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Plant Germplasm Registration Notice*

187 proposals were received online for consideration of registration of germplasm for unique/superior traits. After preliminary screening by member-secretary, Plant Germplasm Registration Committee (PGRC), 108 proposals complete in all respects were got reviewed by the experts and were presented in XXXXIXth meeting of the PGRC held in virtual mode on December 08, 2022. A total of 90 proposals with unique/novel features belonging to 35 species were finally recommended for registration. The information on registered germplasm is published with the purpose to disseminate the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes. Description of the 45 out of the 90 germplasm lines registered after recommendation by PGRC is given below:

1. BPT 2848 (IC645766; INGR22100), a rice germplasm with high protein content (10.5%) in polished kernel

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Even though rice (*Oryza sativa* L.) contains less protein content than wheat or corn, it has superior biological value therefore, the impact of improving the protein content in rice would be enormous in combating the protein energy malnutrition which is prevalent in more than one third of world's children population. BPT 2848 (IET 28692) is a derivative of the cross between RP Bio 226*1 /IRGC 48493 which was developed through pedigree method of breeding at Agricultural Research Station, Bapatla. BPT 2848 was evaluated in IVT- Biofortification trial which was conducted at 9 locations spread over 7 states. In this trial, a total of 38 entries including 4 checks *viz.,* IR 64 and BPT 5204 as yield checks and DRR Dhan 45 and Chittimuthyalu as micronutrient checks were evaluated for grain yield, quality traits and nutritional parameters. The polished rice of all the entries were analysed for nutritional parameters *viz.*, Zinc content, Fe content and Protein content at ICAR-NRRI, Cuttack during *kharif*, 2019. Among all the entries tested, BPT 2848 recorded highest overall mean protein content of 10.5% in polished rice. The two micronutrient checks *viz.*, DRR Dhan 45 and Chitimuthyalu recorded 6.43% and 8.30% mean protein content on over all basis respectively. IET 28692 recorded more than 10.0% protein content in polished rice at 5 locations *viz.*, Jeypore (13.17%), Cuttack (13.33%), Sirsi (10.52%), Aduthurai (12.28%) and Coimbatore (10.36%), out of 9 testing locations (Table 1).

Table 1: Protein content (%) in polished rice samples of BPT 2848 (IET 28692) in Initial Variety Trial- Bio-fortification (IVT-Biofort) analyzed at ICAR-NRRI, Cuttack, *Kharif*, 2019

IET No	*Jeypore*	*Cuttack*	*Sakoli*	*Navsari*	*Sirsi*	*Aduthurai*	*Coimbatore*	*Moncompu*	*Maruteru*	*Overall Mean*
IET 28692 (BPT 2848)	13.17	13.33	7.17	8.83	10.52	12.28	10.36	9.46	9.34	10.50
BPT 5204	8.12	7.79	7.45	6.17	6.00	8.36	8.93	7.92	5.47	7.36
DRR Dhan45	7.11	7.94	4.43	5.53	5.44	6.53	6.59	6.22	8.08	6.43
Chitti- muthyalu	7.85	7.88	8.65	7.17	7.62	9.32	9.10	9.52	7.60	8.30
IR 64	7.82	7.78	5.19	6.65	6.00	6.72	6.86	-	6.32	6.67

Source: AICRP trials data from IVT-Biofortification trial from Varietal Improvement Progress Report Volume 1

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2. Moirang-Phou Khokngangbi (IC350549; INGR22101), a rice germplasm with resistance to leaf blast, mid-early duration and long bold grain type

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Rice (*Oryza sativa* L.) blast caused by *Magnaporthe oryzae* is one of the major diseases causing yield loss up to 20-100% under favourable conditions. The deployment of resistance genes *i.e.* R genes have been the foundation for disease resistance breeding. Till date more than 100 R genes have been identified, of them 31 R genes cloned and characterized. But there is an arm race between host and pathogen showing highly variable and new races are evolving very rapidly resulting in breakdown of resistance. The wild species and land races of rice are treasure trove for many biotic and abiotic stress tolerance genes. The study was conducted for identification of novel source of blast resistance from landraces from North East India. A total of 39 North Eastern land races (India) along with resistant check Tetep a well known donor for blast resistance and susceptible check HR-12 were screened for four successive years (2015, 2016, 2017 and 2018) in specialized uniform blast nursery beds (UBN) at ICAR-IIRR, Hyderabad. The standard method and protocol was followed and scoring was done after 10 to 15 days of post infection depending on the severity of the infection on the susceptible check using standard evaluation system (SES, IRRI, 2013). Among the 39 land races screened for blast resistance, Moirang-Phou-Khokngangbi, Thangjing-Phou and Punshi showed resistance reaction with a score of 2-3, supporting files, IIRR news latter). These three land races were again screened during 2016, 2017 and 2018 for further confirmation and the results were similar with previous season confirming resistance nature of these three landraces. During in-house experiments Moirang-Phou Khokngangbi was identified as a promising leaf blast-resistant and high yielding (IIRR Annual report, 2020). It is a mid-early duration line with 92 days to 50% flowering and long bold (LB) grain type During all the 4 years disease screening (2015, 2016, 2017 and 2018) it recorded a resistant score of 2-3 where as highly susceptible check HR-12 recorded score of 9. In addition to blast resistance this line also has high yield of 33.0 g per plant and reported promising for seedling vigour index (SVI)., under paper roll method and poly house condition, as SVI trait is important for early seedling establishment, nutrient uptake and to compete with weeds under direct seeded rice (DSR) condition. In conclusion, Moirang-Phou Khokngangbi is a potential restorer line with leaf blast resistance and can be exploited further in resistance breeding. Based on this meritorious background, this landrace deserves registration as genetic stock.

3. RP5593-83-12-3-1 (IC645772; INGR22102), a rice germplasm with high nutrient (NPK) uptake and high grain yield under native sodic soil conditions and tolerance to acidic soils

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In the studies of genetic improvement for abiotic stress tolerances like sodicity, soil acidity and aerobic conditions in rice (*Oryza sativa* L.), RP5593-83-12-3-1 (MTP-1) / IET26168, a derivative of MTU1010 × Nagina 22 cross is identified as promising culture based on multi-location AICRP on Rice testing. It was an early duration culture with 82 days to 50% flowering and medium slender (MS) grain type. It was evaluated in AICRP on Rice, Soil science – Sodicity trial (Screening of germplasm for sodicity and management of sodic soils in RBCS) and acidity trial (Screening of rice genotypes for tolerance to soil acidity) during 2019 (ICAR-IIRR Progress Report, 2020). The overall mean grain yield was noted as 3.95 t. ha^{-1} under native sodic conditions without gypsum amendment (pH 8.5 – 10.0). In addition, MTP-1 noted 24% and 8% yield superiority over CSR23 (tolerant check) and MTU1010 (female parent) under native sodic soils; Noted higher nutrient (NPK) uptake (Kg. ha^{-1}) in comparison with CSR23 and MTU1010 across the tested locations under

Table 1: Agro-morphological and yield characters of RP5593-83-12-3-1 (MTP-1) / IET26168 (Based on the AICRP on Rice data).

Trait	*Value*
Plant Height (cm)$^{\#}$	102-105
Days to 50% Flowering$^{\#}$	80-83
Panicles per Square meter$^{\#}$	277-290
Grain Yield (t. ha^{-1})$^{\#}$	4.81 (32)$^{\#}$; 3.95 (4)$^{\$}$; 4.47 (4)*
H (%), M (%) and HRR (%)$^{\#}$	78.15; 69.35; 59
KL, KB and L/B$^{\#}$	5.67; 2.15; 2.64
ASV, AC and GC$^{\#}$	4; 24.34; 37.5

#-Aerobic; $ - Native Sodic soil; *- Unlimed acidic soils. H: Hulling (%); M: Milling (%): HRR: Head Rice Recovery (%); KL: Kernel Length(mm); KB: Kernel Breadth(mm); L/B: Length and breadth ratio; ASV: Alkali Spreading Value; AC: Amylose Content (%); GC: Gel Consistency. Values within the parenthesis indicate the number locations tested during AICRP on Rice trials.

native sodic soils. In addition to sodicity tolerance, this culture also exhibits acidity tolerance in terms of grain yield and lower toxicity score under un-limed acid soils (pH 4.3 – 5.2). MTP-1 exhibits mean grain yield, 4.47 t. ha^{-1} and straw yield, 7.26 t. ha^{-1} under unlimed acidic soils of tested locations (Table 1). MTP-1 exhibits toxicity score of 3.67 under unlimed acidic soils and 3.00 under limed treatment soils. MTP-1 was also evaluated in aerobic trials during 2016, 2017 and 2018 (ICAR-IIRR Progress Report, 2017-2019,). The overall mean grain yield was noted as 4813 Kg. ha^{-1} across the tested locations of aerobic ecosystem which is 2%, 14% and 2% superiority over national (CR Dhan 201), zonal and local checks. MTP-1 also exhibits moderately resistance to Leaf blast and desirable grain and cooking quality characteristics with intermediate amylose content (24.34%). The identified genetic stock, has tolerance to soil sodicity and soil acidity with adaptation to direct seeded aerobic rice cultivation. It can be used as a potential donor in breeding rice for multiple abiotic stress tolerance.

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4. CPE-109 (IC646825; INGR22103), a rice germplasm with complete panicle emergence in elite genetic background of Samba Mahsuri

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Panicle emergence is one of the yield attributing trait which is a limiting factor in BPT 5204 causing an average yield loss of 10-20% as the panicles covered with flag leaf fail to emerge completely. CPE-109 is an EMS derived mutant from Samba Mahsuri, with complete panicle emergence (2-3cm) compared to wild type (BPT5204) which exhibits panicle choking behaviour. This line was tested for three seasons in triplicates during June-2014 (*kharif*), January-2015 (*Rabi*) and june-2015 (*kharif*) at two different locations *viz*., IIRR, Rajendranagar, Hyderabad, and at ICRISAT Patancheru, Hyderabad. At both locations, CPE-109 showed superior agro morphological characters with higher productive tillers per plant (17.0), higher grain number (209) and was also having higher grain yield per plant (24g) compared to wild type (BPT 5204- 15.8g). In addition to CPE traitCPE-109 also exhibited brown spot resistance in NSN-2 trial carried out during *Kharif*, 2020.

Leaf folder, *Cnaphalacroccis medinalis is* an important foliage feeding insect in rice (*Oryza sativa* L.) (Poaceae), causes frequent outbreaks and considerable yield losses of about 63-80% in susceptible high yielding or hybrid rice varieties. A sub-set of 49 M2 EMS Samba Mahsuri mutants with high grain yield potential out of a large set of EMS mutants were characterized for resistance to rice leaf folder to understand basis of resistance. MSM-139 is an EMS derived mutant from Samba Mahsuri (Potupureddi *et al*., 2021). It showed high tolerance to the leaf folder with a minimal damage area of107.22mm2 and with a damage score of 3.7, whereas the wild type (BPT5204) had a damage area of 248.14 mm2 with a damage score of 7. Field experiments were carried out for 2 years during the wet seasons of 2015 and 2016 and during both the years, MSM-139 showed moderate resistance (3.7) compared to wild type (Javvaji *et al*., 2021). Green house experiments were carried out during the dry season of 2015, and the insect (leaf folder adult months) had shown lower ovipositional preference and lower larval settling preference accompanied by more time taken by the larva for leaf selection (3.1 min).

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5. MSM-139 (IC646826; INGR22104), a rice germplasm with tolerance to leaf folder in elite genetic background of Samba Mahsuri

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The rice (*Oryza sativa* L.) leaf folder, *Cnaphalocrocis medinalis Guenee* (Lepidoptera: Crambidae), is an important foliage feeding insect in rice and is widely distributed throughout Asia, causing frequent outbreaks and considerable yield losses.

To develop resistant sources of leaf folder in high yielding variety Samba Mahsuri (BPT- 5204) a mutant population was developed by exposing seeds of BPT-5204 to EMS treatment and a mutant population of 10,500 seeds were developed in collaboration with CSIR-CCMB. A sub-set of 49 M_2 mutants with high grain yield potential (Gopi *et al*., 2017; Suneel *et al*., 2020), were screened for leaf folder resistance during the wet seasons of 2015 and 2016. Mutant SM lines were phenotyped using the rapid field screening method developed at 6-8 tiller stage at 30-45 days after transplanting using ten-day-old larvae. In 2015 and 2016 wet season trials, the mutant MSM-139 exhibited minimal damage area with a mean damage score of 3.7. Green house experiments also displayed lower oviposition rate, lower settling preference of first instars, maximum time for leaf folding, fewer binds per primary fold, maximal leaf length and minimal leaf width. The insect showed minimal reproduction rate, lesser body weight and extended growth period on MSM-139 compared to susceptible check.

Reference

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6. IL-3 (IC646827; INGR22105), a rice germplasm with excellent resistance for leaf and neck blast and tolerance to sheath blight

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Rice (*Oryza sativa* L.) blast is a serious constraint in rice production. However, many resistant genes have been identified of which most of them are not truly broad-spectrum and durable. The wild species of *Oryza* (storehouse of the genes) have been rarely used for the identification of blast resistance genes except for the two genes *i.e.*, *Pi9* and *Pi40*. The maintenance of wild species and their rich genetic pool enables their utilization in resistance breeding programs. The introgression line, IL-3 developed by PAU using *O. nivara* (accession no. 105410) in the genetic background of PR114 (elite Indian variety) was screened under Donor Screening Nursery (DSN) of AICRIP 2013 in replication for multiple disease resistance. The results indicated that the IL-3 has promising resistance for both leaf and neck blast with mean susceptibility index (SI) of 3.6 and 1.4 in 2013. The blast scores were recorded according to standard IRRI SES scale. Also, the line has shown moderate resistance for sheath blight during AICRIP 2013 with SI 4.8.

The IL-3 has been genotyped for the presence of reported blast resistance genes using linked as well as gene-specific markers. A total of 10 blast genes were screened in the IL-3. The results indicate that the IL-3 do not possess any of the tested genes (Devi *et al*., 2015). Further genotyping was carried out using 1233 SSR markers (selected minimum 1 marker per 5Mb) which were spread uniformly across the twelve linkage groups to identify the donor genome introgression. It was found that IL-3 possesses 95.95% recurrent parent genome.

Reference

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7. NH787 (IC626285; INGR22106), a rice germplasm with higher root biomass and number of tillers and tolerance to low phosphorus soil with associated traits

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Nagina 22 (N22) is an early maturing drought and heat tolerant *aus* variety of rice (*Oryza sativa* L.). NH787 is an Ethyl Methane Sulphonate (EMS) induced mutant of N22. M1 seeds of N22 were provided to IIRR as part of the DBT Network Project. The mutant was identified in M3 generation as one of the high yielding mutants under low soil phosphorus (P) field condition at ICAR-Indian Institute of Rice Research, for two years 2010 & 2011. The plant vigour, root growth and panicle size were significantly better in NH787 as compared to N22 under low soil P conditions. Grain yield of NH787 was 2-5- fold higher than N22 under normal and low soil P conditions (Poli *et al*., 2021). The grains of NH787 are darker than N22. Apart from these traits, NH787 showed increased 1000 grain weight and improved grain quality traits (hulling, milling, percent head rice recovery, percent amylose content, alkali spread value, gelatinization temperature, and gel consistency). NH787 showed high grain length, width and area compared to N22 under normal and low P conditions (Poli *et al*. 2021). Histochemical staining showed very less accumulation of reactive oxygen species (ROS) in cut leaves of NH787 plants grown under low soil P, when compared to N22. The antioxidant enzymes assay in root and leaf at vegetative and reproductive stages showed higher SOD and CAT activity in root and leaf at vegetative stage and high CAT activity at reproductive stage in NH787 compared to N22 under low P condition (Poli *et al*., 2021). Apart from these enzyme activities, NH787 has high pN (photosynthesis rate), Fv/Fm (photosystem II activity), and higher pollen viability than N22 under low soil P and normal P conditions (Poli *et al*., 2021). *NH787* was also tested in multi-location field trials (low phosphorus trails) conducted by All India Coordinated Research Project on Rice (AICRPR) in 2018 at 5 locations. The low phosphorus trail included 29 entries along with three checks. IET 28059 (NH787) recorded grain yield of 3162 kg/ha with 82 days to 50% flowering. The mutant NH787 showed 14.31% higher grain yield than early check Rasi in five locations. Among the test entries of early group in Zone II NRRI-Cuttack, IETs 28059 recorded superior yield over early check Rasi by 51.15%, which is best among the 29 entries (AICRIP Vol 1 p1.3672018).

Reference

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8. Dular (IC646829; INGR22107), a rice germplasm highly tolerant to submergence with high anaerobic germination potential

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Dular is a highly drought and phosphorus starvation tolerant aus cultivar of rice (Oryza sativa L.) from West Bengal, India. It has been evaluated for multiple locations/seasons under different abiotic stress conditions: drought, osmotic stress, submergence, anaerobic germination and low phosphorus conditions at NRRI and AICRIP trials. Dular has appeared as a unique genotype possessing tolerance to all these stresses. Under drought conditions it registered low leaf drying (SES score = 2.33), low spikelet sterility (30.13%), high relative leaf water content (82.7%) and high grain yield. It also showed lower reduction in shoot and root dry weight, and chlorophyll content under osmotic stress (1% and 2% Mannitol). In a recent study, we detected qDTY$_{1.3}$ in Dular using DTY QTL linked SSR markers (Roy et al., 2021). Under 14 days of complete submergence at seedling stage, Dular registered a high survival rate (72%) and 78% elongation ability. Molecular marker based survey indicated the presence of Sub1A gene in Dular. It has high anaerobic germination potential and recorded 82% mean germination and higher epicotyl length under anaerobic trials. Dular possessed the Kasalath-type haplotype at the Pup1 locus and showed a high level of tolerance to phosphorus starvation by maintaining higher biomass (Roy et al., 2021). Agro-morphologically, it is early maturing, having intermediate plant height (113.9 cm), low tillering ability (7.8) and low grain yield (2.49 t/ha).

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9. AC43012 (IC645856; INGR22108), a rice germplasm with tolerance to vegetative stage drought stress and associated traits

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The genotype 'AC43012' (Chariesid) was found tolerant to drought and osmotic stresses at vegetative stage (Dash & Swain, 2015) with a drought score of '3' under field and control (AICRIP Annual Reports 2021). 'AC43012' (Chariesid) showed very low transpiration rate (0.046 kg water 2h^{-1}) and high water use efficiency (2.0 – 2.2 g biomass kg^{-1} of water) under field evaluation of drought stress (55% of the F.C.). AC43012 is highly tolerant to osmotic stress (1 and 2% mannitol stress amounting to 3.0 to -4.5 bars osmotic potential) with >90% germination percentage (Dash & Swain, 2015). This genotype can also maintain a good plant vigour in terms of both root and shoot length and plant biomass (Dash & Swain *et al.,* 2015). It was observed that AC43012 had high ROS scavenging potential under osmotic stress characterized by a high peroxidase activity (8.0 U g-1 FW) in this genotype (Dash & Swain *et al.,* 2015). 'AC43012' (Chariesid) was found to be medium yielding (4.5 t/ha) with an average maturity duration of 150 days. It has a short (~105 cm) plant type. It has a well exerted droopy panicle with medium bold grain type. In pan India multi-locational testing including 5 AICRIP locations *viz*., Karjat, Maruteru, Patambi, Titabar and Cuttack it was found that 'AC43012' (Chariesid) is tolerant to mannitol induced osmotic stress (1 and 2% mannitol) at early vegetative stage with minimum reduction in root and shoot length and shoot dry biomass as compared to tolerant checks Vandana and Dular (AICRIP Annual Reports 2021). This valuable rice (*Oryza sativa* L.) germplasm has vegetative drought tolerance and physiologically important traits like low transpiration rate and high water use efficiency (WUE). Besides, this genotype also showed high tolerance against mannitol induced osmotic stress at the germination (>90%) and early seedling stage with good plant vigour under stress conditions. This genotype is medium yielder (4.5 t/ha) with a short plant height and medium bold grain. This material could be used as a valuable donor for developing drought tolerant rice cultivars having specific traits like low transpiration rate and high WUE.

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10. AC43025 (IC645857; INGR22109), a rice germplasm with tolerance to vegetative stage drought stress and associated traits

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The genotype 'AC43025' (Dudha Charisda) was found tolerant to multiple abiotic stresses like drought and osmotic stress at vegetative stage (Dash & Swain, 2015), salinity (12 dS m^{-1}) and submergence (two weeks of complete submergence) at early vegetative stage along with moderate level (>50%) of anaerobic germination potential (AICRIP Annual Reports 2021). 'AC43025' (Dudha Charisda) has lower transpiration rate (0.052 kg water 2h^{-1}) under water stress conditions

(55% of the F.C.) and possess high water use efficiency (WUE) of 2.00 – 2.19 g kg^{-1} water (2015-16; Dash *et al.*, 2015). It was observed that AC43025 had high ROS scavenging potential under osmotic stress characterized by a high peroxidase activity (8.0 U g^{-1} FW) in this genotype (Dash & Swain, 2015). This genotype was also tolerant to vegetative stage submergence stress of about two weeks with mean survival rate of 76% across three AICRIP locations *viz.*, Titabar, Cuttack and Patambi as compared to the 79% mean survival of tolerant check Swarna-Sub1 (AICRIP Annual Reports 2021). Besides, this genotype possesses a moderate level of anaerobic germination potential (>50%) tested across three AICRIP locations *viz.*, Titabar, Cuttack and Masodha (Faizabad) (AICRIP Annual Reports 2021). 'AC43025' (Dudha Charisda) was found to be medium yielding (4.2 t/ha) under normal conditions and 2.3 t/ha under moderate drought stress conditions. The average maturity duration was found long (150 days). In pan India multi-locational testing including 7 AICRIP locations *viz.,* Coimbatore, Masodha (Faizabad), Maruteru, Karaikal, Patambi, Titabar and Cuttack it was found that 'AC43025' (Dudha Charisda) is tolerant to salinity stress (12 dS m^{-1}) at early vegetative stage with a SES score of '3' and shoot Na^+/K^+ ratio of 0.64 as against the Na^+/K^+ ratio of 0.48 of tolerant check FL478 (AICRIP Annual Reports 2021). This valuable rice (*Oryza sativa* L.) germplasm is found to have potential source for multiple abiotic stress tolerance. This genotype is tolerant to individual stresses like drought (with high WUE), salinity (12 dS m^{-1}) and submergence (two weeks of complete submergence) at vegetative stage. Besides, this genotype also possesses a moderate level of anaerobic germination potential (>50%). This genotype is medium yielder (4.2 t/ha) with a medium plant height and medium bold grain. This material could be used as a valuable donor for developing multiple abiotic stress rice having specific traits like high WUE.

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11. AC43037 (IC645858; INGR22110), a rice germplasm with tolerance to vegetative stage drought stress and associated traits

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The genotype 'AC43037' (Gurum) was found tolerant to multiple abiotic stresses *viz.,* drought and osmotic stress at vegetative stage and salinity (12 dS m^{-1}) stress at vegetative stage. This genotype is also moderately tolerant to submergence (two weeks of complete submergence) stress along with moderate level (~40%) of anaerobic germination potential (AICRIP Annual Reports 2021). 'AC43037' (Gurum) has lower transpiration rate (0.050 kg water $2h^{-1}$) under water stress conditions (55% of the F.C.) and possess high water use efficiency (WUE) of 2.00 – 2.19 g kg^{-1} water (ICAR-NRRI Annual Report, 2015-16). Along with drought tolerance (with a drought score of '3') 'AC43037' (Gurum) was found to possess low stomatal density (258.0/mm^2) in the leaf surface (ICAR-NRRI Annual Report, 2015-16). 'AC43037' (Gurum) was found to be medium yielding (4.8 t/ha) under normal conditions and 1.9 t/ha under drought stress conditions. The average maturity duration was found long (145 days). It has a short (~95 cm) plant type with non-lodging culm. It has an intermediate panicle type with medium bold grain type. In pan India multi-locational testing including 7 AICRIP locations *viz.*, Coimbatore, Masodha (Faizabad), Maruteru, Karaikal, Patambi, Titabar and Cuttack, it was found that 'AC43037' (Gurum) is tolerant to salinity stress (12 dS m^{-1}) at early vegetative stage with a SES score of '5' and shoot Na^+/K^+ ratio of 0.82 as against the Na^+/K^+ ratio of 0.48 of tolerant check FL478 (AICRIP Annual Reports 2021). This valuable rice (*Oryza sativa* L.) germplasm is found to have potential source for multiple abiotic stress tolerance. This genotype is tolerant to individual stresses like drought (with high WUE and low stomatal density) and salinity (12 dS m^{-1}) stress at vegetative stage. Besides, this genotype is also moderately tolerant to and submergence (two weeks of complete submergence) stress and possesses moderate level of anaerobic germination potential (~40%). This genotype is medium yielder (4.8 t/ha) with a short plant height, non-lodging culm and medium bold grain. This material could be used as a valuable donor for developing multiple abiotic stress rice having specific traits like high WUE and low stomatal density.

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12. Akhanphou (IC352909; INGR22111), a rice germplasm with resistance to leaf and neck and blast

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In North Eastern India, enormous genetic variability and high selection pressure in pathogen races contributes to the evolution of many novel gene(s) or QTL(s). Among several landraces, Akhanaphou is one of the popular landraces from Manipur has tolerance to biotic and abiotic stresses, adaptation and desirable taste. The germplasm was collected, conserved and maintained at ICAR RC NEH Manipur Centre, Lamphelpat, Imphal. In the extensive and rigorous phenotyping, (Imphal and Hyderabad). Akhanaphou proved resistant against leaf and neck blast. (Agalwe *et al.*, 2018). Akhanphou is one of the unique landraces that has been extensively exploited for development of varieties or breeding lines at ICAR RC NEH Manipur Centre, Imphal. It possesses two blast resistance gene, Pit 38 & Pitp and two novel QTLS qLNBL-5 and qLNBL-7. It is tolerant to low phosphorous and exhibited combined resistance to leaf blast (score 1 on SES scale) and neck blast (score 1 on SES scale). It was extensively used for development of advanced mapping population for exploring the novel gene(s) or QTLs conferring broad spectrum resistance. Recombinant inbred lines (RILs) were developed by crossing Akhanaphou X Leimaphou by single seed descent (SSD) method at ICAR RC NEH Manipur Centre. Two novel QTLs (Quantitative trait loci) i.e. qLNBL-5 and qLNBL-7 were mapped using two consecutive years of phenotyping from multi-location environments and genotyping using polymorphic markers (Agalwe *et al.*, 2017). Both of these QTLs confer broad spectrum resistance toward leaf as well as neck blast by contributing 26% and 25% phenotypic variance toward the resistance. QTLs discovery though immortal mapping population is more reliable and chances of false positive is minimum. Gene profiling was done with positive control of Tadukan and Tetep and revealed the presence of two major blast resistance gene(s) *Pit 38* & *Pitp*. Results of QTL mapping and gene profiling confirm the durable resistance nature of germplasm against leaf and neck blast. Akhanphou was also found tolerant to low phosphorus conditions when screened at ICAR-IIRR, Hyderabad. Therefore, the multi-stress tolerant nature of germplasm insists us for its conservation and successful utilization in breeding programme. Agronomically the plant is erect tall, well exerted panicle, medium bold grain and fitted well for Manipur valley. Keeping in view of the several economic important traits, the germplasm deserve registration with ICAR-NBPGR, New Delhi as genetic stock to enrich the blast resistance breeding programme in rice (*Oryza sativa* L.).

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13. Haosil Mah (IC647170; INGR22112), a rice germplasm with high resistance to leaf and neck blast

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Hosilmah is a unique landrace of hill region of Manipur. The germplasm was collected by a team of scientist from ICAR RC Manipur Centre, Imphal. Hosilmah is cultivated in Ukhrul district of Manipur and some parts of Nagaland. The genotype is very well adapted to jhum cultivation mainly due to weed competiveness and tolerant to low input agriculture. Hoslimah is characterized by tall plant stature, board leaves, high photosynthetic ability, bold grain and long duration maturity. Under high input agriculture the plant is prone to lodge and this indicates that germplasm is well suited for low input management conditions. The material was purified and maintained at ICAR Manipur Centre for its use in hybridization programme. Later, material was screened for reaction to blast under natural epiphytotic conditions. The germplasm exhibited high degree of blast resistance at vegetative as well as at reproductive stages. The genotypes showed high degree of leaf blast resistance and also exhibited tolerance to panicle blast. All form of blast is detrimental to plant health and therefore development of resistant varieties is only sustainable and viable option for managing the disease. Under natural epiphytotic conditions, chances of escape of pathogen are sometimes happens due to incompatible reaction of host, pathogen and environment. Therefore, screenings under controlled conditions are very much important for precise phenotyping of germplasm. For precise phenotyping, germplasm was screened under uniform blast nursery for consecutive two years at ICAR-IIRR, Rajendranagar Hyderabad. Results of UBN are in support of screening under natural epiphytotic conditions. Germplasm exhibited high degree of resistance as compared to resistant checks. Therefore, the valuable material may be explored for presence of major *R* gene or some novel gene through molecular breeding. Highly adaptive virulent strain of the pathogen often poses serious threats on existing deployed *R* genes and thus force us to explore the positive screening and identification of different blast *R* genes in the germplasm collection (Wang *et al*., 2010). Availability of DNA markers has facilitated the breeder for screening of major *R* gene using gene linked or specific markers. The material was later subjected to gene profiling using 12 major blast resistance genes (*Pitp, Pi33, Pi54, Pib, Pi20, Pi38, Pita2, Pi1, Piz, Pi9, Pizt*, and *Pi40*) through linked as well as gene specific markers. Surprisingly, the germplasm was tested positive for two major blast resistance gene, *Pi9, pi33* (Bangale *et al*., 2017). *Pi 9* and *Pi33* in combination exerts high degree of resistance reaction towards a variety of virulent strains imparting broad spectrum resistance. The germplasm may be used as a donor for transferring the R genes in different genetic background of rice (*Oryza sativa* L.) through classical or marker assisted selection.

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14. Phoutum Mah (IC647171; INGR22113), a rice germplasm with high resistance to leaf and neck blast

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Phoutum Mah is a unique rice (*Oryza sativa* L.) landrace from hilly region of Manipur. The germplasm was collected by a team of scientists from ICAR RC Manipur Centre, Imphal from Ukhrul district of Manipur. Phoutum Mah is cultivated in hilly region of Manipur and its neighboring state, Nagaland. The germplasm was evaluated for yield and yield attributing traits at Manipur Centre. In general, landrace is average or poor yielder compared to cultivars, but possess several specific attributes like, tolerant to several biotic and abiotic stresses, low input responsive, weed competitiveness, and well adaptation to specific environment. Identification of resistant landraces from diverse geographical region will help the breeder for better utilization as a donor for improvement of existing high yielding varieties. The explored germplasm was purified and maintained at ICAR Manipur Centre for its future use in rice breeding programme (Annual Reports, 2013, 2014 and 2015). This germplasm was screened for leaf and neck blast reaction under natural epiphytotic conditions at ICAR RC Manipur Centre and found to be high degree of resistance against natural virulent strains of blast pathogen. For confirmation of resistance nature, the germplasm was later rigorously screened for two seasons under uniform blast nursery at ICAR-IIRR, Rajendranagar, Hyderabad where it also exhibited high degree of resistance against the blast disease in both the seasons. Since, this landrace is quite unexplored and untapped, mining of useful major or minor novel genes imparting durable blast resistance would be useful. The germplasm line could serve as an important donor for introgression of blast resistance R gene through classical or innovative plant breeding tools.

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15. Wainem (IC647172; NGR22114), a rice germplasm with leaf and neck and blast resistance

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Wainem is a unique landrace adapted to specific environment of north eastern of India. This landrace was collected from Senapati district of Manipur through an exploration trip by scientists of ICAR RC Manipur Centre. After its collection, the germplasm line was purified and maintained at ICAR RC Manipur Centre, Lamphelpat, Imphal. Wainem is a typical characteristic of upland rice (*Oryza sativa* L.) and cultivated in some pockets of Senapati district of Manipur and parts of Nagaland. It is also grown in jhum farming due to weed tolerant nature, early seedling vigour, tolerant to various biotic and abiotic stresses. Wainem was consistently screened for two seasons at ICAR RC NEH Manpur Centre, Lamphelpet (Natural epiphytotic condition) for leaf and neck blast resistance. It was reported high degree of resistance against leaf as well as neck blast (Anonymous, 2015). Later, this germplasm was sent to ICAR-IIRR, Hyderabad for precise phenotyping under uniform blast nursery (UBN). The germplasm was constantly screened for two seasons under UBN and exhibited high degree of resistance against blast (Bangale *et al*., 2017). Gene profiling was carried out using linked/functional molecular markers corresponded to well-known 12 major blast resistance gene (*Pitp, Pi33, Pi54, Pib, Pi20, Pi38, Pita2, Pi1, Piz, Pi9, Pizt*, and *Pi40*) and surprisingly, the germplasm absence of these 12 major genes. Therefore, this unique landrace can be explored for the discovery of novel gene(s)/QTL(s) for broadening the gene pool to combat the blast pathogen competition.

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16. Mesa Tsuk (IC647174; INGR22115), a rice germplasm with leaf and neck and blast resistance

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Mesa Tusk (syn. Mesao Tsuk) is a rice (*Oryza sativa* L.) landrace distributed in some parts of Nagaland. The germplasm was collected from very remote place of Zunheboto district of Nagaland by a team of scientist of ICAR RC NEH Manipur Centre, Imphal. The germplasm is still cultivated in some parts of Nagaland under Jhum farming or shifting cultivation. Due to global warming and fluctuating climatic conditions, the emergence of new virulent races is imminent, thereby food security is under alarming situation which can potentially be managed through the identification of new durable resistance (*R*) genes and/or superior alleles from landraces and wild relatives. (Susan *et al*., 2018). Mesa Tusk has been characterized for tall stature, broad leaves, late maturity duration and bold seeded grain. The germplasm was later purified, maintained and evaluated at Manipur Centre for its use in breeding programme. The material was rigorously screened for two seasons at ICAR RC NEH Manipur Centre for testing its reaction toward leaf and neck blast disease. Mesa Tusk, identified to have high degree of resistance at vegetative as well as reproductive phases. Along with leaf blast, panicle blast also contributes for significant losses of grain yield. Therefore, identification of germplasm possessing high resistance toward leaf and neck blast is very much important to reduce the losses cause by blast disease. Later genetic material was rigorously screened under uniform blast nursery (UBN) at ICAR-IIRR, Rajendranagar, Hyderabad for consecutive two seasons to decipher the blast resistance nature of germplasm. The germplasm was reported to have degree of resistance and may be utilized in rice (*Oryza sativa* L.) breeding programme. Later, the material was subjected to gene profiling using well characterized 12 major blast *R* resistance genes (*Pitp, Pi33, Pi54, Pib, Pi20, Pi38, Pita2, Pi1, Piz, Pi9, Pizt*, and *Pi40*) and the germplasm was found positive for only *Pizt* gene (Bangale *et al*., 2017).

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17. IC128335 (INGR22116), a wheat germplasm with drought tolerance and higher antioxidant activity

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Drought stress is one of the major limiting factors of wheat (*Triticum aestivum* L.) productivity worldwide. In India, nearly 20% of the total cultivated wheat is grown under rainfed conditions. Both drought and heat stress are responsible for 20-30% reduction in grain yield. Therefore, identification and integration of drought tolerance into new varieties attracts researchers as it helps to develop climate resilient wheat. The wheat genotype IC128335 was identified to be highly tolerant to drought conditions based on extensive evaluation and salient features are mentioned below.

This genotype was also evaluated for two years under irrigated timely, rainfed timely and irrigated late field conditions at ICAR-IIWBR Karnal and have shown low drought sensitivity index (-1.7 and -2.81) and less reduction (%) in thousand grain weight (-49.9 and 14.4). Again this genotype was evaluated at Akola, and Powarkheda under field conditions and at Karnal under controlled conditions (rainout shelter) for two years (2015-16 and 2016-17) and found to be highly tolerant to drought stress (DSI = 0.45). IC128335 is characterized with higher antioxidant activity (1.8fold), total phenolic content (1.6 fold), proline content (2.4 fold) and higher SOD activity and higher upregulation of transcription factors (qTaWRKY2 – 3.49 fold and qTaNAC2a –2.31 fold). This genotype is found to be highly tolerant to drought conditions showing potentialto be used as a donor for enhancing drought tolerance in wheat.

18. DBW325 (IC646830; INGR22117), a wheat germplasm highly resistant to wheat blast, leaf rust and Karnal bunt

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Wheat (*Triticum aestivum* L.) blast (WB) caused by *Magnaporthe oryzae* pathotype *Triticum* (MoT), is one of the most devastating and yield limiting disease in warm and humid wheat production regions. The disease was first identified in Brazil in 1985 and later on spread to wheat growing areas in Bolivia, Paraguay, and Argentina. Recently, WB has been introduced to Bangladesh threatening wheat production in South Asia with the possible further spreading in the Asian continent. Besides this wheat crop is also constrained by rust pathogens. Therefore, breeding wheat for tolerance to biotic and abiotic stresses has been the main breeding objective in any breeding programme. Genotype DBW325 was developed (CHIBIA//PARULA II/CM65531/3/SUPER KAUZ/BAVIACORAM92/4/MUNAL#1) following modified bulk pedigree method. This genotype was evaluated for yield in NIVT-5B and AVT-RI-TS-PZ under restricted irrigated conditions in AICRP on wheat and Barley during 2019-20 and 2020-21. Genotype DBW325 was included in Indian material sent for screening against wheat blast disease and found to be highly resistant (Score «0») against wheat blast when evaluated in three environments Jashore, Bangladesh (two years) and Quirassalis, Bolivia (one year) at two different dates of sowing during 2019-20 and 2020-21 (ICAR-IIWBR, 2020 and 2021).

In addition to this, evaluation for different diseases was also undertaken under Plant Pathological screening nursery (PPSN) and found to be highly resistant to leaf rust (North ACI- 1.6; South ACI- 1.5) when evaluated at fourteen locations *viz*., Delhi, Hisar, Kanpur, Ludhiana, Pantnagar, Faizabad, Wellington, Mahabaleshwar, Niphad, Vijapur, Pune, Junagadh, Powarkheda and Indore. This genotype was also found to be Karnal bunt resistant (average incidence upto 5%) when evaluated at five locations *viz*., Ludhiana, New Delhi, Hisar, Karnal and Jammu during 2020-21. DBW325 is of short stature having an average plant height of 67cm and matures in about 106 days in peninsular zone evaluation. Grains are of semi hard texture, amber colour with a thousand grain weight of 40g. The multiple resistance of DBW325 to wheat blast, leaf rust, and Karnal bunt makes DBW325, a potential donor to be utilized for breeding multiple disease resistance in wheat.

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19. RLBW02 (IC640204; INGR22118), a wheat germplasm with resistance to stripe and leaf rust and tolerance to stem rust

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Wheat (*Triticum aestivum* L.) rusts are devastating diseases, can cause significant yield loss and poor grain quality. The genotype IC640204 (RLBW02) was evaluated in Initial Plant Pathological Screening Nursery (2021-22) for rust diseases following standard AICRP methods (Anonymous 2022). The IPPSN was conducted at 08 centres (Malan, Dhaulakuan, Jammu, Gurdaspur, Ludhiana, Karnal, Hisar and Durgapura) for stripe rust, 08 centres (Ludhiana, Karnal, Delhi, Durgapura, Ayodhya, Kanpur, Sabour and Coochbehar) for leaf rust (north) and 08 centres each namely, Vijapur, Indore, Powarkheda, Niphad, Pune, Mahabaleshwar, Dharwad and Wellington for leaf rust (south) and stem rust. The genotype IC640204 (RLBW02) showed resistance for stripe rust (ACI=3.9), leaf rusts-north (ACI=0), leaf rust-south (ACI=2.0) under field conditions (Table 1). The genotype IC640204 also confirmed seedling resistance against all the races of stripe rust and stem rust in SRT analysis at IIWBR, RS, Flowerdale, Shimla (Table 1). The molecular marker analysis indicated the presence of stripe rust gene YrSP (2BL) in the genotype IC640204, which is closely linked with the gene(s) *Yr5, Yr7, Yr43, Yr44* and *Yr53* (Anonymous, 2021).

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Table 1: Rust reactions in IPPSN (2021-22) and SRT data of IC640204

Genotype	*Leaf rust (north)*		*Leaf rust (south)*		*Stripe rust*		*Stem rust*	
	ACI	*HS*	*ACI*	*HS*	*ACI*	*HS*	*ACI*	*HS*
IC640204 (RLBW02)	0	0	2.0	20MR	3.9	10S	4.4	20S
Infector	80.0	100S	76.0	80S	77.1	80S	81.4	100S
SRT for stripe rust								
Races	110S84	46S119	7S0	T	78S84	110S119	P	238S119
Reaction	;	0;	0;	;	;	;	0;	0;
SRT for stem rust								
Races	11A	40-1	11	117-6	40A	15-1	40-3	40-2
Reaction	;1	;	;1	0;	;1	0;	0;	;-

20. DBW342 (IC646831; INGR22119), a wheat (*Triticum aestivum*) germplasm with resistance to wheat blast, stem rust and leaf rust

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Wheat blast is an emerging threat for wheat (*Triticum aestivum* L.) production and wheat rusts are major devastatingbiotic stresses. DBW342 is an important genetic resource for wheat blast resistance coupled with stem and leaf rust resistance (Anonymous 2021, Anonymous 2022). The genotype DBW342 was evaluated against wheat blast at Bangladesh during 2020-21 and 2021-22 under two environments each year (timely and late sown) and showed complete resistance for wheat blast (Table 1). DBW342 was also evaluated in Plant pathological Nursery (PPSN) during *rabi*, 2020-21 at 09 centres namely, Delhi, Hisar, Jammu, Kanpur, Karnal, Ludhiana, Pantnagar, Durgapura and Faizabad for leaf rust (north) and 09 centres (Wellington, Mahabaleshwar, Niphad, Vijapur, Pune, Junagarh, Powarkheda, Dharwad and Indore) each for leaf rust (south) and stem rust. DBW342 showed resistance against stem rust (ACI=1.5), leaf rust- north (ACI=0) and leaf rust- south (ACI=2.9) in PPSN during *rabi*, 2020-21 (Table 1).

Table 1: Average and highest multi-location rust reactions

Genotype	Wheat blast		Stem rust		Leaf rust (north)		Leaf rust (south)	
	Av	HS	ACI	HS	ACI	HS	ACI	HS
DBW342	0	0	1.5	10MS	0	0	2.9	20MS
Infector	86.0	100	82.5	100S	77.1	100S	82.9	100S

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Anonymous (2021) Progress Report of AICRP on Wheat and Barley, Crop Protection. In: S Kumar, J Kumar, P Jasrotia, PL Kashyap, R Kumar and GP Singh (Eds). ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India. 251 p.

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21. CPIIWBR-121 (IC646832; INGR22120), a wheat germplasm immune or complete field (adult plant) resistance against yellow rust disease

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Yellow rust of wheat (*Triticum aestivum* L.) is considered as one of the devastating fungal diseases of wheat posing considerable yield losses in North western plain zones of India. Host resistance is the most economical way to manage yellow rust. Unfortunately, the resistance genes have become ineffective due to the acquisition of virulence to that particular resistance gene rendering the variety susceptible. Therefore, new and effective resistance sources against yellow rust, either within or outside cultivated wheat are much sought. The diversity of resistance i.e. the genetic base must be broadened involving novel resistance sources for this disease. In this connection, the genotype 14th HRWYT-219 (tested as CPIIWBR-121) having pedigree as PASTOR// TRAP#1/BOW/3/CHEN/AEGILOPS SQUARROSA (TAUS)// BCN (14thHRWYT-219) was screened against yellow rust disease in a coordinated EPPSN nursery constituted under AICRP on Wheat and Barley for screening of promising wheat genotypes against yellow rust of wheat at nine yellow rust hot spot locations (Ludhiana, Durgapura, Jammu, Karnal, Pantnagar, Almora, Dhaulakuan, Hisar and Malan) under artificially created yellow rust epiphytotic conditions during 2021-22 crop season with an aim to identify the genetic resources for resistance to yellow rust for broadening genetic base of wheat crop. During the field disease data recording at all the locations, consistent and uniform immune reaction (ACI for Yellow rust = 0; HS for yellow rust = 0) was noticed for 14th HRWYT-219 (tested as CPIIWBR-121) (Anonymous, 2022). Overall, the germplasm 14th HRWYT-219 (tested as CPIIWBR-121) is identified as resistant germplasm to yellow rust, as displaying immune reaction and can be a novel genetic resource and has the potential to deploy as a donor for incorporation of resistance to yellow rust and broaden the genetic base.

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22. IC416188 (INGR22121), a wheat germplasm with terminal heat tolerance

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A comprehensive study was conducted to identify heat tolerant wheat lines from an association mapping panel of 205 wheat (*Triticum aestivum* L.) accessions, evaluated under late sown conditions in India at three different locations (Delhi, Hisar and Karnal) for 3 consecutive years (2015-2018). Planting was done in three replications on each location. In the field screening, data was recorded for 16 agronomic 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 was 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 favorable alleles for each QTL region were identified by comparing the extreme phenotypic values in association mapping panel. Based on Principal Component Analysis, the first PC was positively correlated with DM, GFD, PHT, PTL, GNM, GW, TGW, and HI. Wheat genotypes were classified into three groups based on biplots of PC1 vs. PC2. IC416488 was considered tolerant genotypes showing high scores for PC1 and PC2 and as classified into group 1 (tolerant type) along with other germplasm. It also had four favorable alleles and were stable at all three locations. This is a potential genetic resource for heat tolerance, which can be further used in wheat improvement programme.

23. IC533742 (INGR22122), a wheat germplasm with high level of salt tolerance

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Salinity stress is a major abiotic stress limiting wheat production in various wheat (*Triticum aestivum* L.) growing regions of the world. Diverse germplasm lines were evaluated for vegetative and adult-stage salt tolerance. The vegetative stage salt tolerance evaluation experiments (experiment 1, 60 accessions; experiment 2: 135 accessions; experiment 3: 44 accessions) were carried out in sand pot culture under glass house conditions at ICAR-NBPGR, New Delhi (Chaurasia *et al*., 2022). The experiments were laid following completely randomized *design* (CRD) with three replications each for two treatments; control (Hoagland solution) and salt stress (Hoagland solution + 100 to 150 mM NaCl or EC ~ 15 dS/m^{-1}). For salt stress treatment, 15 days old seedlings were irrigated with 100 to 150 mM NaCl Hoagland solution at regular intervals. For the adult stage salt tolerance evaluation, wheat genotypes were evaluated in Augmented Randomized Complete Block Design at ICAR-Central Soil Salinity Research Institute Karnal, Haryana, India with two environments, *viz.*, control (ECiw ~ 1.0 dS/m) and saline stress (ECiw ~ 15 dS/ m).

The accession "IC533742" performance was almost at par with the salt-tolerant checks and was far superior over sensitive check in all three glasshouse experiments as well as the field conditions salinity stress. Thus this line can be utilized as a donor for development of high yielding salt tolerant varieties

References

Chaurasia S, A Kumar and AK Singh (2022) Comprehensive Evaluation of Morpho-Physiological and Ionic Traits in Wheat (*Triticum aestivum* L.) Genotypes under Salinity Stress. *Agriculture* 12(11): 1765. https://doi.org/10.3390/agriculture12111765

24. EC178071-428 (EC178071; INGR22123), a wheat germplasm with high salt tolerance

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Diverse germplasm lines were evaluated for vegetative and adult-stage salt tolerance. The vegetative stage salt tolerance evaluation experiments (experiment 1, 60 accessions; experiment 2: 135 accessions; experiment 3: 44 accessions) were carried out in sand pot culture under glass house conditions at ICAR-NBPGR, New Delhi (Chaurasia *et al*., 2022). The experiments were laid following completely randomized *design* (CRD) with three replications each for two treatments; control (Hoagland solution) and salt stress (Hoagland solution + 100 to 150 mM NaCl or EC ~ 15 dS/m^{-1}). Initially, both control and salt-stressed plants were grown without salt stress. For salt stress treatment, 15 days old seedlings were irrigated with 100 to 150 mM NaCl Hoagland solution at regular intervals. Morpho-physiological parameters including shoot dry weight (SDW), membrane stability index (MSI) and chlorophyll [measured using chlorophyll meter SPAD-502plus, Konica-*Minolta*, Osaka, Japan] were recorded after 15 days of salt treatment. Since salt stress drastically reduce shoot biomass, the ability to tolerate salinity stress was defined only the on basis of salt tolerance index (STI). STI= shoot dry weight under NaCl / shoot dry weight under control condition X 100. The genotypes were classified based on the STI value for shoot dry weight as tolerant (STI>70) and susceptible (STI <35).

For the adult stage salt tolerance evaluation (Accessions: 153), wheat (*Triticum aestivum* L.) genotypes were evaluated inAugmented Randomized Complete Block Design at ICAR-Central Soil Salinity Research Institute Karnal,Haryana, India with two environments, *viz*., control (ECiw ~ 1.0 dS/m) and saline stress (ECiw ~ 15 dS/ m). The experiment was set up in row-column order (20R X 9C) in four blocks andfive checks (KRL 210, KH 65, K1006, HD2009 and HD2851) randomized within 45 entries per block.

The accession “EC178071-428” performance was almost at par with the salt-tolerant checks and was far superior over sensitive check in all three glasshouse experiments as well as the field conditions salinity stress. Thus, this line can be expedited for development of the development of high yielding salttolerant varieties

References

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25. DWRB189 (IC632077; INGR22124), a barley germplasm with high anti-oxidant activity and black colour grains

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Barley (*Hordeum vulgare* L.) is one of the important coarse cereals used for food, feed and malting purposes. The grain colour of barley is an important trait and the coloured grains are rich in phenolic acids and anthocyanin. These flavonoid compounds have important free radical scavenging capacity, thereby making coloured barley a popular healthy food. The yellow colour of the barley is due to the accumulation of proanthocyanidins in the testa layer, while the black colour has been attributed to the accumulation of phytomelanins in the lemma and pericarp. Besides dietary benefits, anthocyanin accumulation in grains has been suggested to play a role in tolerance to diverse environmental stresses.

DWRB189 (BCU2336) is a hulled six-row barley genotype, which has unique black grain colour grains with high anti-oxidant activity. DWRB189 showed the highest anti-oxidant activity of 72.3 % discolouration by DPPH method followed by the registered genetic stock Kasota (37.9 % discolouration), check BH946 (32.2 % discolouration) and BH902 (29.9 % discolouration) (Anonymous 2019, Anonymous 2022, Table 1). The genotype DWRB189 is unique

Table 1: Anti-oxidant activity profile of DWRB189 (2021-22) by DPPH method (% discoloration)

Genotype	Karnal*	Karnal	Ludhiana	Hisar	Mean	% Advantage
DWRB189 (IC0632077)	68.92	83.4	47.3	89.7	72.3	-
BK1127 (BCU8173) (c)	31.76	20.6	22.2	17.8	23.1	213.0
Kasota (BCU8176) (c)	57.83	25.5	30.3	NA	37.9	90.8
BH902 (c)	39.21	26.3	27.8	26.4	29.9	141.8
BH946 (c)	45.60	30.6	27.9	24.7	32.2	124.5
DWRB91 (c)	35.24	18.3	26.4	21.5	25.4	184.6
DWRB92 (c)	31.45	19.3	20.7	17.3	22.2	225.7
DWRB137 (c)	46.34	23.5	23.0	20.2	28.3	155.5

*2018-19 data

for black grain colour and high anti-oxidant activity required for free radical scavenging capacity and boosting immunity.

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26. DWRBG-11 (BK 306) (IC646833; INGR22125), a barley germplasm with higher wort free amino nitrogen content and higher malt diastatic power

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Malt is one of the major industrial products of barley (*Hordeum vulgare* L.) and in India approximately 30% of the total production is utilized for this purpose. The nitrogenous compounds available for consumption by yeast during brewing fermentation are known as free amino nitrogen (FAN) and sources of malt barley having better FAN production capability during malting and mashing are required.

The diastatic power of barley malt is the collective activity of starch degrading enzymes, which accumulates or gets activated during malting. Higher diastatic power becomes more important, when adjuncts (*e.g.* wheat grains, rice flakes etc) are used for brewing and barley malt is used as source of starch degrading enzymes. The genotype DWRBG-11 (Tested as BK 306) was found to have these both traits of higher FAN content and higher diastatic power activity in the multi-location testing during the rabi season of 2020-21 (Tables 1 and 2).

Table 1: Free Amino Nitrogen (FAN content, in ppm) in the wort of genotype BK 306 grown at different locations

Genotype	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	*Average*
BK 306	201	197	206	230	244	217	216
DWRUB 52 (c)	192	168	257	174	198	202	199
DWRB 91 (c)	183	151	215	173	199	148	178
DWRB 92 (c)	186	173	235	187	244	143	195
DWRB 101 (c)	200	159	212	188	225	191	196
RD2849 (c)	195	163	186	180	185	124	172
DWRB 123 (c)	166	119	202	176	172	140	162
DWRB-160 (c)	160	134	163	150	189	125	154
DWRB-182 (c)	171	151	218	156	219	140	176
Average	184	157	210	179	208	159	
LSD (5%)							21

Table 2: Diastatic power (°L) in the malt of genotype BK 306 grown at different locations

Genotype	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	*Average*
BK 306	116	102	106	108	106	106	107
DWRUB 52 (c)	94	100	106	99	83	94	96
DWRB 91 (c)	104	109	109	109	98	102	105
DWRB 92 (c)	98	106	102	106	109	104	104
DWRB 101 (c)	104	104	96	83	100	96	97
RD2849 (c)	100	100	94	98	98	79	95
DWRB 123 (c)	111	94	94	96	109	104	101
DWRB-160 (c)	111	96	104	99	109	96	103
DWRB-182 (c)	109	109	109	90	98	98	102
Average	105	102	102	99	101	98	
LSD (5%)							8

27. DWRBG9 (IC118689; INGR22126), a hulled land race of barley with resistance to Corn Leaf Aphid

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Corn leaf aphid (CLA), *Rhopalosiphum maides* (Fitch) is considered as one of the most devastating insect-pest of barley (*Hordeum vulgare* L.) in India, however, genetic resources with resistance to this insect are limited. Preliminary screening of a set of 408-Barley landraces received from ICAR-NBPGR, New Delhi against corn leaf aphid was carried out at ICAR-IIWBR, Karnal under artificial conditions of insect infestation in a net-house during 2020-21 crop season to find out aphid resistant genotypes against this insect. The genetic stock DWRBG9 registered for resistance to CLA is a six-row landrace (IC118689) collected from Pitampur tehsil of Tezpur district of Assam state. It was found to be promising for aphid resistance in the preliminary screening. To confirm its response to CLA, the line HLR-20 was further screened against the insect at hot spot locations (Karnal, Kanpur, Khudwani and Durgapura) during 2021-22 crop season in a coordinated entomology nursery constituted under AICRP on Wheat and Barley. At all the four hot spot locations the aphid score was recorded as 5 in the susceptible check Alfa 63 on 1-5 scale (where 1 is immune/ highly tolerant, while 5 is highly susceptible) (Table 1). This suggested that environmental conditions and insect population was sufficient for meaningful screening of genotypes in the nursery for their response to infestation of aphid. In case of DWRBG9, the aphid score recorded was 2 at all the four testing locations (Table 1), hence, DWRBG9 is characterised as resistant to corn leaf aphid (ICAR-IIWBR, 2022).

The new and effective resistance sources against CLA, either within or outside cultivated barley are much sought after. The diversity of resistance *i.e.* the genetic base must be broadened involving novel resistance sources for this insect. Identification of genetic resources for resistance to CLA in landraces is considered very important for broadening genetic base of barley crop. The germplasm, DWRBG9 (HLR-20) is a landrace found to be resistant to CLA, is a novel genetic resource and can be used as a donor for incorporation of resistance to corn leaf aphid.

Reference

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Table 1: Resistant reaction of DWRBG9 (HLR-20) against infestation of corn leaf aphid at multi-location during *rabi* 2021-22 season

Genotype	*Parentage/ identity No.*	*Corn leaf aphid score ((1-5 scale)*				*Average Score*	*Maximum Score*
		Karnal	*Kanpur*	*Khudwani*	*Durgapura*		
DWRBG9 (HLR-20)	IC118689	2	2	2	2	2	2
Alfa-93	AURORA /QUEEN //BEKA	5	5	5	5	5	5

28. DWRBG 12 (IC646835; INGR22127), a six rowed barley germplasm with low grain protein content (9.2%) and high malt diastatic power(105°L)

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Malt is one of the major industrial products of barley (*Hordeum vulgare* L.) and in India approximately 30% of the total production is utilized for this purpose. The major proportion of malt goes to brewing and distillation industry. Different sectors of the alcohol industry have different malt quality requirements, resulting in different barley varieties being bred for each, whether that be for malt distilling or brewing. For malt spirit distillers, the optimal grain protein concentration is considered to be 9.4% and (protein concentration is inversely related to grain starch concentration) represents the best balance for high starch concentration and potential alcohol yield. Therefore, these attributes are seen as critical determinants of alcohol yield following fermentation of the malted barley wort. Along with low protein content, higher diastatic power (starch degrading activity) is required for maximum solubilisation of starch. However, getting this combination is difficult to get, since the grain protein content is usually positively correlated with malt diastatic power. A barley genotype DWRBG-12 (BCU 6315) has been identified with low grain protein content (average value 9.2% dwb) with reasonably good malt diastatic power (average value 105°L) in the multi-location testing during the rabi season of 2020-21 (Tables 1 & 2). The genotype can be a potential source for these traits for malt barley improvement programme (for distillation use) of the country.

Table 1: Protein content (% dwb) in BCU 6315 at different locations during 2021-22#

Genotype	Durgapura	Hisar	Karnal	Ludhiana	Pantnagar	Kanpur	Mean
BCU 6315	8.8	7.7	10.9	12.2	7.8	8.0	9.2
DWRUB 64 (c)	10.2	8.9	11.5	10.0	9.3	9.0	9.8
DWRUB 52 (c)	11.4	12.0	12.1	9.2	9.8	11.9	11.1
DWRB 101 (c)	11.8	11.9	14.1	9.0	9.9	12.8	11.6

#Predicted values through Near Infrared Reflectance Instrument

Table 2: Malt Diastatic power (°L) in BCU 6315 at different locations during 2021-22

Genotype	Durgapura	Hisar	Karnal	Ludhiana	Pantnagar	Kanpur	Mean
BCU 6315	104	111	111	106	100	100	105
DWRUB 64 (c)	66	89	102	109	98	106	95
DWRUB 52 (c)	40	55	72	79	59	96	67
DWRB 101 (c)	47	59	65	62	68	100	67

29. DWRBG10 (IC356122; INGR22128), a hulless six-rowed landrace of barley with high ß-glucan and starch content

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Barley (*Hordeum vulgare* L.) has been historically an important food source in many parts of the world. However, better product quality and mouth-feel of food products prepared from wheat and rice compared to barley resulted in limited improvement in food processing and product development in this crop. Majority of the barley grown is hulled type which is another important factor that limited the scope of barley for its popularisation as a food crop as it required pearling of barley grains.

The registered genetic stock is a landrace (IC356122). Out of 408 landraces of barley received from ICAR-NBPGR, New Delhi, a set of 78 landraces which were hulless, were screened at ICAR-IIWBR, Karnal during 2020-21 crop season for physical grain quality parameters. Twelve of them were shortlisted and were evaluated at six locations (Karnal, Hisar, Ludhiana, Durgapura, Pantnagar and Kanpur) during *rabi* 2021-22 under 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 multilocation samples was done at quality lab of ICAR-Indian Institute of Wheat and Barley Research, Karnal, for nutritional-quality traits of grains. The genetic stock DWRBG10 was found to be rich in β-glucan (6.4 %) and starch (65.4 %) as compared to 5.9 % β-glucan and 63.5 % starch recorded in the checks PL 891 and Karan 16, respectively on dry weight basis (Table 1). DWRBG10 is a six-row hulless landrace of barley (IC356122) collected from Munsiyari tehsil of Pithoragarh district in Uttrakhand.

Relatively limited efforts to systematically breed and develop hulless varieties for food uses have been devoted to barley. With the increasing awareness about nutraceuticals, the acceptance of barley as health food is slowly and steadily increasing. For higher flour recovery, the higher starch content is essential. The landrace DWRBG10 with higher β-glucan coupled with higher starch contents, making it as valuable combination of traits for food barley improvement programme of the country.

Reference

ICAR-IIWBR (2022) Progress Report of AICRP on Wheat & Barley 2021-22, Barley Improvement. In: RPS Verma, OV Singh, AS Kharub, D Kumar, C Lal, J Singh, R Malik, L Kumar, SK Bishnoi, S Kumar, SC Bhardwaj, P Jasrotia, OP Gangwar, A Verma, A K Sharma, C Singh, S Singh and GP Singh (Eds). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. pp 5.53–5.54 (http:// www.aicrpwheatbarleyicar.in/reports/)

Table 1: Grain beta glucan content (% db) and starch content (%db) in DWRBG10 (HLR-90) at different locations during 2021-22

Genotype	Quality parameter	Row Type	Karnal	Hisar	Ludhiana	*Durgapura*	*Pantnagar*	*Kanpur*	*Mean*
HLR-90	β-glucan	6	6.8	6.4	6.8	6.1	7.0	5.6	6.4
	Starch		61.2	65.2	65.2	67.6	66.2	67.0	65.4
Karan-16 (C)	β-glucan	6	5.2	5.2	6.3	5.5	NA	4.5	5.3
	Starch		59.3	61.4	63.6	68.8	NA*	64.5	63.5
NDB-943 (C)	β-glucan	6	5.6	5.1	5.9	5.8	5.6	4.5	5.4
	Starch		59.7	59.7	65.5	68.3	60.5	64.2	63.0
PL891 (C)	β-glucan	2	5.8	5.2	6.3	6.2	6.5	5.1	5.9
	Starch		61.0	60.0	64.6	66.8	62.9	64.5	63.3

**Not available*

30. BHS 485 (IC646836; INGR22129), a hulless barley germplasm resistant to yellow rust and leaf rusts at the adult plant stage along with high protein and starch content

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BHS 485 (BBM 839) is a naked barley (*Hordeum vulgare* L.) line resistant against leaf and stripe rust. BHS 485 (BBM 839) has shown adult plant resistance to stripe (ACI= 0.1) and leaf rust (highest susceptibility score=TMS) (Table 1). The line has also been reported as a promising source of malt barley in context to protein content 10.3% (dry weight) and starch content of 64.3% (dry weight). This line is developed following pedigree method of breeding involving crosses between released barley variety 'HBL 276' and barley genetic stock 'BHS 369' at ICAR-IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Center, Shimla (H.P.).

BHS 485 (BBM 839) has semi-erect growth habit with medium maturity (170 days) under Northern Hill condition. The average yield is 2.35 t/ha under rainfed condition of Northern Hill Zone of All India Coordinated trials 2020-21. The distinguishing features BHS 485 (BBM 839) are six-rowed; naked; semi-erect growth habit; erect flag leaf attitude; green leaves and thousand grain weight of 38 grams.

Table 1: Reaction to major diseases

Diseases	Condition	Year	Response of Proposed Genetic stock BHS 485 (BBM 839)	Page No.
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2020-21	HS= TMS	3.14 of Reference (i)
Stripe rust (Yellow rust)	NBDSN (APR)	2020-21	Resistant with ACI=0.1 (HS=TMR)	3.14 of Reference (i)
	IBDSN	2019-20	Yellow rust ACI 0.1 (Highest Score TMR)	3.5 of reference (ii)

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

31. BHS 486 (IC646839; INGR22130), a barley germplasm with adult plant resistance to yellow rust as well as resistance to most pathotypes of leaf rust at seedling stage

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BHS 486 (BBM 845) 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 (except *H4* race). The proposed genetic stock also possesses seedling resistance against all the pathotypes of stripe rust (except for *M* and *Q* race showing moderate susceptibility. BHS 486 (BBM 845) also showed adult plant resistance to yellow rust (ACI=5.1) and leaf rust (HS= 5MS). This line is developed following pedigree method of breeding involving crosses between barley variety HBL 276 with BHS 365 at ICAR-IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Center, Shimla (H.P.) (Table 1)

BHS 486 (BBM 845) has a semi-spreading growth habit with medium maturity (169 days) under Northern Hill condition. The average yield is 2.89 t/ha under rainfed condition of Northern Hill Zone of All India Coordinated trials 2020-21. The distinguishing features of BHS 486 (BBM 845) are six-rowed; hulled; semi-spreading growth habit; erect flag leaf attitude; green leaves and thousand grain weight of 42 grams.

Table 1: Reaction to major diseases

Diseases	Condition	Year	Response of Proposed Genetic stock BHS 486 (BBM 845)	Page No.
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2020-21	HS= 5MS	3.14 of Reference (i)
	NBDSN (Seedling)	2020-21	R (Resistant to all races except *H4*)	3.23 of Reference (i)
Stripe rust (Resistant to Yellow rust)	NBDSN (APR)	2020-21	ACI=5.1	3.14 of Reference (i)
	NBDSN (Seedling)	2020-21	R to all races (except for *M* and *Q* showing MS response)	3.23 of Reference (i)
	IBDSN	2019-20	Yellow rust ACI= 7.7	3.5 of reference (ii)

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

32. BHS 483 (IC646840; INGR22131), a hulless barley germplasm with Resistance to yellow and leaf rusts at the adult plant stage

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BHS 483 (BBM 833) is a naked barley (*Hordeum vulgare* L.) line resistant against leaf and stripe rust. BHS 483 (BBM 833) has shown adult plant resistance to stripe (ACI= 4.7) and leaf rust (Highest susceptibility score=0). It has shown seedling resistance to moderately resistance response against all the prevailing pathotypes of stripe rust (except for race *24* and *Q* showing MS reaction). The line has also been reported as a promising source of malt barley in context to protein content (10% dry weight). This line is developed following pedigree method of breeding involving crosses between released naked barley variety 'BHS 352' and barley breeding line 'BHS 366' at ICAR-IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Center, Shimla (H.P.).

BHS 483 (BBM 833) has semi-erect growth habit with medium maturity (170 days) under Northern Hill condition. The average yield is 2.52 t/ha under rainfed condition of Northern Hill Zone of All India Coordinated trials 2020 and 2021 (Table 1). The distinguishing features of BHS 483 (BBM 833) are six-rowed; naked; semi-erect growth habit; erect flag leaf attitude; green leaves and thousand grain weight of 40 grams.

References

ICAR-IIWBR (2021) Progress Report of AICRP on Wheat & Barley 2020-2021, Barley Improvement. In: RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Jogendra Singh, Rekha Malik, Lokendra Kumar, SK Bishnoi, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Ajay Verma, Amit Kumar Sharma, Charan Singh, Satyavir Singh and GP Singh (Eds). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. p 244.

ICAR-IIWBR (2020) Progress Report of AICRP on Wheat & Barley 2019-2020, Barley Improvement. In: RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh (Eds). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. p 230.

Table 1: Reaction to major diseases

Diseases	Condition	Year	Response of Proposed Genetic stock BHS 483 (BBM 833)	Page No.
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2020-21	HS= 0	3.14 of Reference (i)
Stripe rust (Yellow rust)	NBDSN (APR)	2020-21	ACI=4.7	3.14 of Reference (i)
	NBDSN (Seedling)	2020-21	Resistant to moderately resistant response to all races (Except for race *24* and *Q* showing moderately susceptible response)	3.23 of Reference (i)
	IBDSN	2019-20	Yellow rust ACI= 0.7 (Highest Score 10MR)	3.5 of reference (ii)

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

33. IC138120 (INGR22132), a two-rowed barley germplasm with high test weight coupled with early maturity

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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 any crop. In this context, 6778 accessions of barley (*Hordeum vulgare* L.) germplasm from National Genebank (NGB), ICAR-NBPGR, New Delhi

Table 1: Year-wise data of test weight and days to attain physiological maturity (DPM) in barley accession IC138120

Year	*Test weight (100-grain weight; g)*		*Days to physiological maturity*	
	IC138120	*DWRB101 (Check var.)*	*IC138120*	*DWRB101 (Check var.)*
2016-17	6.723	5.13	108	127
2017-18	6.62	4.93	110	129
2018-19	5.739	5.065	117	130
2019-20	6.286	5.001	118	128
2020-21	6.426	5.125	119	129
Mean	6.359**	5.050	114.4**	128.6

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

were characterized for agro-morphological traits, and trait-specific accessions were validated during the years 2016–2021 (Manju *et al*., 2019; Kaur *et al*., 2022). Selection from barley accession IC138120 is a unique combination of high-test weight (hundred-grain weight) and early maturity in two-rowed genetic background. This accession was found significantly superior for hundred-grain weight (6.359 g) coupled with early maturity (114.4 days) compared to check variety DWRB101 recorded with the hundred-grain weight of 5.050 g and 128.6 days to attain maturity based on evaluation data in five consecutive years (*Rabi* 2016-17 to *Rabi* 2020-21) (Table 1). Test weight is an important parameter in two-rowed barley having a major role in yield compensation, grain size uniformity, and quality compared to six-row barley where these factors are limiting. Furthermore, high grain weight and early maturity are a very rare combination as these traits are negatively correlated. The short-duration and fast-growing barley perfectly fit the major cropping system (cereal-legume) in dryland areas of arid/semi-arid zones and escape drought and terminal heat stress. Therefore, the identified accession can be utilized in barley breeding programs for developing improved varieties with high grain weight and earliness.

References

Manju, V Kaur, K Sharma and SR Jacob (2019) Assessment of genetic diversity in cultivated and wild species germplasm of barley based on morpho-agronomical and root architecture traits. *Indian J. Plant Genet. Resour.* 32(3): 360-367. http://dx.doi.org/10.5958/0976-1926.2019.00039.1

Kaur V, J Aravind, Manju, SR Jacob, J Kumari, BS Panwar, N Pal, JC Rana, A Pandey and A Kumar (2022) Phenotypic characterization, genetic diversity assessment in 6,778 accessions of barley (*Hordeum vulgare* L. ssp. *vulgare*) germplasm conserved in National Genebank of India and development of a core set. *Front. Plant Sci.* 13: 771920. doi: 10.3389/fpls.2022.771920

34. GECH 716 (IC472387; INGR22133), a barnyard millet germplasm with early flowering and early maturity

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Barnyard millet [*Echinochloa frumentacea (Roxb.)*] is mainly cultivated for both grains and fodder in northern hilly and central and southern plain areas. It is nutritionally rich in dietary fiber content, Iron and Zinc and vitamins. The most of the genotypes in barnyard millet are of medium to late maturing types with crop duration of 98-119 days (Gupta *et al*., 1999). The trait earliness in flowering and maturity is of present need to develop early maturing cultivars with good grain yielding ability. The genetic stock GECH 716 is a pureline selection from the germplasm line IC472387 identified in the list of 100 accessions evaluated for trait specific germplasm identification. GECH 716 flowers in 38-44 days and matures in 83-87 days as compared to three checks *viz.,* VL 172 (69 and 105 days), VL 207 (64 and 98 days) and DHBM 93-3 (68 and 107 days) flowering and maturity respectively. The identified line produces a fodder yield of up to 5.0-5.4 t/ha and the grain yield of up to 1.7 -2.0t/ha. The genetic stock GECH 716 is having high productive tiller number and it will keep on producing tillers with good panicle size after attaining maturity by main productive tillers, adding to the higher grain yield. The proposed genetic stock GECH 716 may serve as a potential donor parent in the development of early maturing cultivars in barnyard millet and also helpful in developing mapping populations to identify the genomic regions associated with early flowering and maturity.

Reference

Gupta Arun, VP Mani, MK Sinha and VS Chauhan (1999) Agrobiodiversity and crop genetic resources in northwestern Himalayas. *Indian J. Plant Genet. Resour.* 12**:** 410-416.

35. GPU 28-2082 (IC646842; INGR22134), a finger millet germplasm with Neck Blast and Finger Blast Resistance

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Finger millet [*Elusine coracana* (L.) Gaertn], GPU28-2082 is neck and finger blast resistant line developed from induced gamma mutagenesis of GPU 28 variety. GPU 28 were irradiated with gamma rays and M_1 generation was raised during *kharif*, 2015. In M_1 generation, chlorophyll mutants were observed. About 750-1000 panicles from populations obtained from 500Gy and 600Gy gamma irradiation were harvested separately and were raised in panicle to row progeny in M_2 generation along with parental genotype. Selections were done during M_2 and M_3 generation as release of variability were observed up to M_3 generation. Selected lines were advanced till M_7 generation. Sixty one promising mutants along the parental genotypes were evaluated in replicated field trials in four environments during 2019 and 2020 at Indian Institute of Millets Research, Hyderabad in Telangana and during 2020 at Agricultural Research Station, Vizianagaram in Andhra Pradesh and AICRP Small Millets Project Coordinating Unit, Bengaluru in Karnataka.

GPU28_2082 height grows to a height of 100-120cms with days to flowering of 76 days (medium flowering). The mutant recorded 7 number of fingers with a finger length of 8.3 cm. The entry, GPU 28_2082 were screened along with its original variety (GPU 28) and two checks (GPU 67 and MR 6) under high disease pressure under field conditions during *kharif* 2019 and 2020. GPU28_2082 has recorded incidence of 3.2 for neck blast (Grade of 1 to 9) and finger blast 3.3 (Grade of 1 to 9) and is considered as resistant/tolerant individuals. Hence, GPU 28_2082 is unique in terms of neck and finger blast resistance and moreover it is an improved breeding line with superior grain yield which can be used directly for neck and finger blast resistance breeding.

36. ER 41 (IC642429; INGR22135), a finger millet germplasm with early flowering and early maturing

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Finger millet (*Elusine coracana* (L.) Gaertn) is an important nutri-cereal crop of the Semi-arid tropics with significantly higher calcium in the grains. The ICAR-Indian Institute of Millets Research is one of the National Active Germplasm Sites (NAGS) undertaking collection, characterization, evaluation and conservation of millets germplasm in the country. The finger millet germplasm, ER 41 was collected from the state of Tamil Nadu during the year 2018. ER 41 is locally known as "Vellai Suruttai" and it was collected from Narasingapuram village, Vaniyampadi taluk, Vellore district of Tamil Nadu at Latitude of 12.3629 and Longitude of 78.4352 with an altitude of 485 m msl.

The accession, ER 41 was evaluated for qualitative and quantitative traits of importance along with three check varieties at 6 locations *viz.,* Vizianagaram, Waghai, Bengaluru, Mandya, Athiyandal and Perumallepalle under AICRP on Small millets during 2021. It was found that, ER 41 flowered and matured significantly earlier than all the check varieties tested in the trial. ER 41 flowered at 65 days after sowing whereas, the check varieties, VL 376 (71 days), GPU67 (79

Table 1: Data on days to 50% flowering and days to maturity of indigenous finger millet germplasm during *Kharif* 2021 at 6 AICRP on Small millets centres

Acc. No	*Days to 50% flowering*														*Days to maturity*													
	VIZI	*RANK*	*WAGH*	*RANK*	*BENG*	*RANK*	*MAND*	*RANK*	*ATHI*	*RANK*	*PERU*	*RANK*	*INDIA (6)*	*RANK*	*VIZI*	*RANK*	*WAGH*	*RANK*	*BENG*	*RANK*	*MAND*	*RANK*	*ATHI*	*RANK*	*PERU*	*RANK*	*INDIA (6)*	*RANK*
ER41	66	2	77	6	59	7	54	2	65	44	65	1	64	1	93	2	114	7	102	10	89	2	100	41	98	2	99	1
GPU48 (C)	105	62	98	65	63	33	83	62	63	36	91	69	84	67	138	62	131	66	106	34	118	62	97	34	124	68	119	47
GPU67 (C)	101	57	87	37	61	15	81	59	65	43	79	25	79	49	133	57	121	29	103	17	116	59	99	37	112	28	114	47
VL376 (C)	76	7	81	10	62	16	76	36	65	49	65	4	71	9	106	9	114	9	104	18	111	36	99	40	98	1	105	9
Mean	92		88		65		76		62		81		77		123		122		106		111		96		114		112	
CD (5%)	2.7		1.9		0.9		1.6		1.7		1.8		1.1		3.1		1.8		0.9		1.7		2.1		1.7		1.2	
CD (1%)	3.5		2.5		1.2		2.2		2.2		2.3		1.5		4		2.4		1.2		2.2		2.7		2.3		1.5	
CV (%)	13		9.4		6.2		9.5		12		9.5		6.4		11		6.6		3.8		6.5		9.5		6.7		4.6	

days) and GPU48 (84 days) flowered late by at least 6 to 20 days. In terms of days taken for maturity, ER 41 matured early by 6 days compared to the earliest maturing check VL 376 (105 days). The other check varieties matured still later, GPU48 (119 days), GPU67 (114 days) (Table 1).

Several of earlier studies have reported identification of early flowering finger millet lines. Studies also have shown that the accessions from South Asia especially the Indian lines to be early in flowering (Babu *et al*., 2014). The earliness for flowering and maturity are an important criteria necessary for varietal improvement programmes in India where the accessions such as ER 41 could act as a potentialtrait donors for early flowering and maturity. The early lines might also escape from biotic and abiotic stresses

Reference

Babu BK, P Dinesh, PK Agrawal, S Sood, C Chandrashekara, JC Bhatt and A Kumar (2014) Comparative Genomics and Association Mapping Approaches for Blast Resistant Genes in Finger Millet Using SSRs. *PLoS ONE*. 9: e99182

37. IC308859 (INGR22136), a finger millet germplasm with early flowering and maturing

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Finger millet [*Elusine coracana* (L.) Gaertn] is an important nutri-cereal crop of the Semi-arid tropics with significantly higher calcium in the grains. The ICAR-Indian Institute of Millets Research is one of the National Active Germplasm Sites (NAGS) undertaking collection, characterization, evaluation and conservation of millets germplasm in the country. The finger millet germplasm, IC308859 is locally known as "Chodulu" and was collected from the state of Andhra Pradesh.

The accession, IC308859 was evaluated for qualitative and quantitative traits of importance along with four check varieties at 5 locations *viz*., Vizianagaram, Waghai, Bengaluru, Mandya and Athiyandal under AICRP on Small millets during *kharif* 2021. The results indicated that, IC308859 flowered and matured significantly earlier than all the check varieties tested in the trial. IC308859 flowered at 68 days after sowing whereas, the check varieties, PR 202 (74 days), VL376 (75 days), GPU67 (77 days) and GPU48 (76 days) flowered late by at least 6 to 9 days. In terms of days taken for maturity, IC308859 matured early by 7 days compared to the earliest

Table 1: Data on days to 50% flowering and days to maturity of indigenous multi-whorled finger millet germplasm during *Kharif* 2021 at 5 AICRP on Small millets centres

Acc. No.	*Days to 50 % flowering*												*Days to maturity*											
	ATHIYANDAL	*RANK*	*BENGALORE*	*RANK*	*MANDYA*	*RANK*	*VIZIANAGARAM*	*RANK*	*WAGHI*	*RANK*	*INDIA (5)*	*RANK*	*ATHIYANDAL*	*RANK*	*BENGALORE*	*RANK*	*MANDYA*	*RANK*	*VIZIANAGARAM*	*RANK*	*WAGHI*	*RANK*	*INDIA (5)*	*RANK*
IC0308859	63	11	63	27	70	7	74	9	74	1	68	1	95	6	105	34	105	7	103	6	108	1	103	1
GPU 48 (C)	65	28	62	19	83	46	86	34	86	29	76	41	99	27	103	14	118	46	117	32	121	33	111	39
GPU 67 (C)	65	25	65	47	83	47	89	38	83	18	77	46	99	28	106	46	118	47	121	39	116	13	112	42
PR 202 (C)	73	50	63	39	70	10	83	24	82	14	74	22	107	48	103	21	105	10	115	26	119	23	110	26
VL 376 (C)	62	2	63	32	76	26	93	42	82	16	75	30	94	5	105	37	111	26	125	43	115	11	110	28
Mean	65		62		75		83		85		74		98.9		103.6		110.2		114.2		119.3		109.3	
CD (5%)	0.73		0.48		1.4		2.17		1.38		0.71		1.05		0.54		1.4		2.41		1.27		0.76	
CD (1%)	0.96		0.63		1.84		2.86		1.82		0.93		1.38		0.7		1.84		3.17		1.67		1	
CV (%)	4		2.8		6.7		9.4		5.9		3.4		3.8		1.9		4.6		7.6		3.8		2.5	

maturing checks VL 376 and PRL 202 (110 days). The other check varieties matured still later, GPU48 (111 days), GPU67 (112 days). The other quantitative traits recorded on the multi-whorledfinger millet germplasm, IC308859 included plant height (99 cm), grain yield (1709 kg/ha), fodderyield (5571 kg/ha), number of productive tillers (4.0), number of finger (6.8) and finger length (7.3cm) (Table 1).

Several of earlier studies have reported identification of early flowering finger millet lines (Kalyana Babu *et al.*, 2014). Studies also have shown that the accessions from South Asia especially the Indian lines to be early in flowering (Babu *et al.*, 2014). The earliness for flowering and maturity are an important criteria necessary for varietalimprovement programmes in India where the accessions such as ER 41 could act as a potentialtrait donor for early flowering and maturity. The early lines might also escape from biotic and abiotic stresses

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Kalyana Babu B, PK Agrawal, D Pandey, JP Jaiswal and A Kumar (2014) Association mapping of agro- morphological characters among the global collection of finger millet genotypes using genomic SSR markers. *Mol. Biol. Rep.* 41: 5287–5297.

38. IC331688 (INGR22137), a finger millet germplasm with more number of productive tillers (4.7cm) and taller plant (119 cm)

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Finger millet [*Elusine coracana* (L.) Gaertn] is an important nutri-cereal crop of the Semi-arid tropics with significantly higher calcium in the grains. The ICAR-Indian Institute of Millets Research is one of the National Active Germplasm Sites (NAGS) undertaking collection, characterization, evaluation and conservation of millets germplasm in the country. The finger millet germplasm, IC331688 is a local indigenous germplasm collected from Murhu taluk, Khunti district/Jharkhand.

The accession, IC331688 was evaluated for both qualitative and quantitative traits of importance along with four check varieties at 5 locations *viz.*, Vizianagaram, Waghai, Bengaluru, Mandya and Athiyandal under AICRP on Small millets during kharif 2021. The results indicated that, IC331688 has recorded a significantly higher number of productive tillers (4.7) as compared to the popular check varieties GPU48 (3.7), GPU67 (3.9), PR 202 (3.9) and VL 376 (3.6) when tested across 5 locations. Additionally, IC0331688 was also having maximum plant height (119) compared to check varieties GPU 48 (100 cm), GPU 67 (106 cm), PR 202 (104 cm) and VL 376 (101 cm). The other quantitative traits recorded on the multi-whorled finger millet germplasm, IC331688 included days to 50% flowering (76 days), days to maturity (111 days), grain yield (1985 kg/ha), number of finger (7.1), finger length (7.3 cm) and finger length (6.7 cm). It has also recorded an average fodder yield of 6159 kg/ha during kharif 2021 at 5 locations in the AICRP on Small millets.

Several of earlier studies have reported characterization and identification of trait specific finger millet accessions (Kalyana Babu *et al.*, 2014). The previous reports suggest that accessions with high tiller number and plant height may be of great importance for development of dual purpose cultivars which can provide optimum quantity of grain as well as fodder (Babu *et al.*, 2014). Therefore, the identified accession IC331688 may act as a trait donor for higher number of productive tillers and taller plant height for use by plant breeders.

References

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Kalyana Babu B, PK Agrawal, D Pandey, JP Jaiswal and A Kumar (2014) Association mapping of agro- morphological characters among the global collection of finger millet genotypes using genomic SSR markers. *Mol. Biol. Rep.* 41: 5287–5297.

39. IC413273 (INGR22138), a foxtail millet germplasm with early flowering

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Foxtail millet [*Setaria italica* (L.) Beauv]is one of the oldest crops cultivated for food grain, hay and pasture. The ICAR-Indian Institute of Millets Research is one of the National Active Germplasm Sites (NAGS) undertaking collection, characterization, evaluation and conservation of millets germplasm in the country. The foxtail millet germplasm, IC413273 was identified to beearly flowering compared to check varieties in a multi-location trial conducted across six locationsunder the AICRP on Small millets.

The accession, IC413273 was evaluated at 6 locations under the AICRP on Small millets during *kharif* 2021 along with other 73 acc. of foxtail millet germplasm. IC413273

Table 1: Data on days to 50% flowering of indigenous foxtail millet germplasm during Kharif 2021at 6 AICRP on Small millets centres

S.No	*Acc. No.*	*Days to 50% flowering*													
		VIZIANAGARAM	*RANK*	*MANDYA*	*RANK*	*ATHIYANDAL*	*RANK*	*HAGARI*	*RANK*	*NANDYAL*	*RANK*	*SOLAPUR*	*RANK*	*INDIA (6)*	*RANK*
25	IC0413273	44	1	47	2	47	59	34	9	46	3	54	1	45	1
70	DHFt 109-3 (C)	50	54	53	21	46	45	39	48	47	29	64	46	50	47
71	SiA 3156 (C)	50	55	52	11	44	19	35	17	47	22	59	18	48	10
72	SiA 326 (C)	54	69	52	16	46	51	35	15	50	62	61	33	49	45
73	Suryanandi (C)	48	28	58	64	48	66	40	54	48	44	55	3	49	42
	Mean	49.1		54.3		44.7		37.9		47.8		62.3		49.3	
	CD (5%)	0.64		0.69		0.54		0.82		0.36		1.18		0.43	
	CD (1%)	0.85		0.9		0.7		1.08		0.47		1.55		0.56	
	CV (%)	5.7		5.5		5.2		9.5		3.2		8.3		3.8	

has shown early flowering by 3 days (45 days) comparedto check varieties DHFt 109-3 (50 days), SiA 3156 (48 days), SiA 326 (49 days) and Suryanandi (49 days) (Table 1). The other quantitative traits recorded on the foxtail millet germplasm, IC413273 included days to maturityin 79 days, plant height of 111 cm, grain yield of 1989 kg/ha, fodder yield of 3466 kg/ha, numberof productive tillers of 3.9 cm, panicle length of 18.9 cm and 1000-Seed weight of 2.8 g.

Several of earlier studies have reported characterization and identification of trait specific foxtail millet accessions. Many previous reports suggest that early flowering and maturity being highly correlated with grain yield in arid and semiarid regions may be of great importance in foxtail millet improvement (Upadhyaya *et al*., 2011; Ghimire *et al*., 2018) and may also help in escaping drought and cold stresses. Therefore, the identified accession IC413273 may act as a trait donor for early maturityin foxtail millet for use by plant breeders.

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40. IC479598 (INGR22139), a foxtail millet germplasm with high number of productive tillers

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Foxtail millet [*Setaria italica* (L.) Beauv] is one of the oldest crops cultivated for food grain, hay and pasture. The ICAR-Indian Institute of Millets Research is one of the National Active Germplasm Sites (NAGS) undertaking collection, characterization, evaluation and conservation of millets germplasm in the country. The foxtail millet germplasm, IC479598 was identified to be significantly higher number of productive tillers as compared to check varieties in a multilocation trial conducted across six locations under the AICRP on Small millets.

The accession, IC479598 was evaluated for both qualitative and quantitative traits of importance along with other 73 acc. of foxtail millet and four check varieties at 6 locations viz., Vizianagaram, Mandya, Athiyandal, Hagari, Nandyal and Sholapur under AICRP on Small millets during *kharif* 2021. The results indicated that, IC0479598 has recorded a significantly higher number of productive tillers (6.2) as compared to the popular check varieties DHFt 109-3 (4.3), SiA 3156 (4.2), SiA 326 (3.9) and Suryanandi (3.7). The other quantitative traits recorded on the foxtail millet germplasm, IC479598 included days to 50% flowering (48 days), days to maturity (82 days), plant height (109 cm), grain yield (2275 kg/ha), fodder yield (3867 kg/ha), panicle length (18.6 cm) and 1000-Seed weight (2.7 g).

Several of earlier studies have reported characterization and identification of trait specific foxtail millet accessions (Nirmala kumari and Vetriventhan *et al*., 2010). The previous reports suggest that accessions with high tiller number and plant height may be of great importance for development of dual purpose cultivars which can provide optimum quantity of grain as well as fodder (Brunda *et al*., 2014). Therefore, the identified accession IC479598 may act as a trait donor for higher number of productive tillers in foxtail millet for use by plant breeders.

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41. IC480408 (INGR22140), a foxtail millet germplasm with longer panicle

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The foxtail millet (*Setaria italica*) germplasm, IC480408 has recorded a significantly longer panicle length (20.9 cm) as compared to the popular check varieties DHFt 109-3 (16.6 cm), SiA 3156 (17.2 cm), SiA 326 (17.6 cm) and Suryanandi (16.0 cm). The accession, IC480408 was evaluated at 6 locations under the AICRP on Small millets during *kharif* 2021 along with other 73 accessions of foxtail millet germplasm (Table 1). The other quantitative traits recorded on the foxtail millet germplasm, IC480408 included days to 50% flowering of 53 days, days to maturity of 87 days, plant height of 122 cm, grain yield of 2009 kg/ha, fodder yield of 4044 kg/ha, 3.1 average number of productive tillers and 2.7 g of 1000-Seed weight.

Several of earlier studies have reported characterization and identification of trait specific foxtail millet accessions (Xiang *et al*., 2017). Many previous reports suggest that accessions with longer panicles may be of great importance for enhancement of yield in foxtail millet (Xing *et al*., 2010; Xiang *et al*., 2017). Therefore, the identified accession IC480408 may act as a trait donor for higher panicle length in foxtail millet for use by plant breeders.

References

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Table 1: Data on longer panicle of indigenous foxtail millet germplasm during *Kharif* 2021 at 6 AICRP on Small millets centres

S.No	*Acc. No.*	*Panicle length*													
		VIZIANAGARAM	*RANK*	*MANDYA*	*RANK*	*ATHIYANDAL*	*RANK*	*HAGARI*	*RANK*	*NANDYAL*	*RANK*	*SOLAPUR*	*RANK*	*INDIA (6)*	*RANK*
46	IC0480408	22.6	6	22.7	1	17.1	7	23	1	16	43	23.7	5	20.9	1
70	DHFt 109-3 (C)	20.4	14	15.6	50	9.3	73	18.3	26	16.2	40	20.1	22	16.6	44
71	SiA 3156 (C)	18.1	33	18.4	14	13.8	60	17.3	42	17.4	24	18.5	42	17.2	33
72	SiA 326 (C)	18.8	27	15.3	57	16.5	23	20.1	10	17.8	16	17.2	52	17.6	27
73	Suryanandi (C)	14.6	73	16.5	40	17	11	16.1	55	15.4	52	16.7	59	16	61
	Mean	18.3		16.8		15.2		17.5		16.5		18.8		17.2	
	CD (5%)	0.52		0.44		0.4		0.49		0.54		0.58		0.32	
	CD (1%)	0.69		0.57		0.52		0.65		0.71		0.77		0.42	
	CV (%)	12.4		11.4		11.4		12.3		14.3		13.6		8.1	

42. PS176 (IC647175; INGR22141), a kodo millet germplasm with early flowering

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Kodo millet (*Paspalum scrobiculatum*) is one of the species of *Paspalum* native to the Old-World tropics and used as cereal in India. *Paspalum* L. is a large genus of the Poaceae with nearly 310 species that are mainly distributed in the Americas and cultivated for forage and turf. Kodo millet is also referred to as 'ancient grain' as it was cultivated as an annual cereal in India from at least 3000 years ago and looking at its nutritional benefits it is also called as 'Nutri-cereals'. Kodo millet is one such nutri-cereal grown on marginal and degraded lands producing high grain yields even with limited water. In India, it is grown largely in tribal regions and under poor environments, and finds place in the diet of poor people either as whole grains or in the preparation of traditional food products like idli, dosa, chapathi, pongal, soup *etc.* India is the only country contributing to the world's kodo millet production with about 0.08 million ton of grains from an area of 0.2 million ha. In India, it is grown in the states of Madhya Pradesh, Uttar Pradesh, Maharashtra, Chattishgarh, Tamil Nadu and Karnataka. Among all the small millets kodo millet is the long duration crop which takes 4-5 months to mature and also late in flowering. Efforts were made in selecting kodo millet germplasm which can mature <100 days (Hariprasanna *et al.,* 2016; Deepika *et al.,* 2021).

KMV570 is early flowering and maturing genotype selection from germplasm line IPS176.It is 4 days early in flowering and maturity when compared with best check RK390-25for early flowering in the AICRP trial for two years i.e. IVT and AVTI (Table 1). Average plant height is 63cm, 6 productive tillers/plant, good fodder yield (5148kg/ha) and grain yield (2263kg/ha).

The cultivation practices followed for raising crop and recording data was according recommendations given by AICRP on small millets. Data was collected on 10 rows, 3 replications with row length 3m, row to row distance 22.5cm, plant to plant spacing 10cm with gross plot size 2.25x3.0m and 40:20:00 kg NPK/ha fertilizer dose. The trait earliness helps the researchers in many ways like to take up more than two crops in a year (speed breeding), to escape stress conditions like, heavy rainfall coinciding with maturity, terminal moisture stress, terminal high temperature stress, incidence of pests and diseases etc. the early flowering and maturing lines can be effectively used to identify the genomic regions associated with the trait by developing mapping populations using these early lines

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Table 1: Performance of KMV570 genotype in AICRP trials small millets-Breeding

Genotype	2020 IVT		2021 AVTI		Average	
	Flowering	Maturity	Flowering	Maturity	Flowering	Maturity
KMV570	64.21	98	61.88	100.41	63.045	99.205
RK390-25	67.85	103	66.21	103.33	67.03	103.165
TNAU86	73.03	108	70.45	108.56	71.74	108.28
Local check	68.81	102	69.84	107.63	69.325	104.815
CD (5%)	2.96	3.65	3.08	3.66	3.02	3.655

Days to flowering is average of 11 locations for 2020 IVT and 2021 AVT I

Days to maturity is average of 8 locations during 2020 IVT and average of 9 locations for AVTI 2021

43. IPS181 (IC404607; INGR22142), a kodo millet germplasm with early flowering, early maturity and shoot fly resistance

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Kodo millet (*Paspalum scrobiculatum*) KMV571 was identified as early flowering and maturing genotype along with shoot fly resistance when compared with best check RK390-25 in the AICRP trial for two years (Table 1). It is a selection from germplasm line IPS181(IC404607). It was also resistant to shoot fly when compared with the best resistant check BK-36 for two years (Table 2). Average plant height is 63cm, 6 productive tillers/plant, good fodder yield (5785.56kg/ha) and grain yield (2556.19kg/ha). The trait earliness helps the researchers in many ways like to take up more than two crops in a year (speed breeding), to escape stress conditions like, heavy rainfall coinciding with maturity, terminal moisture stress, terminal high temperature stress, incidence of pests and diseases etc. the early maturing with shoot fly resistance lines can be effectively used to identify the genomic regions associated with the shoot fly resistance and early maturity by developing mapping populations using these lines

Days to maturity is average of 8 locations during 2020 IVT and average of 9 locations for AVTI 2021

Days to flowering is average of 11 locations for 2020 IVT and 2021 AVT I

Data is average of 4 locations for 2020 IVT and AVT I

Data is average of 3 locations for 2021 IVT and AVT I

Table 1: Performance of KMV571 genotype in AICRP trials small millets-Breeding

Genotype	*2020 IVT*		*2021 AVTI*		*Average*	
	Flowering	*Maturity*	*Flowering*	*Maturity*	*Flowering*	*Maturity*
KMV571	67.91	103.13	61.36	99.44	64.635	101.285
RK390-25	67.85	102.88	66.21	103.33	67.03	103.105
TNAU86	73.03	108	66.67	108.56	69.85	108.28
Local check	68.81	102.25	67	107.63	67.905	104.94
CD (5%)	2.96	4	3.08	3.43	3.02	3.715

Table 2: Performance of KMV571 genotype in AICRP trials small millets - shoofly resistance

Genotype	2020 IVT		2021 AVTI		Average	
	% deadheart @ 21 DASE	*% deadheart @ 28 DASE*	*% deadheart @ 21 DASE*	*% deadheart @ 28 DASE*	*% deadheart @ 21 DASE*	*% deadheart @ 28 DASE*
KMV571	13.52	18.4	7.16	9.26	10.34	13.83
BK-36 (R)	15.32	25.2	6.86	8.3	11.09	16.75
GPUK-3 (S)	22.82	33.19	11.51	13.73	17.165	23.46
CD (5%)	11.76	16.88	5.37	6.42	8.565	11.65

44. SPV 2602 (IC646841; INGR22143), a sorghum germplasm with high total fresh biomass (59.6 t/ha) and high juice yield (19654 l/ha)

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Sweet sorghum (*Sorghum bicolor* L. Moench), a sugar crop with wider adaptation and high potential for bioenergy and ethanol production is expected to meet food, feed, fodder, fuel and fibre demands. It produces high biomass (50-80 t/ha) and alcohol (1500-2800 l/ha) and multiple income opportunities exist with this crop. This crop has been considered as a potential ethanol production feedstock because it accumulates fermentable sugar in the stalk and is resilient to climate change. Some sweet sorghum lines attain juice yields of about 78% of total plant biomass,

Table 1: Summary data on juice yield and total fresh biomass traits- IAVHT-Sweet sorghum *Kharif* 2018

Traits	*SPV 2602*	*CSV 19SS*	*CSV 24SS*	*CD (5%)*
Juice yield (l/ha)	19654	17037	15351	2776
Total fresh biomass (t/ha)	59	55	53	8.6

(*AICRP on Sorghum trial data*)

containing from 15 to 23% soluble fermentable sugars which are composed mainly of sucrose (70–80%), fructose and glucose (Umakanth *et al.,* 2024).

The sweet sorghum variety SPV 2602 is a derivative of a dual purpose genetic stock SPV 1871 and the most popular sweet sorghum variety SSV 74. It has recorded high total fresh biomass yields, fresh stalk yields, juice yields apart from high juice extraction percentage in comparison to the checks. SPV 2602 is tested under IAVHT-sweet sorghum of AICRP on Sorghum during 2018. This line is identified for uniqueness in having high juice yielding ability 19654 l/ha and total fresh biomass of 59.6 t/ha in comparison with the national checks (Table 1).

Reference

Umakanth, A V, S Paroha, A Kumar, A Ranganathan and D Swain (2024) Sweet Sorghum for Biofuel Production in Sub-Tropical India. *J. Sci. Res. Rep.* 30(4): 1-9.

45. SPV 2700 (IC546931; INGR22144), a sorghum germplasm with high total fresh biomass and high juice yield

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Of late, Sweet sorghum (*Sorghum bicolor* L. Moench) is gaining attention as a potential alternative feedstock for energy and industry, because of its high biomass yield and particularly, higher fermentable sugars in the juice. Sweet sorghum has rich soluble sugar in the stalk which can be converted into a number of products such as ethanol, syrup, fodder, jaggery and paper. It has the capacity to produce a crop with high biomass yield per hectare on marginal lands that are not suitable for food and feed production (Vermerris and Saballos *et al.,* 2012). These unique properties of sweet sorghum provide an opportunity to integrate this crop into world's biofuel industry. The key traits for realizing higher ethanol yields in sweet sorghum are high biomass, juice yield and higher sugar content.

Table 1: Summary data on total fresh biomass and juice yield traits- IAVHT-Sweet sorghum *Kharif* 2020

Trait	SPV 2700	CSV 19SS	CSV 24SS	CD 5%
Total Fresh Biomass (t/ha)	53.8	46.8	46.5	6.1
Juice yield (l/ha)	14318	12264	14154	2867

(AICRP on Sorghum trial data)

The sweet sorghum variety SPV 2700 was developed through pedigree method of breeding by crossing a *kharif* sorghum genetic stock RSCN 2103 with the most popular sweet sorghum variety SSV 84. It has recorded higher total fresh biomass yields and juice yields which are the characters of paramount importance in realizing higher ethanol yields. With a higher total fresh biomass yielding ability (53.8 t/ha) and juice yield (14318 l/ha), this genotype was superior to both the checks for these traits under IAVHT-sweet sorghum of AICRP trials 2020 (Table 1). This genotype is suitable to be grown as a sweet sorghum variety for rainfed *kharif* sorghum growing regions of the country especially in the command areas of sugar mills.

Reference

Vermerris W and A Saballos (2012) Genetic enhancement of sorghum for biomass utilization. In: Paterson, AH (Ed) Genomics of the *Saccharinae*. Springer, New York, pp 391-425.