Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXIXth meeting held on January 28th, 2019 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 32 germplasm lines out of 52 proposals considered. The information on registered germplasm is published with the purpose to disseminate the informationto respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer (s) / author (s) is / are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. CSR51 (Bulk 212) (IC0619319; INGR19001), a Rice (*Oryza sativa*) Germplasm for Tolerant to Alkalinity Stresses up to pH 9.9 and Salinity Stresses up to ECe 10.0 dS/m with Long Slender Grain

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Globally, more than 800 million hectares of land are salt-affected, including both saline and alkaline soils, which are more than 6% of the world's total land area (FAO 2014). In India, 6.73 million ha are affected by salt and 3.77 million ha are affected by alkaline soils. Genetic improvement of salt tolerance in rice appears to be economically feasible and a promising strategy for maintaining stable rice production, globally. The rice (*Oryza sativa* L.) line,CSR 51 (IET 22017), a derivative of the cross CSR23/CSR27 at ICAR-CSSRI, Karnal. The line CSR 51 was developed for saline and alkaline areas where ECe ~ 10.0 dS/m and pH is up to 9.9. Of the two parents, CSR 23 is tolerant to alkalinity (pH ~9.9) and another parent CSR27 is tolerant to salinity (ECe~10.0 dS/m) with high yield potential.

Morpho-agronomic characteristics: This culture recorded good yield under salt stress situations with good initial vigour, strong culm and good tillering ability. The culture is easily distinguishable through its morphological features such as erect flag leaf with long slender grains, strong culm, well exerted panicle with late leaf senescence. This line has been evaluated in AICRIP trial (Alkaline & Inland Stress Tolerant Varietal Trial) during 2011-13. All through the testing years i.e. 2011, 2012 and 2013, IET 22017 performed well in the alkaline stress locations of Haryana (Karnal, Kurukshetra and Jind), Uttar Pradesh (Lucknow and Kanpur) and Tamil Nadu (Annmalainagar); saline stress locations were Haryana (Karnal, Rohtak and Panipat) and Karnataka (Gangavathi) and majority of occasions figured among the top ranked entries of the trial and recorded impressive yield gain over all the checks.

It's interesting to note that none of the entries have qualified in three years of testing other than the entry IET 22017. The proximity of genotype Bulk 212 to saline and alkaline environment indicates its adaptability to salt stress environments. Results of the production environments with low GE interaction can be extrapolated to other environments and used to increase rice productivity in salt-affected areas (Krishnamurthy *et al*., 2015). Across three years 2011, 2012 and 2013, CSR 51 (Bulk 212) showed superiority yield advantage of 29%, 25%, 83%, 79%, 47%, 98%, 78% and 68% CSR 36 (National check), CSR23, Jaya (Yield check), NDRK50021(qualifying variety-2),TR2005-041(qualifying variety-3), TR2005-031(qualifying variety-4) and RP4939-221-16-4-2-2-1-1(qualifying variety-5) respectively across alkalinity locations of Karnal, Kurukshetra and Jind in Haryana, Lucknow and Kanpur in Uttar Pradesh and Annamalai Nagar. Across saline affected locations of Karnal, Rohatak and Panipat in Haryana, Gangavati in Karnataka, CSR 51 (bulk212)

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showed superiority yield advantage of 27%, 95%, 10%, 44%, 37%, 29% and 53% over CSR 36 (National check), Jaya (Yield check), CSR23, NDRK50021 (qualifying variety-1), TR2005-041 (qualifying variety-2), TR2005-031 (qualifying variety-3) and RP4939-221-16-4-2-2-1-1(qualifying variety-4).

Associated Characters and Cultivated Practices: Based on three years screening in NSN1 and NSN2 IET 22017 showed moderate resistance to blast and bacterial leaf blight, green leaf hopper, gall midge and stem borer. Quality parameters studied at IIRR (DRR) showed that IET 22017 has high milling recovery (71.27%) coupled with high head rice recovery (HRR) of 69%. It has long slender grain and alkali spreading value (ASV) of 4.3. It has got intermediate amylose content (24.58%). The above values are indicative of excellent cooking quality of IET 22017.

The performance of CSR 51 (IET 22017) was consistently high under alkalinity and salinity stress locations for three successive years. The alkaline locations were Haryana (Karnal, Kurukshetra and Jind), Uttar Pradesh (Lucknow and Kanpur) and Tamil Nadu (Annmalai nagar); saline stress locations were Haryana (Karnal, Rohtak and Panipat) and Karnataka (Gangavathi). It showed yield superiority over national alkaline check (CSR 36), CSR23, local check and other qualifying checks. This was only an entry promoted to 3rd year of testing. None of the entries qualified for 3rd year of testing in both alkaline and saline stresses. Therefore, CSR 51 (IET 22017) was promising under alkalinity and salinity stresses. This Germplasm can be used as a genetic stock for future breeding programmes aiming at development of high yielding salt tolerant rice varieties for saline and alkaline soils.

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2. Robin Mutant (*Herbicide tolerant mutant*) (IC0628569; INGR19002), a Rice (*Oryza sativa*) Germplasm with Herbicide Tolerance

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Increased water and labour scarcity in major rice growing areas warrants a shift towards direct seeded rice cultivation under which management of weeds is a major issue. A few herbicide tolerant genotypes have been developed using non-transgenic approach, primarily through induced mutagenesis, in crops *viz.,* maize, canola, wheat, rice and sunflower (Anderson and Georgeson, 1989) though transgenic approach is more prevalent.

Table1. Evaluation of *Robin mutant* at Multi locations

Sl.No	Genotypes	Dose of Imazethapyr on 30 Days old seedling	Coimbatore	Cuttack	New Delhi IARI FARM July 2017	New Delhi NRCPB Botany field June 2017
1	N 22	100g ai/ha	0% survival	0% survival	0% survival	0% survival
2	“HTM Robin” mutant	100g ai/ha	100% survival	100% survival	100% survival	100% survival

In the present study, we have successfully identified an induced mutant in rice tolerant to a broad spectrum non-selective herbicide, imazethapyr, considering the ease in registering and commercializing the material developed through non-transgenic approaches.

A mutant population of about 1,00,000 single M_2 plants generated by bulking the progeny of M_1 plants raised from about 1 Kg of EMS treated N22 seeds were grown in the field at Department of Rice, Tamil Nadu Agricultural University, Coimbatore and sprayed with herbicide, Imazethapyr. Three mutant plants putatively resistant to Imazethapyr were identified from the field in the M 2 generation. However, only a single mutant plant was found to be tolerant to subsequent herbicide spray in the re-potting experiments which was named as, ‘HTM-N22’ later it was named as “HTM *Robin” mutant*. Tolerance against the herbicide imazethapyr exhibited by the “HTM *Robin”* mutant was confirmed across subsequent filial generations up to M_5 and found to be true breeding. The true breeding and monogenic nature of the herbicide tolerant mutant identified in the present study was evident from the results of progeny testing, inheritance studies, molecular and DUS characterization.

This mutant was evaluated along with its wild type “N 22” under four locations. The results confirmed that it was resistant to Herbicide Imazethapyr at all four locations *viz.,* Coimbatore, Cuttack, IARI New Delhi and NRCPB, New Delhi (Table 1). The novel imazethapyr tolerant mutant which has been developed indigenously has opened up the possibilities of its extensive usage, without fear of infringement of any IPR, in the public rice breeding programmes in India and elsewhere.

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3. RP 5316-RIL-243 (IC0628571; INGR19003), a Rice (*Oryza sativa*) Germplasm for Potential Donor for Resistance to Planthoppers (Brown Planthoppers and Whitebacked Planthoppers). Exhibits Resistance during Vegetative and Reproductive Stages of Crop Growth

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Planthoppers namely brown planthoppers (*Nilaparvata lugens* Stal) and whitebacked planthoppers (*Sogatella furcifera*) are the major sap sucking insects in rice causing 100% yield loss under hopper- burn.

In an ongoing breeding program at ICAR-IIRR, Hyderabad for developing promising planthopper resistant rice varieties, a RIL (F_9)designated as RP 5316–RIL-243 derived from the cross NDR 359 (Susceptible)/MO1(Resistant) was found to be promising with stable resistance against planthoppers consistently for 3 years. A set of 200 RILs were initially screened at RARS, Maruteru, a natural hotspot for infestation of planthoppers in West Godavari district along with the standard checks (Ptb 33-resistant and TN1-Susceptible) in 6 environments continuously *ie.,* (1) 2012 *rabi,* (2) 2012 *kharif,* (3) 2013 *rabi,* (4) 2013 kharif, (5) 2014 *rabi* and (6) 2014 *kharif.* Among them a RIL namely RP 5316-RIL-243 was found to withstand high insect pressure (200-520 WBPH insects and 35-40 BPH insects per hill) during *kharif*, 2012 whereas 120-459 BPH insects and 10-15 WBPH insects/ hill during rabi, 2012 (IIRR Annual report, 2012-13). Similarly it was found resistant in the presence of as many as 350-515 BPH and 80-130 WBPH insects/hill during *kharif,* 2013, while 500-600 BPH insects and 5-10 WBPH insects/hill during rabi 2013 (IIRR Annual report, 2013-14). Also it showed resistance under heavy infestation of 390 to 450 BPH and 25 to 33 WBPH insects/hill during 2014, *kharif* and 600 to 800 BPH + 30 to 40 WBPH insects/hill during 2014, *rabi* (Fig 1). Thus it showed more or less resistant reaction with an overall mean score of 3.4±0.59 across 3 years, could survive and produced seed.

For confirmation of the observed field resistance, the same RIL was subjected to BPH and WBPH infestation separately during *kharif* and *rabi* seasons of two years (2013 and 2014) in glass house at ICAR-IIRR, Hyderabad during seedling stage using standard seed box screening method. The screening studies could detect RP 5316–RIL-243 with resistance reaction in both years with a mean damage score of 3.6 in 2013 and 3.1 in 2014 for BPH and WBPH respectively. The resistant checks, Ptb 33 and MO1 for BPH and WBPH recorded mean damage scores of 3 and 2.9 respectively. MO1, the donor parent of RIL population showed moderate resistance to BPH (DS = 3.5). Quality point of view it was superior with high head rice recovery (58%) and intermediate amylose content (23 %) and desirable ASV (5 mm).

Since RP 5316–RIL-243 displayed consistent resistance reaction for 3 years (2012 to 2014) continuously involving six seasons, it could be used as an elite resistant genetic stock to dev elop new varieties conferring combined resistance to planthoppers.

4. CHERAYI POKKALI (AC 39416A) (IC0413644; INGR19004), a Rice (*Oryza sativa*) Germplasm for Tolerant to Combined Stress of Drought and Salinity, Tolerant to Vegetative Stage Salt Stress, Tolerant to Vegetative Stage Stagnant Flooding

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Rice production is becoming more vulnerable nowadays due to climate change. Reports have shown that extreme events like longer dry spells or heavy rain have already gone up in las few years. In coastal areas,contamination of agricultural land by intrusion of seawater as a result of rise in sea level and erratic rainfall changing the micro environment in multifaceted manners. On the other hand, in rain-fed upland areas, rice is mostly cultivated as direct seeding due to lower cost of cultivation and other benefits. Water stagnation of even 5-10 cm in the field after sowing impede germination and crop growth. In reality these stresses come simultaneously either or in tandem during crop growth stages. Hence, genotype tolerant to multiple abiotic stresses can be of immense importance for its utilization in crop improvement than genotype with solitary abiotic stress tolerance trait.

Morpho-agronomic characters of AC 39416 (A): AC 39416A was used as check in the for multiple abiotic stress tolerance under multi-locational AICRIP trials during the period from 2013-2016. It was observed that AC 39416A under salinity and water stress was superior in comparison to other rice cultivars and showed moderate tolerance to anaerobic seeding condition. Based on the trial conducted at 9 locations AC 39416A along with other three lines found to be superior and were recommended as multiple stress tolerance rice genotypes based on their superior performance in terms of germination, root, shoot length and seedling vigour.

Associated characters and cultivated practices: AC 39416A is tolerant to vegetative stage salt stress. When tested for salinity stress, this genotype was found to be highly tolerant to vegetative stage salinity stress with a similar salinity evaluation score (SES) like tolerant check FL478. Detailed physiological studies also suggested highly salt tolerant nature of AC 39416A for traits like photosynthesis, chlorophyll fluorescence and Na^+/K^+ ratio (Sarkar et al. 2013; Singh and Sarkar 2014; Sarkar and Ray 2016). Anaerobic germination potential or tolerance to Germination Stage Oxygen Deficiency (GSOD) of this genotype was tested along with 2000 rice genotypes including known checks. AC 39416A showed tolerance to GSOD. The germination % of AC 39416A was 59% under anaerobic condition (10 cm of standing water above soil surface), while the maximum germination of 68% was observed in the tolerant check.

AC 39416A was also found tolerant to vegetative stage stagnant flooding (medium depth ≈ 50 cm). AC 39416A maintained greater stability of yield and yield parameters compared to other genotypes. A mere reduction of 8–10% in panicle number and <5% reduction in panicle weight (per m^2) was observed in AC39416A under vegetative stage stagnant flooding.Two-year experimentation showed that AC 39416A is tolerant to combined stresses of stagnant flooding and salinity. Even after 45 days of the imposition of combined stress of salinity (8 dS m^{-1}) and water stagnation (45 cm depth of water), the injury symptoms were negligible in AC 39416A (score 2) compared to susceptible genotype Gayatri (score 9). Testing of genotypes under combined stresses of Salinity (12 dS m^{-1}) and polyethylene induced moisture stress revealed that AC 39416A showed greater tolerance than susceptible check IR 29 and drought tolerant check CR 143-2-2.

In conclusion, we can say that AC 39416A is tolerant to drought, salinity and stagnant flooding at vegetative stage and moderately tolerant to germination stage oxygen deficiency (anaerobic seeding) and tolerance to combined stress of salinity and drought and water stagnation and salinity.

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5. DHOBANUMBERI (IC0256804) (IC0256804; INGR19005), a Rice (*Oryza sativa*) Germplasm for Resistant to Brown Plant Hopper

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The purified landrace 'Dhobanumberi (CRRI Accession number 35184)' showed resistance to Brown Plant Hopper (BPH) consistently against BPH population of NRRI, Cuttack during the years 2000, 2006 and 2015. Phenotyping showed low survivility rate and low feeding of BPH on the genotype. It was also promising in All India Coordinated Rice Improvement Programme trials (AICRIP) during 2003 and 2004. Since no separate biotype was confirmed location-wise in India, this genotype was tested against populations of different locations as mentioned in the Progress reports of the AICRIP. It was resistant to BPH in all the 5 locations tested during 2003 whereas during 2004, it showed resistant reaction at 4 locations.

Morpho-agronomic characteristics: The data on multilocation tests were generated for four years through AICRIP, ICAR-IIRR, Hyderabad in which the said entry was showing promising results against BPH. In addition, it was also identified as a potential donor for having multiple resistance to several insect pests of rice.

Associated characteristics and cultivated practices: Basing on the performance, the donor has already been utilized in breeding programme of the Institute. The breeding lines thus evolved, are also showing highly resistant reaction against BPH in multi-locational testing. It was recommended by the Institute Research Council (IRC) and Research Advisory Council (RAC) for registration as well as utilization in breeding programme for promotion to yield trial or for utilization in breeding programme for biotic stress like BPH resistance and also for resistance to multiple insect pests of rice. Basing on the recommendations, this donor has been utilized in making different cross combinations in breeding programmes of the ICAR-IRRI collaborative programmes and other rice research stations across the country.

The breeding lines thus evolved were also showing highly resistant reaction against BPH. The promising BPH-resistant breeding lines such as CR 2711-76, CR 2711-149, CR 2711-114 and CR 2711-139 evolved by using the variety as a resistant donor in the background of Tapaswini further confirms it's resistance.

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6. Khora-1 (AC 41620 (IC0574806; INGR19006), a Rice (*Oryza sativa*) Germplasm having High Anaerobic Germination

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In the era of global climate change, rice cultivation especially in the rain-fed shallow lowland ecology faces multi-facet problems. Dominated by poor and marginal farmers in this ecology, direct seeding of rice is becoming a popular option due to lower cultivation cost. But, erratic rainfall leading to water stagnation just after direct seeding of rice causes a lot of problem with excess water in the field. More often than not it creates complete submergence of the field leading to severe hypoxic conditionfor the germinating seed.Fortunately, in nature some of the rice genotypes areblessed with considerable degree of anaerobic germination potential and are tolerant to germination stage oxygen deficiency (GSOD). Interesting, the mechanism of GSOD tolerance found to be quite different than that of *SUB-1* mediated submergence tolerance at early vegetative stage. The QTLs reported for vegetative stage submergence tolerance do not work for anaerobic germination and vice-versa. Though donors for submergence tolerance had been identified long back, but till date we don't have well-established donor for GSOD tolerance. The genotype having high anaerobic germination potential would be of immense use as potential donor for GSOD tolerance trait, for rice crop improvement programme particularly for low-land ecologies.

Morpho-agronomic characters of Khora (AC 41620): AC 41620possesses an erect culm attitude. The plant is tall in nature having plant of125-130 cm and possesses weak leaf pubescence of blade surface, medium leaf sheath intensity of anthocyanin colouration and intensity of green colour, presence of leaf sheath anthocyanin colouration, leaf collar, leaf auricles and leaf ligule. The colour of the coleoptile and basal leaf sheath is green. This genotype was tested under NICRA project for 3 consecutive years (2012-13, 2013-14, 2014-15) and found that the genotype possesses high degree of anaerobic germination potential (NICRA Research Highlights 2012-13, 2013-14, 2014-15). Comparison of AC 41620 for anaerobic germination potential among 21 rice genotypes clearly showed its superior germination ability (>85%) under anaerobic condition, while the germination percentage of tolerant check viz. Rashpanjor was 75% and it was <15% in FR13A, Pokkalietc (Table 1). Further, the genotype was tested against Naveen (GSOD susceptible genotype) and found that it is having considerably higher anaerobic germination potential under 10 cm of water stagnation after sowing. The germination ability, coleoptile elongation and seedling vigour under anaerobic condition was significantly better in AC41620 as compared to Naveen (Vijayan et al. 2015; 2018).

Associated characters and cultivated practices: Our study showed a significantly different mechanism of tolerance to anaerobic germination condition exists in the genotype AC 41620. A more robust genetic regulation as evidenced from comparative transcriptomic study between anaerobic germination susceptible Naveen and tolerant AC 41620 showed, differentially regulated genes were more in case oftolerant genotype, AC 41620 (1130 DEGs), compared to susceptible genotype, Naveen (930 DEGs). Comparisonof transcriptome profiles revealed that 604 genes were uniquely up-regulated and 164 genes were uniquely downregulatedin tolerant genotype, AC 41620, while the corresponding numbers of genes in case of susceptible genotype, Naveen were 520 and 60, respectively. Detailed pathway analysis revealed, efficient use of available resources through energy saving mode imparted anaerobic germination tolerance in AC41620. Moreover, accelerated carbon and nitrogen metabolism (higher NR and NiR activities) in AC41620 under prolonged anoxia provided improve pH-homeostasis and energy source.Interestingly, we didn't find much alteration in any of the AG-QTLs reported till date, rather the study pointed out a few newer mechanism of anaerobic germination tolerance in AC 41620, which wasn't reported in functional validation of AG-QTLs. Perhaps, this genotype can be immense use not only as donor for anaerobic germination tolerance, but also can be used for identifying robust AG-QTL for higher anaerobic germination potential in rice.

Table 1. Effect of complete submergence (10 cm standing water) on germination ability (%) of a few rice genotypes

Genotype	GP under anaerobic condition	Genotype	GP under anaerobic condition	Genotype	GP under anaerobic condition
FR13A	11.5	Ravana	37.5	Pantara	52.5
Pokkali	15.0	AC41647	42.5	AC39416A	57.5
Kamini	27.5	JRS21	45.0	AC40346	60.0
Paloi	27.5	Talmugra	47.5	AC34245	65.0
JRS155	29.0	JRS8	50.0	Rashpanjor	71.0
JRS20	32.5	JRS182	52.5	JRS196	75.0
Panikekua	37.5	AC34280	52.5	AC41620	85.5

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National Innovations on Climate Resilient Agriculture (NICRA) Research Highlights (2012-13, 2013-14, 2014-15). ICAR-CRIDA, Hyderabad.

7. IC536365 (IC0536365; INGR19007), a Wheat (*Triticum aestivum*) Germplasm Resistant to all the Prevailing Stem, Leaf and Stripe Rust Pathotypes of India due to the Synergistic Combination of Minor and Major Rust Resistance Genes, Presence of Leaf Tip Necrosis (LTN), a Phenotypic Marker for the Presence of Minor/APR Genes

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A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of rust and spot blotch resistance. Genebank accessions comprising three species of wheat – *Triticum aestivum, T. durum* and *T. dicoccum* were screened sequentially at multiple disease hotspots, during the 2011-14 crop seasons, carrying only resistant accessions to the next step of evaluation. Initially, all the wheat accessions conserved in the gene bank were simultaneously regenerated and screened at Wellington (Tamil Nadu), a hotspot for stem and leaf rusts. Total of 2, 200 wheat accessions were selected based on leaf tip necrosis (LTN), a phenotypic trait linked to adult plant rust resistance genes viz., *Lr34+, Lr46+, Lr67+, Lr68* etc. having pleiotropic association with multiple disease resistance genes(Kumar*et al*., 2014). Further the LTN wheat accessions and the rest of the accessions were evaluated at Wellington. Identified 4,925 resistant accessions (including 1,526 LTN wheat accessions as well) were further evaluated at Gurdaspur (Punjab), a hotspot for stripe rust and Cooch Behar (West Bengal), a hotspot for spot blotch. Wheat accession (IC536365) displayed resistance reaction to all the three rusts in all the tested location at adult plant stage wherein stem rust pathotypes: 40A (62G29) & 40-1 (62G29-1); leaf rust pathotypes:17 (61R24), 77A(109R31), 77-5 (121R63-1), 77-7 (121R127) & 77-8 (253R31); stripe rust pathotypes: 46S119, 78S84 & I is commonly prevalent.

Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance and profiled using molecular markers. Evaluation of rust resistant accessions (IC536365) for seedling resistance test (SRT) against seven virulent pathotypes (stem rust pathotypes: 40-1 (62G29-1), 11 (79G31 & 117-3 (167G3); leaf rust pathotypes: 77-5 (121R63-1) & 104-2 (21R55); stripe rust pathotypes: 46S119 & 78S84) of three rusts under artificial epiphytotic conditions in glass house showed resistance reaction. Molecular analysis to identify different combinations of genetic loci imparting resistance to leaf, stem and stripe rust using linked molecular markers for the resistant accessions (IC536365) revealed the presence of two minor/adult plant rust resistance genes (APR) for stripe rust (*Yr36* & *Yr48*) and one each for stem rust (*Sr2/Yr30/Lr27*) and leaf rust (*Lr*46/*Sr*58/*Yr*29/*Pm*39/*Ltn2*) and two major gene for stripe rust (*Yr5* & *Yr15*) and one each for leaf rust (*Lr50*) and stem rust (*Sr13*).

Germplasm accession (IC536365) carries combination of two minor/adult plant rust resistance genes (APR) for stripe rust (*Yr36*&*Yr48*) and one each for stem rust (*Sr2/Yr30/Lr27*)and leaf rust (*Lr*46/*Sr*58/*Yr*29/*Pm*39/*Ltn2*) and two major gene for stripe rust (*Yr5* & *Yr15*) and one each for leaf rust (*Lr50*) and stem rust (*Sr13*). Moreover, APR genes have pleiotropic association with stem and stripe rust resistance along with powdery mildew which is an added advantage. Synergistic combination of minor and major rust resistance genes made the accession resistance to the prevailing rust pathotypes in India. APR genes are pathotype non-specific resistance based on horizontal type of resistance mechanism. Development of new pathotype(s) is slow/remote compared to major gene resistance which leads to durable resistance. So, the germplasm could be vital source for imparting durable rust resistance in wheat.

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8. EC574482 (EC574482; INGR19008), a Wheat (*Triticum aestivum*) Germplasm Resistant to the Entire Prevailing Stem, Leaf and Stripe Rust Pathotypes of India due to the Synergistic Combination of Minor and Major Rust Resistance Genes. Presence of Leaf Tip Necrosis (LTN), a Phenotypic Marker for the Presence of Minor/APR Genes

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A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of rust and spot blotch resistance. Genebank accessions comprising three species of wheat–*Triticum aestivum, T. durum* and *T. dicoccum* were screened sequentially at multiple disease hotspots, during the 2011-14 crop seasons, carrying only resistant accessions to the next step of evaluation. Initially, all the wheat accessions conserved in the gene bank were simultaneously regenerated and screened at Wellington (Tamil Nadu), a hotspot for stem and leaf rusts. Total of 2,200 wheat accessions were selected based on leaf tip necrosis (LTN), a phenotypic trait linked to adult plant rust resistance genes viz., *Lr34+, Lr46+, Lr67+, Lr68* etc. having pleiotropic association with multiple disease resistance genes(Kumar*et al*., 2014). Further the LTN wheat accessions and the rest of the accessions were evaluated at Wellington. Identified 4,925 resistant accessions (includes 1,526 LTN wheat accessions as well) were further evaluated at Gurdaspur (Punjab), a hotspot for stripe rust and Cooch Behar (West Bengal), a hotspot for spot blotch. Wheat accession (EC574482) displayed resistance reaction to all the three rusts in all the tested location at adult plant stage wherein stem rust pathotypes: 40A(62G29) & 40-1(62G29-1); leaf rust pathotypes:17(61R24), 77A(109R31), 77-5(121R63-1), 77-7(121R127) & 77-8(253R31) ; stripe rust pathotypes: 46S119, 78S84 & I is commonly prevalent.

Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance and profiled using molecular markers. Evaluation of rust resistant accessions (EC574482) for seedling resistance test (SRT) against the stripe rust pathotypes, 46S119 & 78S84 under artificial epiphytotic conditions in glass house showed resistance reaction. Molecular analysis to identify different combinations of genetic loci imparting resistance to leaf, stem and stripe rust using linked molecular markers for the resistant ace ssions (EC574482) revealed the presence of three minor/adult plant rust resistance genes (APR) for leaf rust *Lr46*/*Sr*58/*Yr*29/*Pm*39/*Ltn2, Lr*67/*Sr*55/*Yr*46/*Pm*46/*Ltn3* and *Lr68*) and one for stripe rust (*Yr48*) and two major genes for stripe rust (*Yr5*&*Yr15*) and one for leaf rust (*Lr50*).

Germplasm accession (EC574482) carries combination of three minor/adult plant rust resistance genes (APR) for leaf rust *Lr*46/*Sr*58/*Yr*29/*Pm*39/*Ltn2, Lr*67/*Sr*55/*Yr*46/*Pm*46/*Ltn3* and *Lr68*) and one for stripe rust (*Yr48*) and two major genes for stripe rust (*Yr5*&*Yr15*) and one for leaf rust (*Lr50*). Moreover, APR genes have pleiotropic association with stem and stripe rust resistance along with powdery mildew which is an added advantage. Synergistic combination of minor and major rust resistance genes made the accession resistance to the prevailing rust pathotypes in India. APR genes are pathotype non-specific resistance based on horizontal type of resistance mechanism. Development of new pathotype(s) is slow/remote compared to major gene resistance which leads to durable resistance. So, the germplasm could be vital source for imparting durable rust resistance in wheat.

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9. HI 8774 (IC0628570; INGR19009), a Wheat (*Triticum durum*) Germplasm for Resistant to Stripe Rusts with Additional Resistance to Karnal Bunt and Powdery Mildew

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Durum wheat is the second most important wheat species produced in India. Biotic stresses like stripe rusts, flag smut, Powdery mildew and Karnal bunt affect world wheat production significantly. Karnal bunt affects the wheat export prospect of the country to a great extent as it is quarantined diseases in many parts of the world. The pathogens' continued evolution and appearance of newer pathotypes leading to breakdown of new varieties in couple of years is a cause of concern and hence, broadening of genetic base for host resistance is a continuous process.

HI 8774 **(**HI 8863/HI 8498**)**,durum wheat genotype developed at ICAR-Indian Agricultural Research Institute, Regional Station, Indore was identified to be resistant to stripe rust, Karnal bunt and powdery mildew in multi-location testing *viz*., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2015 to 2018 (Table 1). This genotypes showed high levels of adult-plant resistance to most prevalent and virulent pathotypes like 46S119 (5MS) and 78S84 (10MS) of stripe rust in isolated nurseries. In seedling test, it showed moderate resistance reaction to both these pathotypes and also showed resistance responses to many new pathotypes like 238S119, 111S68 and 38S102 (Anonymous, 2016). It also showed resistance to other diseases like Karnal bunt and powdery mildew (Table 1). HI 8774 showed significant superiority in grain yield of 7% in NIVT and AVT-I in comparison to zonal check variety HI 8498 in Central Zone (Anonymous 2015b and 2016b).It has soft grains (grain hardness index of 7) which is suitable for biscuit making (Anonymous 2016b).As the availability of multiple disease resistant high yielding genotypes is rare, HI 8774 could be utilized as a potential resistance donor to breed varieties against these multiple pathogens along with quality and high grain yield.

Table 1. Field responses of HI 8774 to stripe rust, Karnal bunt and Powdery mildew

Year of testing	Trial	Stripe rust		Karnal bunt (%)		Powdery Mildew	
		HS	ACI	HS	Avg.	HS	Avg.
2014-15	NIVT 4	20S	5.3	1.1	-	-	-
2015-16	AVT I	5S	1.2	9.3	3.8	7	5
2016-17	EPPSN	5MS	1.7	-	-	-	-
2016-17	MDSN	5S	1.0	4.0	-	4	2

(HS-Highest score, ACI-Average Coefficient of Infection)

Source: AICW&BIP - Crop Protection Report (2015-18)

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10. QLD 84 (IC0628572; INGR19010), a Wheat (*Triticum aestivum*) Germplasm with Soft Grain Genotype (Very Low Grain Hardness Index). Suitable for Better Biscuit Making

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Grain hardness is an important trait in wheat quality with a profound effect on milling, baking and end-use qualities of wheat. It is common to differentiate soft and hard wheat in the world trade for product specific utility. Soft wheat is more friable, requires less energy to mill, and produces flours and meals with finer particles and lower starch damage, which are suitable for cake and biscuit production. Soft grain textured wheat produces tender and larger biscuits.

QLD84 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing 37thIBWSN05/36thIBWSN138 (Pedigree: MIANYANG20/3/CMH84.3379/ CMH78.578// MILAN). The genotype was evaluated at 13 centers in Quality Component Screening Nursery (QCSN) for three consecutive years (2015-16, 2016-17 and 2017-18). QLD84 was found to be superior with 18 grain hardness index over the years and locations to all the testing genotypes and soft grain check variety HS490 (31: grain hardness index) (Table 1). QLD84 recorded the lowest grain hardness index in all the 13 tested centers compared to the best check variety (HS490) for low grain index. QLD84 recorded lowest grain hardness index of 19, 18 and 18, respectively during 2015-16, 2016-17 and 2017-18. Whereas, the check variety HS490 tested in 2015-16 (grain hardness index: 27) and 2017-18 (grain hardness index: 35). QLD84 was 41.9% superior over check variety HS490. Low grain hardness index is very important factor to obtain high spread factor of biscuit and better biscuit quality. Thus, QLD84 would be a potential source to be utilized in future breeding programs to develop bread wheat varieties suitable for better biscuit making.

Table 1. Grain hardness index of QLD84 at 13 locations during three years as compared to the best available check HS490

Zone	Location	QLD84			HS490 (Check)	
		2015-16	2016-17	2017-18	2015-16	2017-18
NHZ	Almora	18	16	-	24	-
NWPZ	Ludhiana	19	13	-	26	-
	Durgapura	13	17	-	33	-
	Delhi	15	19	20	27	39
	Pantnagar	18	22	-	29	-
	Karnal	21	22	-	29	-
NEPZ	Pusa	20	23	-	26	-
	Kanpur	22	-	18	21	30
CZ	Junagadh	20	16	-	25	-
	Vijapur	20	19	16	24	35
PZ	Pune	20	19	-	21	-
	Dharwad	26	11	-	37	-
	Niphad	-	-	18	-	35
Mean (National)		19	18	18	27	35
Three years mean			18		31	
%Superiority of QLD84 over best check variety HS490						41.90%

11. QLD 11 (IC0628573; INGR19011), a Wheat (*Triticum aestivum*) Germplasm with High Grain Protein Content

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Grain protein is an important trait that determines the nutritional quality and baking properties of wheat. It is one of the major pricing factors for wheat trading at global market, and is an important nutritional factor for human health. Protein is an essential component of cells and it supports muscle growth, immune and enzymatic reactions; protein-energy malnutrition causes marasmus and kwashiorkor. Grain yield and grain protein content through its contribution to end-use quality, are the two most important characters determining the economic value of a bread wheat crop.

QLD11, a promising bread wheat genotype was selected from 15th High Rainfall Wheat Screening Nursery (HRWSN) with the parentage of MURGA. The genotype was evaluated at 12 locations along with high protein check variety (UP2672) during 2015-16 and 2016-17 under Quality Component Screening Nursery (QCSN). QLD11 found to be superior with 14.48% protein content over the years and locations to all the testing genotypes and check variety UP2672 (14.06%) (Table 1). QLD11 recorded the high grain protein content in all the 12 tested centers compared to best check variety (UP2672) for high grain protein content. QLD11 was recorded high grain protein content of 14.83% and 14.13%, respectively during 2015-16 and 2016-17. Whereas, the check variety UP2672 recorded 14.39% and 13.72%, respectively during 2015-16 and 2016-17. Thus, QLD11 would be a potential source to be utilized in future breeding programs to improve grain protein content of bread wheat varieties.

Table 1. Grain protein content of QLD11 and UP2672 (C) at 12 locations during 2015-16 and 2016-17

Zone	Location	QLD11		UP2672 (C)	
		2015-16	2016-17	2015-16	2016-17
NHZ	Almora	14.60	14.46	13.27	12.64
NWPZ	Ludhiana	12.70	13.02	12.73	13.26
	Durgapura	15.80	14.80	15.67	13.64
	Delhi	15.10	14.77	14.70	14.24
	Pantnagar	14.20	11.74	12.90	11.84
	Karnal	13.80	14.94	14.00	12.85
NEPZ	Pusa	15.30	12.65	15.10	13.91
	Kanpur	14.00	-	13.83	-
CZ	Junagadh	16.00	14.79	15.33	14.99
	Vijapur	15.70	15.39	14.63	13.89
PZ	Pune	15.10	15.60	14.80	15.00
	Dharwad	15.60	13.30	15.70	14.63
Mean (National)		14.83	14.13	14.39	13.72
Two years mean		14.48		14.06	

12. DWRB191 (IC0626293; INGR19012), a Barley (*Hordeum vulgare*) Germplasm with High Grain Zinc Content

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Large portion of human diet consists of cereals which are important sources of minerals especially micro nutrients like iron (Fe), zinc (Zn), iodine (I) and selenium (Se). Identifying genotypes with higher contents of micronutrients is thus very important and useful in improving nutritional quality of crops and in turn human and livestock health. Barley flour is used with wheat and gram flour to make *chapattis* more nutritious in rural areas of north western plains particularly in Rajasthan, Uttar Pradesh and Bihar since old time. While hulless barley grains are mostly used as food in cold and arid regions of Leh and Laddakh. In this direction new initiatives were taken to develop bio-fortified hulless barley genotypes with enriched zinc content at ICAR-IIWBR, Karnal.

A hulless barley genotype DWRB191 was developed from hybridization BHS352/HBL113, which possesses high grain zinc content and desirable agro-botanic characters in hulless genetic background. A set of 18 genotypes was evaluated during 2016-17 and based on grain zinc data, disease tolerance and agro-morphological characters the genotype DWRB191 was selected. The grain zinc content was estimated by atomic absorption spectroscopy (AAS) method at ICAR-IIWBR, Karnal. The multi-location data of DWRB191with promising checks namely BHS352 and Karan 16 are presented in the Table 1.

The studies on grain zinc and iron content bio-fortification in barley are lacking under Indian conditions. Even no germplasm and variety has been registered/release for enriched grain zinc content. The genotype DWRB191 showed grain zinc content of 44.9 ppm and while the elite hulless checks viz., BHS352 and Karan16 exhibited grain zinc content of 39.9 ppm and 36.6 ppm, respectively (Anonymous, 2018; Kumar *et al.,* 2018). The barley germplasm DWRB191 revealed 12.5% and 22.7 % superiority for grain zinc content over the checks BHS352 and Karan16, respectively.

Table 1. Grain zinc content (ppm) of DWRB191 and checks

Location	DWRB191	BHS352 (c)	Karan16 (c)
Karnal	35.2	33.2	34.0
Hisar	46.7	40.7	38.1
Durgapura	47.8	44.0	37.6
Jobner	49.7	41.5	36.5
Mean	44.9*	39.9	36.6
% advantage	-	12.5	22.7
LSD (0.05)		4.65	

*Significantly superior to the checks (CD at 5 %) & locations considered as replications

The genotype DWRB191 was observed with semi-erect growth habit and showed 1000 grain weight of 38 g (35-39 g). Barley grains are used in different industrial purposes *i.e.* food, multi-grain *atta,* health drinks etc. and the availability of high grain zinc content genotype DWRB191 will be certainly helpful for health benefits.

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13. DWRB192 (IC0626294; INGR19013), a Barley (*Hordeum vulgare*) Germplasm with High Grain Iron Content

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Barley is used for human food, cattle feed and malting purposes. Barley is called as poor man's crop due to its low input requirement and better adaptability to harsh environments and saline and alkaline soils. The hulless barley grains are mostly used as food in cold and arid regions of Leh and Laddakh and parts of plains in Rajasthan, Uttar Pradesh and Bihar etc. Barley flour in combination of wheat and gram flour is used to make nutritious *chapattis* in different parts of the country. Cereals constitute major portion of human diet and are important sources of minerals especially micro nutrients like iron (Fe), zinc (Zn), iodine (I) and selenium (Se). Therefore, the development of genotypes with higher grain iron content is one of the main objectives in the present time.

DWRB192 is a hulless barley genotype, which was developed from cross BHS352/HBL113 and possesses higher grain iron content. Different hulless barley genotypes were evaluated during 2016-17 and based on grain iron data, disease tolerance and agro-morphological characters the genotype DWRB192 was selected. The grain iron content was estimated by atomic absorption spectroscopy (AAS) method. The multi-location data of DWRB192 are presented in the Table 1 below-

Table 1. Grain iron content (ppm) of DWRB192 and checks

Location	DWRB192	BHS352 (c)	Karan16 (c)
Karnal	44.9	32.9	32.9
Hisar	43.9	39.9	39.9
Durgapura	51.0	42.9	36.9
Jobner	49.9	43.2	41.3
Mean	47.4**	39.7	37.8
% advantage	-	19.4	25.4
LSD (0.01)	6.66		

**Significantly superior to the checks (C.D. at 1 %) & locations considered as replications

Barley grains are used in different industrial purposes *i.e.* food, multi-grain *atta,* health drinks etc. and the availability of high grain iron content genotype DWRB192 will be certainly helpful for health benefits. The genotype DWRB192 showed grain iron content of 47.4 ppm and while the elite hulless checks viz., BHS352 and Karan16 exhibited grain iron content of 39.7 ppm and 37.8 ppm, respectively (Anonymous, 2018; Kumar *et al.,* 2018). The studies on grain zinc and iron content and bio-fortification in barley are lacking under Indian conditions. Even no germplasm and variety has been registered / release for enriched grain iron content. The barley germplasm DWRB192 revealed 19.4% and 25.4

% superiority for grain iron content over the checks BHS352 and Karan16, respectively. The genotype DWRB192 was observed with erect growth habit and showed 1000 grain weight of 40 g (38-41 g).

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14. GJG 0904 (IC0627616; INGR19014), a Chickpea (*Cicer arietinum*) Germplasm with Wilt Resistant, Semi Erect Plant Type, Single Pink Coloured Flower per Peduncle. Tuberculated Seed Texta with Large Sized Brown Colour Desi Type Seed

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Chickpea (*Cicer arietinum* L.) is an important pulse crop grown during *rabi* season in tropics and spring in the temperate region of the world. Chickpea is grown on about 8.39 million ha producing 7.06 million tonnes of seed with productivity of 840 kg/ha in India (Anonymous, 2017). *Fusarium oxysporum* have different races and it causes the wilt disease in chickpea and affects the all major chickpea cultivars (Gurjar *et al*., 2009). As per survey conducted by Sunit *et al*. (2012), the yield loss was up to 72.16 per cent due to this disease. This genotype was found to be resistant in wilt sick plot at ICRISAT, Jabalpur, Rahuri, Sehore and Junagadh during different years (2012-13, 2013-14, 2015-16) of testing.

The line GJG 0904**,** was developed at Pulses Research Station, Junagadh Agricultural University, Junagadh using wilt resistant source by pedigree method of selection in a segregating population of a cross (GJG 0105×Phule G 92926).

Morpho-agronomic characteristics of GJG 0904

Entry	Year	Yield (Kg/ha)	Maturity days	100 seed wt. (g)
GJG 0904	2011-12	2110	108	28.6
	2012-13	2207	105	27.0
Mean		2158.5	106.5	27.8

(Source: AICRP report 2011-12 & 2012-13)

Associated characters and cultivation practices:

• Resistant to *Fusarium* wilt disease	• Semi spreading growth habit
• Medium maturity (106.5 days)	• Single flower per peduncle
• Average Yield (2158.5 Kg/ha)	• Brown seed colour
• Large seed size (27.8 g/100 seeds)	• Angular seed shape

Recommended cultivation practices:

Seed rate: 60 Kg/ha; Spacing: 45×10 cm; Fertilizer dose: 20:40:00 N:P:K

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15. EC390977 (EC390977; INGR19015), a Soybean (*Glycine max*) Germplasm with Photoperiod Insensitivity. Source of Recessive Alleles e3 and e4, Early Maturity

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Soybean (*Glycine max* (L.) Merr.) is a photoperiod sensitive short-day plant and its different accessions starts flowering when the day length, which depends on latitudes, is less than their critical day length. Although soybean adapts to a very wide range of latitudes, its individual accessions adapt to a narrow latitudinal band. India lies in the latitudes between 6°-37° and latitude specific adaptation is observed in soybean accessions and varieties (Bhatia *et al.*, 2003). Soybean germplasm accession EC 390977 has been acquired from Taiwan and its photoinsensitive nature has been confirmed at ICAR-IISR, Indore.

At ICAR-IISR, 2071 soybean accessions were evaluated for their response to photoperiod by growing them in ambient and extended day length conditions (17 hrs). Under extended photoperiod, only 7 germplasm accessions including EC 390977 showed no significant delay in flowering and could reach to physiological maturity and hence, was identified as photoperiod insensitive(Bhatia *et al.*, 2003; Singh *et al.*, 2008a,b,c; Gupta *et al.*, 2017). Among rest of the germplasm accessions, about 30% showed delay in flowering ranging from 10 to 100 days while rest of the accessions did not flower under extended photoperiod indicating a very high degree of sensitivity to photoperiod. From 30% of the accessions that could flower under extended photoperiod, none of the accessions could reach to physiological maturity. This clearly indicated that besides flowering other reproductive stages were also sensitive to day length in soybean.

EC 390977 has been evaluated at different latitudes along with photosensitive varieties (Dharwar, Pune, Indore and Pantnagar) and has shown consistent flowering response. Delayed flowering response has been observed at higher latitudes in photosensitive varieties (Fig. 1). EC 390977 has semi-determinate growth habit with

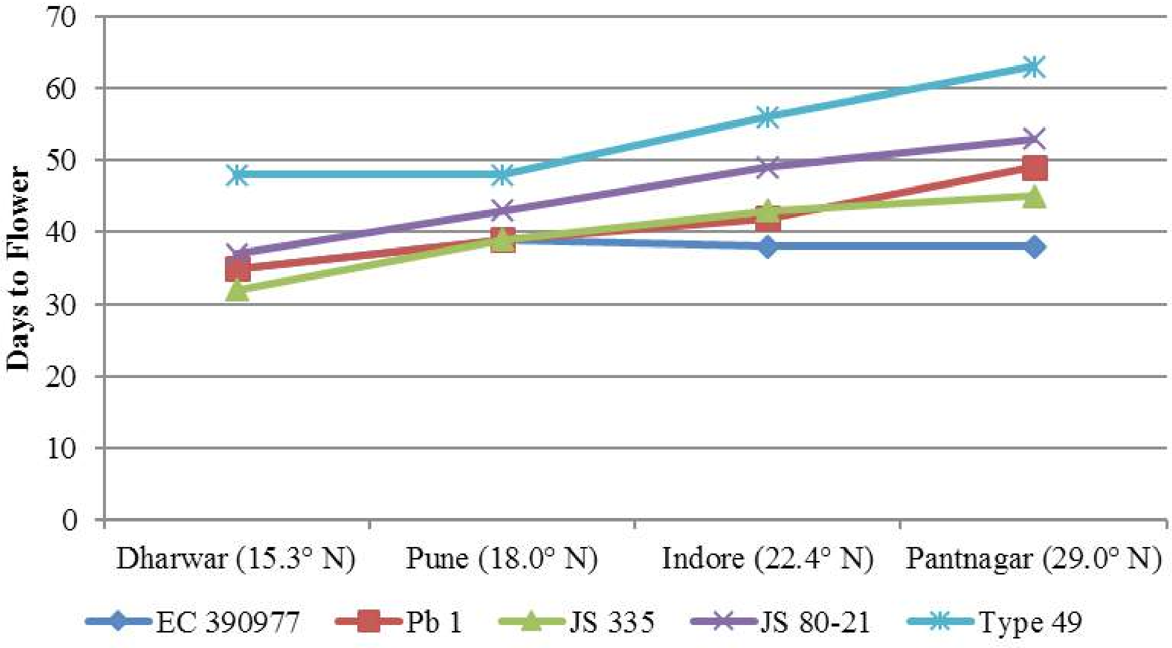

Fig. 1. Latitudinal consistency of EC 390977 in days to flowering

plant height of 60-65 cm, purple hypocotyl, purple fowers with flowering and maturity of 37-39 and 85-87 days, respectively. Its pod shatter at maturity and have tawny pubescence, seeds are yellowish green with light brown hilum. EC 390977 has been characterized for genes underlying photoperiod insensitivity, maturity and growth habit traits using sequencing and allele specific markers, and its genotype has been determined as *E1E1E2E2e3e3e4e4* (Gupta *et al.*, 2017). EC 390977 has allele specific markers for recessive alleles of *E3* and *E4* and dominant allele of *Dt1* and it has been used as a donor of these alleles for marker assisted back cross breeding in ICAR-IISR, Indore.

Genotype EC 390977 is a useful germplasm source for breeding of photo-insensitivity, earliness and semi- and indeterminate growth habit in soybean. These traits are desirable for development of soybean cultivars for growing in new areas across latitudes for wider adaptation and increasing cropping intensity & harvest index of the crop. Identified allele specific markers would be useful for gene pyramiding for earliness and photo-insensitivity using marker assisted breeding.

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16. MACS 330 (IC538550; INGR19016), a Soybean (*Glycine max* Germplasm with Photoperiod Insensitivity. Source of Recessive Alleles e2, e3-tr, Extra Early Maturity

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Soybean (*Glycine max* (L.) Merr.) is a photoperiod sensitive short-day plant and its different accessions starts flowering when the day length, which depends on latitudes, is less than their critical day length. Although soybean adapts to a very wide range of latitudes, its individual accessions adapt to a narrow latitudinal band. India lies in the latitudes between 6°-37° and latitude specific adaptation is observed in soybean accessions and varieties (Bhatia *et al*., 2003). Soybean breeding line MACS 330 was received for Initial Varietal Yield Trial in All India Coordinated Research Project on Soybean and conserved at the National genebank with National identity IC 538550. The MACS 330 is an advance generation selection from the cross Monetta × EC 95937, developed at Agharkar Research Institute, MACS, Pune.

At ICAR-IISR, 2071 soybean accessions were evaluated for their response to photoperiod by growing them in ambient and extended day length conditions (17 hrs). Under extended photoperiod, only 7 germplasm accessions including MACS 330 showed no significant delay in flowering and could reach to physiological maturity and hence, was identified as photoperiod insensitive (Bhatia *et al*., 2003; Singh *et al*., 2008a,b,c; Gupta *et al*., 2017). Among rest of the germplasm accessions, about 30% showed delay in flowering ranging from 10 to 100 days while rest of the accessions did not flower under extended photoperiod indicating a very high degree of sensitivity to photoperiod. From 30% of the accessions that could flower under extended photoperiod, none of the accessions could reach to physiological maturity. This clearly indicated that besides flowering

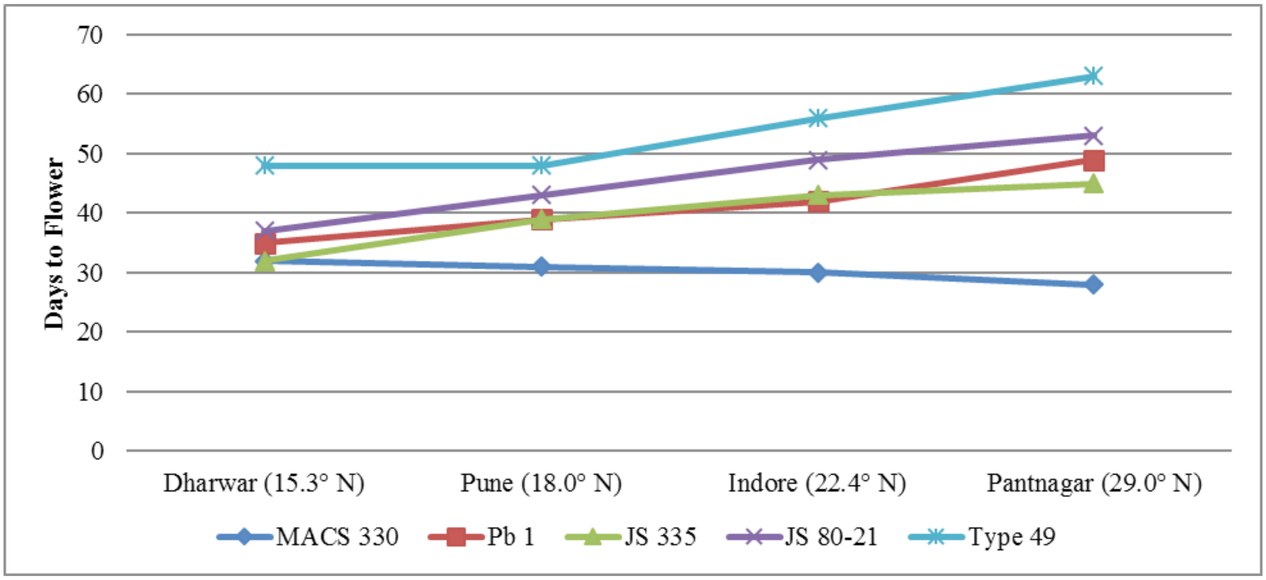

Fig. 1. Latitudinal consistency of MACS 330 in days to flowering

other reproductive stages were also sensitive to day length in soybean.

MACS 330 has been evaluated at different latitudes along with photosensitive varieties (Dharwar, Pune, Indore and Pantnagar) and has shown consistent flowering response. Delayed flowering response has been observed at higher latitudes in photosensitive varieties (Fig. 1). MACS 330 has determinate growth habit with 20-25 cm plant height, green hypocotyl, white flowers with flowering and maturity of 30 and 75 days, respectively. Its pods have tawny pubescence, seeds are yellow with gray hilum and being a breeding line it has a yield potential of up to 2 t/ha. Photoinsensitivity and determinate growth habit of MACS 330 has been confirmed through its characterization at photoperiodic, maturity and growth habit loci using sequencing and allele specific markers. Its genotype has been determined as *E1E1e2e2e3e3E4E4dt1dt1* (Gupta *et al.*, 2017). Recessive alleles of *E2* and *E3* confer earliness and photoperiod insensitivity and *dt1* makes this genotype determinate in growth habit.

Genotype MACS 330 is a useful germplasm source for breeding of photo-insensitivity, earliness and determinate growth habit in soybean. These traits are desirable for development of soybean cultivars for growing in new areas across latitudes for wider adaptation of crop, and increasing cropping intensity & harvest index. Identified allele specific markers would be useful for gene pyramiding for earliness and photo-insensitivity using marker assisted breeding.

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17. IPC-15 (DPC-15) (IC0625992; INGR19017), a Castor (*Ricinus communis*) Pistillate Line with Papaya Leaf Type, Non-spiny Capsules

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Mechanism of pistillate lines in castor is based on N, S and NES type. Majority of the pistillate lines are based on S type-dominant and epistatic in nature while NES mechanism is based on recessive genes for pistillate trait (Lavanya 2002 and Lavanya *et al.,* 2006). The present genetic stock, IPC-15 (DPC-15), is developed through conventional breeding technique *viz*., intra varietal hybridization followed by pedigree method of selection and generation advancement. Pistillate trait is from a NES source viz., NES-6, distinct with non-spiny capsules while DCS-12 is used for incorporating a distinct leaf type called "papaya leaf type" which is characterized by deep lascination of the leaf. Pistillate plants were identified in the segregating population of the cross, NES-6 x DCS-12 with the unique traits like non-spiny capsules and papaya leaf type. The pistillate trait was further stabilized by selfing the pistillate line with the male flower at the base of the spike. Heritability of the pistillate trait was observed up to 98 % in a population of nearly 60-100 plants every year. In a trial on stability of pistillate character of three pistillate lines viz., DPC-14, DPC-15 (IPC-15) and DPC-16 in three dates of sowing viz., 1st November 2006, 22nd December 2006 and 14th February 2007, the proposed pistillate line recorded mostly female plants and a few plants with 100 % monoecious and 100 % interspersed staminate flowers, necessary for the maintenance of the pistillate line (Anonymous, 2007).

IPC-15 has other distinct morphological characters like red stem, double bloom, very short plant height up to primary spike (16-18 cm) and very short primary spike (15-20 cm). The pistillate line flowers in 28-30 days and matures in 85-90 days. Primary spike emerges by 7 nodes while the secondary spikes emerge in 5-6 nodes (Table 1). The pistillate line is also distinct due to its

Table 1. Chief botanical and morpho-agronomic description of the proposed pistillate line along with DPC-9 and M-574 for comparison

Characteristic	IPC-15 (DPC-15)	DPC-9	M-574
Stem color	Red	Green	Green
Presence of bloom	Double	Zero	Triple
Type of internodes	Elongated	Elongated	Condensed
Number of nodes up to primary spike (Mean)	7	14	15
Leaf shape	Flat	Flat	Deep Cup
Leaf lascination	Deep (papaya / okra type)	Shallow	Shallow
Branching pattern	Divergent	Divergent	Convergent
Spike shape	Cylindrical	Cylindrical	Conical
Spike length of primary	Small (15-20 cm)	Long (41-60 cm)	Long (41-70 cm)
Spike compactness	Loose	Semi-compact	Semi-compact
Stigma color	Bright red	Greenish yellow	Red
Sex expression	Pistillate with ISF	Pistillate with ISF	Pistillate with ISF
Capsule: spines	Non-spiny	Spiny	Spiny
100-seed weight (g)	30	29	29
Seed: shape	Oval	Oval	Oval
Seed: base color	Brown	Light brown	Light brown
Seed: mottling	High	Low	High
Seed: caruncle	Inconspicuous	Conspicuous	Conspicuous

loose spike and non-spiny capsules. Among 34 parental lines and three checks screened, five lines viz., DPC-15, DPC-21, DPC-25, M-571 and M-574 were found highly resistant to leafhopper (grade 0) compared to susceptible checks DPC-9 and DCH-177 (grade 4.0) (DOR Annual Report, 2013-14). Molecular diversity study of 20 castor genotypes indicated that IPC-15 (DPC-15) is grouped along with pistillate lines like NES-6, NES-22 and DPC-16 which were developed using NES source of pistillateness (Ushakiran and Lavanya, 2016).

IPC-15, a genetically diverse, stable pistillate line with distinct morphological characters like papaya leaf type, non-spiny capsules, early maturity and short plant height has a good potential as a female line for the development of castor hybrids. Among the several preliminary hybrids developed using IPC-15 as female, two hybrids *viz*., PHT-12-2 (DPC-15 × DCS-105), PHT-12-3 (DPC-15 × DCS-107) with early maturity (100 days to the primary spike) and high yielding (2332 kg/ha) compared to the best check, GCH-7 (2188 kg/ha) were promising.

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18. RG-631 (IC0546708; INGR19018), a Castor (*Ricinus communis*) Germplasm Resistant to Leafhopper [(*Empoasca flavescens* (Fabr) (*Cicadellidae: Hemiptera*)]

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Castor (*Ricinus communis* L.) is an important non-edible industrial oilseed crop. India is the leading castor growing country in the world. Leafhopper, *Empoasca flavescens* Fabr. (Cicadellidae: Homoptera) is an important sucking pest and could cause yield loss to the extent of 22-89% in castor (Jayaraj, 1966; Lakshminarayana and Duraimurugan, 2014). In order to manage this pest, growing a resistant castor cultivar is an effective and economic measure. Availability of a stable resistance source is a prerequisite in leafhopper resistance breeding programmes. In order to identify sources of resistance to leafhopper, several genotypes were screened against leafhopper. RG-631, which was derived from a segregating population of a local collection, Punjab-1 through pedigree selection followed by inbreeding for about 12 years, has showed resistance to leafhopper in the first year. Its resistance reaction was tested at Palem, Yethapur and Hyderabad for four years using infester-row method under heavy leafhopper infestation condition.

Morpho-agronomic characteristics: RG-631 is a medium duration (55 days to flowering and 120-125 days to maturity), tall plant (124 cm) type having 16-17 nodes on green coloured stem with heavy triple bloom. Its capsules are green, non-spiny and non-dehiscent; its 100-seed weight is 30.3 g and oil content is 51%.

Associated character and utility: RG-631 was found to be stably resistant to leafhopper (0-1 hopper burn on 0-4 score) at Palem, Yethapur and Hyderabad locations in all the four years of testing. This would serve as a stable source of leafhopper resistance to castor breeders in All India Coordinated Research Project on Castor and other castor breeders in the country. It would also serve as genetically uniform base material to develop mapping populations for identifying molecular markers flanked to leafhopper resistance, and for developing RILs as well as for tagging the gene(s) controlling leafhopper resistance.

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19. RG-57 (IC0628058; INGR19019), a Castor (*Ricinus communis*) Germplasm Morphologically Distinct Selection from a Wild Type Collection, 1077-2 from Dantiwada, Gujarat

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India is the largest producer of castor (*Ricinus communis* L.) in the world and secured a virtual monopoly in castor production. Castor oil is the only natural oil possessing ricinoleic acid in high percentage. Ricinoleic acid in commercial cultivars is 85-88%; ricinoleic acid makes castor oil a unique source for preparation of thousands of high globally demanding industrial derivatives (Ogunniyi, 2006).An increase in ricinoleic acid from the existing level would increase value of castor oil as it would be highly beneficial to industry and the country. In order to identify sources of high ricinoleic acid type genotypes, germplasm was assayed for fatty acid profile. The accession, RG-57 giving more than 90% ricinoleic acid was further tested at four locations under rainfed and irrigated conditions for two years in RBD with two replications to test its stability for ricinoleic acid content. It was developed through progeny selection and inbreeding from a semi-wild type castor collection (1077-2) collected from Dantiwada, Gujarat.

Morpho-agronomic characteristics: RG-57 is a short plant type (78-85 cm) having green stem with bloom and 14 nodes on it. It has green spiny capsules and reaches to 50% flowering in 54-66 days and maturity in 109-126 days. Its 100-seed weight is 27-29 g and oil content is 45-47%

Associated character and utility: RG-57 possessed 91% mean ricinoleic acid content when tested for two years at four locations under rainfed and irrigated conditions indicating its high stability for high ricinoleic acid content. RG-57 is a unique source of high ricinoleic acid, and serves as a donor for high ricinoleic acid content for developing high ricinoleic type castor cultivars.

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20. DRMR 1-5 (IC0625996; INGR19020), an Indian Mustard (*Brassica juncea*) Germplasm with Double Low (<2%) Erucic Acid in Oil &< 30 µmoles Glucosinolate/g of Defatted Seed Meal). White Rust Resistant. Yellow Seed Coat

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DRMR 1-5 is a yellow seeded Indian mustard (*Brassica juncea* L.) genotype possessing white rust resistance with double low characteristics along with at par oil content in comparison to checks. DRMR 1-5 derived as single plant selection from the cross NUDHYJ-3 x Varuna, was evaluated along with 11 lines derived from the same cross and 2 checks varieties, namely Kranti (national check) and Pusa Mustard-21 (quality check) for morphological and biochemical characters in RCBD with 3 replications during 2012-13.The erucic acid content was determined by preparing methyl ester of oil sample (Sarin *et al*., 2009) in SP 2300 + 2310 SS column of Nucon model 5765 gas chromatograph. The glucosinolate content in the seed meal was determined by complex formation between glucosinolates and sodium tetra-chloropalladate solution using spectrophotometer at 405 nm as per Kumar *et al*., 2004. The oil content was determined in a Soxhlet apparatus (AOAC, 1997). DRMR 1-5 showed double low quality trait under IVT and AVT-I trial of AICRP-RM programme during

Table 1. Description of quality traits and white rust resistance of DRMR 1-5

Average over centers (Bharatpur, Ludhiana and New Delhi) and years (2012-13 to 2016-17)			
	Erucic acid (%)	Glucosinolate (µmoles/g of defatted seed meal)	Oil content (%)
Kranti (National Check)	40.71	92.5	40.17
Pusa-Mustard-21 (Quality check)	2.0	78.1	37.37
DRMR 1-5	1.29	23.2	40.72
% White Rust severity average over AICRP-RM centers and years (2012-13 to 2016-17)			
	75DAS	100DAS	Staghead
Rohini (Susceptible check)	26.0	30.8	12.9
DLSC-1 (Resistant check)	1.2	0.0	0.0
DRMR 1-5	2.8	1.6	0.0

2013-14 and 2014-15 at different locations. DRMR 1-5 also showed resistance for white rust disease caused by *Albugo candida* under both natural and artificial condition in the experiment conducted in different locations under AICRP-RM testing during 2013-14 to 2016-17, while screening against white rust disease along with other strains and checks including susceptible checks repeated after every 2 test rows. Observations on white rust disease were recorded on 75 and/or 90-100 DAS and number of stag head was recorded 15 days before harvesting. Double low quality trait for DRMR 1-5 was further confirmed during 2016-17 at DRMR, Bharatpur. DRMR 1-5 was included in the Brassica germplasm during year 2015-16 under AICRP-RM and in the year 2016-17 it was identified as white rust resistant source of *B. juncea* for use in breeding programmes. DRMR 1-5 showed 1.3 per cent erucic acid and 23.2 µmoles glucosinolate per gram of defatted seed meal with 41 per cent oil content along with resistance against white rust, in mean over locations of AICRP-RM trials and DRMR (Table 1).

Morpho-agronomic characters: Morpho-agronomic characters of the germplasm DRMR 1-5 are as follows: plant height (196.9 cm), main shoot length (62.7 cm), number of primary branches (6.1), number of siliqua on main shoot (60.5), number of siliqua per plant (822.9), 1000-seed weight (2.8 g), seed yield per plant (23.5 g), seed yield (1884 kg/ha) and oil yield (795 kg/ha). It completes 50 per cent flowering in 55 days and reaches to physiological maturity in around 132 to 138 days. Its seed coat colour is yellow.

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21. DRMRIJ 12-48 (IC0628059; INGR19021), an Indian Mustard (*Brassica juncea*) Germplasm with Multiple Disease Resistance (White Rust, Powdery Mildew and Alternaria Blight)

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White rust caused by *Albugo candida* (Pers. ex Lev.) Kuntze, Alternaria blight caused by *Alternaria brassicae* (Berk.) Sacc., and powdery mildew caused by *Erysiphe cruciferarum*are the most devastating diseases of Crucifers and cause severe yield losses in Indian mustard (*Brassica juncea*). Resistant sources are available for white rust in *Brassica juncea* but resistant sources are not available for Alternaria blight and powdery mildew in *B. juncea,* though have been reported in related / wild species. Further developing a genetic stock with resistance/ tolerance against all the three diseases will be an advantage in preventing the losses caused by these diseases. DRMRIJ 12-48 is an inbred line derived from a cross between OJR 2 and Zem 2 (exotic

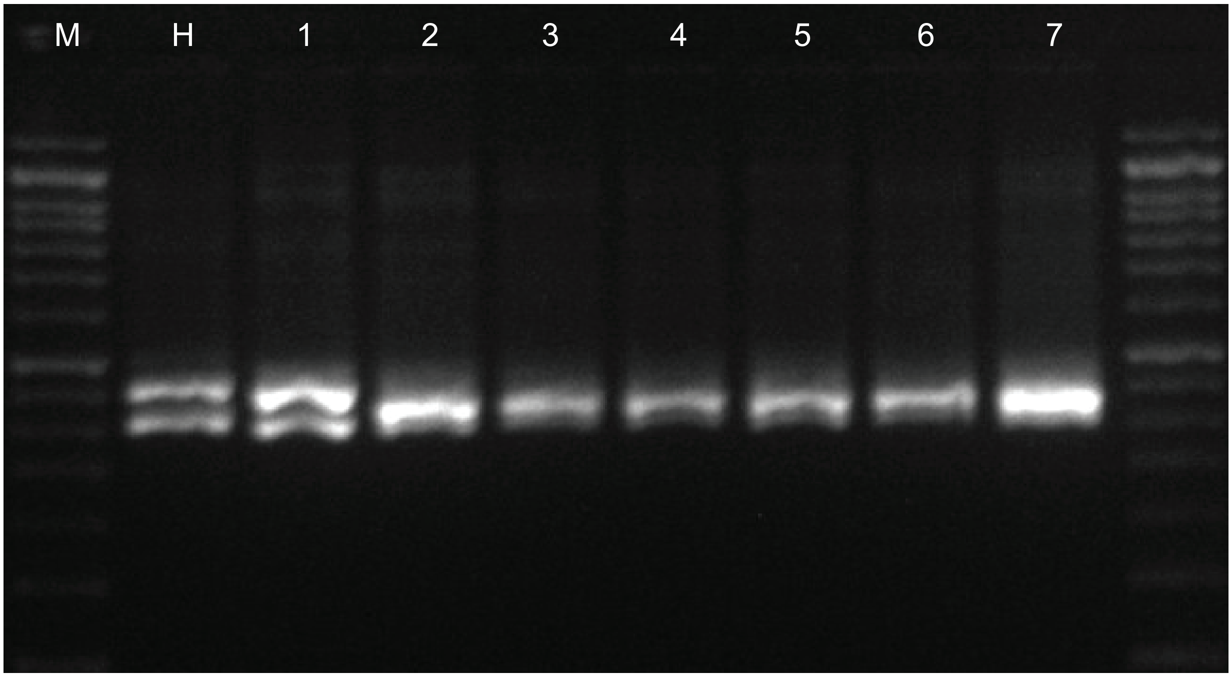

Fig. 1. Validation of IP marker (At5g41560) tagged to white rust resistance loci (AcB1-A4.1) in DRMRIJ 12-48
M: 50 bp DNA ladder; H: Heera, 1: DRMRIJ 12-48; 2: Varuna; 3: Rohini; 4: Kranti; 5: NRCHB 101; 6: Giriraj & 7: RH 749

germplasm) followed by individual plant selection. Cross was attempted during 2008-09 between OJR 2 and Zem 2.

Morpho-agronomic characteristics: Strain DRMRIJ 12-48 was characterized for agronomic traits viz., days to flower initiation (57 days), plant height (169 cm), length of main raceme (47 cm), days to flower senescence (107 days), days to maturity (136 days), oil content (38.7%), 1000-seed weight (4.7 g), number of seeds per siliquae (16.5) and siliquae length (4.4 cm). DRMRIJ 12-48 was inducted to AICRP-RM during 2014-15 and have been evaluated against white rust, alternaria blight and powdery mildew continuously for three years during 2014-15. 2015-16 and 2016-17.

Associated characters and cultivated practices: White rust reaction at leaves was recorded at two different stages viz., 75 and 100 days, while staghead formation was recorded at flowering stage. Candidate strain DRMRIJ 12-48 expressed resistant reaction against white rust at 75 days stage which was at par with resistant check BIO YSR during all three years of testing at Hisar. Disease reaction against white rust on leaves at 100 days stage was recorded at five locations viz., Bharatpur, Kangra, Kanpur, Pantnagar and Morena which included three hot spots (Kangra, Pantnagar and Morena). On the basis of mean disease index over all five locations for three years, candidate strain DRMRIJ 12-48 expressed 3.4 % which was better than the resistant check BIO YSR (8.9%) and susceptible check Varuna (42.9%) and Rohini (32.3%). A perusal of location wise disease reaction data revealed that candidate strain DRMRIJ12-48 had immune reaction at Hisar, Bharatpur, Pantnagar and Morena centres during all three years of testing. Resistant reaction against white rust was confirmed with already reported IP marker also (Fig. 1).

Reaction against alternaria blight was recorded on leaves at 100 days stage at five locations viz., Kangra, Kanpur, Morena, Hisar and Bharatpur and on pods at three locations; Kangra, Hisar and Morena over three years of testing. Disease incidence as indicated by percent Alternaria blight severity on leaves was lesser (27.2%) than both resistant (38.4% in BIO YSR) and susceptible checks (34.1 % in Varuna and 46.1% in Rohini). Considering less disease incidence on leaves on the basis of average of three years than the check cutlivars and at pods also at two locations, DRMRIJ 12-48 was found tolerant to alternaria blight.

Observations on powdery mildew incidence were recorded at Morena centre during all three years of testing, while at Kanpur for one year *i.e.* during 2016-17, hence representing performance of four environments. Percent powdery mildew severity was 0.6 % in DRMRIJ 12-48, which was better than all existing check cultivars viz., BIO YSR (47.1%), Varuna (51.5%) and Rohini (44.0%), indicating resistant reaction of candidate strain DRMRIJ 12-48 against powdery mildew.

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22. Mutant 85 (IC0621697; INGR19022), a Linseed (*Linum usitatissimumm*) Germplasm for Early Maturity for Southern Zone

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A substantial part of rice fallows during the *rabi* (post rainy) season are left uncropped because of limited availability of soil moisture. Late maturity is a major inconvenience to utilize the residual moisture after paddy harvest, where plants must mature within a muchshorter growing season. The objective of this study was to develop early maturing linseed mutants for efficient utilization of available residual moisture after paddy harvest.

Morpho-agronomic characters: The mutant line 85 derived from 0.3 per cent EMS treatment recorded early days to fifty per cent flowering (35 days) and maturity at and 95 days respectively, compared to mean value of 40.00 days for fifty per cent flowering and 110 days for maturity in corresponding control NL- 115. This genotype with shorter duration is suited for its cultivation in paddy fallows utilizing the residual moisture.

Associated characters and cultivated practices: In the present study, promising mutants for early maturity (Mutant No. 85) derived from 0.3 per cent EMS treatment recorded an early days to 50 per cent flowering and maturity at 35 days and 95 days respectively, compared to mean value of 45.20 days for 50 per cent flowering and 104 days for maturity in corresponding control (Plate 1). This mutant has recorded significantly higher number of secondary branches per plant (75) compared to the parent with 23 secondary branches, significantly higher number of capsules per plant (230), while its non mutant parent has recorded 56 capsules. This genotype has recorded significantly higher yield of 10 q/ha compared to 7.35q/ha recorded by the initial variety NL-115. The performance of other early maturing mutants is presented in Table 1.

Table 1. Performance of early mutants for seed yield and test weight

Mutants	Seed yield (kg/ha)	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	Number of secondary branches/ plant	Number of capsules/ plant	Number of seeds/ capsule	Test weight (g)	Oil (%)
85	1000*	35*	95*	40	5	75*	230*	6	13.83	40.30
79-4	740	35*	98*	41 40	9*	73*	215*	5	11.83	40.43
60-4	655	35*	98*	38	12*	103*	438*	5	15.37	39.40
26-3	800*	35*	94*	36	19*	209*	325*	4	8.64	40.13
Control Mean	735	45.2	110	46.64	4.37	23.25	56.01	6	9.45	39.74
CD at 5%	12.23	1.78	1.895	7.989	4.121	17.871	22.34	2.027	8.21	1.94

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23. SFS-9943 (IC0625999; INGR19023), a Safflower (*Carthamus tinctorius*) Germplasm with High Oil Content (34.7%)

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Safflower (*Carthamus tinctorius* L.) is a multipurpose oilseed crop grown in winter season in India, which is the major safflower growing country in the world. The cultivars from the major safflower growing countries *viz.,* India and China are of low oil type (28-29%) (Smith, 1996). Low oil content in Indian safflower varieties has necessitated development of safflower genotypes with enhanced oil content. An inbred line, SFS-9943 derived from [(537701 × 544042) × 560165) × 537701] × 537701 was tested at 16 locations under rainfed and irrigated conditions under All India Research Project on Safflower.

Morpho-agronomic characteristics: SFS-9943 is spiny in nature, flowers are yellow at bloomand orange when dried. Seeds are white in colour (100 seed weight: 3.6 g). It reaches to 50% flowering in 88 days and maturity in 132 days.

Associated character and utility: SFS-9963 had an average oil content of 34.7% while thecheck varieties, A1, PBNS-12 and NARI-6 had 26.8, 27.4 and 29.8%, respectively. Oil content had ranged from 28.6-38.9% in SFS-9943, 23.7-29.1% in A1, 23.3-31.2% in PBNS-12 and 25.8-33.1% in Nari-6 across 16 locations. SFS-9943 had 34.6-38.9% oil content at 11 locations, 30-31.3% oil content at four locations and 28.6% at one location out of 16. It ranked 1st at 12 locations with respect to oil content among the 25 entries tested in AICRP (Safflower) (Ann. Rep. Safflower, 2015). Variation in oil content across locations was attributed to influence of environment on oil content (Mahali and Carapetian, 2013; Mustafa *et al*., 2016). SFS-9943 is anindigenous source of high oil content and would serve as a high oil parent in breeding aiming to enhance oil content in safflower.

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24. IISR 7548 (IC0619910; INGR19024), a Black Pepper (*Piper nigrum*) Germplasm for Black Pepper Cultivar with Very Long Spike (29.3 cm; reported Range is 3.7 to 17.1 cm)

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Black pepper (*Piper nigrum* L.) originated in the Western Ghats of South India. This region is endowed with many landraces besides the progenitors of cultivated black pepper. Landraces, natural mutants, improved varieties and even true seedlings constitute the primary genepool of this tropical vine (Sasikumar *et al.*, 2007, 2011; Ravindran *et al.*, 2000). The ICAR-Indian Institute of Spices Research (Kozhikode, Kerala, India), the apex organization for black pepper research, has been involved in the mapping, collection, characterization and conservation of the diversity of black pepper from its centers of diversity/ domestication of the country. A unique black pepper accession with very long spike was collected from a tea estate at Wayanad district and registered for its unique character.

Morpho-agronomic characteristics: A black pepper germplasm survey and collection programme was undertaken Coottanadu Estate, Wayanad, Kerala, bordering the evergreen forest of the Western Ghats (latitude: 11°34'42''N; longitude: 76° 06'70''E; altitude: 800m mean sea level. Collection number 7548 (IC-0619910) is given to the specimen. This accession is characterized by very long spike with a maximum length of 29.3 cm, hitherto unreported in the primary genepool of black pepper. The morphological characters of the crop based on DUS guidelines is given in Table 1.

Table 1. Morphological characters of IC- IC-0619910

Character	Remark/Value
Shoot tip color	Light purple
Leaf length (cm)	12.30 (medium)
Leaf width (cm)	5.55 (narrow)
Leaf petiole length (cm)	1.05 (short)
Spike length (cm)	29.3
Spike peduncle length (cm)	1.31 (medium)
No. of berries/spike	17.6 (less)
Piperine (%)	3.4
Essential oil (%)	2.7

Spike length is an important yield contributing trait in black pepper and amenable for selection (Sujatha and Namboodiri, 1995; Pillai *et al.,* 1979). Reported spike length in cultivated black pepper ranges from 3.7 to 17.1 cm (Ravindran *et al.,* 2000). The present new collection with unusually long spike length is thus a unique line which will be a source of new genes for spike length improvement in black pepper.

Associated characters and cultivated practices: Besides its unique feature, the accession is characterised by a loose setting; purple to light purple shoot tips; drooping/hanging lateral branches; ovate–lanceolate to ovate leaves with acuminate tips; medium-quality, round, small berries. The fresh yield per vine was 2–3 kg.

Being blessed with excellent vegetative multiplication method black pepper can be easily propagated using rooted cuttings. Runner shoots of the accession is rooted in the nursery and planted in live standards to conserve the genotype following the practice in vogue. It is being further screened against biotic and abiotic stresses.

Acknowledgements

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25. DPO185 (IC0627267; INGR19025), an Isabgol (*Plantago ovata*) Germplasm with Yellow Leaf Tip. Downy Mildew Resistance

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Isabgol (*Plantago ovata* Forsk.) belongs to *Plantaginaceae* family, is an important medicinal plant commercially grown in India. The external seed coat, 'psyllium husk' of commerce is an excellent dietary fibre and is commonly known as "Isabgol" in Hindi and "Blonde Psyllium" in English. The isabgol husk (epicarp of seed) has medicinal properties and is used against constipation and irritation of digestive tract. It is hydrophilic in nature and upon absorbing water, increases by 10-15 times in volume. Consequently, it is a very good dietary fibre, which stimulates peristalsis and helps in bowel clearance. The husk, which is about 25 to 30% of the seed, has the property of absorbing and retaining water and hence, it works as an anti-diarrheal drug. The husk is also used in calico printing, dyeing, agar-agar media preparation, gum and jelly making, as binder in tablets, as thickner and a fixative in ice-cream, confectionary and in cosmetics industries. It has been used as a deflocculant in paper and textile manufacturing, as an emulsifying agent, as binder or lubricant in meat products, and as a replacement of fat in low-calorie foods. Downy mildew (DM) disease caused by fungal pathogen *Peronospora plantaginis* Underwood., is one of the most important and destructive diseases of Isabgol. The oomycete pathogen *P. plantaginis* is a typical obligate biotroph, solely depend on the host constituents for its nutrients and survival. Development of high yielding varieties with distinct morphological marker (s) and resistance of Downy mildew are the major breeding objectives in this crop. In this direction, a mutation breeding was attempted using chemical mutagens like DES, EMS and colchicine in the popular variety GI-2. Several morphologically distinct mutants were obtained. The Isabgol genotype DPO-185 is a mutant of GI-2, a popular cultivar of Isabgol grown in India bred at ICAR-Directorate of Medicinal and Aromatic Plants Research (ICAR-DMAPR), Anand, Gujarat, India. The genotype, DPO-185 is erect, shows distinct yellow leaf tip coloration followed by tip drying during flowering, resistant to DM disease, late maturing (130-140 days) and low yielding. DOP-185 was challenged with the fungal stains causing Downy mildew disease during flowering to ascertain the disease resistance from 2014 to 2017 and was compared with DPO-14 (INGR11035), a DM susceptible and early genotype and a registered germplasm. Visual disease score was recorded 10 days after the pathogen challenge on 1 to 9 scales on the basis of area under DM infection through visual observations. The genotype DPO-185 recorded mean score of 3.3 with score ranging from 3.0 to 4.0 across seasons indicating the resistance to DM disease. DPO-185 is late maturing (130-140 days) from the date of sowing as compared to 100 days in DPO-14 and its parent GI-2 (110-120 days). The resistant genotype can be a potential allelic donor to improve host plant resistance to DM disease in Isabgol. Further, the genotype is useful for unravelling genetic mechanisms underlie DM-host interaction. Yellow leaf tip trait can be used as DUS character for identification of elite germplasm lines and cultivars.

26. DTPO6-6 (IC0627269;INGR19026), Tetraploid Isabgol (*Plantago ovata*) Germplasm

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Isabgol (*Plantago ovata* Forsk, Plantaginaceae, diploid species with 2n = 8) is an important medicinal plant cultivated in India and regularly being exported in the world market. Isabgol seed husk has the property of absorbing and retaining water which accounts for its utility in stopping diarrhea and it is a diuretic, alleviates kidney and bladder complaints, gonorrhea, arthritis and hemorrhoids. Being an introduced crop from Mediterranean region to India, the available genetic variability is very low and hence attempt have made to induce variability through mutation and polyploidy. A stable tetraploid (2n = 4x = 16) (DTPO6-6) line of isabgol was developed from the variety GI 2 using colchicine (0.1 to 0.5%) seed treatment. The tetraploidy was confirmed throughflow cytometry, root anatomy phenotypic observation and cytology. Further, tetraploid genotype was compared with its counterpart diploid parent for qualitative and quantitative morphological traits. The tetraploids were fertile and stable over years (2010-2017). Morphologically the tetraploids were more vigorous than the diploids but were late maturing. The anatomical comparison revealed that the size xylem and phloem of stem and inflorescence stalk were larger in tetraploids than diploids. The seed yield was also higher in tetraploids than thediploids. Further, selection and breeding can be done in tetraploid lines for the qualitative and quantitative improvement of Isabgol after inter crossing between tetraploid lines.

27. DWS-10 (IC0627268; INGR19027), a Withania/Ashwagandha (*Withania somnifera*) Germplasm with Male Sterility at 10-30^{o}C at RH50-60% and 20-40^{o}C at RH40-50%

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Ashwagandha [*Withania somnifera* (L.) Dunal] belongs to family Solanaceae and its somatic chromosome number 2n=48. It is considered as wonder herb with multiple medicinal properties. It is cultivated in the North western and Central India besides some parts in peninsular region as post rainy crop. The species is annual to perennial, branched under shrub to herb of about 30 to 120 cm height. Roots are the major medicinally important part in addition to leaves and seeds. In 2009, in one of the germplasm of ashwagandha, RAS 23, a spontaneous male-sterile plant (DWS10) was found which produced male-sterile pollens under short-day (winter) condition and fertile pollens under long-day (summer) condition. The seeds obtained from this plant were grown in the next season and compare with its counter fertile plant (Parent) for morphological, anatomical, flower biology and physiological parameters. This sterile material can reproduce itself by selfing under long-day condition (summer season; temperature >35^{o}C), and becomes male sterile during winter; temperature 10-30^{o}C and RH 40-50%. Crosses can be effected during winter to produce F_1 hybrids. Significant differences between male sterile and its counter parts were observed for morphological and floral traits. Crosses were made were made between male sterile and male fertile plants during winter season. Per cent berry setting ranged from 14.29 (DWS10 x MWS204) to 54.17% (DWS10 x MWS139) and the number of seeds per berry ranged from 3.50 (DWS10 x MWS204) to 22 (DWS10 x MWS139). DWS10 can form base for commercial exploitation of hybrid vigour in Ashwagandha.

28. AKSM-08 (IC0586912; INGR19028), a Safed Musli (*Chlorophytum borivilianum*) Germplasm for High Root Weight and High Saponin

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Safed musli (*Chlorophytum borivilianum Sant*. & Fernandez) an herbaceous plant belonging to the family liliaceae commonly called as Safed musli belongs to the genus *Chlorophytum.* Mostly collected from wild sources as its tubers are in high demand in indigenous systems of medicine in the preparation of an aphrodisiac drug for curing general debility.

The present study compiled with four years data (*Kharif* 2011-15) wiht thirteen genotypes and present germplasm AKSM-08 (IC586912) have been collected from Bordi village, in Akola District in Maharashtra. These germplasm are maintained and evaluated in Nagarjun Medicinal Plants Garden, Dr.Panjabrao Deshmukh Krishi Vidyapeeth., Akola. The pure line selection method of plant breeding was applied.

Table 1. Yield performance of IC586912 accession

Year of testing	Root yield(g/plant)	AKSM-8 (IC586912) Root yield (q/ha)
2011-12	22.07	45.20
2012-13	22.53	48.96
2013-14	19.47	44.05
2014-15	18.20	37.65
Mean	20.57	43.97

Source: AICRP Report Dr. P.D.K.V., Akola.

The study revealed that, the root weight (g/plant) of AKSM-8(IC586912) was (20.57) however the root yield per hectare was significantly higher (43.97). AICRP Report of 2011-15).

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29. BMS-122/NIC-718(IC0112532; INGR19029), a Barbados Aloe (*Aloe barbadensis*) Germplasm with High Leaf Weight, High Mucilage Content

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Aloe barbadensis (2n=14) are perennial succulents or Xerophytes belongs to the family Liliaceous. Aloes have green fleshy leaves covered by thick cuticle, under which a thin vascular layer covering an inner clear pulp (Boudreau *et al*., 2013a). Though there is much diversity in Aloes the cultivators are unable to choose the best ecotype genetically differentiated is restricted to a specific habitat for commercial cultivation. Hence the present study carried out.

The present study compiled with four years data (*Kharif* 2011-15) with seventeen genotypes. In which nines were collected throughout the Maharashtra and eight genotypes were collected from National Research Centre, Boriavi (Anand), Gujarat. This germplasm were maintained and evaluated by Nagarjun Medicinal Plants Garden, Dr. Panjabrao Deshmukh Krishi Vidyapeeth., Akola. The pure line selection method of plant breeding was applied. In the present study the germplasm has been registered for its unique characteristics of high leaf weight and high mucilage content.

The study revealed that, the leaf weight (g/plant) of IC112532 (BMS-122) was (344.60), however the mucilage content was significantly higher (65.37) and also exhibits light blotches on young leaves were identified as a marker characters (AICRP Report of 2011-15).

Table 1. Yield performance of IC 112532 accession

Year of testing	IC 112532	
	Leaf weight (g/plant)	Mucilage (%)
2011-12	393.60	62.34
2012-13	291.50	62.40
2013-14	325.70	70.63
2014-15	367.60	66.15
Mean	344.60	65.37

Source: AICRP Report Dr. P.D.K.V., Akola.

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30. Nishkantak Prickleless (IC0629502; INGR19030), a *Solanum viarum* Germplasm for Prickleless, Alkaloids Content Higher than the Prickly Plant Type

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Solanum viarum Dunal (Family Solanaceae) is commonly known as tropical soda apple, while in India its local common name is 'kantha kari'. *S.viarum* is a medicinal plant having high contents of medicinally important steroidal alkaloids such as solasodine, α-solanine, solamargine, solasonine, solanidine, khasianine etc. used for commercial production of solasodine in India. These steroidal alkaloids exhibit a variety of biological activities including anti-cancerous, anti-fungal, anti-microbial, anti-viral, insecticidal, anti-inflammatory, anthelmintic, anti-herpes activities and are also major raw materials for commercial production of pharmaceutically important contraceptive steroids.

S. viarum is an economically important woody shrub of South American origin and widely distributed in the Asian subcontinent. In India,it is reported from Khasi hills, Naga hills, West Bengal, Nilgiris, Orissa, Sikkim, and the Upper Gangetic plains. The aerial parts of *S. viarum* including the calyx are packed with sharp prickles which renders harvesting of fruits diffucult and expensive. Due to nonsynchronous maturity of berries, mechanized harvesting is not possible. Therefore, the harvesting is done by hand plucking which is very difficult due to large and hard prickles. CSIR-National Botanical Research Institute, Lucknow, has obtained a prickleless spontaneous mutant under *S. viarum* breeding program (Khanna and Singh, 1985; Singh *et al*., 1998) and named as NBRI-Sel. The mutant was latterly christened 'Nishkantak'. The prickleless genotype is important not only for devoid of prickles but also for better yield and alkaloid contents. The highest alkaloid content is reported in the berries as compared to any of the other plant parts, eg., leaf, stem or root. The yellowish berries, a particular ripening stage contain the highest alkaloid contents.Germplasms of both the prickly and prickleless mutant of *S. viarum* have been conserved under *in vitro* condition for last ~35 years maintaining their prickly/prickleless nature and plants are stable under field conditions also.

The prickleless mutant, 'Nishkantak' has no prickles on the stem throughout the year but 2-4 prickles appeared on mature leaves during winter months. The finding to develop prickleless strain is novel in overcoming the constraint for adapting high density planting, easy harvesting and there by getting high yield. The berries yield is 1.29 tonnes/ hectare in prickly WT and 1.57 tonnes/ hectare in prickleless mutant.Single-nucleotide polymorphisms (SNPs) analysis measured that the prickly and prickleless genotypes were 99.92% genetically similar (Pandey *et al.,* 2018).

The various morphological characters of field-grown mature plants were recorded with five replicates for three consecutive years (2016-18). The data on different parameters of field-grown plants alongwith yield/plant were presented in Table 1. For alkaloid profiling of solasodine, solanidine and α-solanine contents different plant parts (leaf, stem and roots) of field-grown mature plants, *in vitro*-grown shoot cultures and yellowish coloured berries (II stage of ripening) were used (Table 1).

Table 1. Alkaloid contents(solasodine, solanidine, and α-solanine) in various plant parts of field and *in vitro*-grown prickly and prickleless genotypes of S. viarum

Type of Material	Alkaloids analysed (mg/g DW)	Prickly (WT)			Prickleless (Mutant)		
		*Avg±S.E.			*Avg±S.E.		
		2016	2017	2018	2016	2017	2018
Field-grown L+S+R[2]	Solasodine	1.71±0.14	1.89±0.12	1.88±0.11	2.22±0.42	2.34±0.33	2.32±0.25
	Solanidine	2.96±0.41	2.94±0.35	2.99±0.33	2.48±0.47	2.59±0.25	2.44±0.34
	α-solanine	3.96±0.25	3.99±0.28	3.84±0.31	4.09±0.31	4.12±0.53	4.21±0.22
	Total	**8.64**	**8.82**	**8.71**	**8.81**	**9.05**	**8.97**
Field-grown Berries[3]	Solasodine	1.00±0.13	1.10±0.11	1.08±0.05	1.17±0.37	1.18±0.28	1.15±0.22
	Solanidine	1.02±0.04	1.04±0.08	1.06±0.12	0.76±0.01	0.87±0.05	0.92±0.08
	α-solanine	4.91±1.23	4.99±0.09	4.88±1.22	5.61±0.87	5.66±0.12	5.45±0.99
	Total	**6.93**	**7.13**	**7.02**	**7.44**	**7.71**	**7.52**
[4]*In vitro*-grown L+S+R	Solasodine	1.34±0.07	1.31±0.05	1.25±0.03	1.90±0.24	2.01±0.33	1.98±0.21
	Solanidine	2.30±0.13	2.64±0.22	2.48±0.11	2.41±0.21	2.49±0.22	2.78±0.36
	α-solanine	1.19±0.02	1.04±0.04	1.18±0.09	2.31±0.09	2.22±0.06	2.28±0.02
	Total	**4.83**	**4.99**	**4.91**	**6.62**	**6.72**	**6.74**
Plant height (cm)		119±2.81	125±1.73	132.52±1.29	103±2.19	104.6±2.49	115±1.71
Prickles/young leaf*		13.6±0.68	14.6±1.08	17.6±0.68	nil	nil	nil
Prickles/mature leaf*		23.6±1.08	26.4±0.93	26±1.00	nil	nil	3.2±0.83
Prickles/ petiole of young leaf*		10.2±0.75	8.8±0.97	9.6±1.08	nil	nil	nil
Prickles/ petiole of mature leaf *		7.6±0.37	10.4±1.7	11±0.71	nil	nil	nil
Prickle/ Internode*		21.2± 0.11	20.4±1.44	18. 4±0.82	nil	nil	nil
Berries/ plant		57.20±3.47	52.80±3.15	54.00±3.39	63.20±0.28	64.20±2.97	65.60±1.96
Yield/plant (g)		129.04±7.83	125.56±7.50	123.01±5.98	148.27±5.11	159.34±7.38	162.03±4.85

*Average of 3 replicates ± Standard Error;
[2] L+S+R = Leaf + Stem + Roots in total
[3] Second stage of berries, i.e. yellowish green
[4] Culture incubation: 45 days

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31. Swadi Palas (IC0629501; INGR19031), a Flame of Forest (*Butea monosperma*) Germplasm with Trifoilate Leaflet and Acute Apex (occasionally penta foliate). Larger flower with Dull Orange Colour with Early Biological Maturity

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Palas (*Butea monosperma* Lam.) Taub. commonly known as 'Flame of the forest' (Sanjappa, 1987; Shah 2011). Tree is very useful for local people in terms of medicine, pharmaceutical industry and several nontimber forest products (NTFP) (Pal and Bose, 2011; Sanjappa, 1987). Besides NTFPs, in association with *rangeeni* strain of Indian lac insect (*Kerria lacca* Kerr.) it also yields a resin called lac, extensively cultivated by tribal communitiesfrom Jharkhand, Chhattisgarh, Madhya Pradesh, West Bengal, etc. (eds. K.K. Sharma and R. Ramani, 2010) and has commercial importance. A new variant of *palas*strain from Putadag village (N 23^0 25.746' and E $85^0$43.391') in Ranchi (Jharkhand) has been identifiedfor raising *kusmi*strain of Indian lac insect (*Kerria lacca* Kerr.). This variant not only differs in terms of lac insect strain preference but also differs morphologically from commonly available Palas. Locally, it is known as *Swadi Palas* due to its preference by *kusmi*strain of lac insect. The comparative morphological account, its keys for identification is presented in Table 1. Thus, identification of *Palas* variant'*Swadi'*will increase the industrially superior *kusmi*lac production.*Kusmi* lac fetches high value in the marketdue to its superior quality over *rangeeni* lacthereby, augmenting the earningsof lac growers.

Table 1. Comparative morphological characters of Palas variant 'swadi' and common Palas

Morphological Characters	Palas variant 'Swadi'	Common Palas
Tree height (meter)	16-20	8-15
Trunk diameter (cm)	40-80	25-50
Bark colour	Whitish	Blackish-brown
Leaflets	Pinnately trifoliate (rarely 5-foliate)	Pinnately trifoliate (rarely unifoliate)
Terminal leaflet	Rhomboid	Suborbicula or obovate
Apex	Acute apex	Obtuse to round or emarginate
Pedicel length (mm)	28 to 31	17 to 22
Calyx diameter (mm)	16 to 18	14 to 16
Calyx length (mm)	16 to 21	13 to 17
Flower length (cm)	5.5 to 6.3	4.5 to 5.0 cm
Stamen length (mm)	68-78	49-62
Style (mm)	73-86	49-61
Anther length (mm)	1.3-1.74	1
Pod length	13-14 cm	10-16
Seed size (cm)	3.0-3.7 x 1.8-2.3	2.5-4 x 2-3
Flower Colour	Orange	Scarlet flowers (orange-red/Indian-orange)
Flowering time	January-February	March- April
Fruiting	March -April	April-May

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32. HTW 63 (IC36761A; INGR19032), a Wheat (*Triticum aestivum*) Germplasm for Drought Tolerance

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Wheat is grown in a wide range of environments and is affected by biotic and abiotic factors. Worldwide, it was estimated that about 65 million hectares of wheat area is under water limited environments, wheat yields are generally reduced to 50% or even less of its yield potential under normal irrigation. In India, nearly 80% wheat is cultivated under irrigated conditions, 66% of it receives only partial (1-2) irrigations, and the remaining 20% is grown under rainfed environments.Both drought and heat stress are responsible for 20-30% reduction in grain yield. Therefore, it is necessary to identify tolerant genotypes followed by introgression of the tolerance into elite agronomic background.

The genotype HTW 63 was found to be tolerant to both heat as well as drought tolerance (Sareen *et al.,* 2014). To reconfirm the drought tolerance of HTW 63, a trial was conducted under timely sown, late sown, rainfed timely and rainfed late sown conditions at four locations (Akola, Dharwad, Karnal and Powarkheda) for two years (2015-16 and 2016-17) under NICRA project. This genotype was found tolerant to drought as well as heat under field conditions as indicated by values of stress indices DSI (-0.18), HSI (0.98) and DHSI (0.92). In addition to this, this genotype along with checks was evaluated under controlled conditions (rainout shelter for drought stress tolerance and temperature controlled glasshouse for heat tolerance). HTW 63 had shown tolerance to both drought as well as heat stress as depicted by the stress indices DSI (0.68) and HSI (0.90) (Table 1).

The performance of HTW 63 under rainfed timely sown conditions with respect to other desirable agronomic features namely: days to heading (63 days), days to maturity (114 days0, plant height (104cm) and thousand grain weight (46.6g) has also indicated its suitability to be used in crossing programmes (Table 2).

Table 1. Evaluation of HTW 63 along with checks for drought tolerance

Drought susceptibility index (DSI) of HTW 63 and checks under field (pooled over 4 locations and 2 years) and controlled (rainout shelter and glasshouse) conditions

Entry	Field conditions			Controlled conditions	
	TS IR	LS IR	LS RF	Rainout shelter	Temp controlled glasshouse
	DSI	HSI	DHSI	DSI	HSI
HTW 63 (IC 36761A)	-0.18	0.98	0.92	0.68	0.90
Checks (Registered genetic stocks for heat and drought)					
AKAW 2862-1	1.25	0.66	1.10	2.77	2.61
HTW11	1.05	1.61	1.18	1.89	0.96
HTW 6	0.82	0.80	0.89	0.45	0.69
C 306	0.52	0.64	0.94	0.35	0.93
C 306 M10	1.23	1.10	1.05	1.60	3.39
HINDI 62	0.97	1.25	1.16	0.84	2.34

*DSI- Drought susceptibility index HSI- Heat stress sensitivity index and DHSI- Drought & heat sensitivity index; TSIR – Timely sown irrigated; LSIR- late sown irrigated; LSRF- Late sown rainfed

Table 2. Agronomic characteristics of the drought tolerant genotype, HTW 63 pooled over two years under field conditions

Genotypes	Days to heading		Days to maturity		Plant height (cm)		Thousand grain weight (g)	
	IR-TS	RF-TS	IR-TS	RF-TS	IR-TS	RF-TS	IR-TS	RF-TS
HTW63	68	63	119	114	123	104	42.0	46.6
Checks								
AKW2862-1	70	66	120	114	101	79	49.5	48.2
C 306	82	76	126	121	118	105	43.4	41.8
C 306 M10	74	71	123	120	124	104	44.9	45.5
HINDI 62	87	79	129	121	99	91	36.4	42.5
HTW11	82	76	124	119	94	84	41.6	39.4
HTW6	84	77	127	122	103	86	38.8	41.3

The high level of drought tolerance in HTW 63 makes it a potential donor for use in hybridization programmes targeted to improving drought tolerance in future wheat genotypes.

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