stage flooding, these accessions showed high anaerobic germination (AG) potential of 75% and maintained superior seedling vigour. IC640862 is positive for *PSTOL1* and carries Kasalath-type gene haplotype at the *Pup1* locus responsible for higher phosphorus uptake efficiency under low-P conditions. Hydroponic experiment showed that this Black gora accession produces higher root and shoot biomass and longer roots under P-limited conditions. Furthermore, IC640862 is characterised as resistant to blast disease at Hazaribag location and is found positive for the *Pi- 54* locus based on gene-specific InDel marker. Agro-morphologically, IC640862 has high vegetative vigour, intermediate plant height (121 cm), early maturing (90-95 days) and short bold kernels

References

Roy S, A Banerjee, J Kumar, BC Verma and NP Mandal (2021a) Morpho-agronomic and Genetic Diversity of Gora Rice (*Oryza sativa* L.) Landraces of Chotanagpur Plateau Region in Eastern India. *Indian J. Plant Genet. Resour.* 34(2): 196-205.

Roy S, BC Verma, A Banerjee, J Kumar, US Ray and NP Mandal (2021b) Genetic diversity for drought and low phosphorus tolerance in rice (*Oryza sativa* L.) varieties and donors adapted to rainfed drought prone ecologies. *Sci. Rep.* 11: 13671.

5. RPbio4918-166S (IC648977; INGR23005), a rice germplasm with high photosynthetic rate and high seedling vigour

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Leaf photosynthetic traits (Fig. 4) were evaluated in a set of high-yielding *Oryza sativa* cv. Swarna / *Oryza nivara* backcross introgression lines (BILs) along with recurrent parent Swarna, both in wet (*Kharif*) and dry (*Rabi)* seasons in normal irrigated field conditions. BILs 166s with high and consistent photosynthetic rate exhibited stable high yield levels and biomass production in both the seasons compared to the recurrent parent Swarna (Rao *et al.,* 2018). 166S showed high PN (23.58 lmol (CO2) m-2 s -1]) and gs 0.501 [mmol (H2O) m-2 s -1] in *Kharif* and transpiration rate (E) [mmol (H2O) m-2 s -1.

Fifteen BILs were evaluated for three seasons (*kharif* 2014, *rabi* 2015 and *kharif* 2015) for seedling vigour and yield-related traits. 166S showed higher germination percentage, Root length, seedling vigour index, and harvest index than 248S (DRRDhan40) and Swarna. Of all these 15 BILs, 166S and derived lines were already identified as stable genotypes in the previous study and showed good seedling vigour. High-yielding BIL 166S showed higher seedling vigour indices compared with checks Tulasi and Sahbhagidhan. 166S showed a QTL region linked to seedling vigour from *O. nivara* at the chromosomal region between RM223 and RM210. In terms of vigour, 166S and derived lines were better compared to checks. Introgressions of *O. nivara* into Swarna revealed transgressive segregants for all the traits studied. 166S (G6) were identified to be stable and ideal genotypes for bulk yield, grain number and number of filled grains. 166S (G6) proved significantly superior in yield over the recurrent parent Swarna and on par with the best check MTU1010. G6 (166S) showed yield stability across the seasons along with high mean yield performance. G6 is a late duration genotype, with strong culm strength, high grain number and panicle weight. G6 has a higher yield and stability than Swarna but has the Swarna grain type. 166S exhibited superior performance under direct seeded condition and conservation agriculture practices. BIL 166S, designated as IET21938 (RPBio4918-166S), was tested in 12 saline, alkaline locations in India and it was better than best check CSR36 for alkaline areas at one location, Kumarganj (UP). 166s was reported as salinity-tolerant based on their seed germination and seedling growth response under different salinity treatments. The attenuation in yield potential was comparatively low in 166S due to its efficient compartmentalization of Na+ in leaf tissue (Ganeshan *et al.,* 2016).

References

Ganeshan P, J Ajay, B Parmar, AR Rao, K Sreenu and P Mishra (2016) Identification of salt tolerant rice lines among interspecific BILs developed by crossing *Oryza sativa/O. rufipogon* and *O. sativa/O. nivara*. *Aust. J. Crop Sci.* 10:

220–228.

Rao YV, D Balakrishnan, KR Addanki, S Mesapogu, TV Kiran, D Subrahmanyam, S Neelamraju and SR Voleti (2018) Characterization of backcross introgression lines derived from *Oryza nivara* accessions for photosynthesis and yield. *Physiol Mol Biol Plants.* 24: 1147- 1164.

6. IR 129477-902-121-10-1-1 (IC648593; INGR23006), a rice germplasm with multiple biotic stress resistance genes

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The traditional system of rice (*Oryza sativa* L.) cultivation is largely dependent upon labour, water, and energy. The higher cost of pumps, depletion of groundwater, increasing labour wages, and changing climatic conditions are the most important constraints to the puddled system of rice cultivation. Direct seeding of rice is becoming the most popular method for the production of rice, as it requires less water, labour, and energy for the production of rice compared to the traditional method. To combine anaerobic germination, blast resistance, brown plant hopper resistance, bacterial blight resistance, gall midge resistance, grain yield under direct-seeded cultivation conditions, early vigour, nodal roots, and early and uniform emergence in the background of high-yielding irrigated rice cultivar IR09N538 (IRRI 132/PR 30138-35-2//IR04N114) with preferable grain type, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct seeded aerobic-adapted traits (Sandhu *et al.,* 2021). A total of 38 promising breeding lines were tested at PAU Ludhiana (3 years), ISARC Varanasi (3 years) and BAU Sabour (2 years). The breeding line IR 129477-902-121-10-1-1 showed grain-yield and had the following genes as assessed by molecular markers: **Xa4*: gene for BLB resistance, *BPH3*: gene for resistance to brown plant hopper, *GM4*: gene for resistance to gall midge, *Pita:* gene for blast resistance, *qAG9.1*: QTL for anaerobic germination, *qDTY3.1*: QTL for increased yield under drought conditions, *qGY6.1, qGY10.1*: QTL for increased yield under direct seeded cultivation condition, *qNR5.1, qNR4.1:* QTL associated with nodal root number facilitating nutrient uptake under variable anaerobic aerobic soil conditions. This germplasm can serve as a valuable donor for future breeding programmes

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

7. IR 129477-709-375-3-5-7 (IC648594; INGR23007), a rice germplasm with multiple biotic stress resistance genes

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The traditional system of rice (*Oryza sativa* L.) cultivation is largely dependent upon labour, water, and energy. The higher cost of pumps, depletion of groundwater, increasing labour wages, and changing climatic conditions are the most important constraints to the puddled system of rice cultivation. Direct seeding of rice is becoming the most popular method for the production of rice as it requires less water labour, and energy for the production of rice compared to the traditional method. To combine anaerobic germination, blast resistance, brown plant hopper resistance, bacterial blight resistance, gall midge resistance, grain yield under direct-seeded cultivation conditions, early vigour, nodal roots, and early and uniform emergence in the background of high-yielding irrigated rice cultivar IR09N538 (IRRI 132/PR 30138-35-2//IR04N114) with preferable grain type, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct seeded aerobic-adapted traits (Sandhu *et al.*, 2021). A total of 38 promising breeding lines were tested at PAU Ludhiana (3 years), ISARC Varanasi (3 years) and BAU Sabour (2 years). The breeding line IR 129477-709-375-3-5-7 showed grain-yield and had the following genes as assessed by molecular markers: **GM4*: gene for resistance to gall midge, *Pita:* gene for blast resistance, *qAG9.1*: QTL for anaerobic germination, *qDTY3.1, qDTY12.1*: QTL for increased yield under drought conditions, *qGY6.1:* QTL for increased yield under direct seeded aerobic cultivation conditions *qNR5.1:* QTL associated with nodal root number facilitating nutrient uptake under variable anaerobic aerobic soil conditions. Thus, this germplasm can serve as a valuable donor for future breeding programmes.

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

8. IR 129477-1629-14-1-4-2 (IC648595; INGR23008), a rice germplasm with biotic resistance genes

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Direct-seeded rice (DSR) is a sustainable alternative to puddled transplanted rice (PTR) due to its better adaptability to the future labour-water shortage scenario. The DSR method of rice (*Oryza sativa* L.) cultivation is better suited to bring mechanization opportunities in agriculture and attract youths to select farming as a career. To combine anaerobic germination, blast resistance, brown plant hopper resistance, bacterial blight resistance, gall midge resistance, grain yield under direct-seeded cultivation conditions, early vigour, nodal roots, and early and uniform emergence in the background of high-yielding irrigated rice cultivar IR09N538 (IRRI 132/PR 30138-35-2//IR04N114) with preferable grain type, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct seeded aerobic-adapted traits. At each generation, phenotypic plant selection was conducted initially based on plant type, duration, plant height, number of tillers, grain type, and visual yield, and then selected plants were evaluated genotypically with the trait-associated markers (Sandhu *et al.,* 2021). A total of 38 promising breeding lines were selected and evaluated in multi-environments. The breeding line IR 129477-1629-14-1-4-2 showed better grain-yield with preferable grain type (Length/Breadth ratio: 3.62) and quality traits (milled rice recovery: 68.82%, head rice recovery: 59.76%) under direct seeded aerobic cultivation conditions across years. The breeding line IR 129477-709-375-3-5-7 showed grain-yield and had the following genes as assessed by molecular markers: **Xa4, xa5, Xa21*: genes for BLB resistance, *BPH3*: gene for resistance to brown plant hopper, Pi9, *Pita:* gene for resistance to blast, *qAG9.1*: QTL for anaerobic germination, *qDTY3.1*: QTL for increased yield under drought conditions, *qNR5.1, qRHD1.1:* QTL associated with nodal root number and root hair density facilitating nutrient uptake under variable anaerobic aerobic soil conditions, *qEMM1.1*: QTL for early and uniform emergence early uniform emergence

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

9. IR 129477-1629-210-4-4-4 (IC648596; INGR23009), a rice germplasm with multiple biotic resistance genes

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Direct-seeded rice (DSR) is a sustainable alternative to puddled transplanted rice (PTR) due to its better adaptability to the future labour-water shortage scenario. The DSR method of rice (*Oryza sativa* L.) cultivation is better suited to bring mechanization opportunities in agriculture and attract youths to select farming as a career. To combine anaerobic germination, blast resistance, brown plant hopper resistance, bacterial blight resistance, gall midge resistance, grain yield under direct-seeded cultivation conditions, early vigour, nodal roots, and early and uniform emergence in the background of high-yielding irrigated rice cultivar IR09N538 (IRRI 132/PR 30138-35-2//IR04N114) with preferable grain type, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct seeded aerobic-adapted traits. At each generation, phenotypic plant selection was conducted initially based on plant type, duration, plant height, number of tillers, grain type, and visual yield, and then selected plants were evaluated genotypically with the trait-associated markers (Sandhu *et al*., 2021)· A total of 38 promising breeding lines were selected and evaluated in multi-environments. The breeding line IR 129477-1629-210-4-4-4 showed better grain yield with a preferable grain type (Length/Breadth ratio: 3.67) and quality traits (milled rice recovery: 68.17%, head rice recovery: 54%) under direct-seeded aerobic cultivation conditions across years. The developed advanced breeding line possesses the QTL/gene for biotic and abiotic stress resistance/tolerance, a genomic region conferring early and uniform seedling establishment and root traits improving nutrient uptake under DSR. It also tested positive for markers of the following genes: **xa5, Xa21*: genes for BLB resistance, *BPH3*: gene for resistance to brown plant hopper, *Pita:* gene for resistance to blast *qAG9.1*: QTL for anaerobic germination, *qDTY2.1, qDTY3.1*: QTL for increased yield under drought conditions, *qNR5.1, qRHD1.1:* QTL associated with nodal root number and root hair density facilitating nutrient uptake under variable anaerobic aerobic soil conditions, *qEMM1.1*: QTL for early and uniform emergence early uniform emergence.

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.* 12: 1-17.

10. IR 129477-3343-500-36-5-1 (IC648597; INGR23010), a rice germplasm with biotic resistance genes *Xa4+xa5+xa13 +GM4+Pita.* QTL markers (*AG9.1, qDTY3.1, qRHD1.1 and qEMM11.1*)

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In view of the urgency to save groundwater resources on one hand and food security as well as farmers' livelihood on the other, technologies aimed at saving water in rice (*Oryza sativa* L.) cultivation hold significance. Direct Seeded Rice (DSR) is a promising technology with water and labour-saving possibilities. (Sandhu *et al.,* 2021). To combine anaerobic germination, blast resistance, brown plant hopper resistance, bacterial blight resistance, gall midge resistance, grain yield under direct-seeded cultivation conditions, early vigour, nodal roots, and early and uniform emergence in the background of high-yielding irrigated rice cultivar IR09N538 (IRRI 132/PR 30138-35-2//IR04N114) with preferable grain type, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct seeded aerobic-adapted traits. At each generation, phenotypic plant selection was conducted initially based on plant type, duration, plant height, number of tillers, grain type, and visual yield, and then selected plants were evaluated genotypically with the trait-associated markers (Sandhu *et al.,* 2021). A total of 38 promising breeding lines were selected and evaluated in multi-environments. The breeding line IR 129477-3343-500-36-5-1 showed better grain-yield and preferable grain type (Length/Breadth ratio: 3.50) and quality traits (milled rice recovery: 64.16%, head rice recovery: 77.44%) under direct seeded aerobic cultivation conditions across years. It also tested positive for markers of the following genes: *Xa4, xa5, xa13*: genes for BLB resistance, *GM4*: gene for resistance to gall midge, *Pita:* gene for blast resistance, *qAG9.1*: QTL for anaerobic germination, *qDTY3.1*: QTL for increased yield under drought conditions, *qRHD1.1:* QTL associated with root hair density facilitating nutrient uptake under variable anaerobic aerobic soil conditions, *qEMM11.1*: QTL for early and uniform emergence.

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

11. IR 129477-4026-249-15-1-2 (IC648598; INGR23011), a rice germplasm with multiple biotic resistance genes

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The transition of the traditional puddled system of rice (*Oryza sativa* L.) cultivation to direct seeded cultivation system will be greatly facilitated by the development and adoption of new direct seeded aerobic adapted rice varieties. At PAU, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct seeded aerobic-adapted traits. At each generation, phenotypic plant selection was conducted initially based on plant type, duration, plant height, number of tillers, grain type, and visual yield, and then selected plants were evaluated genotypically with the trait associated markers (Sandhu *et al.,* 2021). A total of 38 promising breeding lines were selected and evaluated in multi-environments. The breeding line IR 129477-4026-249-15-1-2 carrying multiple QTL/genes viz. *Xa4, Xa21*: gene for BLB resistance, *BPH3*: resistance to brown plant hopper, *GM4*: resistance to gall midge, *qAG9.1*: QTL for anaerobic germination, *qDTY3.1, qDTY12.1*: QTL for increased yield under drought conditions, *qRHD1.1, qRHD5.1:* QTL associated with root hair density facilitating nutrient uptake under variable anaerobic aerobic soil conditions, *qEMM11.1*: QTL for early and uniform emergence early uniform emergence, performed well in terms of grain yield and adaptability under DSR and also exhibited phenotypically high levels of tolerance/ resistance to abiotic and biotic stresses with desired grain quality characteristics.

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

12. IR 129477-4139-439-1-1-2 (IC648599; INGR23012), a rice germplasm with Biotic resistance genes *Xa4, xa5, Xa21, Pi9, Pita.* QTL markers (*AG9.1, qDTY3.1, qDTY12.1 and qEMM11.1*)

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Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

13. IR 129477-3343-500-36-5-1 (IC648597; INGR23010), a rice germplasm with biotic resistance genes Xa4+xa5+xa13 +GM4+Pita. QTL markers (AG9.1, qDTY3.1, qRHD1.1 and qEMM11.1)

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The transition of the traditional puddled system of rice (*Oryza sativa* L.) cultivation to direct seeded cultivation system will be greatly facilitated by the development and adoption of new direct-seeded aerobic-adapted rice varieties. At PAU, a complex crossing program began in the 2014DS at IRRI with 12 donors, including donors for biotic and abiotic stress tolerance and direct-seeded aerobic-adapted traits. At each generation, phenotypic plant selection was conducted initially based on plant type, duration, plant height, number of tillers, grain type, and visual yield, and then selected plants were evaluated genotypically with the trait-associated markers (Sandhu *et al.,* 2021). A total of 38 promising breeding lines were selected and evaluated in multi-environments. The breeding line IR 129477-4197-209-2-2-2 introgressed with multiple genes, *viz.* 8 QTL/genes* (*Xa4+xa5+ Xa21+Pita+Pita2+qAG9.1+ qDTY3.1+qNR5.1*) showed grain-yield of 5.9 t ha-1 in Philippines (4.4 t ha- 1 IR09N538) and 4.5 t ha-1 in Ludhiana location of Punjab (4.2 t ha-1 PR126) and 5.1 t ha-1 at ISRAC, Varanasi (UP) (4.4 t ha-1 IR09N538, 4.0 t ha-1 Sahbhagi dhan, 4.2 t ha-1 MTU1010) with preferable grain type (Length/Breadth ratio: 3.57) and quality traits (milled rice recovery: 71.58%, head rice recovery: 60.28%) under direct seeded aerobic cultivation conditions across years. The genomics-assisted breeding line with a combination of root traits improving nutrient uptake, anaerobic germination and biotic/abiotic stress tolerance/resistance QTL/genes showed better yield advantages, viz. 34% in the Philippines, 5% in Punjab and 16% at ISARC Varanasi over the best performing check/recipient variety with better grain quality under direct seeded cultivation condition *viz., Xa4, xa5, Xa21*: genes for BLB resistance, *Pita, Pita2:* genes for blast resistance, *qAG9.1*: QTL for anaerobic germination, *qDTY3.1*: QTL for increased yield under drought conditions, *qNR5.1:* QTL associated with nodal root number facilitating nutrient uptake under variable anaerobic aerobic soil conditions.

Reference

Sandhu N, S Yadav, M Catolos, MT Cruz and A Kumar (2021) Developing climate-resilient, direct-Seeded, adapted multiple-stress-tolerant rice applying genomics-assisted breeding. *Front. Plant Sci.*12: 1-17.

14. MTU 1184 (IC648601; INGR23014), a rice germplasm with Submergence tolerance

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Coastal rice (*Oryza sativa* var. indica) ecosystems, covering more than 16 per cent of rice area worldwide (20 million ha), are adversely affected by annual flooding (Panda and Barik *et al.,* 2021). Paddy fields in these flood-prone lowlands are subjected to either flash floods (a few days to two weeks) or stagnant flooding with water levels of 30-50 cm in the fields (Sem-Deep Water). In recent years, climate change has contributed to the increased incidence of both types of floods and the yield loss under such situations ranges from 10 to 100%, depending on the cultivated variety, stage of the crop, flood duration, and depth of the floodwater (Sukantha *et al.,* 2020). Keeping this in view, Regional Agricultural Research Station (RARS), Maruteru of Acharya NG Ranga Agricultural University (ANGRAU) has developed flood-tolerant variety MTU 1184 by conventional Plant Breeding using PLA 1100, released and widely cultivated as flood and submergence tolerant variety and BM 71, BPH resistant genotype, as parents from 2008 to 2011. The flood tolerant rice culture was intensively evaluated for yield at the research station and different locations under AICRIP system, in semi-deep-water ecosystem.

The entry MTU 1184 (IET 24486) was tested in station yield trials from *kharif* 2012 to *kharif* 2014 under a semi-deep-water ecosystem at RARS, Maruteru. It had 150 days duration, is tolerant to flash floods for 15 days at tillering stage and is also suitable for stagnant flooding (30-50 cm). It has medium slender grain with brown glume. The plant is semi-tall with 130 cm height and has moderate elongation ability, kneeing ability, two weeks of seed dormancy and good grain quality characteristics.

MTU 1184 is also moderately tolerant to Brown Plant Hopper (Score 5), Blast (Score 5), possessing blast resistant genes *piks, pikh, pi1, pi39, pi2* and Bacterial Leaf Blight (Score 5) as per the data from National Screening Nurseries of AICRIP.

References

Panda D and J Barik (2021) Flooding Tolerance in Rice: Focus on Mechanisms and Approaches. *Rice Sci.* 28 (1): 43-47.

Sakanta KS, SS Sarangi, B Maji, PC Sharma, AK Srivastava, D Burman, S Mandal, SL Krishnamurthy, US Singh and AM Ismail (2020) *SUB1* varieties increased rice (*Oryza sativa*) yield in flood-prone rainfed lowlands of coastal regions. *Indian J. of Agric. Sci.* 90 (11): 2064-70.

15. MTU IJ 206-7-4-1; (BM 71) (IC648602; INGR23015), a rice germplasm with resistance to Brown Plant Hopper

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The line, MTU IJ 206-7-4-1 (BM 71) is of medium duration (135 days), average height (140cm), profuse tillering, good grain number (205/panicle), average test weight (21.5g), long slender (3.2 L/B ratio) with light brown husk, translucent kernel and resistant to Brown Plant Hopper. The resistance was confirmed in the screening studies at different locations in the All India Co-ordinated Rice Improvement Program from 2003 to 2005. The resistance was stable across locations and years during the different periods of testing. Antixenosis (Non-preference) and antibiosis resistance mechanisms were found to be responsible for BPH resistance in BM 71. Molecular studies revealed the presence of *Bph3* and *Bph6* BPH resistance genes in MTU IJ 206-7-4-1(BM 71).

MTU IJ 206-7-4-1 (BM 71) is resistant to Brown Plant Hopper with a damage score of 3.0. Further, the resistance was confirmed in the screening studies at different locations in the All India Co-ordinated Rice Improvement Program from 2003 to 2005 (DRR Annual Progress Report 2003, 2004 and 2005). Vijaya Lakshmi *et al.,* (2010) in their studies on phenotypic response of 16 rice genotypes to brown plant hoppers (BPH) at flowering stage under field conditions reported damage score of 1 for BM 71 on 0-9 scale of SES for rice (IRRI, 2014) on par with the resistant check, PTB 33. (Vasanthabhanu *et al.,* 2014) reported antixenosis (Non-preference) and antibiosis as the resistance mechanisms operating in BM 71 for BPH resistance. (Sri Chandana *et al.,* 2015) in their molecular studies revealed the presence of *Bph3* and *Bph6* BPH resistance genes.

References

Chandana Bhogadhi, JS Bentur, Ch V Durga Rani, G Thappeta, KN Yamini, N Arun Prem Kumar, Md. Jamaloddin, G Swathi, V Jhansi Lakshmi, K Vasantha Bhanu and PV Satynarayana (2015) Screening of Rice Genotypes for Resistance to Brown Plant Hopper Biotype 4 and Detection of BPH Resistance Genes. *Int. J. Life Sci. Biotech. and Pharma Res.* 4 **(**2): 90-95.

Vasanta Bhanu K, PV Satyanarayana, P Satyanarayana Reddy and A Vishnu Vardhan Reddy (2014) MTU IJ 206-7-4-1 (BM 71), A New Brown Planthopper Resistant Donor with high levels of antixenosis and antibiosis effects. *Int. J. Innov. Appl. Res.* 2 (12): 35- 41.

16. CSAR 7-9-2020 (IET 29356) (IC648979; INGR23016), a rice germplasm with tolerance against soil sodicity

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In order to develop superior and stress tolerant rice (*Oryza sativa L.*) genotypes under medium to high alkalinity stress with a pH range of 8.5 to 10.9, rigorous screening and selections were made during Kharif 2019 in the breeding materials supplied by ICAR-IIRR, Hyderabad. After evaluation of the selected lines in the station trial, two promising genotypes, i.e. CSAR 7-9-2020 and CSAR 12-10-2020, were nominated for testing in coordinated varietal trials in Kharif 2020. Advanced Varietal Trial-1 (AL & ISTVT) comprising fourteen entries excluding six checks was conducted at 18 locations during Kharif 2021but data from six locations, namely Kurukshetra, Anjanteli, Kanpur, Lucknow, Annamalainagar and Karaikal, were found suitable for statistical analysis (Table 1). Promising genotypes were identified based on a significant critical difference of the test entries over the checks-either best check or the early check. On an overall basis, the mean grain yield ranged from 1735 kg/ha (Pusa 44) to 3337 kg/ha (IET 29356), and days to 50% flowering varied from 79 days (IET 28606) - 99 days (Pusa 44). Plant height of the entries ranged from 81.8 cm (CSR 10) to 102.2 cm (Local

Table 1: General information about soil stress parameters and yield performance of entries under alkalinity and inland salinity in AVT 1-AL & ISTVT, *Kharif,* 2021

Location/state Alkalinity	Soil pH	Soil EC (dSm-1)	Exptl. mean (Kg/ha)	Grain Yield Range (Kg/ha)	CV%	Remarks
Kurukshetra (Haryana)	9.7	1.0	3335	1527-4107	13.3	Data considered for analysis
Anjanteli (Haryana)	9.7	0.9	3375	1400-4240	10.29	Data considered for analysis
Annamalainagar (Tamil Nadu) (Tamil Nadu)	8.5	1.5	2896	1616-3350	10.1	Data considered for analysis
Lucknow (Uttar Pradesh)	9.6	0.96	2491	1014-3722	23.85	Data considered for analysis
Kanpur (Uttar Pradesh)	9.8	0.7	2235	1318-2929	19.2	Data considered for analysis
Karaikal (Puducherry)	8.5	1.8	2822	1833-3618	12.9	Data considered for analysis

Source: Annual Progress Report 2021 Vol. 1- Varietal Improvement, page no.– 1.517 (ICAR-IIRR, Hyderabad). Soft copy of the report is available on the IIRR website.

check), and the panicles/m2 varied from 288 (Pusa 44) to 349 (IET 29353). Among the checks, local check (2908 kg/ha) recorded the highest yield followed by CSR 10 (2668 kg/ha), FL 478 (2529 kg/ha), CSR 36 (2518 kg/ha), CSR 23(2424 kg/ha) and Pusa 44 (1735 kg/ha).

Among the test entries, IET 29356 (CSAR-7-9-2020), a selection from BC-3-7-9 (CST7-1/IRGC- 69861//Pusa-1601), recorded a mean grain yield of 3337 kg/ha, 91 days to 50% flowering, 97 cm plant height and 329 panicles/m^2 and ranked first on an overall basis with 15% yield superiority over the best check. This culture is also found to be superior in zone II encompassing Uttar Pradesh and Haryana states, with a mean grain yield of 3604 kg/ha and 84 days to 50% flowering. Quality-wise, IET 29356 recorded long bold grains with 68.1% head rice recovery, low amylose content of 19.36%, medium GC (47 mm) and high ASV (7).

17. DBW400 (IC648603; INGR23017), a wheat germplasm with resistant to leaf rust

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Wheat (*Triticum aestivum* L.) is prone to a number of rust diseases, namely leaf rust, stem rust and stripe rust. This rust can cause yield losses up to 80% under favourable environmental conditions. There is a need to identify the genotypes with built tolerance against rusts. These resistant genotypes can be used in the breeding programme as a donor for the development of rust resistant, high yielding wheat varieties. Leaf rust is one of the important diseases of wheat, prevailing in all the wheat growing zones of the country.

DBW400(KUTZ//KFA/2*KACHU) was selected from the CIMMYT nursery 12th STEMRRSN6023. This genotype was found highly resistant to leaf rust during different years of multi-location testing in coordinated trials (EIGN, IPPSN and PPSN) conducted under artificial epiphytotic conditions. This genotype was tested in 12 hotspot locations (Table 1) for leaf rust in IPPSN and PPSN. The proposed genotype was found to be highly resistant to leaf rust across locations and years.

Table 1: Leaf rust in IPPSN and PPSN

Year	Number of locations	Leaf rust (South)		Leaf rust (North South)	
		HS	ACI	HS	ACI
2020(IPPSN)	12	5S	1	5S	1.5
2021(PPSN)	12	tR	0.1	10S	2.9

HS: Highest score; ACI: Average coefficient of infection

Additionally, the genotype was also resistant to stem rust with HS:20S; ACI:6.1 in 2021 and HS:10S andACI:305 in IPPSN and PPSN during 2020 and 2021. Therefore, DBW400 will be a potential source to be used as a donor to incorporate genes for leaf rust resistance in an improved wheat variety.

18. UASQ 332 (IC648604; INGR23018), a wheat germplasm with high zinc content

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Worldwide, over 2 billion people suffer from iron (Fe), zinc (Zn) and/or other (multiple) micronutrient deficiencies. In India, 48% of children aged 5-10 years have zinc/iron or other micronutrient deficiencies. Zinc is one of the important micronutrients for normal growth and development. Dicoccum wheat is known to accumulate more Zn and Fe than bread and durum wheat. It also has a higher content of Protein, lysine, and crude fibre. As a consequence of these nutritional characteristics, Dicoccum wheat (DDK 1001) was used as donor for improvement of Durum wheat (HD4501). Wheat (Triticum aestivum L.) UASQ 332 was developed at the University of Agricultural Sciences, Dharwad by Gamma irradiation of F1 (DDK 1001/HD 4501) with 150Gy. The genotype was evaluated along with 53 entries at 13 different locations across the country for different quality traits in Quality Component and Wheat Bio-fortification Nursery (QCWBN), and the grain zinc data is presented in Table 1. UASQ 332 was found to be superior for grain zinc concentration (47.3 ppm) over all the check varieties. UASQ 332 was found to be superior to all 4 checks in all 4 zones. The per cent superiority of UASQ 332 over the check varieties WB02, DBW187, DBW222, and GW322 was 16.8%, 43.4%,32.3%, and 25.4%, respectively (Table 1).

The genotype also contains relatively higher grain iron concentration and grain protein content.

Thus, UASQ 332 would be a potential source to be utilized in future breeding programs to develop high yielding durum wheat varieties with enhanced grain zinc concentration.

Table 1: Grain Zinc content (ppm) of QCWBN entries

Zone	Location	Genotype	Check Varieties			
		UASQ 332	Wb02	DBW187	DBW222	Gw322
NWPZ	Zonal Mean	52.8	44.4	36.8	39.2	40.0
NEPZ	Kanpur	44.4	31.1	28.5	32.3	35.6
	Varanasi	36.7	27	26.8	25.7	29.8
	Sabour	33.3	27.1	23.9	25.1	28.3

	Zonal Mean	38.1	28.4	26.4	27.7	31.2
CZ	Indore	41.3	42.6	36.2	39.7	43.7
	Vijapur	55	53	33.1	34.7	43.4
	Powarkheda	39.7	35.2	28.2	36.2	35.6
	Zonal Mean	45.3	43.6	32.5	36.9	40.9
PZ	Pune	57.8	54.7	44.1	35.8	51.0
	Dharwad	59.8	42.8	36.3	49.1	32.8
	Niphad	43.4	41.6	29.6	35.2	36.1
	Zonal Mean	53.7	46.4	36.7	40.0	40.0
Mean (National)		47.9	41.0	33.4	36.2	38.2
% Superiority Over Checks		16.8	43.4	32.3	25.4	

19. IC112049 (INGR23019), a wheat germplasm with Terminal heat tolerance, high productive tiller numbers, thousand grain weight and harvest index

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A comprehensive study was conducted to identify heat tolerant wheat lines from an association mapping panel of 205 wheat accessions, evaluated under late sown conditions in India at three different locations (Delhi, Hisar and Karnal) for 3 consecutive years (2015-16, 2016-17 and 2017-18). Planting was done in three replications at each location. In the field screening, data was recorded for 16 agronomic and physiological traits such as days to heading (DH), days to anthesis (DA), days to physiological maturity (DM), chlorophyll fluorescence (CFL), cell membrane stability (CMS), grain filling duration (GFD), grain weight/spike (GW, g), grain numbers/spike (GN), grain numbers/m (GNM), productive tillers/m (PTL), plant height (PHT, cm), 1,000 grain weight (TGW, g), biomass (BM, gm−2), grain yield (GY, gm−2), grain filling rate (GFR), and harvest index (HI, %) to find out the variation among studied wheat accessions. Stability analysis and AMMI biplot were also performed to analyze the stable performance of genotypes across the environment and years. Genotyping using a high density 35 K array revealed a large number of SNPs that could be used for the GWAS analysis. In total, 69 QTLs were identified for the ten agronomic traits. The favourable alleles for each QTL region were identified by comparing the extreme phenotypic values in association mapping panel. GY is the most desirable agronomic trait; however, its genetic regulation is very complex, controlled by a number of genes whose expressions are influenced by environmental conditions. In GGE biplot analysis, HI, PTL, GFD, GN, GY, and TGW traits were performed for yield components to identify the best genotypes and stability across the 3-locations i.e., Delhi, Hisar and Karnal. For PTL, TGW and HI, IC112049 germplasm was the best performing genotype at Delhi and Karnal. The analysis revealed heat tolerant germplasm lines based on the presence of high favourable alleles for the IC112049 germplasm line. This is a potential genetic resource for heat tolerance, which can be further used in the wheat improvement programme.

20. PAU16076 (IC648605; INGR23020), a wheat germplasm with resistant to yellow rust with gene *Yr5*

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The quality of wheat (*Triticum aestivum* L.) grain-based products is determined mainly by prolamins consisting of polymeric glutenin and monomeric gliadins proteins. The balanced ratio of these monomeric and polymeric proteins provides the required amount of strength and viscosity for the dough (Wang *et al.,* 2009). Wheat varieties with 1BL/1RS chromosomal translocation are quite popular throughout the world due to their better yield and adaptation, but this translocation is also responsible for lowering bread making quality. The presence of *Sec- 1* locus on the translocated arm 1RS causes dough stickiness (`sticky dough syndrome') due to presence of ω-and γ-secalins proteins encoded by 1RS locus (Lukaszewski *et al.,* 2014). To replace this locus in a popular Indian wheat cultivar PBW550 (PBW550+*Yr5*) with corresponding locus from 1BS, one NIL with absence of secalin locus (*Sec-1-*) in cultivar Pavon background was used as donor (called Pavon 44:38). BC2F5 and BC2F6 NILs with absence of secalin locus were evaluated for two years in replicated yield trial and NILs were tested for bread making quality. NILs were identified having reduced dough stickiness with performance of NIL pau16076 (NIL 72) for bread making characteristics was superior to parental line PBW550 with better loaf volume in the range of 580cc. This line is giving yield of 21.0 qt/acre. In the process of marker assisted transfer of 1BS locus for the absence of *Sec-1*, care was taken to keep rest of 1RS chromosomal arm intact with the help of markers. The presence of rye specific chromatin in NIL 16075 was tested positive with the help of markers rye F3/R3. Besides the NIL was also tested positive for important genes of *Lr26/Yr9/Sr31* and *Pm8* of 1RS chromosomal arm. Beside the line is positive for stripe rust resistance gene *Yr5*.

References

Lukaszewski AJ (2014) Manipulation of the 1RS.1BL translocation in wheat by induced homoelogous recombination. *Crop Sci.* 40: 216–222.

Wang LH, XL Zhao, ZH He, W Ma, R Appels and RJ Peña (2009) Characterization of low- molecular-weight glutenin subunit Glu-B3 genes and development of STS markers in common wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* 118: 525–539.

21. PAU16077 (IC648606; INGR23021), a wheat germplasm with possesses genes for resistant to leaf rust-stripe rust (*Lr57-Yr40*) and stripe rust (*Yr15*)

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Wheat (*Triticum aestivum* L.) is the most widely consumed food grain, and like other cereal crops, the yield is a complex quantitative trait determined by different parameters of tiller number, grain number, grain weight, etc. Grain or kernel weight (thousand grain weight- TGW), consisting of grain length, width, and area, has high heritability, which not only translates into higher yields but also has a favourable effect on flour yield (Gegas *et al.,* 2010)**.** Moreover, uniform and larger sized grains are visually appealing and fetch higher market prices. In the present study, pyramiding of three rust resistance genes, *viz. Yr15* and linked genes *Lr57-Yr40* along with high TGW, into wheat variety PBW550 using a "transfer first and assemble later" strategy (Ishii and Yonezawa *et al.,* 2007). High TGW has been transferred from Rye selection 111, through conventional breeding methods while the three rust resistance genes were transferred through marker assisted selection (MAS).

High TGW was transferred into PBW550 through conventional backcross breeding with high grain weight version of PBW343. High grain weight in PBW343 has been transferred from a selection called Rye SelIII. Phenotypic selections in three-year replicated trials led to an increase in TGW of 18%. Improved versions of PBW550 with increased TGW of 45.5 was crossed sequentially with PBW550+*Yr5* (PBW746), with stripe rust resistance and

PBW550+*Lr57-Yr40* (BWL5236) line, having linked stripe rust- leaf rust resistance genes. The line PAU16077 has been tested at three locations in Punjab for two years, and an average yield of 22.1 qt/acre was recorded.

Resistance to leaf rust and stripe rust has been incorporated in the high TGW version of PBW550 through marker assisted pyramiding of stripe rust resistance gene *Yr15* using marker *Xuhw302*, and a pair of linked leaf rust and stripe rust resistance genes *Lr57-Yr40* using marker *Ta5DS- 2754099_kasp23* one by one.

References

Gegas VC, A Nazari, S Griffiths, J Simmonds, L Fish, S Orford, L Sayers, JH Doonan and JW Shape (2010) A genetic framework for grain size and shape variation in wheat. *Plant Cell* 22: 1046–1056. doi: 10.1105/tpc.110.074153

Ishii T and K Yonezawa (2007) Optimization of the marker-based procedures for pyramiding genes from multiple donor lines: II. Strategies for selecting the objective homozygous plant. *Crop Sci.* 47: 1878–1886. doi: 10.2135/ cropsci2006.11.0750

22. PAU16078 (IC648607; INGR23022), a wheat germplasm with resistance to leaf rust and stripe rusts

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Among the different biotic stresses of wheat (*Triticum aestivum* L.), the stripe rust and leaf rust impose major threats to yield (Singh *et al.,* 2020). As the pathogen evolves quickly, leading to the breakdown of many major genes, a strong backup of resistance genes is required to tackle the future threats quickly. *Aegilops triuncialis* (UtUtCtCt), the non-progenitor of wheat, is an excellent source of biotic and abiotic stress resistance. The leaf rust (LR) and stripe rust (YR) resistant accession of *Ae. triuncialis*, pau 3462 was crossed and backcrossed susceptible cultivar WL711(NN) by inducing homeologous pairing using CS *ph1*. BC2F7 introgression line with 2n chromosome number of 42, with resistance to LR and YR, was selected and named as IL*tri*. IL*tri* was crossed with leaf rust and stripe rust susceptible cultivar WL711(NN), and F2 and F2:3 mapping populations were developed. These populations were screened against leaf rust and stripe rust pathotypes at the seedling and adult plant stage and found to be segregated into 3R:1S (F2) and 1HR:2Seg:1HS ratios (in F3), for both leaf rust and stripe rust, indicating inheritance of a single dominant all-stage resistance gene working against both the rusts. The leaf rust and stripe rust resistance genes were temporarily designated as *Lrtri* and *Yrtri,* respectively, and found to be inherited independently of each other. Molecular mapping with 614 SSR markers from the whole genome of wheat mapped the *Lrtri* at a distance of 11.2 cM from SSR marker *Xwmc*606. These two genes, *Lrtri* and *Yrtri,* are showing resistance to all the prevalent races of leaf rust and stripe rust.

Reference

Singh H, J Kaur, R Bala, P Srivastava and NS Bains (2020) Virulence and genetic diversity of *Puccinia striiformis f. sp. tritici* isolates in sub-mountainous area of Punjab, India. *Phytoparasitica* 48: 383– 395.

23. PAU16075 (IC648608; INGR23023), a wheat germplasm with Glu-B3/GliB1 locus transfer on 1RS chromosomal arm, resistant to stripe rust with transfer of gene *Yr5*

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Wheat with 1BL/1RS translocation is known for providing better yield and adaptation, but is also responsible for lowering bread making quality due to reduced dough strength. This is due to absence of wheat 1BS locus *Glu-B3/Gli-B1* encoding low molecular weight glutenins and gliadins (Wang *et al.,* 2016). In present work marker assisted selection has been utilized to introduce Glu-*B3/Gli-B1* locus in 1RS arm in wheat variety PBW550 (PBW550+*Yr*5). The donor for Glu-*B3/Gli-B1* locus was a NIL in the background of cultivar Pavon, carrying a modified 1RS arm with presence of *Glu-B3/Gli-B1* (called Pavon 40:9) (Lukaszewski *et al.,* 2014).

The phenotypic evaluation of BC2F5 and BC2F6 NILs with *Glu-B3/GliB1* positive locus was done for two years in a replicated yield trial. NILs PAU16075 was selected with an average yield of 20.6 qt/acre, having plant height of 90cm. The line is having improved dough strength with protein content of 11.76%, SDS sedimentation value of 37.72cc, dry gluten 11.50% and gluten index of 81.70. The loaf volume 565cc, dough consistency, and crumb texture of this NIL is superior to the recurrent parent PBW550 because of the retained glutenins and gliadins.

The care was taken for the retention of 1RS arm during the back-cross assisted transfer of *Glu-B3/GliB1* locus. The presence of rye specific chromatin in NIL 16075 was tested with help of markers rye F3/R3 while the important genes on 1RS arm viz. *Lr26/Yr9/Sr31* and *Pm8* were also tested positive with respective markers. The line is also resistant to stripe rust due to presence of gene *Yr5*.

References

Lukaszewski AJ (2014) Manipulation of the 1RS.1BL translocation in wheat by induced homoeologous recombination. *Crop Sci.* 40: 216–222.

Wang Y, S Zhen, N Luo, C Han, X Lu, X Li, X Xia, Z He and Y Yan (2016) Low molecular weight glutenin subunit gene *Glu-B3h* confers superior dough strength and bread making quality in wheat (*Triticum aestivum* L.). *Sci. Rep.* 6: 1–12.

24. BFKW-2 (EC787008; INGR23024), a wheat germplasm with high grain protein (16.7%), Iron (45.7 ppm) and Zinc (47.8 ppm) content

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Zinc is one of the important micronutrients for the normal growth and development of plants and animals. A set of 14 Amphidiploids with 4 international checks received from the University of Nottingham, United Kingdom, under DBT-BBSRC project and 2 Indian checks (1 aestivum + 1 durum) were evaluated for zinc, iron, protein content, agronomic traits and disease resistance. They were planted continuously for 2 years during 2018-19 and 2019-20 in a simple randomized block design with 4 rows of 2.5 meter plots in replication at ICAR-IIWBR Hisar and ICAR- IIWBR Karnal. Pooled and environment-wise grain protein, iron, and zinc content are presented in Table 1. Agronomic traits like days to heading (DTH), days to maturity (DTM), plant height (PHT), thousand grain weight (TKW), tiller/meter, spike length (cm). Zinc and iron estimations were performed using an Oxford instrument X-Supreme 8000. BFKW-2 found to be superior with 16.7% grain protein, 45.7 ppm grain iron and 47.8 grain zinc content in comparison to check

Table 1: Pooled grain protein, iron, and zinc content in wheat genotypes

Trait	**Testing genotype**	**Check**	
	BFKW-2	DBW 187	HI 8498
Grain Protein (%)	16.7	13.7	12.8
Grain Iron (ppm)	45.7	37.3	44.8
Grain Zinc (ppm)	47.8	35.8	40.6
Per cent Superiority Over Checks			
Grain Protein	-	21.9	30.5
Grain Iron	-	22.5	2.0
Grain Zinc	-	33.5	17.7

varieties DBW 187 (Protein: 13.8%; Iron: 37.3 ppm; Zinc: 35.8 ppm) and HI 8498 (Protein: 12.8%; Iron: 44.8 ppm; Zinc: 40.6 ppm). Per cent superiority ranges from 21.9-30.5, 2.0-22.5, and - 17.7-33.5 over check varieties for grain protein, grain iron, and grain zinc, respectively.

Thus, BFKW-2 would be a potential source as high grain protein, iron and zinc donor parent. This valuable germplasm may be utilized in breeding programs to develop bread wheat varieties with high protein and micronutrient content.

25. BFKW-7 (EC787015; INGR23025), a wheat germplasm with high grain protein and Zinc content

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Worldwide, over 2 billion people suffer from iron (Fe), zinc (Zn) and/or other (multiple) micronutrient deficiencies. In India, 48% of children aged 5-10 years have zinc/iron or other micronutrient deficiencies. Zinc is one of the important micronutrients for normal growth and development. A set of 14 Amphidiploids with 4 international checks received from the University of Nottingham, United Kingdom, under DBT-BBSRC project and 2 Indian checks (1 *aestivum* + 1 *durum*) were evaluated for zinc, iron, protein content, agronomic traits and disease resistance. They were planted continuously for 2 years during 2018-19 and 2019-20 in a simple randomized block design with 4 rows of 2.5 meter plots in replication at ICAR-IIWBR Hisar and ICAR-IIWBR Karnal.

Pooled and environment-wise grain protein, iron, and zinc content is presented in Table 1. Agronomic traits like days to heading (DTH), days to maturity (DTM), plant height, (PHT), thousand grain weight (TKW), tiller/meter, spike length (cm). Zinc and iron estimations were performed using an Oxford instrument X-Supreme 8000. BFKW-7 found to be superior with 17.1% grain protein, 53.3 ppm grain iron and 54.2 grain zinc content in comparison to check varieties DBW 187 (Protein: 13.8%; Iron: 37.3 ppm; Zinc: 35.8 ppm) and HI 8498 (Protein: 12.8%; Iron: 44.8 ppm; Zinc: 40.6 ppm). Per cent superiority ranges from 24.8–33.6, 18.9–42.9, and 33.5–51.4 over check varieties for grain protein, grain iron, and grain zinc, respectively.

Thus, BFKW-7 would be a potential source of high grain protein, iron and zinc donor parent. This valuable germplasm may be utilized in breeding programs to develop bread wheat varieties with high protein and micronutrient content.

Table 1: Pooled grain protein, iron and zinc content in wheat genotypes

Traits	**Testing Genotype**	**Checks**	
	BFKW-7	DBW 187	HI 8498
Grain Protein (%)	17.1	13.7	12.8
Grain Iron (ppm)	53.3	37.3	44.8
Grain Zinc (ppm)	54.2	35.8	40.6
Percent Superiority Over Checks			
Grain Protein	-	24.8	33.6
Grain Iron	-	42.9	18.9
Grain Zinc	-	51.4	33.5

26. GW A 2019-957 (IC0642305; INGR23026), a wheat germplasm with high zinc content

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All living organisms require an optimum intake of essential mineral micronutrients for their normal growth and development, and human beings obtain these essential nutrients from their daily diet (Welch and Graham *et al.,* 2004). Malnutrition due to insufficient intake of micronutrients, including Fe and Zn, has been identified as one of the major global health issues, particularly in children aged 0–5 years, and pregnant and lactating women, affecting nearly 1.5 to 2 billion people across the globe. The intensity of the risk is much higher in countries dominated by cereal-based diets, particularly in Asia and Africa (Kumssa *et al*., 2015). Genetic biofortification makes use of plant breeding techniques to produce genotypes with higher micronutrient levels, reducing levels of anti-nutrients and increasing the levels of substances that promote nutrient absorption. Accordingly, GW A 2019-957 was developed (cross DBW 31/WR 1873) and identified as a high zinc content genotype possessing high yield. The grain yield of GW A 2019-957 (64.4 q/ha) was significantly superior to the best zonal check GW 322 (50.8 q/ha) over the location in Quality Component and Wheat Biofortification Nursery (QCWBN) in the central zone, and also possessed high zinc content (47.0 ppm) as compared to the best check UP 2672 (41.7 ppm).

The mean performance of the GW A 2019-957 under QCWBN central zones revealed its superiority for a combination of traits like high zinc concentration and grain yield (Table 1), establishing its usefulness as a potential donor for biofortification in wheat.

References

Kumssa DB, EJM Joy, EL Ander, MJ Watts, SD Young, S Walker and MR Broadley (2015) Dietary calcium and zinc deficiency risks are decreasing but remain prevalent. *Sci. Rep*. 5: 10974. doi:10.1038/srep10974

Welch RM and RD Graham (2004). Breeding for micronutrients in staple food crops from a human nutrition perspective. *J. Exp. Bot*. 55: 353–364. doi:10.1093/jxb/erh064

Table 1: Overall performance of GW A 2019-957 in QCWBN during 2020-2021

Genotype	Grain yield (q/ha)	Zinc content (ppm)
GW A 2019-957	64.4	47.0
UP 2672 (c)	51.0	41.7
MACS 6222 (c)	67.9	40.1
DBW 187 (c)	60.2	34.4
WB 2 (c)	63.1	39.0
HD 3086 (c)	49.1	36.4
GW 322 (c)	50.8	39.5
HS 490 (c)	48.6	38.3
CD at 10 %	6.9	2.4

27. HS545 (IC648609; INGR23027), a wheat germplasm with resistant to all pathotypes of Brown Rust

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Leaf rust or brown rust caused by the fungus *Puccinia triticina* Eriks has its impact on the wheat (*Triticum aestivum* L.) crop grown in 30 million hectares (mha) area of India, Pakistan, Bengladesh and Nepal (Huerta-Espino *et al.,* 2011). The pathogen is very dynamic and renders wheat cultivars susceptible by evolving new pathotypes. To counter such threats, diverse wheat germplasm carrying brown rust resistance genes effective at different stages of growth are required. In this direction, a rust resistant wheat germplasm HS545 was developed from a cross "HD2819/HS435" Bulk-Pedigree method of breeding to have parental choice with the wheat breeders. HS545 has been found resistant against all the pathotypes of brown rust, including 77-8 and 77-10, known virulence for *Lr19* and *Lr28* under seedling resistance test. Rust resistance gene complex *Lr24/Sr24,* derived from *Agropyron elongatum*, located on 3DL, confers resistance to all the currently prevalent pathotypes of brown rust in the Indian Sub-continent (Bhardwaj *et al.,* 2021). HS545 has been validated for the presence of *Lr24/Sr24* using molecular marker *Sr24#12*. Inheritance studies revealed the presence of single dominant gene pair for controlling brown rust against the virulent pathotype 77-5. HS545 possesses agronomic features *viz*., semi-erect growth habit, green foliage, waxy flag leaf sheath, waxy peduncle with bent attitude, tapering ear shape, 94cm plant height, brown ear with brown medium awns, matures in 157 days, the grains are semi-hard and ovate shaped, amber in colour with thousand grain weight of 40 g. Broad spectrum resistance present in HS545, along with good agronomic features, would serve as desirable choice for breeding brown rust resistant wheat varieties in India.

References

Bhardwaj SC, S Kumar, OP Gangwar, P Prasad, PL Kashyap, H Khan, S Savadi, GP Singh, N Gupta and R Thakur (2021) Physiologic specialization and genetic differentiation of *Puccinia triticina* causing leaf rust of wheat in the Indian Sub-continent during 2016-2019. *Plant Disease* http://doi.org/10.1094/PDIS- 06-20-1382-RE

Huerta-Espino J, RP Singh, S German, BD McCallum, RF Park, WQ Chen, SC Bhardwaj and H Goyeau (2011) Global status of wheat leaf rust caused by *Puccinia triticina*. *Euphytica* 179: 143-160.

28. DWRBG-13 (IC646834; INGR23028), a barley germplasm with higher malt beta glucanase activity (384 Units/kg malt), lower wort beta glucan content (130 ppm)

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Malt is one of the major industrial products from barley (*Hordeum vulgare* L.), which is further utilized mainly for beer production. The malt producing industry requires certain minimum quality parameters in the barley to get higher recovery and better quality. The higher beta glucans content in grain may reduce water uptake during steeping, while in wort it adversely affects filtration rate and quality of malt extract. DWRBG-13 (ICARDA-11), along with four checks, was grown at six locations during the *rabi* season of 2020-21, and grains were malted and mashed. The genotype ICARDA-11, registered the highest malt beta-glucanase activity as compared to the checks, with an average value of 384U/kg of malt (Table 1). It had a lower wort beta-glucan content of 130 ppm (Table 2). This genotype can be a potential source of these two traits in the malt improvement programme of the country.

Table 1: Activity of Beta-Glucanase (Units/kg) in malt of different barley genotypes

Genotype	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Average	Average*
ICARDA-11	380	360	382	487	369	315	382	384
DWRUB 52(c)	260	279	309	308	239	280	279	286
DWRB 101 (c)	175	186	197	263	256	140	203	194
DWRB-182 (c)	167	264	257	299	240	167	232	231
DWR 37 (c)	195	223	208	269	272	272	240	235

Table 2: Wort Beta-Glucan content (ppm) in different barley genotypes

Genotype	Karnal	Hisar	Ludhiana	Durgapura	Pantnagar	Kanpur	Average	Average*
ICARDA-11	198	92	167	101	39	107	117	130
DWRUB 52 (c)	552	397	404	392	261	280	381	401
DWRB 101 (c)	471	370	602	447	232	176	383	408
DWRB-182 (c)	368	325	432	441	234	321	353	373
DWR 37 (c)	683	856	633	462	269	239	524	566

**Average values excluding Pantnagar location, which registered exceptionally low wort beta glucan content*

29. BHS 479 (IC646838; INGR23029), a barley germplasm resistant to most pathotypes of leaf rust and stripe rust at the seedling stage

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BHS 479 (BBM 798) is a barley (*Hordeum vulgare* L.) line resistant against leaf, stripe and stem rust. It has shown seedling resistance against all the prevailing pathotypes of leaf rust. The proposed genetic stock also possesses seedling resistance against all the pathotypes of stripe rust (except for 24, showing a moderately resistant response). BHS 479 (BBM 798) also showed adult plant resistance to leaf (highest score TMS), stem rust (highest score 0) and stripe rust (ACI 5.8). This line is developed following the pedigree method of breeding involving three- way crosses between barley breeding line BBM 556 with BHS 169 and a registered barley genetic stock BHS 369 at ICAR-IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Centre, Shimla (H.P.).

BHS 479 (BBM 798) has a semi-erect growth habit with medium maturity (165 days) under Northern Hill conditions. The average yield is 3.46 t/ha under the rainfed condition of the Northern Hill Zone of All India Co-ordinated trials 2019-20 (Table 1). The distinguishing features of BHS 479 (BBM 798) are six-rowed, hulled; semi-erect growth habit; erect flag leaf attitude; green leaves and 1000-grain weight of 42 g.

Table 1: Reaction of BHS 369 to major diseases

Diseases	Condition	Year	Response of Proposed Genetic stock BHS 479 (BBM 798)
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2019-20	HS= TMS
	NBDSN (Seedling)	2019-20	R (Resistant to all races)
Stem Rust (Resistant to black rust)	NBDSN (APR)	2019-20	HS=0
Stripe rust (Resistant to Yellow rust)	NBDSN (APR)	2019-20	ACI=5.8
	NBDSN (Seedling)	2019-20	R to all races (except for *24* showing MR response)
	IBDSB	2018-19	Yellow rust ACI 1.0 (Highest Score 5S)

ACI= Average Coefficient of incidence HS= Highest Score
IBDSN= Initial Barley Disease Screening Nursery NBDSN= National Barley Disease Screening Nursery

30. VR 1143 (IC647589; INGR23030), a finger millet germplasm with early duration combined with neck and finger blast resistance

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Finger millet [*Eleusine coracana* (L.) Gaertn.] is drought resistant nutri cereal grown for food & fodder. The future improvement of the crop depends upon the amount of valuable trait-specific germplasm available for different traits. Finger millet, VR 1143, is early duration entry developed by crossing VR 708 with GPU 48 and followed by the pedigree method of selection. It belongs to early maturity with medium plant height and a larger number of productive tillers/plant.

The proposed entry, along with other test entries and two checks were evaluated during the four years from 2017 to 2020. VR 1143 matures six days earlier than the national early check, VL 352, while it was on par with the very early check, VR 708. The check, VR708 (63.9% & 56.2%), is highly susceptible to neck and finger blast, while the entry, VR 1143 (5.7% & 4.9%) was resistant to neck & finger blast disease, and hence this entry can be used in crop improvement for the development of early maturity varieties with resistance to blast disease.

31. VR 1135 (IC647590; INGR23031), a finger millet germplasm with banded blight resistance

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Finger millet [*Eleusine coracana* (L.) Gaertn.], VR 1135 is a Banded blight resistant line developed by crossing PS1 with VL 315 and following pedigree method of selection. The entry, VR 1135 was evaluated with other promising entries along with local (VR 847) & national checks (PR 202, VL 350) for yield and also with disease resistant (GE4999) & disease susceptible (VR 708) checks. It was tested in consecutive years from 2017 to 2020 during Kharif season in Randomized block design with three replications at the Agricultural Research Station, Vizianagaram (lat 18^0 10'N, long $83^0$39' E and altitude of 74 msl), Andhra Pradesh, which is hot spot for blast & banded blight disease.

The entry, VR 1135 belongs to medium maturity (121 days) as like the local check VR 847 (124 days). The entry VR 1135 was evaluated from 2017 to 2020 for the disease severity. Scoring for the disease severity during all four years of testing was done. The entry, VR 1135 recorded significantly lower score of banded blight over all the checks during all four years of testing. It recorded 71.80%, 40.96% and 87.10% less incidence of banded blight over Local check VR 847, Resistant check (GE 4999) and Susceptible check (VR 708), respectively. It recorded fewer incidences of banded blight (3.8%) among all the 30 entries tested for banded blight resistance, and it also showed resistance to neck & finger blast (4.0% each). VR 1135 is unique in terms of banded blight resistance and also possesses resistance to neck and finger blast. Since it is an advanced breeding line, it can be used directly as a source for the development of high-yielding banded blight and blast resistant varieties.

32. VR 1125 (IC647592; INGR23032), a finger millet germplasm with neck blast resistance and finger blast resistance

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Finger millet [*Eleusine coracana* (L.) Gaertn.] is one of the small millets that is highly valued for its nutrient composition. It is a crop of both food and nutritional security. Blast is a major problem in the finger millet crop, which can hamper the production up to 70% in severe cases. Hence, finger millet improvement is oriented towards the development of blast resistant high yielding varieties. Finger millet, VR 1125 is neck and finger blast resistant, high yielding variety developed by crossing Udurumallige with GPU 48 during 2010, followed by the pedigree method of selection up to F6 generation. It was evaluated with other 23 promising lines along with local and national check for yield; resistant and susceptible check for blast disease resistance in Randomized block design with three replications during consecutive four years (*Kharif*, 2017 to 2020) at Agricultural Research Station, Vizianagaram (lat 180 10'N, long 83039' E and altitude of 74 msl), Andhra Pradesh which is hot spot for blast disease. The proposed entry, along with other test entries and two checks, was tested under high-pressure conditions under field conditions during the four consecutive four years from 2017 to 2020.

The entry VR 1125 belongs to medium maturity (115 days) with longer ear & finger length (9.1 cm & 8.5 cm) compared to the check VR 847 (7.9 cm & 7.3 cm) respectively. It recorded a significantly lower score of neck and finger blast over all the checks during all four years of testing. VR 1125 (3.5%) recorded 71.6%, 60.1% and 94.6% less incidence of neck blast over Local check (12.6%), Resistant check (8.7%) and Susceptible check (63.9%) respectively. VR 1125 (3.0%) also recorded 76.0%, 54.4% and 94.7% less incidence of finger blast over Local check (14.5%), Resistant check (6.4%) and Susceptible check (56.1%), respectively. Moreover, the entry has recorded higher fodder yield & grain yield compared to the local check, VR 847. VR 1125 is unique in terms of neck and finger blast resistance. Hence, it can be used directly as a source for the development of high yielding blast resistant variety.

33. PPR 2885 (IC595249; INGR23033), a finger millet germplasm with non-lodging having uniform maturity

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Finger millet [*Eleusine coracana* (L.) Gaertn.] line PPR 2885, a cross derivative of PPR 2709 and Kalyani, developed through the pedigree selection method, was elevated in multi-environments. It was found to be highly tolerant to blast (leaf blast, neck blast and finger blast), brown spot, leaf sheath blight and stem borer. The culture matures within 115-120 days and attains 50% flowering in 85-98 days after sowing. It has an erect plant type with semi dwarf (85-90 cm) plant height. It has light purple pigmentation at nodes. The ear head is semi compact nature and has many lengthy, top curved fingers. The colour of the grain is light purple brown with a test weight of 3.0 g. Quality of grain is good, having high calcium and Total free amino acids. At maturity, it is resistant to lodging due to culm strength semi dwarf nature of the plant.

34. WN 630 (IC648610; INGR23034), a finger millet germplasm with High number of fingers and longer ear head length

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A total of 38 finger millet [*Eleusine coracana* (L.) Gaertn.] accessions constituted of 25 promising landraces of long earhead and thirteen released varieties were evaluated for 12 morphological characters, including grain yield. Based on mean performance over three years (*Kharif* 2019, 2020 and 2021) at two locations, the genotype WN-630 showed a very high number of fingers per earhead *i.e.* 12.50, which is >8 (high) as per DUS testing guidelines and very long earhead length, *i.e.* 13.43 cm, which is >12 cm (very long) as per DUS testing guidelines. This morphological trait, such as the number of fingers per earhead, main earhead length and length of finger, has direct contributions towards the high grain yield per plant. The best promising finger millet genotypes, *viz.* WNN-630, for a high number of fingers per earhead and very long earhead length, with moderate resistance to pests and diseases found during three years of genetic evaluation at three different locations, which was used as a promising parent in a further breeding programme.