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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXXIIIrd meeting held on March 18th, 2021 at the National Bureau of Plant Genetic Resources, New Delhi. A total of 125 proposals were received for registration. Out of that, 105 proposals were considered for registration. Finally, 90 applications covering 35 crop species were approved for registration. The information on registered germplasm is published with the purpose to disseminate the information to 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. Pant CMS3A & Pant CMS3B (IC0635012 & IC0635013; INGR21001), a Rice (*Oryza sativa*) Germplasm with Fully Exserted Panicle. High Number (305.31) of Grains Per Panicle. Excellent Outcrossing Rate

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Hybrid rice cultivation is gaining world wide popularity. Research on hybrid rice in China was initiated in 1964 (Yuan, 1966). The genetic tools essential for breeding hybrid rice varieties are as the male sterile line (A-line), maintainer lines (B-line) and restorer (R-line) were developed during 1973 (Yuan and Virmani, 1988). Use of gibberelic acid (GA3) at proper stage with proper dose enhances the seed set on seed parent (Virmani, 2005), but the use of GA3 also enhances the cost of seed that farmers or seed producers has to bear. The cost of one gram of GA3 in the local market varies between Rs. 120-150 depending upon the purity and company. With a view to improve the seed set of CMS lines in rice, a conversion programme in the background of an improved rice genotype, “NAT 990-99” was initiated at GB Pant University in 2003 by using widely used CMS line “IR58025A” as non recurrent parent. Progenies in each backcross generation were checked for pollen sterilityand morphological traits. In BC6 generation progeny with desired morphological traits, that is fully exterted panicles, complete sterile plants were selected and allowed to cross pollination with the maintainer line NAT 990-99 in isolation, to get the genetically pure seed of cytoplasmic male sterile line. The conversion procedure was followed as in the development of Pant CMS 2A (Nautiyal *et al.,* 2011).

Morpho-agronomic charcteristic: Newly developed PantCMS3A has got complete exserted panicle with the dark green leaves plant height 120-125 cm with sturdy stem which prevents the lodging the crop. Yield (kg/ha) was found maximum with mean value in Pant CMS3A 2043.00 kg/ha in natural conditions without using supplementary pollination in four years.

Associated characters and cultivation practices: Newly developed Cytoplasmic Genetic Male Sterile Line Pant CMS3A has 12-15 effective tillers per plant. The leaves are dark green. It is moderately resistant to bacterial leaf blight disease and tolerant to stem borer. It can be cultivated in the rice growing areas under irrigated under high fertility conditions.

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Table 1: Panicle length, Number of filled grains, Total number of grains and Yield (Kg/ha) in different CMS lines

CMS Line	*Panicle length (cm)*					*Number of filled grains*					*Total number of grains*					*Yield (kg/ha)*				
	2011	*2012*	*2013*	*2014*	*Mean*	*2011*	*2012*	*2013*	*2014*	*Mean*	*2011*	*2012*	*2013*	*2014*	*Mean*	*2011*	*2012*	*2013*	*2014*	*Mean*
IR58 025 A	20.66	21.66	20.88	21.66	21.21	23.36	27.30	23.86	27.60	25.53	174.33	175.96	174.33	172.66	174.32	1231.00	1176.00	1178.00	1231.00	1204.00
IR58 025 B	21.46	21.90	21.34	21.64	21.58	147.16	154.20	148.00	154.00	150.84	168.16	171.46	170.16	172.42	170.61	2616.00	2693.00	2700.00	2764.00	2693.25
Pusa 6A	24.73	24.93	24.80	24.93	25.59	24.72	28.90	24.20	29.00	26.70	136.40	142.00	138.62	140.00	139.25	1153.00	1193.00	1155.00	1196.00	1174.25
Pusa 6B	25.63	26.56	25.83	26.54	26.14	137.83	155.16	138.00	160.00	147.74	150.40	168.66	154.60	169.00	160.66	2393.00	2483.00	2492.00	2420.00	2447.00
Pant CM S 3A	29.13	30.66	29.30	30.66	29.93	109.20	110.50	111.00	113.25	110.98	340.26	349.83	338.40	348.20	344.17	1953.00	2043.00	2053.00	2043.00	2023.00
Pant CMS 3B	31.43	32.60	31.83	32.40	32.06	305.43	303.83	302.00	310.00	305.31	321.40	322.33	324.60	326.20	323.63	4633.00	4833.00	4833.00	5022.00	4830.25
IR79 156 A	22.46	23.00	23.34	23.00	22,95	24.96	29.00	29.20	28.60	27.94	178.23	180.20	176.33	179.20	178.49	1168.00	1180.00	1199.00	1265.00	1203.00
IR79 156 B	21.80	23.26	23.84	24.20	23.27	158.60	159.80	160.00	158.00	159.1	179.23	180.21	178.40	180.20	179.51	2899.00	2762.00	2792.00	2692.00	2786.25
CD at 5%	1.22	0.95	1.20	0.92	-	7.13	4.07	7.11	4.06	-	4.77	1.96	4.78	1.92	-	1.92	1.65	1.91	1.61	-
CV	2.63	1.98	2.60	1.96	-	3.14	1.72	3.12	1.70	-	1.22	0.48	1.20	0.49	-	4.54	3.79	4.49	3.72	-

2. AC 42997 (IC0576152; INGR21002), a Rice (*Oryza sativa*) Germplasm with Vegetative Stage Drought Tolerance. Prolific Roots. High Water Use Efficiency.

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The germplasm line (AC 42997) was collected and conserved at NRRI Rice gene bank. This showed tolerance to vegetative stage drought stress consistently for five years (2011 onwards) after rigorous screening under simulated moisture stress in NRRI. Under simulated stress during vegetative stage, AC 42997 was observed to be tolerant withleast leaf rolling SES "1", leaf death score of SES "3", had high root length density, root dry weight and root to shoot dry weight ratio (CRRI Ann. Rep 2012-13, pp- 97; Dash *et al*. 2017), high water retention capacity (>70%), at 10-13% soil moisture content and soil moisture tension of -55 to -60 kPa during the stress period. The germplasm line was tested in NRRI, Cuttack from 2011-2016 for multiple years under NICRA Project. It is identified promising and unique withmany traits compared to other genotypes.

It has high *per se* performance for more than one root traits under control and stress condition. Though many germplasm lines have been identified for drought tolerance, there is also urgency to identify more and more donors with specific traits to evolve better varieties with higher drought tolerance coupled with higher grain yields, in view of the fast-changing environments. Same level of resistance does not mean the gene (s) responsible for tolerance will be same. Hence this germplasm line/landrace may be registered as a donor for vegetativestage drought tolerance with specific root traits responsible for drought tolerance.

Table 1: Performance of AC42997 for different drought related physiological traits

Traits	*Significance*	*Reference*
Drought score	Resistant (R), SES "3"	Dash *et al.,* 2017
Root Traits	Root and shoot length: Increase in maximum rootlength under drought Root thickness: Moderateiii) Root length density: high Root biomass: High Root to shoot dry wt ratio: High under drought comparedto control root volume: high Root length density: high	Dash *et al.,* 2017, Acta Physiol. Plant (2017) 39:8 DOI10.1007/s11738-016-2297-1 CRRI Annual Report 2012-13, Pg No. 97 ARRW Golden Jubilee International Symposium on "Sustainable rice production and livelihood security: challenges and opportunities" held during 2-5 March 2013 at Central Rice Research Institute, Cuttack, Odisha. Pg No. 262-263. National Conference of Plant Physiology (NCPP) on "Frontiers of plant physiology research: food security and environmental challenges" held during 23-25 Nov 2014 at OUAT, Bhubaneswar, Odisha. Pg No. 226.
Germination percentage	High percent of germination(>90%) under 1% and 2% mannitol induced osmotic stress.	Dash GK and Swain P (2015). Oryza 52 (4): 307-312.
Water use efficiency	High water use efficiency (3.26 g biomass/kg water) under drought stress and well-watered (2.55 g biomass/kg water) condition.	International Rice Symposium on "Rice Science for Global Food and Nutritional Security" held during 18-20th Nov 2015 at Hyderabad. Pg No. 238
Transpiration rate	Slow transpiration rate per unit leaf area under well-watered (3.69 g/cm^2) and water stressed condition (3.11g/cm^2)	International Rice Symposium 2015 on "Rice Science for Global Food and Nutritional Security" held on 18-20th Nov 2015at Hyderabad. Pg No. 238
Stomatal density	Low stomatal density (352.2/mm^2)	International Rice Symposium (IRS) 2015 on "Rice Sciencefor Global food and Nutritional Security" held during 18-20th Nov 2015 at Hyderabad. Pg No. 238

3. IC330611 (IC0330611; INGR21003), a Rice (*Oryza nivara*) Germplasm Vegetative stage drought tolerance.

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The wild species of the cultivated rice are a good reservoir of genetic variability for various biotic and abiotic characters. They harbour significantly higher genetic diversity than the cultivated species. During 1999-2001, a total of 483 accessions of two common wild rice species, namely *Oryza nivara* and *O. rufipogon* were collected from south east India – where they occur abundantly. On evaluation against abiotic stress specifically to drought, two accessions of *O. nivara* (IC330611) were found tolerant to moisture stress with SES score of 0 & 1. These germplasms were collected from West Bengal and were screened under field condition at NRRI during dry season of 2003 & 2004 in augmented design. Five checks *viz*. Salumpikit, Vandana, Vanaprabha and CR 143-2-2 as tolerant and IR 20 as susceptible check were used during screening trial. Plants were grown for 35 days after germination with sprinkler irrigation. The irrigation was withdrawn for 30 or more days till the susceptible checkshowed permanent wilting followed by watering for recovery. Peizometers were fixed to monitor ground water table at 15, 30 and 45 cm depth at periodic intervals after suspension ofsprinkler irrigation. Ground water table was below 100 cm during the period of drought stressand soil moisture decreased from 30 to 5% up to 45 cm soil depth. The drought scores and recovery data was taken as per SES method (1 to 9 scale). The lines with early leaf rolling after suspension of sprinkler irrigation showed higher score for drought tolerance (7-9) and lines with delayed leaf rolling recovered faster after rewatering. The scoring of this tolerant wild riceis 1 in SES scale.

It is of significance in the context of drought situation, as the habitat of wild rice species is usually swampy places like seasonal ditches. Root length of *O. nivara* was 20.2 cm under normal condition while it was 25.7 cm under moisture stress. Root penetration in *O. nivara*, an annual wild rice species was deeper while in *O. rufipogon*, a perennial wild species, it was shallow and adventitious. Under simulated stress during vegetative stage, it is observed to be tolerant with least leaf rolling SES "1", leaf death score of SES "3" had high root length density,root dry weight and root to shoot dry weight ratio, high water retention capacity (>70%), at 10-13% soil moisture content and soil moisture tension of -55 to -60 kPa. Though many germplasm lines have been identified for drought tolerance, there is still urgency to identify more and more donors with specific traits to evolve better varieties with higher drought tolerance in view of the fast-changing environments. Same level of resistance does not mean the gene (s) responsible for tolerance will be same. Hence this germplasm line/landrace can beused as a donor for vegetative stage drought tolerance.

4. IC330470 (IC0330470; INGR21004), a Rice (*Oryza nivara*) Germplasm with Vegetative Stage Drought Tolerance

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5. Dubaraj (IC301206) (IC0301206; INGR21005), a Rice (*Oryza sativa*) Germplasm with Very High 1000-Grain Weight (50.4g).

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Rice is one of the major crops of India, where there is considerable range of variability exists. Its cultivation dates back to 6000 years ago, as it has its mention in ancient scriptures. The records claim more than 1,50,000 rice landraces which were in cultivation in India. Owing to the popularization of the fertilizer responsive, high yielding varieties, many of these landraces have vanished from the geography of India. However, the socio-economic, ethnic cultures prevailing around the rice cultivation and the thoughtful collection and conservation of the landrace diversity, more than 55,000 rice landraces are conserved in the National Genebank.

Apart from their remarkable adaptability to the local climate change, some of the landraces areknown for their unique traits. Dubaraj is one such landrace collected from the Chattisgarh region, which is one of the aromatic rice. The characterization of the germplasm collection has shown that the one of the accessions of Dubaraj, IC 301206 which has its source from Raipur,Chattisgarh, has recorded high 1000 grain weight, i.e., 50.4g.

IC301206 is a long grain rice, whose morphological characters are given below

Characteristics	*Description*
Early Plant Vigour	Very Good
Coleoptile Colour	Green
Basal Leaf Sheath Colour	Green
Leaf Blade Colour	Green
Leaf Pubescence	Pubescent
Stigma Colour	White
Ligule Shape	2-Cleft
Auricle (Pres/Abs)	Green
Awning	Long fully awned
Panicle Type	Intermediate
Panicle Exsertion	Medium well exserted
Flag Leaf Angle	Erect
Apiculus Colour	White
Leaf Senescence	Slow
Panicle Threshability	Intermediate
Husk Colour	White
Sterile Lemma Colour	Straw
Kernel Colour	White
Aroma	No scent
Seedling Height (cm)	22.8
Leaf Length (cm)	58.0
Leaf Width	1.14
Days to 50% Flowering	131 days
No. of Effective Tillers	4.4
Plant Height (cm)	177.4
Panicle Length (cm)	29
Days to Maturity	162 days
Grain Length/Breadth	4.7
1000 grain weight (gm)	50.4
Grain yield per Plant (gm)	11.01

Table continued...

6. Karuppunel (IC0637545; INGR21006), a Rice (*Oryza sativa* var. *indica*) Germplasm with High Grain Zinc Content (41.05 ppm)

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It is accepted across the global scientific community that modern day rice cultivars are high yielding but low in micronutrient status which is predisposing rice eating population to micronutrient malnutrition. The situation is grim in poor and developing nations who cannot afford to diverse diets to meet their nutrient requirements. Hence rice is the choice crop for bio fortification programmes to address the hidden hunger among poor rural populations. The rich genetic diversity of rice preserved in landraces offer huge potential for improving the nutritional status of high yielding modern rice cultivars. Karuppunel is one such landrace which has huge potential for enriching the endosperm zinc content of popular rice varieties. The accession was collected from Tamil Nadu state, purified and being maintained as part of breeders collection in the Division of Genetics, ICAR-Indian Agricultural Research Institute (IARI), New Delhi.

Morpho-agronomic characteristics: Upon evaluation of a set of 192 rice accessions for grain iron and zinc concentrations, Karuppunel recorded as high as 46.2 ppm in brown rice and 40.9 ppm in polished rice (Bollinedi *et al*. 2020a & 2020b), the values significantly higher than the recommended target of 28 ppm for biofortication programmes as per the Harvest Plus guidelines (Bouis *et al.* 2011). The accession was further nominated for testing at multiple locations under a biofortification donor trial conducted under the consortium research project (CRP) on Biofortication and it out-performed all the promising donors in the trial with a range of 29.1 ppm to 49.67 across the environments. It has also recorded considerably high mean concentration of 4.3 ppm iron in polished rice as against to 2 ppm in popular cultivars. The other agro- morphological characteristics of Karuppunel are plant height (146 cm), days to 50% flowering (98 days), panicle length (23.2 cm). It has black husk and red pericarp due to accumulation pro-anthocyanidins with beneficial health impact.

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7. IET17948 (IC0637546; INGR21007), a Rice (*Oryza* sp.) Germplasm Bacterial Blight Resistant with Three Bacterial Blight Resistance Genes, *xa5, xa13* and *Xa21* Pyramided in PR106

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Bacterial blight (BB) of rice, caused by gram-negative bacteria *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most destructive disease worldwide leading up to 60% of the yield loss undersevere condition (Jiang *et al*. 2020). Pyramiding of two or more genes will be more effective in pathogen evolution at lower rate (Singh *et al.* 2001). Here, we want to register the rice line IET- 17948 (PR106 / IRBB62 // 2*PR106) with three bacterial blight resistance genes *viz xa5*, *xa13* and *Xa21* pyramided into an Indica rice cultivar PR106 at PAU. The crosses were made between high yielding bacterial blight susceptible cultivar PR106 and IRBB62 (having 3 resistance genes). F_1 plants were backcrossed with PR106 to generate BC_1F_1's. PCR based molecular markers linked to *xa5*, *xa13* and *Xa21* resistance alleles were used to select plants from BC_1F_1 onwards. The BC_2F_3 lines having 2 or 3 homozygous genes for resistance to BB were identified on the basis of molecular marker analysis and inoculated with BB isolates/races to determine disease reaction. Genes in combinations were found to provide high levels of resistance to predominant *Xoo* isolates.

Morpho-agronomic characteristics: BC_2F_4 progenies were evaluated in commercial fields (Ludhiana, Sangrur, Jallandhar and Ferozpur) against the pathogen populations prevalent in the region. Lines of PR106 with three pyramided genes were evaluated against 17 isolates from the Punjab and six races of *Xoo* from the Philippines under natural conditions at 31 sites. The lines with three genes showed superior level of resistance as compared to the lines with either single or double bacterial blight resistance genes.

Associated characters and cultivation practices: IET17948 carries three bacterial blight resistance genes which gives complete resistance at the seedling and adult plant stage to *Xanthomonas* pathotype seven.

References

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8. ILPAUGS_BPH34 (IC0637548; INGR21008), a Rice (*Oryza* sp.) Germplasm Resistance against BPH Biotype 4 Prevalent in India carrying the novel Brown plant hopper resistant gene BPH 34 from *Oryza nivara* acc. IRGC104646 on rice chromosome 4

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Brown Planthopper (BPH, *Nilaparvata lugen* Stål) is one of the most destructive insects of rice (*Oryza sativa* L.) causing significant yield losses annually. Exploiting host plant resistance to BPH and incorporating resistant genes in susceptible commercial cultivars is economical and environmentally friendly approach to manage this pest. Here, we want to register a stable F8 recombinant inbred line, PAUGS_ BPH (34) with brown plant hopper resistance. This gene was introgressed from *Oryza nivara* accession IRGC104646 to the indica rice cultivar Punjab Rice 122 (Kishor *et al.,* 2017, Sarao *et al.,* 2016). This accession was found resistant against BPH biotype 4, prevalent in Indian subcontinent. Inheritance study using F_2 and $F_{2:3}$ populations revealed the presence of single dominant gene. This novel BPH resistant gene wasmapped on long arm of rice chromosome 4 and designated as *Bph34*. Two of the SSR markers RM16994 and RM17007 were found co-segregating with the *Bph34*. We have generated homozygous resistant F9 progenies (PR122/ *O. nivara* IRGC 104646) with good agronomic background. This genetic stock could be used by plant breeders for further transfer of BPH resistance to other elite cultivars using marker assisted selection.

Morpho-agronomic characteristics: The Agro-morphological features include green sheath, acute-white ligule, erect leaf blade, whitte stigma, straight panicle, white lemma, yellowish white awns at tip and erect to semi-erect panicle branches on straight main axis of panicle.

Associated characters and cultivation practices: The genetic stock IL PAUGS_ BPH (34) has brown plant hopper resistance against BPH biotype 4 prevalent in India. Standard rice agronomic practices can be used.

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9. PAU_CB28 (PR114_Xa38) (IC0637549; INGR21009), a Rice (*Oryza sativa*) Germplasm Carries Bacterial Blight Resistance Gene from *Oryza nivara*

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Bacterial blight (BB) of rice caused by *Xanthomonas oryzae pv oryzae (Xoo)* is one of the major Constrain to the productivity in South-East Asia (Cheema *et al.,* 2008, Bhasin *et al.,* 2012). Anaccession of *Oryza nivara* (IRGC 81825) was found resistant to all the seven *Xoo* pathotypesprevalent in northern states of India. The inheritance studies was conducted using F_2, BC_2F_2,BC_3F_1 and BC_3F_2 progenies of the cross involving *Oryza sativa* cv PR114 and the *O. nivara* acc.81825 using the most virulent *Xoo* pathotype seven. Genetic analysis of the segregating progenies revealed that the BB resistance in O. nivara was conditioned by a single dominant gene. This novel bacterial blight resistance gene was mapped on long arm of chromosome 4 and designated as *Xa-38*. The PCR-based sequence-tagged site marker was developed for effective transfer of the *Xa-38* bacterial blight resistance gene. The homozygous resistant BC3F3 progenies with smallest introgression region have been identified and single seed decent method was used for the generation advancement till BC3F10.Here, we want to register PAU_CB28 (PR114/O. nivara IRGC81825//2*PR114) with bacterial blight resistance.

Morpho-agronomic characteristics: The Agro-morphological features include green basal leaf sheath color. Leaf pubescence of blade surface was absent. The shape and color of the ligule were acute and white, respectively. Early and late observation showed that the flag leaf (attitude of the blade) was erect. Spikelet density of pubescence of lemma was weak. Anthocyanin colorof both lemma at the apex and stem at the nodes was absent. Spikelet's color of stigma was white. The panicle curvature of the main axis was straight. The color of the tip of the lemma in the spikelet was white. The awns were absent or very small. The attitude of branches of panicle was erect to semi-erect.

Associated characters and cultivation practices: PAU_CB28 (PR114_*Xa* 38) carries bacterial blight resistance gene *Xa38* from *Oryza nivara* acc.IRGC 81825 which gives complete resistance at the seedling and adult plant stage to *Xanthomonas* pathotype seven. Standard agronomic practices for rice growing can be used.

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10. IET19339 (IC0637550; INGR21010), a Rice (*Oryza* sp.) Germplasm IET19339 carries three Bacterial Blight Resistance Genes *xa5, xa13* and *Xa21*, Pyramided into cv. Pusa 44

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Bacterial blight (BB) of rice, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is major yield limiting biotic stress in rice production in the Punjab state as rice is grown under irrigated and high fertilizer input conditions that are conducive to the disease development (Lore *et al*. 2011) The identification and exploitation of resistant germplasm is one of the effective and environmentally acceptable approaches to counteract the damage caused by this pathogen. Pyramiding of two or more genes will be more effective in pathogen evolution at lower rate. Here, we report the pyramiding of three bacterial blight resistance genes *viz xa5*, *xa13* and *Xa21* into *indica* rice cultivar Pusa 44 at PAU. F_1 plants were backcrossed with Pusa 44 to generate BC_1F_1's. PCR based molecular markers linked to *xa5*, *xa13* and *Xa21* resistance alleles wereused to select plants from BC_1F_1 onwards. The BC_2F_3 lines having 2 or 3 homozygous genes for resistance to BB were identified on the basis of molecular marker analysis and inoculated with BB isolates/races to determine disease reaction. We want to register a stable backcrossed introgression line with bacterial blight resistance. Genes in combinations were found to provide high levels of resistance to predominant *Xoo* isolates.

Morpho-agronomic characteristics: The basal leaf sheath color of plants was green. Leaf pubescence of blade surface was absent.The shape and color of the ligule were acute and white respectively. Early and late observation showed that the flag leaf (attitude of the blade) was erect. Spikelet density of pubescence of lemma was weak. Anthocyanin color of both lemma at the apex and stem at the nodes wasabsent. Spikelet's color of stigma was white. The panicle curvature of the main axis was straight. The color of the tip of the lemma in the spikelet was white. Panicle awns were present. Late observation showed the yellowish-white color of awns and was present only at the tip. The attitude of branches of panicle was erect to semi-erect.v

Associated characters and cultivation practices: The rice genetic stock ITE19339 carries three bacterial blight pyramided resistance gene and provides complete resistance at the seedling and adult plant stage to *Xanthomonas* pathotype seven. Standard agronomic practices for rice growing can be used.

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11. EC670488 (EC670488; INGR21011), a Rice (*Oryza sativa* x *O. glaberrima*) Germplasm Tolerant to High Temperature Stress (>35ºC) at Reproductive Stage with Very High Spikelet Fertility Particularly Under High Temperature Stress

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Climate change and global warming are posting a serious threat to agricultural productivity worldwide. India is projected to suffer from temperature spike to a tune of 4.7-5.5°C by 2100 paralleling global climate change. Rice is sensitive to heat stress especially at anthesis stage which will be directly reflected in significant grain yield reduction. A new reproductive stage heat stress tolerant (RSHT) genotype NERICA

L 44 (NL 44) shows tolerance levels almost at par with the upland aus rice variety, Nagina 22, which is one of the most reported for heat stress tolerance in rice. The unique nature of this genotype is, its peak anthesis falls around 10.00 am when the ambient temperature has already begun to raise making ita truly RSHT genotype. NL 44 is a NERICA rice variety developed from the inter-specific cross between *Oryza glaberrima* (African rice) and *O. sativa* (Asian rice). In our screening for reproductive stage heat stress tolerance, the rice genotypes, NL 44 consistently showed superior spikelet fertility and grain yield under heat stress evaluated at two locations, Aduthurai and Cuttack during two consecutive seasons (off-season) 2019-20 and 2020-21. The performance of NL 44 in comparison with popular checks in various heat stress trials are summarized in Table 1. The genotype maintained a spikelet fertility percentage of ~85% under heat stress (> 35°C) and grain yield plant^{-1} of ~20g (Ravikiran *et al.* 2020). A representative picture showing the panicles and grains (filled and unfilled) under normal (33–35°C) and heat stress (>35°C) in the heat stress tolerant rice genotype, NL44 and the sensitive rice variety, Pusa Basmati 1 is presented in Figure 1. Trait specific validation was carried out using 113 SSR markers linked to the 54 different QTLs previously reported for reproductive stage heat stress (RSHS) tolerance, identified NL44 as a novel donor for RSHS tolerance in rice (Ravikiran *et al.* 2020).Additionally, unlike N22, NL 44 possesses other desirable characteristics such as photo insensitivity, short stature, good grain quality attributes, etc. The grain quality characteristics of this genotype are acceptable (long slender with moderate amylose content) making it an invaluable donor to breed RSHT rice varieties.

The following are salient characteristics of this genotype:

- Under normal conditions shows a spikelet fertility ~ 90%, while under heat stress (>35^{0}C)maintains 80-85% spikelet fertility
- Photo-insensitive, short stature (90-95 cm) and medium duration (days to 50% flowering – 105-110 days) genotype
- Well exerted, erect to semi-erect, long (28-30 cm) panicles (13-15 in number per plant) awnless grains
- Grain yield at normal temperatures is 26-28g per plant while under heat stress it is 19-22g.
- Long slender grain type with medium test weight (20-23g), elongation ratio (~1.57) and amylose content.

Table 1: Relative performance of NL 44 during off-season, 2018-19 and 2019-20 at two locations, Aduthurai and Cuttack

Season	*Trait*	*Treatment*	*NL44*	*Nagina 22*	*IR64*	*Pusa Basmati 1*
Off Season2018-2019, Aduthurai	GYPP (g)	Control	25.75	18	25.5	26.05
		Heat Stress	20.64	17.45	14.4	14.79
	Spikelet Fertility (%)	Control	87.71	92.52	85.83	74.66
		Heat Stress	84.35	91.46	70.76	42.85
Off Season2019-2020, Aduthurai	GYPP (g)	Control	24.33	17.05	26.84	22.85
		Heat Stress	19.3	12.58	12.3	8.76
	Spikelet Fertility (%)	Control	91.16	94.39	85.38	81.34
		Heat Stress	84.35	91.79	72.41	41.62
Off Season2018-2019, Cuttack	GYPP (g)	Control	20.31	16.53	20	20.7
		Heat Stress	12.25	8.03	8.63	4.67
	Spikelet Fertility (%)	Control	84.08	90.58	84.08	85.88
		Heat Stress	78.23	89.15	62.37	45.61
Off Season2019-2020, Cuttack	GYPP (g)	Control	25.66	18.27	25.27	23.86
		Heat Stress	85.7	92.41	91.12	71.27
	Spikelet Fertility (%)	Control	17.71	13.3	10.63	12.27
		Heat Stress	78.17	88.52	62.68	40.22

12. Pusa Rice Restorer 402 (PRR 402) (IC0637551; INGR21012), a Rice (*Oryza sativa* var. indica) Germplasm Tropical japonica based NPT line, which is a restorer of WA cytoplasm possessing the restorer gene, Rf4, developed in the background of a popular indica rice variety Pusa 44.

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Rice is grown in an area of about 44 million hectares in India with an annual production of about 105 million tonnes of milled rice and average productivity of 2,500 kg of paddy per ha. But the present trend of rice production and productivity will be inadequate to meet the future demand of the fast-growing Indian population. Therefore adoption of hybrid rice is one of the alternate tools to mitigate the yield barrier. Hybrid rice technology in India so far was exclusively dependent on the *indica* germplasm but the level of heterosis is low. Parental lines of the *indica* background are relatively less diverse compared to *japonica* types. Among the various available rice germplasm lines, Tropical *japonica* (TRJ) rice germplasm enjoys special reference as an alternative source for increasing heterosis level in rice. While introducing the new plant type (NPT) concept at the International Rice Research Institute, Philippines (IRRI), Khush (1995) suggested that the ideotype approach is effective for breaking the yield ceiling of an irrigated rice crop.

Keeping this in mind, a series of cross combinations were made between Pusa 44, a popular non-aromatic rice variety released from ICAR-Indian Agricultural Research Institute (ICAR-IARI), New Delhi with diverse TRJ lines sourced from IRRI. The pedigree breeding approach was followed to develop NPT lines. Selection was focussed primarily on NPT characters. A total of 310 lines possessing desirable NPT traits were identified through an evaluation conducted at New Delhi in the ICAR-IARI research farm. The selected lines were further screened by molecular markers namely DRRM-RF3-5, DRRM-Rf3-10 and RMS-SF21-5 linked with fertility restorer genes *Rf3* and RMS-SF21-5 and RM 6100 linked with *Rf4*. Based on marker data 42 restorers were shortlisted and field evaluated during *Kharif* 2017 at three diverse locations *viz.*, New Delhi, Gerua (Assam) and Aduthurai (Tamil Nadu). The restorers were also crossed to a WA-CMS line "Pusa 6A", to understand their restoration ability and evaluated at the aforesaid 3 different aforesaid locations.

Morpho-agronomic characteristics: Based on the multilocation evaluation Pusa Rice Restorer 402 (PRR 402), a tropical *japonica* based NPT line, which is a restorer of WA cytoplasm possessing the restorer gene *Rf4* (Shidenur *et al* 2019), developed in the background of a popular *indica* rice variety Pusa 44 has been identified as one of the promising line. It has all NPT characters such as plant height of 85–92 cm, 10 to 13 productive tillers, sparse unproductive tillers, sturdy culm, heavy panicles having 200 to 250 grains, dark green leaves, and growth duration of 110 to 130 days. The potential of PRR402 as an efficient NPT based rice restorer for exploitation of heterosis has also been demonstrated (Shidenur *et al*. 2020). It produced fertile hybrid (pollen fertility- 91.44% to 96.46% and spikelet fertility- 80.07% to 85.32%) when crossed with a male sterile line, Pusa 6A (Table 1).

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Table 1: Level of heterosis of PRR 402 derived hybrid over the three locations

Combination	*New Delhi*		*Aduturai*		*Assam*		*Across location*	
	SH (%)	AH (%)	SH (%)	AH (%)	SH (%)	AH (%)	SH (%)	AH (%)
Pusa6A/PRR402	49.23**	68.67**	15.72*	32.63*	14.49**	26.87*	26.89**	43.12**

*P<0.05 and **P<0.01; SH: Standard heterosis (for yield per plant); AH: Average heterosis (for yield per plant)

13. Improved White ponni (IWP)-Saltol (IC0638602; INGR21013), a Rice (*Oryza sativa* var. indica) Germplasm Salinity Tolerant line.

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Salinity is one of the major abiotic stresses limiting rice productivity under marginal environments. The progress in development of salinity tolerant rice through Conventional breeding is slow due to complex nature of tolerance mechanisms. In the present study, efforts have been taken to generate NILs of a popular rice variety Improved White Ponni exhibiting increased tolerance against salinity through marker assisted introgression of a major effect QTL 'Saltol' from FL478. The hybridization was between these two parents during *Kharif* 2013. Three backcrosses were performed by using foreground, recombinant and background markers. Genotyping and phenotyping of BC3F1 progenies resulted in the identification of elite NILs of IWP harboring Saltol loci and with >90% of recurrent parent genome recovery. IWP-Sal tol NILs *viz.,*5-35, 5-36 and 5-45 exhibited enhanced tolerance against salinity under hydroponic conditions. The selected NILs were screened under field conditions for their agronomic traits. NIL # 5-36 exhibited superior agronomic performance (58% increased yield over IWP under saline conditions) and superior grain/cooking quality traits than that of IWP. Evaluation of Nils for grain quality traits showed that NILs were found to possess comparable grain quality and cooking quality traits as that of Improved White Ponni. All the three NILs found to possess slender grain type with L/B ratio ranging between 2.65 and 2.86. Overall this study led to the development of salinity tolerant versions of Improved White Ponni through Marker Assisted Back Cross Breeding. (Valarmathi et al., 2019). Under AICRP, IWP- Sal tol was tested under moderate coastal saline tolerant variety trial (CSTVT) at three locations namely Goa (GOA), Kerala (KE) and AP (Andhra Pradesh). Results revealed that IWP-Saltol recorded 1108 kg/ha under salinity stress which is 57.6% over recurrent parent IWP (703 kg/ha). Pooled analysis of data under Multi Location Trials conducted in various locations of Tamil Nadu revealed that IWP-Sal tol recorded 3595 kg/ha which is 16.6% over IWP (RP) (3111 kg/ha). Newly developed salinity tolerant version of Improved white ponni will help in sustaining rice yield under salinity prone areas and it will serve as ideal genetic material for functional genomic studies.

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14. Kolajoha (IC00298323; INGR21014), a Rice (*Oryza sativa* var. *indica*) Germplasm Salinity tolerant.

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Kolajoha is a popular small grain non-Basmati type aromatic rice genotype cultivated in the North-Eastern state of Assam, India. It is selected for its notable aroma in grain and its salinity tolerant status. It has given the GI tagged due to its unique aroma.

Morpho-agronomic characteristics: The genotype is diploid with awnless seed. Seeds are having black coat colour and yellowish white superfine kernel. Kernel length is < 5.5 mm and length to breadth ratio is <3. Grains have strong aroma with 100-200% kernel elongation after cooking. It is tall, photosensitive, takes long duration to mature (160 days).]

Associated characters and cultivation practices: The genotype is low yielding but preferred for preparing table rice, Kheer, Pulao and frumenty. The most commonly present compound in Kola Joha is 2-acetyl-1- pyrroline which is responsible for its aroma. It resulted in lower SES, Na^+ concentration, ratio of Na^+/ K^+ and higher K^+ content under 100 mM salt (NaCl) stress at seedling stage which shows it is highly salinity tolerant. It is adapted to local conditions in Assam where Basmati cannot be grown.

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15. Negheri bao 1 (IC0394535; INGR21015), a Rice (*Oryza sativa*) Germplasm Anaerobic germination tolerant.

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Negheri bao is the indigenous landrace variety collected from North Lakhimpur of Assam. It is selected for its ability to germinate and survive under anaerobic conditions. The SNP genotyping of this landraces has been done by using 50K SNP rice genic chip (Rohilla *et. al.* 2020).

Morpho-agronomic characteristics: Negheri bao 1 is diploid rice plant (2n=24) which underflooding conditions can grow up to a height of 2 meter. It has a large sized leaf, longer panicle,and a large number of spikelets per panicle compared to crops grown without deep water situation. The culm or stem of this bao does not grow entirely erect, rather it becomes zigzag under deep-water condition. Branching does not take place under water. Adventitious roots first develop from the uppermost nodes below the water surface to extract nutrients from the water.

Associated characters and cultivation practices: The crude protein content of this brown rice is significantly high thus it is important from nutritional point of view (Mudoi and Das, 2018). The Sowing of this variety in Assam is done during March to April, as they take more than 300 days to mature. Seeds are normally sown directly in the soil before the rainy season and harvesting is done after the flood water recedes. Chemical fertilizers are not used for cultivation of this rice.

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16. Saragphala-2 (IC0591486; INGR21016), a Rice (*Oryza sativa*) Germplasm Anaerobic germination tolerant.

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Saragphala-2 is a bao rice which is indigenous landrace variety collected from North Lakhimpur of Assam. It is selected for its ability to germinate and survive under anaerobic conditions. The SNP genotyping of this landraces has been done by using 50K SNP rice genic chip (Rohilla *et. al*. 2020).

Morpho-agronomic characteristics: Saragphala bao is diploid rice plant (2n=24) which under flooding condition can grow up to a height of more than 1 meter. It has a large sized leaf, longer panicle, and a large number of spikelets per panicle compared to crops grown without deep water situation. The culm or stem of this bao does not grow entirely erect, rather it becomes zigzag under deep-water condition. Branching does not take place under water. Adventitious roots first develop from the uppermost nodes below the water surface to extract nutrients from the water.

Associated characters and cultivation practices: Under submergence stress conditions at germination stage, this genotype have ability to get enough oxygen for their metabolic activity and rapid coleoptile elongation ability. It is anaerobic germination tolerant genotype also having high anaerobic index than national positive check (Nanhi and Kalongchi). Its anaerobic germination tolerance ability makes this genotype very useful in direct seed sowing cultivation (Rohilla *et. al*. 2020). The Sowing of this variety in Assam is done during March to April, as they take more than 300 days to mature. Seeds are normally sown directly in the soil before the rainy season and harvesting is done after the flood water recedes. Chemical fertilizers are not used for cultivation of this rice.

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17. BRW3806 (IC0637552; INGR21017), a Wheat (*Triticum aestivum*) Germplasm Resistant to wheat blast disease.

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Wheat is an important food crop in India often seriously affected by biotic and abiotic constraints causing serious yield losses. Additionally, the incidence of wheat blast in Bangladesh poses a threat to the wheat crop in the tropical and subtropical regions of Asia in sustaining food security. Therefore breeding wheat for tolerance to biotic and abiotic stresses has been the main breeding objective in any breeding programme. Genotype BRW 3806 was developed at ICAR-IIWBR, Karnal from the cross NI 5439/MACS 2496 following pureline breeding method and later on was selected by BAU-Sabour for testing in the Restricted irrigation trials under AICRP on wheat and Barley for three consecutive years from 2016-17 to 2018-19. Genotype BRW 3806 was included in Indian material sent for screening against wheat blast disease and was identified to be resistant to wheat blast disease at Jessore, Bangladesh and Bolivia under artificial screening. BRW 3806 was also found to be resistant to all the races of *Puccinia graminis tritici* tested at seedling stage having gene combination *Sr28*+5+ against stem rust. This genotype carries *Yr2* against yellow rust and *Lr13*+1+ against leaf rust.

Besides this, the genotype has shown superior performance (51.6 q/ha) under restricted irrigation condition as compared to the checks WH 1080 (45.3 q/ha), PBW 644 (45.32 q/ha) and HD 3043 (43.41 q/ha), WH 1142 (47.9 q/ha) and HD 3237 (50.0 q/ha) (~14 locations in NWPZ) (Table 1; pooled over three years). This genotype flowers and matures in about 105 days and 151 days, respectively. This genotypes had a plant height of 110cm and thousand grain weight of 43g.

Table 1: Summary of yield data for BRW 3806 along with checks in the coordinated trials.

Item	*Year*	*Sites*	*Geneticstock BRW 3806*	*Check varieties*				
				WH1080	*PBW644*	*HD 3042*	*WH1142*	*HD 3237*
Meanyield (q/ha)	2016-17	8	56.5	-	-	-	51.6	-
	2017-18	13	48.5	44.8	44.7	41.7	45.5	-
	2018-19	14	49.8	45.7	45.9	45.0	47.9	50.0
	Mean		51.60	45.25	45.3	43.35	48.33	50.0

Table 2: Yield performance of BRW 3806 in the NWPZ- RIR-TS-TAS trial during 2018-19.

Variety	*Zero irrigation*	*One irrigation*	*Two irrigation*	*Mean Yield*
BRW 3806	41.85	49.06	54.39	48.43
Checks				
WH1142	40.46	48.2	52.10	46.92
HD 3043	37.32	44.01	49.25	43.53
PBW 644	38.72	48.2	52.10	44.54
WH 1080	39.06	46.66	50.82	45.10

During 2018-19, this genotype was also evaluated in the agronomy trial (NWPZ- RIR-TS- TAS) and BRW 3806 (48.43 q/ha) top ranked among all the test and check varieties (ten locations) (Table 2). BRW 3806 has shown good chapatti making quality (7.60) and biscuit making quality (7.79) with the gluten index of 95.

The resistant to wheat blast disease and superior performance under restricted irrigation conditions makes BRW 3806, a potential donor to be utilized for breeding wheat for blast resistance and moisture tolerance.

18. ER9-700 (IC0637553; INGR21018), a Wheat (*Triticum aestivum*) Germplasm with Novel Leaf Rust Resistance introgressed from *Aegilops markgrafii*.

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Plant germplasm registration of ER9-700, a *T. aestivum* genetic stock carrying *Ae. markgrafii* introgression. ER9-700 is highly resistant to leaf rust pathogen *Puccinia triticina* and the resistance gene (*LrM*) is mapped to telomeric end of short arm of 2A chromosome. *LrM* can be utilized for imparting disease resistance in wheat breeding programmes.

ER9-700 is highly resistant to leaf rust (*Puccinia triticina* Eriks.) showing infection types “0” or “0;” against 15 leaf rust races. It was developed with the intent of transferring novel gene(s) from C genome of *Aegilops markgrafii* (CC; $2n=2x=14$) to bread wheat at Division of Genetics, IARI, New Delhi. The 5B nullisomy method was used to induce homoeologous pairing and recombination between wheat and *Ae. markgrafii* chromosomes (Riley and Chapman 1958; Sears and Okamoto 1958). A 5B monosomic plant (mono 5B, $2n - 1 = 41$) in bread wheat cultivar Lal Bahadur was emasculated and pollinated using *Ae. markgrafii* (Accession No. EC331770, PI 369571) pollen. The interspecific F_1 plants with 27 chromosomes were cytologically identified at metaphase I of meiosis following the method described earlier (Niranjana *et al.* 2017) and were backcrossed using pollen of Lal Bahadur ($2n=6x=42$). Leaf rust resistant BC_1F_1 plants were backcrossed with Lal Bahadur and selfed to develop BC_2F_5 generation. One of the lines ($BC_2F_{4:5}$) *viz.*, ER-9 was homozygous for leaf rust resistance showing 3:1 (resistant: susceptible) segregation. But it exhibited sterility in a few spikelets. Hence, fresh pollen from a few individual plants of ER-9 (BC_2F_9 generation) were used to pollinate Agra Local. One of the F_2 populations showed complete fertility and segregated into 3 resistant: 1 susceptible, was advanced to the next generation and maintained by self-pollination. One of the resistant F_4 plants showed normal 21 bivalent configurations in all the PMCs which was named ‘ER9-700’. Genetic analysis revealed that a single dominant gene (*LrM*) imparts leaf rust resistance in ER9-700. This gene was mapped to short arm of chromosome 2A using two SSR and three SNP-based PCR markers. Three SNP based PCR markers *viz.*, SNP_AX-948171722AS, SNP_AX-945380402AS and SNP_AX-945219402AS were closest at a distance of 2.0 cM from *LrM*. Genomic in situ hybridization confirmed the presence of C genome toward the telomeric end of a pair of chromosomes (Kirti *et al.* 2020). Several leaf rust resistance genes have been derived from wild species, however, there is no report of introgression of leaf rust resistance genes from *Ae. markgrafii* (McIntosh *et al.* 2017). This novel leaf rust resistance gene (*LrM*) will diversify the repertoire of rust resistance genes useful in wheat rust resistance breeding.

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19. TMD6-4 (IC0637554; INGR21019), a Wheat (*Triticum aestivum*) Germplasm with Leaf Rust Resistance from *Triticum militinae* introgression.

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Plant germplasm registration of TMD6-4, *T. aestivum* genetic stock carrying *T. militinae* introgression. TMD6-4 exhibited resistance to leaf rust pathogen *Puccinia triticina* Eriks. and exhibits infection types ranging from '0;' to '1+' against fifteen pathotypes from five diverse groups and can be utilized for broadening the genetic base and rust resistance in wheat breeding programmes.

T. militinae Zhuk. et Migusch. (A^tG, $2n=4x=28$) is a tetraploid wild species belonging to the secondary gene pool of wheat. It is a free-threshing form of *T. timopheevii* and was discovered by Zhukovsky in 1950 (Zhukovsky and Migushova1969; Jakobson *et al*. 2006). A *T. militinae* accession (117001) was received from Institute of Plant Science Research, Norwich, England in 1993. TMD6-4 is derived from the cross CS/*T. militinae*//3*NI5439. Meiotic analysis of TMD6-4 showed 21 bivalents indicating its cytological stability (Nataraj *et al.* 2018). TMD6-4 exhibited high degree of seedling stage resistance with infection type (IT) ranging from '0;' to '1+' against fifteen pathotypes from five diverse groups (12, 77, 104, 108, 162) indicating broad-spectrum resistance towards leaf rust. Further, to identify the *T. militinae* introgressions in TMD6-4, molecular characterization was carried out using SSR markers (Nataraj *et al.* 2018). Results indicated that TMD6-4 carried 2.8% of introgression from *T. militinae*. Genome wise analysis of introgression in TMD6-4 showed maximum introgression (3.7%) in B genome, 2.5% in A genome and 2.2% in D genome. The pairing of chromosomes during meiosis between "A" of Chinese Spring and "A^t " of *T. militinae* is primarily homologous, while B and G genomes are similar and shows homoeologous pairing (Gill and Chen 1987). Hence transfer of genes from both A^t and G genomes of *T. militinae* is possible. TMD6-4 is a good source of novel leaf rust resistance and can be used as donor for imparting leaf rust resistance in wheat improvement programme.

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20. TMD 11-5 (IC0637555; INGR21020), a Wheat (*Triticum aestivum*) Germplasm with Leaf Rust Resistance from *Triticum militinae* introgression.

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Plant germplasm registration of TMD11-5, a *T. aestivum* genetic stock carrying *T. militinae* introgressions. TMD11-5 is highly resistant to leaf rust pathogen *Puccinia triticina* and exhibits infection types ranging from '0;' to '1+' against fifteen pathotypes from five diverse groups. The resistance can be utilized for imparting disease resistance in wheat breeding programmes.

TMD11-5 is a genetic stock derived from the cross CS/T. *militinae* acc. no. 117001//3*CS and was found to be cytologically stable (Nataraj *et al.* 2018). *T. militinae* Zhuk. et Migusch. (A^tG, $2n=4x=28$) belongs to the secondary gene pool and is a free-threshing form of *T. timopheevii* which was discovered by Zhukovsky in 1950 (Zhukovsky and Migushova 1969; Jakobson *et al.* 2006). Some consider it as a spontaneous mutant of *T. timopheevii* (Dorofeev *et al.* 1987) and others believe it to have originated from an introgressive hybridization between *T. timopheevii* and *T. carthlicum* Nevski (*T. persicum* Vav.) (Navruzbekov 1981; Jarve *et al.* 2002). T. militinae acc. no. 117001 was received in 1993 from Institute of Plant Science Research, Norwich, Norfolk, England, Great Britain. TMD11-5 showed high degree of seedling stage resistance with infection type (IT) ranging from '0;' to '1+' against fifteen pathotypes from five diverse groups *viz*., 12, 77, 104, 108, 162. Analysis of SSR genotyping data confirmed the introgression of 8.6% genomic regions from *T. militinae* into TMD11-5 (Nataraj *et al.* 2018). TMD11-5 showed maximum introgression of 12.2% in A genome, 6.8% in B genome, 6.8% in D genome. Since B and G genome share greater homology between them than with any other genome of the Triticeae (Gill and Chen 1987), gene transfer from timopheevii wheat to common wheat is possible by direct hybridization. The pairing of chromosomes during meiosis between A and A^t genomes is primarily homologous while pairing between B and G genomes is homoeologous (Gill and Chen 1987) enabling transfer of genes from both A^t and G genomes of timopheevii wheat.

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21. DWAP 1608 (IC0638605; INGR21021), a Wheat (*Triticum aestivum*) Germplasm with Heat and Drought Tolerance.

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The wheat growing areas in the country are exposed to several abiotic stresses during crop growth stages in India. Among these, heat stress becoming important which affects grain filling and thereby lowering the yield potential of the genotypes. Simultaneously the wheat areas in central and peninsular India are experiencing water deficit conditions resulting in drought conditions. Keeping in view a systematic research effort as wheat improvement for warmer areas was initiated at ICAR-IIWBR, Karnal with focus on development of early maturing wheat genotypes that can withstand terminal heat stress during grain growth period and yield more than the other traditional cultivars. This programme has major component of shuttle breeding approach that resulted in development of heat stress as well as drought stress tolerant varieties. In this programme, a number of advanced genotypes were developed and contributed to yield trials and nurseries.

The genetic stock DWAP 1608 (28 ESWYT 107/RAJ 4037) was developed through modified pedigree method. The female parental line 28ESWYT107 (BL1496/Milan/3/Croc_1/

Performance of entries in multi-locational station trial under late sown condition

Entry	Yield (q ha^{-1})	Leaf rust (ACI)	Black rust (ACI)
DWAP 1608	41.9	5S (1.7)	20MS (8.2)
DBW 71 (C)	39.6	5S (1.0)	20MS (7.0)
DBW 14 (C)	37.8	10S (3.2)	60S (22.7)

Ae. squarrosa (205)//Kauz) was germplasm line selected from CIMMYT nursery in 2007-08. The male parental line Raj 4037 was high yielding variety released for timely sown irrigated conditions of Peninsular zone (PZ). As PZ is the only zone where crop exposed to early heat, terminal heat stress in addition to drought conditions, this cross was made to develop heat as well as drought tolerant genotype. DWAP 1608 was evaluated in IIWBR station trial 3 meant for late sown irrigated conditions. Based on its superior performance to the checks, it was promoted in NIVT 3B as DBW 271 during 2017-18 crop season.

At the same time, this genotype was contributed in multilocational NICRA trials and was evaluated for two consecutive crop seasons 2017-18 and 2018-19. The trial was conducted under different production conditions namely timely sown irrigated, timely sown rainfed, late sown irrigated and late sown rainfed conditions at Akola, Karnal and Powarkheda alongwith six heat and drought tolerant check genotypes. Simultaneously same set was also evaluated under rain out shelter during both the crop seasons at Karnal. Data on yield components and phenological traits were recorded under all the three conditions. Susceptibility index was calculated considering irrigated timely sown as control or non-stressed condition, timely rainfed as droughtstress, irrigated late sown as heat stress and rainfed late as heat and drought stress together. Based on pooled data of two crop seasons across three locations namely Akola of PZ, Powarkhedaof CZ and Karnal in NWPZ under late sown irrigated conditions, DWAP 1608 was identified as heat tolerant genotype (Sareen *et al.,* 2019). Similarly, pooled data under late sown rainfed condition also categorized DWAP 1608 as drought and heat tolerant genotype.

It is concluded that the genotype DWAP 1608 is highly tolerant to heat as well as drought stress conditions which may be a potential donor in future wheat improvement programmes for tolerance to abiotic stress conditions.

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Pooled susceptibility index of promising entries in multilocation trial during 2017-18 & 2018-19

Genotype	Akola (PZ)	Powarkheda (CZ)	Karnal (NWPZ)	Pooled
Heat susceptibility index (HSI) under late sown irrigated conditions				
DWAP 1608	2.74	-1.29	1.01	0.42
AKW 2862-1 (C)	1.72	0.61	0.87	0.74
HTW 11 (C)	1.55	0.00	0.97	0.81
HINDI 62 (C)	-0.71	2.19	0.53	0.86
DHTW 60 (C)	0.77	2.17	0.52	0.90
Drought & heat susceptibility index (DHSI) under late sown rainfed conditions				
DWAP 1608	1.00	0.12	0.87	0.77
AKW 3717 (C)	0.70	1.05	0.84	0.85
HINDI 62 (C)	0.59	1.37	0.85	0.94
HTW 11 (C)	0.97	0.60	1.10	0.98
HTW 6 (C)	0.86	1.01	1.07	1.00

22. KHTW-1 (BST1 (ST 1A) (IC0637557; INGR21022), a Wheat (*Triticum aestivum* subsp. *aestivum*) Germplasm with Heat Tolerance and Better Heat Susceptibility Index.

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As global climate change is becoming evident, the staple food crops such as wheat are facing the brunt of increased events of high temperature stress. High temperature stress especially at grain filling duration is affecting wheat yield significantly. Identification and development of heat tolerant wheat germplasm lines is therefore of prime importance nowadays. In this direction under the NICRA project, 42 wheat germplasm lines along with 4 heat tolerant checks were screened for heat tolerance under timely and late sown conditions.

The experiment was conducted at three locations *viz*., Akola, Powarkheda and Karnal during two years i.e. 2017-18 and 2018-19. Grain yield and related phenological parameters were recorded. Heat susceptibility index (HSI) was calculated considering timely sown irrigated condition as control. Based on the mean HSI over years and locations it was found that, BST1(ST 1A) was having significantly lower HSI values than that of the checks.

BST1 (ST 1A) found to be superior with HSI of 0.24 in comparison to all the four heat tolerant check varieties *viz*., AKW2862-1 (HSI=0.74), HTW11 (HSI=0.81), Hindi 62 (HSI=0.86) and HTW60 (HSI=0.9). BST1 (ST 1A) was also superior to all the test genotypes. Therefore, BST1 (ST 1A) would be a potential source as heat tolerance donor parent. This valuable germplasm may be utilized in breeding programs to develop bread wheat varieties suitable for terminal heat tolerance.

Table 1: Heat susceptibility index (HSI) of genotypes tolerant to heat stress under late sown irrigated conditions (pooled over three locations and two crop seasons)

Genotypes	*Karnal*	*Powarkheda*	*Akola*	*Pooled*
KHTW-1 (BST1 (ST 1A))	0.42	0.24	1.91	0.24
QBP 1606	0.56	-0.17	-1.41	0.27
HTW 65	0.86	0.81	0.16	0.35
DWAP 1608	1.01	-1.29	2.74	0.42
HTW 67	1.04	-0.53	0.72	0.46
WS 2016-12	0.64	0.12	2.42	0.50
CNM 16-Jan	0.3	0.88	1.52	0.53
QBP 1605	0.5	0.54	1.63	0.53
QBP 1608	1	-0.18	1.21	0.58
WS 2016-4	0.6	0.57	0.14	0.59
HTW 64	0.8	0.8	-1.03	0.62
DWAP 1607	1.08	-0.09	0.39	0.70
RWP 2016-10	0.84	0.91	2.6	0.79
LBP 2016-9	1.18	0.82	-0.81	0.96
AKW 2862-1 (C)	0.87	0.61	1.72	0.74
HTW 11 (C)	0.97	0	1.55	0.81
HINDI 62 (C)	0.53	2.19	-0.71	0.86
DHTW 60 (C)	0.52	2.17	0.77	0.9

23. DBW 243 (IC0637558; INGR21023), a Wheat (*Triticum aestivum*) Germplasm High Water Use Efficiency.

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India is the second largest wheat producer in the world and it cultivated in an area of about 30 mha (GOI, 2017). The assured supplemental irrigation is major factor during rabi season helps is harvesting the potential of the crop. During the recent decades it has been experienced a steady increase in the depth of the groundwater table in wheat growing regions of Indo Gangetic plains (Hira,2009; Rodell *et al.,* 2009). The current water productivity of wheat is estimated to be about 0.8 - 1.06 kg m^{-3} in India (Meena *et al.,* 2015; Zwart *et al.,* 2010). Uncontrolled irrigation supported by subsidized/free electricity clubbed with low water productivity is leading to unsustainability of the traditional wheat cultivation (Humphreys *et al.,* 2010; Meena *et al.,* 2019). The situation therefore calls for development of improved agronomic management options as well as identification of water use efficient genotypes with better yield. Looking at the necessity for wheat genotypes with high water productivity which can be readily adoptable at farmer's field, the present study has been undertaken aiming at identifying high WUE wheat genotypes under limited moisture conditions.Seventy-one genetically diverse wheat genotypes were screened for high water use efficiency (WUE) under limited soil moisture level at 60 % of Cumulative Pan Evaporation (CPE) during 2015-16. Out of these best performing sixteen high WUE genotypes were shortlisted for a detailed field studyduring 2016-17 and 2017-18. Tukey's test of significance led ranking and GGE biplot analysis identified DBW243 as high water use efficient genotype with a water use efficiency of 2.40 kg m^{-3} at 60% CPE over check variety HD2967 (1.99 kg m^{-3}) during two years of testing.

Table 1: Average Water Use Efficiency of wheat genotype DBW243 in comparison on the basis of experiment during 2016-17 and 2017-18

	WUE 60%			*WUE 80%*			*WUE Avg*
Genotypes	*16-17*	*17-18*	*Avg*	*16-17*	*17-18*	*Avg.*	
	kg m^{-3}			kg m^{-3}			kg m^{-3}
DBW243	2.85	1.94	2.40	2.25	1.62	1.94	2.17
HD2967 (C)	2.19	1.78	1.99	2.15	1.42	1.79	1.89
PBW 550 (C)	2.03	1.43	1.73	1.65	1.26	1.46	1.59
WH1105 (C)	2.22	1.69	1.95	1.91	1.54	1.72	1.84
DBW 88 (C)	2.42	1.69	2.06	2.00	1.59	1.79	1.93
LSD at P< 0.05	0.34	0.19		0.18	0.25		

Table 2: Average Wheat grain yield, of wheat genotype DBW243 in comparison on the basis of experiment during 2016-17 and 2017-18

	GY at 60%CPE		*GY at 80% CPE*		*Avg GY*
Genotypes	*16-17*	*17-18*	*16-17*	*17-18*	
	kg ha^{-1}		kg ha^{-}		
DBW243	5074	4874	5326	4968	5060
HD2967 (C)	3899	4467	5104	4350	4455
PBW 550 (C)	3619	3579	3919	3875	3748
WH1105 (C)	3945	4241	4519	4719	4356
DBW 88 (C)	4315	4255	4731	4869	4542
LSD at P< 0.05	607	486	438	762.6	

24. DCMS 17A & DCMS 17B (IC0637559 & IC0637560; INGR21024), a New CMS (A) Line of Wheat (*Triticum aestivum*) in DBW17 Background with CMS Source (Chuan 18A) along with Maintainer (B) Line.

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Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re- oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The genetic stock DCMS 17A was developed using CHUAN 18A based CMS line CMS21A (CHUAN18A/6/7*KAUZ*2/4/CAR//KAL/BB/3/NAC/5/KAUZ) as female parent in firstcross with Indian advanced variety DBW 17 as male parent. DBW 17 was a landmark variety for north western plains zone as well as north eastern plains zone for timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with DBW 17 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of theCMS lines. This indicated complete male sterility in the new CMS line DCMS 17A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 17A ranged from 92-103 days with mean of 96 days whereas average plant height was 90 cm with range of 84-96 cm. Compared to this, the maintainer line DCMS 17B showed average days to heading of 97 days and plant height of 90 cm which is in tune to CMS line. This similar feature is helpful in synchronised flowering and pollen movement for maximum seed set.

Table 2: Performance of DCMS 17A and its maintainer DCMS 17B for morphological traits

Traits	*DCMS 17A*	*DCMS 17B (DBW 17)*
Coleoptile Colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage Colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber
Spike length (cm)	9	10
Spikelet number	20	22
Days to maturity	143	144

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line DBW 17 (Table 2). The results also indicated similarity in spikelet number per spike, spike length and maturity period in DCMS 17A as compared to the maintainer line.

It may be concluded that the genetic stock DCMS 17A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS 17A and its maintainer for quantitative traits

Year	DCMS17A (CMS- A line)			DCMS 17B (DBW 17: B line)	
	Male sterility(%)	Days toheading	Plant height(cm)	Days toheading	Plant height(cm)
2015-16	100	97	86	97	88
2016-17	100	93	84	93	90
2017-18	100	92	96	94	87
2018-19	100	103	94	102	94
Mean	100	96	90	97	90

25. DCMS 24A & DCMS 24B (IC0637561 & IC0637562; INGR21025), a New CMS (A) line of Wheat (*Triticum aestivum*)in DBW 16 Background with CMS Source (Chuan 18A) alongwith Maintainer (B) Line

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Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re- oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The genetic stock DCMS 24A was developed using CHUAN 18A based CMS line CMS 10A (CHUAN 18A/CHUAN 18B//7*KAUZ/HEVO) as female parent in first cross with Indianadvanced variety DBW 16 as male parent. DBW 16 was a high yielding variety for north westernplains zone for late sown irrigated condition. After initial cross, 8 generations of backcrosses were made with DBW 16 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of theCMS lines. This indicated complete male sterility in the new CMS line DCMS 24A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 24A ranged from 95-108 days with mean of 100 days whereas average plant height was 98 cm with range of 91-102 cm. Compared to this, the maintainer line DCMS 24B showed average days to heading of 100 days and plant height of 97 cm which is in tune to CMS line. This similar feature is helpful in synchronised flowering and pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line DBW 16 (Table 2). The results also indicated similarity in spikelet number per spike, spike length and maturity period in DCMS 24A as compared to the maintainer line DBW 16.

It may be concluded that the genetic stock DCMS 24A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 2: Performance of DCMS 24A and its maintainer DCMS 24B for agro-morphological traits

Traits	*DCMS 24A*	*DCMS 24B (DBW 16)*
Coleoptile Colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage Colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber
Spike length (cm)	10	9
Spikelet number	19	19
Days to maturity	149	148

Table 1: Performance of DCMS24A and its maintainer for quantitative traits

Year	DCMS24A (CMS- A line)			DCMS 24B (DBW 16: B line)	
	Male sterility(%)	Days toheading	Plant height(cm)	Days toheading	Plant height(cm)
2015-16	100	99	91	101	96
2016-17	100	95	100	95	101
2017-18	100	97	98	97	97
2018-19	100	108	102	108	92
Mean	100	100	98	100	97

26. DCMS 34A and 34B (IC0637563 & IC0637564; INGR21026), a New CMS (A) Line of Wheat (*Triticum aestivum*) in PBW 502 Background with CMS Source (Chuan 18A) alongwith Maintainer (B) Line

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Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields. Indian hybrid wheat programme has re- oriented in 1995 with introduction of some cytoplasmic male sterile (CMS) lines from CIMMYT, Mexico but these could not be utilized due to their un-adapted agronomic background. In 2005, the diversification of CMS lines received from CIMMYT was initiated with the objective to develop new CMS lines in the agronomic background of Indian wheat varieties so that these can be further utilized in hybrid wheat development programme. The basic *Triticum Timopheevii* based cytoplasm sources were MTSA 2A, Chuan 13A and Chuan 18A which were transferred in the background of diverse CIMMYT advance lines. These CMS lines from CIMMYT were introduced in India as source of cytoplasmic male sterility for hybrid wheat development programme.

The genetic stock DCMS 34A was developed using CHUAN 18A based CMS line CMS21A (CHUAN18A/6/7*KAUZ*2/4/CAR//KAL/BB/3/NAC/5/KAUZ) as female parent in firstcross with Indian advanced variety PBW 502 as male parent. PBW 502 was a released variety for north western plains zone for timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with PBW 502 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of theCMS lines. This indicated complete male sterility in the new CMS line DCMS 34A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in

Table 2: Performance of DCMS 34A and its maintainer DCMS 34B for morphological traits

Traits	*DCMS 34A*	*DCMS 34B (PBW 502)*
Coleoptile Colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage Colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber
Spike length (cm)	11	11
Spikelet number	20	20
Days to maturity	149	147

Table 1: Performance of DCMS 34A and its maintainer for quantitative traits

Year	DCMS34A (CMS- A line)			DCMS 34B (PBW 502: B line)	
	Male sterility(%)	Days toheading	Plant height(cm)	Days toheading	Plant height(cm)
2015-16	100	102	104	102	95
2016-17	100	94	98	94	96
2017-18	100	97	97	97	97
2018-19	100	105	102	106	107
Mean	100	100	100	100	99

DCMS 34A was ranged from 94-105 days with mean of 100 days whereas average plantheight was 100 cm with range of 97-104 cm. Compared to this, the maintainer line DCMS 34B (PBW 502) showed average days to heading of 100 days and plant height of 99 cm which is in tune to CMS line. This similar feature is helpful in synchronised flowering and pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line PBW 502 (Table.2). The results also indicated similarity in spikelet number per spike, spike length and maturity period in DCMS 34A as compared to the maintainer line PBW 502. The maturity days was more in the DCMS 34AA which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

It may be concluded that the genetic stock DCMS 34A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

27. DCMS 37A and 37B (IC0637565 & IC0637566; INGR21027), a New CMS Line of Wheat (*Triticum aestivum*) in DBW 55 Background With CMS Source (Chuan 18A) alongwith Maintainer (B) Line

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The genetic stock DCMS 37A was developed using CHUAN 18A based CMS line CMS15A (CHUAN18A//7*ATTILA/3BCN) as female parent in first cross with Indian advanced variety DBW 55 as male parent. DBW 55 was a high yielding elite line evaluated in NIVT 1A meantfor north western plains zone as well as north eastern plains zone under timely sown irrigated condition. under timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with DBW 55 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 37A (Table 1).

Table 1: Performance of DCMS 37A and its maintainer for quantitative traits

Year	DCMS 37A (CMS- A line)			DCMS 37B (DBW 55: B line)	
	Male sterility(%)	Days toheading	Plant height(cm)	Days toheading	Plant height(cm)
2015-16	100	93	97	93	98
2016-17	100	94	95	94	100
2017-18	100	97	100	97	103
2018-19	100	104	92	104	99
Mean	100	97	96	97	100

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 37A was ranged from 93-104 days with mean of 97 days whereas average plant height was 96 cm with range of 92-100 cm. Compared to this, the maintainer line DCMS 37B (DBW55) showed average days to heading of 97 days and plant height of 100 cm which is in tune to CMS line. This similar feature is helpful in synchronised flowering and pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line DBW 55 (Table.2). The results also indicated comparable spikelet number per spike, spike length and maturity period in DCMS 37A as compared to the maintainer line DBW 55. The maturity days was more in the DCMS37A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

Table 2: Performance of DCMS 37A and its maintainer DCMS 37B for morphological traits

Traits	*DCMS 37A*	*DCMS 37B (DBW 55)*
Coleoptile Colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage Colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber
Spike length (cm)	10	11
Spikelet number	21	23
Days to maturity	148	146

It may be concluded that the genetic stock DCMS 37A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

28. DCMS 46A and 46B (IC0637567 & IC0637568; INGR21028), a New CMS(A) Line of Wheat (*Triticum aestivum*) in CBW 38 Background with CMS Source (Chuan 18A) along with Maintainer (B) Line

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The genetic stock DCMS 46A was developed using CHUAN 18A based CMS line CMS 15A (CHUAN18A//7*ATTILA/3BCN) as female parent in first cross with Indian advanced variety CBW 38 as male parent. CBW 38 was released variety for north eastern plains zone for timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with CBW 38 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results

Table 1: Performance of DCMS 46A and its maintainer for quantitative traits

Year	DCMS 46A (CMS- A line)			DCMS 46B (CBW 38: B line)	
	Male sterility (%)	Days to heading	Plant height (cm)	Days to heading	Plant height (cm)
2015-16	100	93	101	94	102
2016-17	100	94	103	94	105
2017-18	100	97	111	95	121
2018-19	100	103	104	106	111
Mean	100	97	105	97	110

Table 2: Performance of DCMS 46A and its maintainer DCMS 46B for agro-morphological traits

S.no.	*Traits*	*DCMS 46A*	*DCMS 46B (CBW 38)*
1	Coleoptile Colour	Absent	Absent
2	Growth habit	Semi erect	Semi erect
3	Foliage Colour	Green	Green
4	Spike colour	white	white
5	Spike shape	Tapering	Tapering
6	Awn colour	White	White
7	Grain colour	Amber	Amber
8	Spike length (cm)	9	10
9	Spikelet number	21	22
10	Days to maturity	149	147

indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 46A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 46A was ranged from 93-103 days with mean of 97 days whereas average plant height was 105 cm with range of 101-111 cm. Compared to this, the maintainer line DCMS 46B (CBW 38) showed average days to heading of 97 days and plant height of 110 cm which is in tune to CMS line. This similar heading is helpful in synchronised flowering whereas more height in maintainer line facilitates better pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line CBW 38 (Table.2). The results also indicated comparable spikelet number per spike, spike length and maturity period in DCMS 46A as compared to the maintainer line CBW 38. The maturity days was more in the DCMS 46A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

DCMS 46A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

29. DCMS 51A and 51B (IC0638603 & IC0638604; INGR21029), a New CMS (A) line of Wheat (*Triticum aestivum*) in DBW 76 Background with CMS Source (Chuan 18A) along with Maintainer (B) Line.

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The genetic stock DCMS 51A was developed using CHUAN 18A based CMS line CMS21A (CHUAN18A/6/7*KAUZ*2/4/CAR//KAL/BB/3/NAC/5/KAUZ) as female parent in first cross with Indian advanced variety DBW 76 as male parent. DBW 76 was a high yielding elite genotype evaluated in NIVT

Table 1: Performance of DCMS 51A and its maintainer for quantitative traits

Year	DCMS51A (CMS- A line)			DCMS 51B (DBW 76: B line)	
	Male sterility (%)	Days to heading	Plant height (cm)	Days to heading	Plant height (cm)
2015-16	100	88	103	92	107
2016-17	100	84	109	84	112
2017-18	100	91	100	88	104
2018-19	100	100	124	95	126
Mean	100	91	109	90	112

Table 2: Performance of DCMS 51A and its maintainer DCMS 51B for agro-morphological traits

Traits	*DCMS 51A*	*DCMS 51B (DBW 76)*
Coleoptile Colour	Absent	Absent
Growth habit	Semi erect	Semi erect
Foliage Colour	Green	Green
Spike colour	white	white
Spike shape	Tapering	Tapering
Awn colour	White	White
Grain colour	Amber	Amber
Spike length (cm)	13	13
Spikelet number	23	22
Days to maturity	148	145

1B meant for north western plains zone as well as north eastern plains zone under timely sown irrigated condition. After initial cross, 8 generations of backcrosses were made with DBW 76 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 51A (Table 1).

In hybrid development programme based on three-line system, the maintenance of CMS lines is very crucial. The similarity in days to heading and plant height in CMS and maintainer lines is needed to facilitate pollination and get maximum seed set in the CMS line. The heading period in DCMS 51A was ranged from 84-100 days with mean of 91 days whereas average plant height was 109 cm with range of 100-124 cm. Compared to this, the maintainer line DCMS 51B (DBW 76) showed average days to heading of 90 days and plant height of 112 cm which is in tune to CMS line. This similar heading is helpful in synchronised flowering whereas more height in maintainer line facilitates better pollen movement for maximum seed set.

In addition, few additional agro-morphological traits namely coleoptile colour, growth habit, foliage colour, awn colour, spike colour and shape and grain colour were observed over these years which showed similar pattern to the parental maintainer line DBW 76 (Table.2). The results also indicated almost similar spikelet number per spike, spike length and maturity period in DCMS 51A as compared to the maintainer line DBW 76. The maturity days was more in the DCMS 51A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

It may be concluded that the genetic stock DCMS 51A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

30. IC128565 (IC0128565; INGR21030), a Wheat (*Triticum aestivum*) Germplasm Resistant to Leaf Rust.

Sundeep Kumar*[1], BS Phogat[1], VK Vikas[2], LP Tiwari[3], AK Sharma[4], MS Saharan[5], Amit Kumar Singh[1], Jyoti Kumari[1], Rakesh Singh[1], Sherry Rachel Jacob[1], M Sivasamy[2], M Meeta[6], JP Jaiswal[7], Deep Shikha[7], SP Singh[8], PC Mishra[9], GP Singh[4] and Kuldeep Singh[1]

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A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of leaf rust. Field testing for leaf rust resistance was carried out at 10 different locations Pantnagar (Uttarakhand), Ludhiana (Punjab), Karnal (Haryana), Varanasi (Uttar Pradesh), Kumarganj (Uttar Pradesh), Vijapur (Gujarat), Powarkheda (Madhya Pradesh), Pune (Maharashtra), Dharwad (Karnataka) and Wellington (Tamilnadu) for two years followed by molecular screening to detect the presence of APR genes *Lr34+*, *Lr46+*, *Lr67+* and *Lr68* in Indian wheat germplasm. 190 wheat germplasm lines which were selected from 6319 accessions based on *Ltn* disease screening and average coefficient of infection. Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance. Molecular analysis of 190 selected germplasm lines was done to identify different combinations of APR genes imparting resistance to leaf rust. 49 accessions were identified which were carrying either two or three APR genes were evaluated for yield stability across four different locations in India *viz*., Pantnagar, Varanasi, Powarkheda and Pune, using additive main effects and multiplicative interaction (AMMI) model.

Among identified 49 germplasm lines, IC128565 which showed the presence of leaf rust resistance genes *Lr34+ (Lr34/Yr18/Sr57/Pm38)*, *Lr46+ (Lr46/Yr29/Sr58/Pm39)* and *Lr68* may be considered promising multiple disease resistant germplasm and could be included in breeding program as parents for developing new durable multiple rust resistant cultivars.

31. IC128638 (IC0128638; INGR21031), a Wheat (*Triticum aestivum*) Germplasm Resistant to Leaf Rust and Yield Stability across the Locations

Sundeep Kumar*[1], BS Phogat[1], VK Vikas[2], LP Tiwari[3], AK Sharma[4], MS Saharan[5], Amit Kumar Singh[1], Jyoti Kumari[1], Rakesh Singh[1], Sherry Rachel Jacob[1], M Sivasamy[2], P Jayaprakash[2], M Meeta[6], JP Jaiswal[7], Deep Shikha[7], GP Singh[4] and Kuldeep Singh[1]

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(Tamilnadu) for two years followed by molecular screening to detect the presence of APR genes *Lr34*+, *Lr46*+, *Lr67*+ and *Lr68* in Indian wheat germplasm. 190 wheat germplasm lines which were selected from 6319 accessions based on *Ltn* disease screening and average coefficient of infection. Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance. Molecular analysis of 190 selected germplasm lines was done to identify different combinations of APR genes imparting resistance to leaf rust. 49 accessions were identified which were carrying either two or three APR genes were evaluated for yield stability across four different locations in India *viz*., Pantnagar, Varanasi, Powarkheda and Pune, using additive main effects and multiplicative interaction (AMMI) model.

Among identified 49 germplasm lines, IC128638 which showed the presence of leaf rust resistance genes *Lr46*+ *(Lr46/Yr29/Sr58/Pm39)*, *Lr67*+ *(Lr67/Yr46/Sr55/Pm46)* and *Lr68* may be considered promising multiple disease resistant germplasm and could be included in breeding program as parents for developing new durable multiple rust resistant cultivars.

32. PML 35 (IC0637577; INGR21032), a Maize (*Zea mays*) Germplasm Tolerant to High Density Planting. Stable high yielding (2.29 t/ha) Under normal density. Medium in maturity (95 days).

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Globally, as additional land for maize production is limited, it is essential to increase the maize productivity to cope with the increasing demand for grains. High-density planting is a practical approach for increasing maize yield per unit area (Lee EA, and M Tollenaar, 2007). For instance, the average maize yield is approximately 6,000 kg/ha with a planting density of 52, 500–67,500 plants/ha in China, both parameters are lower than those in the United States. If maize planting density is increased by 15,000 plants/ha, the total maize yield is predicted to be enhanced by 20% (Gong *et al.,* 2015). However, maize varieties/hybrids that are suitable for high-density planting are still lacking in most of the developing countries due to various factors including non availability of suitable genotypes (Andrivon, 2013). Thus, identification of such varieties is an important task in enhancing productivity of maize.

Genotypes were evaluated in randomized block design with two replications. Inter and intra row spacing was adjusted to fit the prescribed density for the evaluation. To attain 66666 plants/ ha, plants were grownin 75 X 20 cm spacing, 60 X 20 cm spacing was followed to attain 83333 plant density per hectare. We ensured the plant density of 88888 plants /ha by following plant geometry of 75 X 15 cm. The highest density of 111111 plants/ha was attain by adjusting genotypes in 60 X 15 cm spacing. Data were recordedon yield component traits.

Among the tested lines, PML 35, PML 46, PML 76, PML 93, KRN-2-5-2, and UMI 1200 significantly out yielded over the trial mean at type III density *ie*, 88888 plants/ha. These lines can be designated as density tolerant lines for grain yield. Among the tolerant line for density stress, PML 35 had high yielding ability (4.07 t/ha).

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33. UMI1230ß+-1 (IC0637575; INGR21033), a Maize (*Zea mays*) Germplasm with Improved Beta Carotene (9.248µg/g)

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Vitamin A deficiency (VAD) is a global health problem. Many people around the world, especially children and pregnant women are VAD deficient. Maize is known as an important source of provitamin A (Baveja *et al.,* 2020) Hence the enrichment of pro vitamin A in maize through breeding is a best option to alleviate the vitamin A deficiency (Mehta *et al.,* 2020).

For this purpose UMI1230 is an elite maize inbred which is widely adapted to the tropical region and serves as a male parent for CO6 maize hybrid was taken to improve the beta carotene concentration through marker assisted breeding. Donor parent called HP467-15 obtained from CIMMYT, having beta carotene content of 10.525µg/g was used as a donor parent to transfer the beta carotene trait in to the inbred UMI1230 through marker assisted backcross breeding. Crossing was initiated during *rabi* (2011-12). The BC1F1 and BC2F1 were obtained by backcrossing the F1's and BC1F1's to its recurrent parent (UMI1230) and evaluated in *Kharif* 2012 and *rabi* (2012-2013) respectively, using the gene specific marker crtRB1, to identify the heterozygous plants having both the favourable allele (543bp) and unfavourable allele (296bp).In *Kharif 2013* the BC2F1 plants were selfed to produce BC2F2. Further BC2F2 plants were raised in *rabi* (2013-14) and were screened for the targ*et al*lele (543bp) to fix the homozygous plants for beta carotene trait and selfed to produce BC2F3. Background screening was done with 214 polymorphic SSR markers and revealed 90.41% – 92.21% recovery of recurrent parent genome in BC2F3and more than 80% of morphological resemblance with its recurrent parent. Similar results in accordance with Chandran *et al.,* 2019. In addition, beta carotene estimation was performed on the parents (UMI1230 and HP467-15) and the identified improved lines using High Performance Liquid Chromatography (HPLC). The mean beta carotene value of recurrent parent from seven locations was 1.468 µg/g and the donor parent was 10.525 µg/g (Senthil *et al.,* 2020). The improved beta carotene line UMI1230β^{+}-1 recorded the mean beta carotene content of 9.248 µg/g from seven locations. Thus the improved line recorded mean beta carotene value comparable to that of the donor parent involved in the backcross breeding programme. Also the improved high beta carotene line UMI1230β^{+}-1 recorded curved type of leaf attitude, lax spikelet of tassel and flint kernel as in case of recurrent parent (UMI1230).

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34. UMI1200ß+-2 (IC0637576; INGR21034), a Maize (*Zea mays*) Germplasm with Improved Beta Carotene (8.286 µg/g)

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Maize is an excellent nutritional source and is consumed as a staple food in different partsof the world, including India. Developing maize genotype with high concentration of betacarotene can help to alleviate the problem of vitamin A deficiency (Muthusamy *et al.,* 2014). For this purpose, UMI1200 is an elite maize inbred which is widely adapted to the tropical region and serves as a male parent for CO6 maize hybrid. Donor parent called HP467-15 obtained from CIMMYT, having beta carotene content of 10.525µg/g was used as a donor parent to transfer the beta carotene trait in to the inbred UMI1200 through marker assisted backcross breeding. Crossing was initiated during *rabi* (2011-12). The BC1F1 and BC2F1 were obtained by backcrossing the F1's and BC1F1's to its recurrent parent (UMI1230) and evaluated in *Kharif* 2012 and *rabi* (2012-2013) respectively, using the gene specific marker crtRB1, to identify the heterozygous plants having both the favourable allele (543bp) and unfavourable allele (296bp).In *Kharif 2013* the BC2F1 plants were selfed to produce BC2F2. Further BC2F2 plants were raised in *rabi* (2013-14) and were screened for the targ*et al*lele (543bp) to fix the homozygous plants for beta carotene trait and selfed to produce BC2F3. Background screening was done with 214 polymorphic SSR markers and revealed 90.24% – 92.42% recovery of recurrent parent genome in BC2F3 and more than 80% of morphological resemblance with its recurrent parent. Similar results in accordance with Chandran *et al.,* 2019. In addition, beta carotene estimation was performed on the parents (UMI1200 and HP467-15) and the identified improved lines using High Performance Liquid Chromatography (HPLC). The mean beta carotene value of recurrent parent from seven locations was 0.783 µg/g and the donor parent was 10.525 µg/g (Senthil *et al.,* 2020). The improved beta carotene line UMI1200β^{+}-2 recorded the mean beta carotene content of 8.286 µg/g from seven locations. Thus the improved line recorded mean beta carotene value comparable to that of the donor parent involved in the backcross breeding programme. Also the improved high beta carotene line UMI1200β^{+}-2 recorded narrow type of leaf attitude, dense spikelet of tassel and dent kernel as in case of recurrent parent used (UMI1200)

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35. OIN-456 (IC00503729; INGR21035), a Jute (*Corchorus olitorius*) Germplasm Susceptible to Stem rot disease caused by *Macrophomina phaseolina*

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Among all diseases of jute, stem rot caused by *Macrophomina phaseolina* is economically most serious disease in both cultivated species. Although it's commonly known as stem rot, but any part of the plant may be infected by the pathogen at any stage of growth right from germination to harvest leading to reduced fiber yield and quality. Breeding for host-plant resistance can reduce reliance on chemical fungicides and facilitate environmentally safe organic jute production. Several disease resistant varieties in different crops have been released for commercial cultivation using MAS in different parts of the world.

While breeding for biotic stress resistance, a stable disease resistance and susceptible sources are required to capitalize the molecular markers for identification and mapping of resistant genes/QTLs. Susceptible genetic stocks have several applications in resistance breeding like they were often used as negative control while screening for resistant source, as a source of inoculum for spreading the disease on test accessions in screening plots and for development mapping populations.

In tossa jute (*C. olitorius* L.), resistant sources for stem rot resistance were identified by De and Mandal (2012) and Meena *et al*, (2015) and in white jute (*C. capsularis* L.) by Mandal *et al.,* (2000). Whereas susceptible source was identified only in capsularis germplasm (Mandal *et al.,* 2000), no stem rot susceptible line was reported in olitorius jute. So, to advance the resistance breeding programmes in tossa jute we have screened around 100 olitorius germplasm lines of different geographic origin through artificial stem inoculation method and selected lines were screened under sick plot conditions. Among the olitorius germplasm OIN-456 is consistently recorded as highly susceptible (Table 1). This line could be useful in developing mapping population for understanding genetics and identification of genes/QTLs responsible for disease resistance. OIN-456 is a red pigmented line with glossy leaf and this line was collected from Madhya Pradesh state (Dandakaranya), India.

Table 1: Disease reaction of the OIN-456 during 2015-2018 under sick plot conditions expressed as AUDPC values

Germplasm line	Species	2015	2016	2017	2018
OIN-456	*C.olitorius*	748	1385	609	939
OIN-154-1	*C.olitorius*	62	201	44	190
WCIN-136-1	*C.aestuans*	0	0	0	0
WCIJ-150-1	*C.fascicularis*	0	0	0	0

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36. WCIN-136-1 (IC0637579; INGR21036), a Jute (*Corchorus aestuans*) Germplasm Highly Resistant to Stem Rot caused by *Macrophomina phaseolina*

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Identification of stable biotic resistance sources has paramount importance in resistance breeding for the development of resistance varieties and identification of resistant genes/QTLs. In jute only few stem rot disease resistance sources were reported. In cultivated tossa jute (*Corchorus olitorius* L.) only moderate stem rot resistance was reported by De and Mandal (2012) and Meena *et al.*, (2015) and resistance in white jute (*Corchorus capsularis* L.) by Mandal *et al.,* (2000). Lack of highly resistant sources and cross incompatibility between *C. olitorius* and *C. capsularis* germplasm lines hampered development of high yielding, stem rot resistant tossa jute varieties.

In this back drop we have identified a wild jute germplasm line (WCIN-136-1) of *Corchorus aestuans* L. with stable disease resistance (zero AUDPC values, Area Under Disease Progressive Curve) reaction during screening for four consecutive years (2015-2018) under sick plot conditions at ICAR-CRIJAF, Barrackpore (Table 1). WCIN-136-1 (*Corchorus aestuans* L.) is a unique wild jute germplasm line with resistant to major disease and insect pest in jute *i.e*, stem rot (caused by *Macrophomina phaseolina* (Tassi) Goid., bihar hairy caterpillar (*Spilosoma obliqua)* resistance and high fiber fineness. WCIN-136-1 was developed through pure line selection from indigenous germplasm line WCIN-136 collected from Sundarban, West Bengal, India.

This germplasm line was first identified as resistant for stem rot disease by artificial stem inoculation method and in subsequent years WCIN-136-1 tested for its stable resistance under sick plot conditions over the years. The genotype WCIN-136-1 not only showed resistant to stem rot disease but it also showed resistant reaction to bihar hairy caterpillar with 100% larval mortality and 0% pupation along with high fiber fineness (0.5 tex). So, this line can be useful as a donor parent to transfer both stem rot, bihar hairy caterpillar resistant and fiber fineness to cultivated tossa jute as it is cross compatible with cultivated tossa jute.

Table 1: Resistant reaction of the WCIJ-136-1 during 2015-2018 under sick plot conditions expressed as AUDPC values

Germplasm line	*Species*	*2015*	*2016*	*2017*	*2018*
OIN-456	*C.olitorius*	748	1385	609	939
OIN-154-1	*C.olitorius*	62	201	44	190
WCIN-136-1	*C.aestuans*	0	0	0	0
WCIJ-150-1	*C.fascicularis*	0	0	0	0

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37. SPV 2438 (PSV 316) (IC0637580; INGR21037), a Sorghum (*Sorghum bicolor*) Germplasm High Protein Content (11.73%).

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Sorghum is an important climate resilient crop of dry lands and integral component of varied agro ecologies and cropping systems. In the context of climate change and prevailing protein energy malnutrition there is a need to identify resilient cultivars with enhanced protein content. Due to systematic breeding efforts at Regional Agricultural Research Station, Palem in collaboration with Indian Institute of Millets Research (IIMR) Hyderabad high yielding culture SPV 2438 was developed. This culture was derived from a cross between SPV-504 x ICSR103 through Pedigree method of breeding at Regional Agricultural Research Station, Palem, PJTSAU, Telangana state of India. It was evaluated in 15 AICRP trials from 2016 to 2018 and recorded significantly superior grain yield (22.16%) and fodder yield (72.18%) over check CSV 17. The normal range of protein content in white sorghum ranges from 8.5 to 10 percent. Where as in quality analysis SPV2438 recorded highest protein content (11.73%) among all the entries and national checks evaluated during the period at all the locations across the country. This entry also showed stable and moderately resistant reaction against grain mold with 3.23 field grade and 4.37 threshed grade during three years of AICRP evaluation. SPV 2438 matures, on an average, in 104 days and takes 67 days to flower. It produces semi compact panicles with medium sized grains (seed weight of 2.66 g/100 seeds) of elliptic shape. The culture attains the height of 227 cm with 21.0-28.0 cm length panicles.

38. GMN 16-5 (IC0635028; INGR21038), a Sorghum (*Sorghum bicolor*) Germplasm with Grain Mold Resistance (3.8).

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Sorghum grain molds is an important disease that affects the quality of the produceand ultimately reduces market price making sorghum cultivation non profitable. Heavy rains at the time of maturity cause severe damage to the sorghum grain, which affects its market price. The deterioration is mainly due to infection caused by a complex of fungi, collectively known as "grain molds". The genetics of grain mold resistance is very complex, governed by major and minor genes showing significant GxE interactions and is hampering the progress in the breeding for grain mold resistance. In India, during the past five decades, the area under rainy season sorghum cultivation has come down from 10.9 to 2.7 million hectares, the main reasons for this decline being poor quality of the rainy season produce, low market value and stagnant yields. The problem of grain mold is encountered throughout the humid tropical and subtropical regions. It remains as a major constraint to sorghum production in most parts of India, Africa, Latin America, and USA. It is necessary to develop new varieties or hybrids that possess resistance to this pest.

In order to incorporate resistance into sorghum parental lines, intensive breeding efforts were initiated at IIMR. Since this is a very complex disease involving many traits and high GxE interactions, population breeding was initiated during 2000 involving elite B and R lines and grain mold resistance sources. Three years of random mating and three cycles of half sib selections were carried out before making selections from the population. Individual selections were made from the population and these were stabilized over 4-5 generations. These stable lines were evaluated for their performance for grain mold resistance and agronomy in station trials.

The seed of the promising selections with grain mold resistance was multiplied and the genotypes were tested in multilocation under AICSIP grain mold nursery.

GMN 16-5 was a population breeding derivative with better level of grain mold tolerance compared to the one of their parents, 296B and agronomically better compared to the grain mold resistant source, B 58586. GMN16-5 was better than the B58586 in desirable agronomic characters like more grain size, less plant height and more compactness of panicles. It is a short and early improved genetic stock with grain mold tolerance better than check, 296B. Bold seed compared to the resistant check, B 58586 with desirable plant height and more compact panicle .GMN 16-5 can be used as resistant source in the grain mold resistance breeding program aiming at development of parental lines and genotypes with grain mold resistance along with agronomic acceptability.

Table 1: Performance of GMN 16-5 for grain mold resistance in AICSIP GMN trials over three years (2016- 3 Env; 2017- 4Env; 2018- 3 Env)

GMN line	Days to flower				Grain mold score (FG)				Grain mold (TG)				100 Seed weight (g)				PC*
	2016	2017	2018	Av	2016	2017	2018	Av	2016	2017	2018	Av	2016	2017	2018	Av	
GMN16-5	68	59	67	65	3.5	3.6	4.2	3.8	3.7	3.0	4.3	3.7	2.1	2.7	2.9	2.6	2.0
B 58586	70	66	72	69	2.2	2.9	1.8	2.3	2	2.3	1.5	1.9	1.8	2.1	1.9	1.9	1.0
Bulk Y	71	63	66	67	6	6.8	7.0	6.6	8	6.3	6.5	6.9	1.7	3.1	3.5	2.8	2.0
296 B	77	-	79	78	5.5	-	5.1	5.3	6.3	-	5.3	5.8	2	-	2.8	2.4	3.0
CD 5%	9.2	5.0	5.8		1.8	0.7	1.3		1.9	1.3	1.8		0.49	0.9	0.6		0.2
CV (%)	6.2	4.3	6.3		22.8	10.9	23.2		29.4	23.9	21.0		11.9	19.5	11.4		4.9

*PC- Panicle compactness

Table 2: Performance of GMN 16-5 for presence of individual grain mold fungi and other traits in AICSIP GMN trials over three years (2016- 3 Env; 2017- 4 Env; 2018- 3 Env)

	Fusarium (%)				Curvularia (%)				Germination (%)				Plant height (cm)		
	2016	2017	2018	Av	2016	2017	2018	Av	2016	2017	2018	Av	2017	2018	Av
GMN16-5	16	16	9	14	26	18	9	17	60	68	80	69	150	130	140
B58586	10	17	4	10	16	21	4	14	80	56	87	74	221	220	221
BulkY	27	14	18	20	23	22	8	18	38	71	71	60	125	100	112
296B	37	22	8	22	16	31	11	19	35	48	72	51	103	103	103
CD 5%	11.5	9.0	6.3		10.1	9.6	4.0		18.0	15.0	10.2		58.7	37.1	
CD 1%	15.5	12.6	8.5		13.6	13.4	5.4		24.2	20.3	13.8		79.6	49.5	
CV (%)	29.5	23.2	44.7		25.1	23.2	23.1		13.7	13.6	6.1		17.7	13.0	

39. SPV 2481 (IC0338975; INGR21039), a Sorghum (*Sorghum bicolor*) Germplasm with High Seed Weight (3.54 g) and High Dry-Fodder Yield (9798 kg/ha)

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Sorghum [*Sorghum bicolor* (L.) Moench] is one of the important dry-land crops of semiarid tropics. It is mainly grown in the drought prone areas to meet the food and fodder security of the region especially Maharashtra, Karnataka, Andhra Pradesh and Telangana where occurrence of drought is very common. Subalakhshmi *et al*, 2019 observed that the characters *viz*., leaf width, panicle length, and hundred seed weight are important traits for grain yield improvement. Elangovan and Kiran Babu (2015) observed PCV and GCV were higher for 100-seed weight and other traits. High amount of GCV and PCV suggested greater scope for selection of superior genotypes for these traits. Dry fodder yield was positively associated with GFY, plant height, stem girth, the no. of tillers, IVDMD, DDM and protein yield and negatively with panicle length visible above sheath. These traits could be considered as the best selection criteria in sorghum breeding programmes for the development of high yielding varieties(Rohila *et al*, 2020).

The sorghum genotype SPV 2481 was evaluated in the Initial Advanced Varietal Trial (Deep Soil) during Rabi 2016-17 at 14 locations and identified as second genotype for more 100-Seed weight with (3.54 g) as compared to 23 genotypes tested including 4 checks. In addition to that the genotype SPV 2481 was evaluated in Initial Advanced Varietal Trial (Deep Soil) during Rabi 2016-17 at 14 locations and identified as first genotype for more dry fodder yield with (9798 kg/ha) as compared to 23 genotypes tested including 4 checks.

The sorghum germplasm SPV 2481 has been identified as new sources for seed weight and higher dryfodder yield in post-rainy (*rabi*) sorghum. It has been proved as a source for more seed weight in IAVTduring 2016-17. It can be used as a parent in the *rabi* sorghum improvement programme to develop *rabi* varieties.

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40. SPV 2412 (IC0415833; INGR21040), a Sorghum (*Sorghum bicolor*) Germplasm with High Seed Weight (3.61 g) and High Dry-Fodder Yield (9720 kg/ha)

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Sorghum [*Sorghum bicolor* (L.) Moench] is one of the important dry-land crops of semiarid tropics. It is mainly grown in the drought prone areas to meet the food and fodder security of the region especially Maharashtra, Karnataka, Andhra Pradesh and Telangana where occurrence of drought is very common. Subalakhshmi *et al*, 2019 observed that the characters *viz.*, leaf width, panicle length, and hundred seed weight are important traits for grain yield improvement. Elangovan and Kiran Babu (2015) observed PCV and GCV were higher for 100-seed weight and other traits. High amount of GCV and PCV suggested greater scope for selection of superior genotypes for these traits.

The sorghum genotype SPV 2412 was evaluated in the Initial Advanced Varietal and Hybrid Trial (Deep Soil) during Rabi 2015-16 at 10 locations and identified with third genotype for more 100-Seed weight with (3.00 g) as compared to 28 genotypes tested including 5 checks (IIMR Publication Number 1/2016-17). In the next year SPV 2412 was evaluated in Initial Advanced Varietal and Hybrid Trial (Deep Soil) during Rabi 2016-17 at 14 locations and identified with first genotype for more 100-Seed weight with (3.61 g) and superior fodder yield (6593 kg/ha) as compared to 23 genotypes tested including 4 checks (IIMR Publication Number 1/2017-18).

The sorghum genotype SPV 2412 is a selection from the local landrace E 142 (IC 415833) from Uttar Pradesh has consistently proved as a potential sorghum genotype for more seed weight in IVT and AVT trials. It can be used as a parent in the sorghum improvement programme.

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41. SPV 2612 (IIMR Red); E-142 (IC0415833; INGR21041), a Red Grain ed Sorghum (*Sorghum bicolor*) Germplasm with High Tannin Content Of (4.51mg ce/g). Adaptability to both *Kharif* and *Rabi*. High Grain Yield

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SPV 2612 is an outcome of the colored sorghum improvement program at Indian Institute of Millets Research, Hyderabad aiming at developing high yielding red sorghum varieties. To promote colored sorghum improvement for feed industry and export purpose, breeding was initiated to develop high yielding colored sorghum lines. The project developed stable lines in different grain color background. To develop red sorghum lines, a number of germplasm lines with red grain were selected from the gene bank and they were crossed to the elite lines. The line SPV 2612 was derived from one such cross between a popular grain sorghum variety, CSV 15 which has white grain and the red germplasm line IS 23514 from Sudan belonging to the race, *Caudatum*. The initial crossing program was made during *rabi* 14 and the F1, F2 and further generations were raised subsequently. In each generation, selections were made based on the color of the grain, maturity duration and productivity.

The selected lines were stabilized and a station trial of the selected lines along with checks was taken up during *kharif* 2017. In the station trials, IIMR red, which was the name given to SPV 2612 at station, was evaluated in a trial where twenty-five colored sorghum genotypes were evaluated in RCBD with CSV 20 as check. Preliminary evaluation identified red sorghum lines with grain yield on par with the high yielding white grain sorghum. IIMR red, a derivative of CSV 15 crossed with a colored germplasm line, IS 23514 was the

Table 1: Performance of SPV 2612 (IIMR Red) in AICSIP trials over two years (2018-*Kharif* 4 env, Rabi- 5 env; 2019-*Kharif* 4 env, Rabi 5env)

Genotype	Grain Yield (kg/ha)						100 Seed weight (g)				Av
	Kharif			Rabi			Kharif		Rabi		
	2018	2019	Av	2018	2019	AV	2018	2019	2018	2019	
SPV 2612	4761.9	4426.2	4594	3103	2837	2970	2.99	2.51	2.7	2.64	2.71
CSV 20	4597.1	3262.8	3929.9	2550	2864	2707	3.01	2.42	2.42	1.96	2.45
CD 5%	1188	1417.1		700	503		0.38	0.43	0.48	0.29	
CV (%)	16.67	15.0		22.57	10.4		9.97	13.15	15.03	10.9	

Table 2: Performance of SPV 2612 (IIMR Red) in AICSIP trials for biochemical traits in 4 environments (2018-2 env; 2019-2 env)

Genotype	*Protein*			*Tannin*		
	2018	2019	Av	2018	2019	Av
SPV2612	9.88	8.2	9.04	4.48	4.53	4.51
CSV 20	8.99	7.14	8.07	0.80	1.44	1.12
CV	7.54	9.21		105.5	54.9	
CD	2.38	1.96		7.14	2.93	

best line with yield numerically and better than CSV 20 and bold seed. Then this entry was submitted for multilocation evaluation in AICRP- Sorghum which was tested under the specialty sorghum category. It was tested in a total of 18 environments over two years. It was tested in 4 locations during *kharif* 2018; 5 locations in *rabi* 2015; 4 locations in *kharif* 2019 and 5 locations in *rabi* 2019. In both the seasons, SPV 2612 has given grain yield on par with the popular variety, CSV 20 (Table 1).

SPV 2612 was analyzed for biochemical constituents like protein and tannin for samples from 4 environments: two in 2018 and two in 2019 and it was found to have high tannin content (Table 2). Tannin content indicates the presence of polyphenols and antioxidant activity which is very good for human health

42. EJN 11 (IC0585181) (IC0585181; INGR21042), a Sorghum (*Sorghum bicolor*) Germplasm with Early Flowering (<56 days).

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Sorghum [*Sorghum bicolor* (L.) Moench] is one of the important dry-land crops of semiarid tropics. It is mainly grown in the drought prone areas to meet the food and fodder security of the region especially Maharashtra, Karnataka, Andhra Pradesh and Telangana. Ezeaku, *et al.,* (1999) evaluated 352 accessions of sorghum germplasm originated from Nigeria and Chad and classified into three flowering groups *viz*., early medium and late flowering. Elangovan, *et al.,*(2013) reported that preliminary characterization of 107 accessions of sorghum germplasm during 2008-2010 and identified EJN 11 one of the early maturing germplasm.

The sorghum germplasm EJN 11 (IC0585181) was evaluated at the AICRP on Sorghum- Deesa centre during *Kharif* 2010 and identified as early flowering germplasm as compared to 103 *kharif* landraces along with 3 checks. The germplasm EJN 11 (IC0585181) again evaluatedin AICRP on Sorghum-Deesa, Indore and Hyderabad during *Kharif* 20110 and identified as early flowering germplasm across three locations as compared to 103 *kharif* landraces along with 3 checks. The local name of EJN 11 (IC0585181) is *Utavali* and collected from Kankraj taluk, Banaskantha district of Gujarat during 2009. This is mainly used for fodder purpose.

The sorghum germplasm EJN 11 (IC0585181) has been identified as new sources for early flowering and can be used in the sorghum improvement programme to develop early variety.

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43. AKGMR 117 (IC0637581; INGR21043), a *kharif* Sorghum (*Sorghum bicolor*) Germplasm with Grain Mold Resistance with Field Grade Grain Mold Score of 3.10 and Threshed Grade Grain Mold Score of 3.53.

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Sorghum (*Sorghum bicolor*) is the fourth most important cereal following rice, wheat and maize and staple food in the semi-arid parts of the world. Grain mold is the major biotic constrain in the way of production, marketing and utilization of *kharif* grain sorghum. It is one of the most important diseased of sorghum in many countries in Asia, Africa, North America, South America. The term Grain Mold Disease Complex (GDMC) has been used in few instances to describe this disease conditions (Prom *et al.* 2003). The disease is particularly important on improved, short- and medium-duration sorghum cultivars that mature during the rainy season in humid, tropical and subtropical climates. Several fungal species of the genera *Fusarium, Curvularia, Alternaria, Phoma, Bipolaris* and *Colletotrichum* have been reported to be associated with grain mold. *Curvularia lunata* and *Fusarium monoliforme* secrete amylase, cellulose and pectinases resulting in the disintegration of endosperm and germ tissues. These fungi also interfere with carbohydrate translocation to developing kernels causing reduction in size and weight of the kernels and ultimately germination of these grains. Therefore, identification of the resistant sources of grain mold in kharif sorghum is if prime importance. Considering this, a multilocation and multi season grain mold screening trial entitled "National Grain Mold Nursery (NGN)" was formulated at national level by Indian Institute of Millets Research (IIMR), Hyderabad.

A national level trial was formulated by Indian Institute of Millets Research (IIMR), Hyderabad consisting of the entries contributed by the all the major centers of the AICSIP (All India Coordinated Sorghum Improvement Project) and conducted during the three years of 2016, 2017 and 2018 at the hot spot centers for grain mold i.e. Akola, Parbhani and Dharwad. Inthis connection, massive breeding programme for grain mold resistance has been continued at AICSIP Akola center and by utilizing the resistance sources identified in the programme, grain mold resistant lines have been developed at Akola center. AKGMR 117 contributed by Sorghum Research Unit, Dr. PDKV, Akola was tested for three years in the "National Grain Mold Nursery (NGN)" trial formulated at national level by Indian Institute of Millets Research (IIMR), Hyderabad. Trial consisted of the testing entries along with one resistant check for grain mold (B 58586) in loose panicle background and one susceptible check (Bulky yellow). The experiments were sown in randomized block design with three replications.

For the character grain mold field grade the resistant check B 58586 recorded the lowest grain mold infestation of 2.29, while the susceptible check exhibited the highest grain mold field grade of 6 66. The best promising entry was AKGMR117 with the grain mold field grade of 3.10 followed by AKGMR 118 (3.50) and AKGMR 119 (3.65). For the character grain mold threshed grade, the resistant check B 58586 recorded the lowest grain mold infestation of 1.83, while the susceptible check exhibited the highest grain mold field grade of 6.83. The best promising entry was AKGMR117 with the grain mold threshed grade of 3.53 followed by AKGMR 118 (3.45) and AKGMR 119 (4.08).

The promising genotypes AKGMR 117 and the resistant check B 58586 exhibited Grain mold disease resistant reaction towards both field grade mold rating and threshed grain mold rating. This resistant reaction can be attributed to the lower percentage of both the fungi i.e. Fusarium and *Curvularia*. Thus, it was concluded form the present study that considering the resistant reaction as confirmed by AICSIP three years report against the grain mold disease, the promising genotype AKGMR 117 showing Grain mold disease resistance need to be exploited in breeding for grain mold resistance in sorghum as the donor parent in the crossing programme.

44. VR 1062 (IC0635026; INGR21044), a Finger Millet (*Eleusine coracana*) Germplasm with Neck Blast Resistance (2.5%) and Finger Blast Resistance (3.0%).

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Finger millet, VR 1062 is neck and finger blast resistant line developed by crossing blast resistant germplasm GE 3076 with improved breeding line VR 855. The cross was performed in 2004 for developing blast resistant high yielding variety and subsequent selections were made through pedegree method from F_2 to F_6. At F_7 stage, it was promoted to Preliminary Yield Trial in 2011. It comes to maturity earlier than check Sri Chaitanya (VR 847) and is on par with Champavthi (VR 708). The plant height is short with medium number of productive tillers/plant. It has more number of fingers/ear head compared to both the checks.

The entry, VR 1062 along with other test entries and two checks were tested under high disease pressure under field conditions for consecutive five years from 2014 to 2018. It ranked first among all the 3000 entries tested for neck blast resistance (2.5% Pooled data) and also showed resistance to finger blast (3.0% Pooled data). VR 1062 has recorded -37.5% &

-97.41 % (less incidence) of neck blast over resistant check, Sri Chaitanya (VR 847) & susceptible check, Champavathi (VR 708) respectively while it recorded 23.08% & 96.85% less incidence offinger blast over Sri Chaitanya (VR 847) & Champavathi (VR 708) respectively. Hence, VR 1062 is unique in terms of neck and finger blast resistance and moreover it is a breeding line and hence it can be used directly for neck and finger blast resistance breeding.

45. FMV1155 (IC00403065; INGR21045), a Finger Millet (*Eleusine coracana*) Germplasm with Early Flowering (65 days), Early Maturity(105 days) and Higher Grain Yield (2188 kg/ha)

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Finger millet has the highest grain productivity among millets and the crop can thrive under a variety of harsh environmental conditions. The crop is also known for its nutritional superiority and the notable is highest calcium content (344 mg/100g) of grains which is about 10-15 times than that of any cereal. Breeding short duration (95-100 days) varieties with desirable grain andfodder yield is one of the major objectives in finger millet. Short duration varieties withcomparable yield can fit it multiple cropping systems and limited water resources and other inputs

Morpho-agronomic characters: The line FMV1155 was tested in All India Coordinated Small Millets Trial during 2018. The mean days to 50% flowering recorded by the entry is 65 days as compared to the similar early maturing check VL376 which recorded 69 days. For days to maturity, the mean days to maturity recorded by the entry is 105 days as compared to the early maturing check VL 376 which recorded 112 days. The entry also recorded higher grain yield of 2188 kg/ha as aganist the similar maturity check VL 376 which recorded 2155 kg/ha

Associated characters: The genotype FMV1155 recorded mean fodder yield of 8261 kg/ha as compared to similar maturing check VL376 which recorded fodder yield of 8075 kg/ha. The entry recorded plant height of 96 cm (semi-dwarf). The mean number of productive tillers recorded by FMV 1155 is three which is same as the check VL376. The entry also recorded highest ear finger length (9 cm) as compared to check VL 376 which recorded 8 cm. The mean number of ears recorded by FMV1155 is 6 which is similar to check VL376. The line can be animportant genetic stock while breeding for early duration variety with high grain yield especiallysuitable for growing in the Northern finger millet growing regions of the country.

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46. VL 384 (IC0637583; INGR21046), a Finger Millet (*Eleusine coracana*) Germplasm with White Grain. Blast Resistance, Medium Maturity and High Grain Yield

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Finger millet is an annual self-pollinated crop grown in Asia and Africa. In India, finger millet is grown in 1.2 million ha area with average productivity of 1706 kg/ha (Joshi *et al.* 2021). Most of the finger millet production is from brown grain varieties except few areas like Karnataka, Maharashtra, Jharkhand and Orissa where state released white grain varieties are cultivated in small scale. All the available white grained finger millet genotypes are late maturing and highly blast susceptible. Blast caused by *Magnaporthe grisea* is a major constraint to finger millet production (Sood *et al.*, 2019). Blast affects finger millet at all stages of growth and most of the landraces and a number of varieties are highly susceptible. Brown grained resistant genotypes have been developed and released for cultivation. However, the dark colour of grains has been the major hindrance for its acceptability in baking and food industry (Sharathbabu *et*

Table 1: Distinguishing characteristics of VL 384 compared to checks in All India Coordinated trials from 2013-2015

Character name	*VL 384 (White grain)*	*VL Mandua 352 (Brown grain)*	*VR 708 (Brown grain)*	*GPU 45 (Brown grain)*
Pigmentation on node	Absent	Absent	Absent	Absent
Growth habit	Erect	Erect	Erect	Erect
Leaf blade pubescence	Present	Present	Present	Present
Number of fingers/ear	7	8	7	7
Ear length (cm)	7.2-7.7	7.3-7.7	6.3-6.4	6.6-7.2
Days to Maturity	110-116	103-107	101-106	104-112
Plant height (cm)	93-97	94-98	84-90	88-96
Grain color	White	Copper Brown	Copper Brown	Copper Brown
Reaction to finger blast (%) (mean of MLT conducted from *kharif* 2013-2015)	9.15	8.10	15.38	5.35
Reaction to neck blast (%) (mean of MLT conducted from *kharif* 2013-2015)	9.66	9.45	18 .38	5.23

al., 2008). Thus, the preference for white grain finger millet genotypes is increasing recently in the urban areas and baking industry because of low tannins, high protein, low fibre, and higher consumer acceptability (Sharathbabu *et al.,* 2008). However, the available white grain types have been observed to be late maturing and highly susceptible to neck and finger blast in comparison to brown grain types. Till date there is no white grain finger millet released genotype available in the early and medium group in the country matching to brown grain for resistance as well as yield potential.

VL 384 has been indigenously developed from a cross between OUAT 2 (White grain late maturing variety released for the State of Orissa, blast susceptible) and GE 4415 (Early maturing core germplasm line from Bihar). It has maturity duration of 110-116 days and found resistant to finger (9.15%) blast disease compared to the early maturing (101-106 days) brown grain national check VR 708 (15.38%) in all India coordinated trials (*kharif* 2013-2015). Likewise, the percent damage due to neck blast in VL 384 (9.66%) was very low compared to the early maturing brown grain check VR 708 (18.38%). VL 384 fell in the same disease scale category of 5-10% with other brown grain national check varieties (VL 352 and GPU 45) in all India coordinated trials. Moreover, its average grain yield over the years and locations in coordinated trials was 27.19 q/ha which was 5.10 per cent higher than the best brown grained national check VL *Mandua* 352 (25.87 q/ha).

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47. IE-2871 (IC0473958; INGR21047), a Finger Millet (*Eleusine coracana*) Germplasm Resistant to Neck Blast (3.71 score in 1-9 scale)

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Blast of finger millet, *Pyricularia grisea*, causes significant loss of production worldwide. The average loss has been reported to be around 28–36% and as high as 80–90% in endemic areas (Ramappa *et al.,* 2002; Nagaraja and Mantur, 2007). So far there was no stable source of resistance available against finger and neck blast. 'IE-2871 selection' was a pure line selection from the Zambian germplasm IE-2871. Selections were made under disease pressure (finger and neck blast) situations at Hyderabad.This selection along with 114 other finger millet genotypes including germplasm of African and Asian origin and a few improved cultivars were evaluated for finger and neck blast resistance across three locations in India representing major finger millet areas. Evaluation was conducted under natural field conditions,

Table 1: Performance and stability of resistance of IE-2871 for finger and neck blast resistance over four environments (Source: Das *et al*. 2021: Crop Protection, 139)

	Finger blast (1-9 scale)							Neck Blast (1-9 scale)						
Genotype	H'16	H'17	V'17	B'18	Mean	*bi*‡	S^2di†	H'16	H'17	V'17	B'18	Mean	*bi*‡	S^2di†
IE-2871	3.5	2.5	4.0	2.5	3.1	0.80	-0.04	2.0	2.0	3.0	2.0	2.3	0.90	-0.16
IE-2883	2.5	2.5	3.5	3.0	2.9	0.91	-0.03	2.0	2.0	4.0	2.0	2.5	1.08	-0.11
GPU-67	4.6	5.0	4.5	2.0	4.0	1.87	-0.19	3.5	3.5	5.5	2.0	3.6	0.83	-0.14
GE-4449 (RC)	3.5	3.5	4.0	3.5	3.6	0.11	-0.29	3.0	3.5	3.5	3.0	3.3	-0.45	-0.17
UM (SC)	8.5	8.0	7.0	6.0	7.4	0.89	0.24	6.5	6.5	6.5	5.5	6.3	0.32	0.16
CD (5%)	0.96	0.93	0.48	0.55				0.81	0.51	0.43	0.48			

Disease severity was measured on a 1–9 scale, where 1= <1% plants/finger (plant for NB; finger for FB) infected with disease, and 9= >75% infected. H'16: Hyderabad 2016, H'17: Hyderabad 2017, V'17: *Viz*ianagaram 2017, B'18: Bengaluru 2018. ‡bi: regression coefficient; †S2di: variance deviation regression.

supplemented with artificial inoculation of earhead with blast pathogen at pre-anthesis stage. IE-2871 was stable for both finger and neck blast resistance. Its resistance to neck blast is far superior (2.3 on a scale of 1-9) than the best available resistance source GE-4449 (3.3) (Table 1) (Das *et al.,* 2021). Additionally it also possesses better resistance for finger blast (3.1) than the resistant check GE-4449 (3.6).

IE-2871 also possesses desirable agronomic characters like medium plant height (103 cm), medium maturity (120 days) compared to early maturity in the presently available resistant check GE-9994 (99 days). Medium maturity is a desirable trait in finger millet. This stable sources of neck blast resistance in finger millet, will serve as an important genetic material in a finger millet resistance breeding programme.

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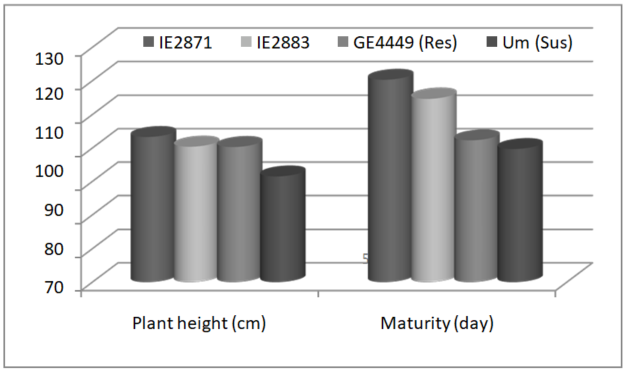

Figure 1: Agro-morphological characteristics of IE-2871

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48. IE-2883 (IC00473970; INGR21048), a Finger Millet (*Eleusine coracana*) Germplasm Resistant to Finger Blast (2.9 score in 1-9 scale)

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Blast of finger millet, *Pyricularia grisea*, causes significant loss of production worldwide. The average loss has been reported to be around 28–36% and as high as 80–90% in endemic areas (Ramappa *et al.,* 2002; Nagaraja and Mantur, 2007). So far there was no stable source of resistance available against finger and neck blast. 'IE-2883 selection' was a pure line selection from the Zambian germplasm IE- 2883. Selections were made under disease pressure (finger and neck blast) situations at Hyderabad. This selection along with 114 other finger millet genotypes including germplasm of African and Asian origin and a few improved cultivars were evaluated for finger and neck blast resistance across three locations in India representing major finger millet areas. Evaluation was conducted under natural field conditions, supplemented with artificial inoculation of earhead with blast pathogen at pre-anthesis stage. IE-2883

Table 1: Performance and stability of resistance of IE-2871 for finger and neck blast resistance over four environments (Source: Das *et al*. 2021: Crop Protection, 139)

Genotype	Finger blast (1-9 scale)							Neck Blast (1-9 scale)						
	H'16	H'17	V'17	B'18	Mean	*bi*ǂ	S^2di†	H'16	H'17	V'17	B'18	Mean	*bi*ǂ	S^2di†
IE-2871	3.5	2.5	4.0	2.5	3.1	0.80	-0.04	2.0	2.0	3.0	2.0	2.3	0.90	-0.16
IE-2883	2.5	2.5	3.5	3.0	2.9	0.91	-0.03	2.0	2.0	4.0	2.0	2.5	1.08	-0.11
GPU-67	4.6	5.0	4.5	2.0	4.0	1.87	-0.19	3.5	3.5	5.5	2.0	3.6	0.83	-0.14
GE-4449 (RC)	3.5	3.5	4.0	3.5	3.6	0.11	-0.29	3.0	3.5	3.5	3.0	3.3	-0.45	-0.17
UM (SC)	8.5	8.0	7.0	6.0	7.4	0.89	0.24	6.5	6.5	6.5	5.5	6.3	0.32	0.16
CD (5%)	0.96	0.93	0.48	0.55				0.81	0.51	0.43	0.48			

Disease severity was measured on a 1–9 scale, where 1= <1% plants/finger (plant for NB; finger for FB) infected with disease, and 9= >75% infected. H'16: Hyderabad 2016, H'17: Hyderabad 2017, V'17: *Viz*ianagaram 2017, B'18: Bengaluru 2018. ǂbi: regression coefficient; †S2di: variance deviation regression.

was stable for both finger and neck blast resistance. Its resistance to finger blast is far superior (2.9 on a scale of 1-9) than the best available resistance source GE-4449 (3.6) (Table 1) (Das *et al.,* 2021). Additionally, it also possesses better resistance for neck blast (2.5) than the resistant check GE-4449 (3.6).

IE-2883 also possesses desirable agronomic characters like semi-compact earhead, medium plant height (100 cm), medium maturity (115 days) compared to early maturity in the presently available resistant check GE-9994 (99 days). Medium maturity is a desirable trait in finger millet. This stable sources of neck blast resistance in finger millet, will serve as an important genetic material in a finger millet resistance breeding programme.

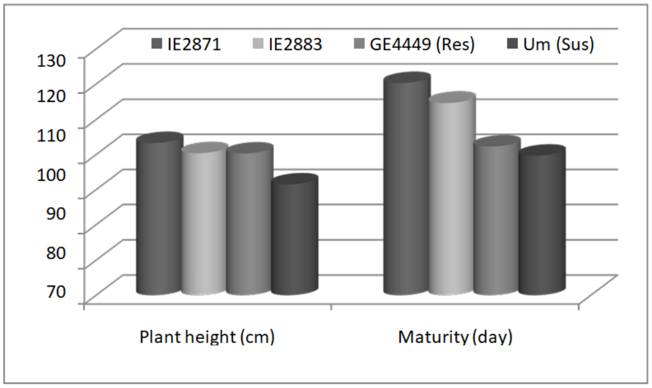

Figure 1: Agro-morphological characteristics of IE-2883

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49. VB 19-16 (IC0637584; INGR21049), a Barnyard Millet (*Echinochloa esculenta*) Germplasm with Awnless Panicle in the Genetic Background of Japanese Barnyard Millet Species (*E. esculenta*). Semidwarf. Green Glumes

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Towards the development of new plat types, isolation of awnless semi-dwarf genotype of Japanese barnyard millet (*E. esculenta*) is the promising development at ICAR-Vivekananda Institute of Hill Agriculture, Almora, India. In Indian barnyard millet (*E. frumentacea*), lodging is a major production constraint causing substantial losses in grain yield. In general, Japanese barnyard millet (*E. esculenta*) genotype PRJ 1 (originally ICRISAT gen bank accession, IEc 542) exhibit semi-dwarf growth habit (tolerant to lodging), posses' panicles with large awns and well adapted to North West Himalaya (Sood *et al*., 2015). However, introgression of these traits in Indian barnyard millet (*E. frumentacea*) (cultivar VL 207) through interspecific hybridization was largely failed due to the presence of strong incompatibility barriers between the species (Sood *et al.,* 2020). Therefore, intraspecific hybridization between the diverse genotypes of *E. esculenta* is one potential strategy to develop transgressive segregants for agronomic traits. Keeping this in view, both way crosses were attempted between two genotypes (PRB 903 and PRJ 1) of *E. esculenta* at ICAR- VPKAS, Almora to exploit their high yield potential and agronomic superiority. The effort has resulted in obtaining F_6 progenies, characterized by large awnless panicles (27.5–35cm), more number of panicle branches (> 30) and medium plant height (120–148 cm) compared to the parents. In general, panicles of *E. esculenta* genotypes are characterized by large awns. Interestingly, the intraspecific hybridization attempt resulted in development of stable awnless segregants in the genetic background of PRJ 1, which are more vigorous than parental line. To the best of our knowledge, this is the first report of isolating awnless Japanese barnyard millet genotypes through hybridization. These awnless *E. esculenta/E. esculenta* derivatives with reduced plant height with uncompromised fodder potential are the positive developments towards generating dual purpose genetic material of barnyard millet.

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50. IIMR FxM-5 (FXV 632) (IC0479823; INGR21050), a Foxtail Millet (*Setaria italica)* Germplasm with Early Flowering (44 days). Early Duration (76 days) with Desirable Grain Yield.

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Foxtail millet (*Setaria italica* (L.) Beauv.), a self-pollinating cereal, belonging to Family *Poaceae* is one of the oldest of the cultivated millets in the world. It is cultivated in about 23 countries in Asia, Africa and America. It is adapted to a wide range of elevations, soils and temperatures. At present globally it is distributed in Eurasia, Ethiopia, Zimbabwe, Japan, China, Nepal and India with around 4 - 5 m ha area. Foxtail millet is grown for food, feed and fodder purpose. Because of the drought tolerance, it was once an indispensable crop of vast rainfed areas in semi-arid regions in India. The area under this crop in India has come down by more than half during 1990's mainly due to introduction of more remunerative crops like sunflower and soybean in black soils. At present, foxtail millet is cultivated on a limited area in Andhra Pradesh, Telangana, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and North Eastern states. It is mostly grown to meet the domestic needs of the rural people. It is widely used as an energy source for pregnant and lactating women, and also for sick people and children, and especially for diabetics. Foxtail millet is highly nutritious and even superior to rice and wheat in certain constituents. Grains of foxtail millet have low glycaemic index (GI) and high fibre (8%) content, because of which it is gaining popularity as diabetic food. The protein content is higher (12.3%) among millets. Because of short duration foxtail millet is ideal as a contingency crop whenever the monsoon delays in semi-arid regions. A number of high yielding varieties have been released, but the yield potential is not fully expressed in farmers' fields due to various management aspects.

There is a need to develop further high yielding early maturing varieties through recombination breeding, which can mature early enough to avoid late season moisture stress in regions where monsoon withdraws early. Such varieties can utilize the short duration moisture availability, especially when onset of monsoon is delayed, and still can provide grains and fodder to the dryland farmers.

Morpho-agronomic characteristics: IIMR FxM-5 (FXV 632) is a foxtail millet selection from GS 957 with significantly early flowering (44 days) and early maturity (76 days), with desirable productivity (2664 kg/ha). Out of 14 locations tested, in 10 locations it flowered early compared to all other entries and in 6 locations it matured first as well as at all India level (Table 1 a & b). The average per day productivity in this genotype was 35.05 kg/ha/day compared to check, DHFt 109-3 (34.38 kg/ha/day) (Table 2). It has cylindrical panicles with medium compact inflorescence lobes and good yield potential. It can be used as a donor parent for incorporating earliness in recombination breeding to combine high yield and short duration. The early flowering and maturity can help in avoiding terminal moisture stress in locations where rainy season withdraws early. Also in regions where foxtail millet followed by pulses cropping pattern is followed, this helps in early sowing of second crop thus ensuring better germination and crop stand.

Associated characters: The shoot fly dead hearts in IIMR FxM-5 (FXV 632) at 21 DASE was 20.52% compared to 23.68% in resistant check. It recorded 3% less incidence of dead hearts compared to SiA 3179 (23.68%), resistant check and 5% lesser than the susceptible check (SiA 907). The tolerance level was on parwith the national checks. IIMR FxM-5 (FXV 632) will be highly beneficial as a donor parent for breaking the yield ceiling and further foxtail millet improvement and consolidation of gains already achieved through conventional breeding.

Table 1a: Flowering duration of IIMR FxM-5 (FXV 632) Vs. checks

Trait	*Location*	*Variety IIMR FxM-5 (FXV 632)*	*Rank*	*Check variety 1 (SiA 3156)*	*Rank*	*Check variety 2 (DHFt 109-3)*	*Rank*	*CD (5%)*
Days to flowering	Nandyal	45	2	48	4	51	15	3
	*Vizi*anagaram	40	1	48	15	46	11	2
	Andhra Pradesh	43	1	48	10	49	13	3
	Dholi	41	1	46	8	49	11	7
	Ranchi	43	2	415	6	50	16	2
	Bangaluru	50	1	52	4	55	13	3
	Hagari	42	1	58	20	49	9	-
	Hanumanamatti	43	1	51	15	49	11	2
	Mandya	38	1	46	22	46	20	5
	Karnataka	43	1	50	14	50	16	3
	Dindori	42	1	49	20	47	8	2
	Rewa	47	3	50	7	51	16	4
	Madhya Pradesh	45	1	50	20	49	11	3
	Solapur	44	1	50	9	52	14	3
	Athiyandal	51	20	49	16	49	14	7
	Hyderabad	51	1	53	3	60	16	5
	Palem	42	1	46	2	53	18	6
	Telangana	47	1	50	2	57	19	5
	All India	44	1	49	9	51	16	2

Table 1b: Maturity duration of IIMR FxM-5 (FXV 632) Vs. checks

Trait	*Location*	*Variety IIMR FxM-5 (FXV 632)*	*Rank*	*Check variety 1 (SiA 3156)*	*Rank*	*Check variety 2 (DHFt 109-3)*	*Rank*	*CD (5%)*
Days to Maturity	Nandyal	75	2	78	4	81	16	3
	*Vizi*anagaram	69	1	78	15	77	10	3
	Andhra Pradesh	72	1	78	10	79	12	3
	Dholi	74	1	78	4	81	13	6
	Ranchi	75	1	80	15	80	12	3
	Bangaluru	88	1	91	4	94	13	3
	Mandya	76	11	76	13	76	13	6
	Karnataka	82	5	84	8	85	14	5
	Dindori	75	2	81	20	78	10	3
	Rewa	74	3	76	5	76	7	4
	Madhya Pradesh	74	1	78	18	77	8	4
	Solapur	72	1	86	5	90	20	5
	Athiyandal	84	21	79	3	83	17	5
	Palem	75	1	78	3	84	15	6
	All India	76	1	80	6	82	13	2

Table 2: Grain yield and per day productivity in IIMR FxM-5 (FXV 632) vs. Checks

No.	*Entry*	*Centre code*	*Grain yield (kg/ha)*	*Days to maturity*	*Rank*	*Per day productivity (kg/ha/day)*
1	FXV 606	SIA 3220	2700	81	12	33.22
2	FXV 607	FXV 607	2744	81	8	34.03
3	FXV 615	SIA 3159	2823	82	14	34.62
4	FXV 616	IIMR FxM-2	2718	81	9	33.59
5	FXV 620	GPUF 2	2727	81	15	33.63
6	FXV 622	FXV662	2666	80	7	33.19
7	FXV 624	PKS 22	2577	80	4	32.03
8	FXV 625	SIA 3303	3104	79	2	39.54
9	FXV 626	SIA 4200	2925	83	22	35.11
10	FXV 627	GPUF 3	2753	82	16	33.39
11	FXV 628	GPUF 4	2997	83	18	36.23
13	FXV 630	TNSI 364	2682	81	11	33.31
14	FXV 631	IIMR FxM-4	2785	83	21	33.62
15	FXV 632	IIMR FxM-5	2664	76	1	35.05
16	FXV 633	IIMR FT 1	2537	79	3	32.08
17	FXV 634	F0XTAIL	2422	83	20	29.10
18	FXV 635	DHFT 109-3-1	2854	82	19	34.60
19	FXV 636	DHFT 109-3-2	2987	82	17	36.39
20	DHFt 109-3 (C)		2817	82	13	34.38
21	SiA 3156 (C)		2938	80	6	36.68
	Mean		2789	81		34.43
	CD (5%)		349	2		-

51. IPU19-27 (IC0636672; INGR21051), a Black gram (*Vigna mungo*) Germplasm, Extra Early (60-62 days) Resistant to Yellow Mosaic Disease (MYMV)

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Urdbean [*Vigna mungo*] also known as blackgram, is an important pulse crop among *Vigna* pulses including mungbean and cowpea in India. Under varying climate change scenario short duration pulses are in demand in different growing regions. Under the All India Co-ordinated Research Project (AICRP) several varieties have been released which are meeting the national and local needs. Initially, semi-determinate to indeterminate plant types alongwith longer duration (90-120 days) were desirable for rainy season (Pratap *et al*. 2013; Gupta *et al*. 2001; Saxena and Yadav 1975). Sixty days maturing pulses including urdbean can fit in any cropping system thereby increase the cropping intensity. One urdbean genotype, IPU19-27, was developed at ICAR- Indian Institute of Pulses Research, Kanpur which mature significantly early (60-65 days) during summer as well as rainy seasons as compared to other released urdbean varieties (70-80 days) in North-Eastern Plain Zone (NEPZ). This genotype was developed from the cross 'SPS 5 x IPU02-33' following the pedigree method of selection. This urdbean genotype showed resistance to mungbean yellow mosaic India virus (MYMIV) under high natural disease pressure conditions as evidenced in susceptible genotypes of urdbean. The major morphological characteristics of this newly developed genotype are medium height and erect plant type, light green lanceolate leaves, bright yellow flowers, medium length black pods on maturity with pubescence, and dull black seeds. This genotype has the potential to be released as a cultivar after multi-location testing and can also be a useful donor for earliness and MYMIV resistance.

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52. RKG-13-55 (IC0633092; INGR21052), a Chickpea (*Cicer arietinum*) Germplasm Resistant against Wilt. Good yield and Early

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The *desi* chickpea genotype RKG 13-55 has been developed by crossing of RSG 931 with RKG 143 at ARS, Kota in the year 2011-12 with the objective of combining high yield with disease resistance. It was tested in station trials and later evaluated in coordinated trials of AICRP on Chickpea across the zones in Initial Varietal Trial (IVT-Desi) in the year 2017-18. It was at par with the checks in yield but showed resistant reaction against fusarium wilt disease. Based on its resistant reaction, it was further evaluated for second year in 2018-19 in sickplots of plant pathological trials where it again showed the resistant reaction against wilt. The chickpea genotype RKG 13-55 was found resistant against wilt for consecutive two years (2017-18 and 2018-19) in Central and South zone; as per the results of the coordinated plant pathological trials of AICRP on Chickpea conducted in sick plots, as compared to checks GNG 2171, CSJ 515 and JG 315

Besides being resistant, RKG 13-55 also gave good yield, higher or at par with the leadind checks *viz*., GNG 1581, GNG 2171, JG 16, GCP 101, GCP 105, KWR 108and JAKI 9218 (dataenclosed). It was evaluated in Initial Varietal Trial (Desi) across the zones during the year 2017-18. In NWPZ, it yielded 2324 kg/ha which was at par with the checks GNG 1581 and GNG 2171 (2328 kg/ha and 2682 kg/ha, respectively). It yielded 1419 kg/ha in NEPZ which wasat par with the checks KWR 108 and GCP 105 (1370 kg/ha and 1670 kg/ha, respectively). The genotype RKG 13-55 gave 2184 kg/ha yield in WCZ which was at par with the checks JG 16 and GCP 101 (2085 kg/ha and 2179 kg/ha). The genotype RKG 13- 55 gave 1922 kg/ha yield in ECZ which was at par with the checks JG 16 and JAKI 9218 (1997 kg/ha and 1430 kg/ha). The genotype RKG 13-55 gave 1386 kg/ha yield in SZ which was at par with the checks JG 11 and JAKI 9218 (1865 kg/ha and 1833 kg/ha). The genotype RKG 13-55 matures in 139 days in North West Plain Zone, 130 days in North Eastern Plain Zone, 111 days in West Central Zone, 102 days in East Central Zone and 95 days in South Zone. It is early or at par with the checks GNG 1581, GNG 2171, JG 16, GCP 101, GCP 105 and KWR 108 in NWPZ, NEPZ, WCZ, ECZ and SZ (data enclosed). The genotype RKG 13-55 has brown, wrinkled, medium bold seed size. The 100-seed weight of RKG 13-55 was 24.2g in NWPZ, 23g in NEPZ, 23.2g in WCZ, 20g in ECZ and 24.8 g in SZ.

53. EC720481 (ILWC246) (EC720481; INGR21053), a Chickpea (*Cicer echinospermum*) Germplasm Resistant against Botrytis Gray Mold

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The wild chickpea accession EC720481 (ILWC246) was selected after preliminary characterization and evaluation of wild annual *Cicer* species for important agro- morphological and major biotic stress related traits during winter 2011-12 and summer 2012. All available global wild *Cicer* species were also evaluated against Ascochyta Blight, Botrytis Gray Mold and Root Knot Nematode, which had resulted into the identification of some resistant accessions against the target

Table 1: Descriptor and descriptor state of EC720481 (ILWC246) for important qualitative characters

Descriptor	*Descriptor state*
Plant pigmentation	Absent
Plant hairiness	Lightly pubescent
No. of leaflets leaf^{-1}	11-13
Flower colour	Light blue
Seed shape	Angular
Seed colour	Black
Testa texture	Tuberculated

traits. The highly resistant accession EC720481 (ILWC246) was further validated twice under controlled screening test using cut-twig screening technique, in which water was used as supportive medium. Twigs were inoculated by spraying spore suspension of *Botrytis cinerea* (10,000 spores ml^{-1}) and covered gently with moist chambers for 144 hrs. An incubation period of 8 hrs. dark and 16 hrs. light was provided with fluorescent lamps. Further observations on disease incidence were recorded using 1-9 rating scale. Based on the disease score, an accession EC720481 (ILWC246) belonging to *Cicer echinospermum* has been reported highly resistant against the BGM (Singh *et al*. 2014.).

Morpho-agronomic characteristics: Besides possessing resistance against Botrytis Gray Mold (BGM), an accession EC720481 (ILWC246) was also reported promising for other agro- morphological traits *viz*; number of branches/ plant (13), number of pods/ plant (31) and number of seeds/plant (33). As far as distinct morphological traits are concerned, the following qualitative features were also reported using chickpea descriptor states developed by IBPGR/ICARDA (Table 1).

The above mentioned important characters have their special significant value for enhancing genetic gains of cultivated varieties, which need to be considered while planning future chickpea genetic improvement programme for introgressing resistance against BGM as well as agronomic improvement of cultivated gene pool.

References

IBPGR/ICARDA (1993) Chickpea descriptors: IBPGR Secretariat, Rome, Italy pp 15.

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54. EC720438 (ILWC229) (EC720438; INGR21054), a Chickpea (*Cicer reticulatum*) Germplasm Resistant to Ascochyta Blight

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The wild chickpea accession EC720438 (ILWC229) was selected after preliminary characterization and evaluation of wild annual *Cicer* species for important agro- morphological and major biotic stress related traits during winter 2011-12 and summer 2012. All available global wild *Cicer* species were also evaluated against Ascochyta Blight, Botrytis Gray Mold and Root Knot Nematode, which had resulted into the identification of some resistant accessions against the target traits. The highly tolerant accession EC720438 (ILWC229) was further validated twice under real filed hot spot at CSKHPKV Research and Extension Centre at Dhaulakuan. It was then artificially inoculated by frequently spraying with ascosporic suspension (1x10^6 spores ml^{-1}) using local isolates of *Ascochyta rabiei*. Further observations on disease incidence were recorded using 1-9 rating scale. Based on the disease score, an accession EC720438 (ILWC229) belonging to *Cicer reticulatum* has been reported highly resistant against the Ascochyta blight (Singh *et al.* 2014, *Crop Sci.*).

Morpho-agronomic characteristics: Besides possessing resistance against Ascochyta blight, an accession EC720438 (ILWC229) was also reported promising for other agro-morphological traits *viz*; number of branches/ plant (12), number of pods/ plant (37) and number of seeds/plant (39). As far as distinct morphological traits are concerned,

Table 1: Descriptor and descriptor state of EC720438 (ILWC229) for important qualitative characters

Descriptor	*Descriptor state*
Plant pigmentation	Low anthocyanin
Plant hairiness	Lightly pubescent
No. of leaflets leaf^{-1}	09-11
Flower colour	Light pink
Seed shape	Angular
Seed colour	Brown
Testa texture	Rough

the following qualitative featureswere also reported using chickpea descriptor states developed by IBPGR/ICARDA (Table 1).

The above mentioned important characters have their special significant value for enhancing genetic gains of cultivated varieties, which need to be considered while planning future chickpea genetic improvement programme for introgressing resistance against Ascochyta blight as well as agronomic improvement of cultivated gene pool

References

IBPGR/ICARDA (1993) Chickpea descriptors: IBPGR Secretariat, Rome, Italy pp 15.

Singh *et al*. (2014) *Crop Science*, **54:**229-239.

55. IC259504 (IC0259504; INGR21055), a Wild Bean (*Vigna vexillata*) Germplasm High protein content (9.5%) in tuber. Bold seededness. Fodder type.

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Tuber cowpea, *Vigna vexillata* (L.) A. Rich. is an underutilized tuberous resilient legume which is known for its multiple uses in India. Being a leguminous tuber, protein is the most important useful trait for enhancing utilization of this crop. A total of 108 accessions of *V. vexillata* were obtained in the form of seed from the Indian national genebank, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi. After screening for agronomic and biochemical traits, the accession IC259504 was found with more than 9.5% protein content in tuber.

Besides high protein content, this accession also has superior agronomic traits *viz*. tuber weight, pod length, number of seed per pod and bold seededness (5.01g). Nutritional compositions were also compared with other major tuber crops *viz*.., sweet potato, cassava and soh-phlong, a minor leguminous tuber from India. In comparison to other crops, tuber cowpea was found to have seven-fold and nine-fold higher amount of protein content than sweet potato and cassava respectively but threefold to soh-phlong.

Sasikumar and Sardana (1988) reported proximate compositions on seeds of tuber cowpea, but they did not give any information on tubers. This is the first study allows a glimpse into the variability in tubers of the Indian region. *V. vexillata* is widely distributed in all four biodiversity hotspots designated in India. Despite low variability in tubers reported globally, this investigation revealed sufficient variation for tuber morphology, nutritional traits and habitat study. Utilization of this underutilized legume can lead to improvement in tuber cowpea as a root crop besides pulse, vegetable and forage crop.

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56. IPC HT2A & IPC HT2B (IC0635034 & IC0635035; INGR21056), a Carrot (*Daucus carota*) CMS line IPC HT2A is First Red Colour Heat Tolerant Tropical Carrot Developed Indigenously. Roots are of Acceptable Size, Red Colour and Self Core. Suitable for Early Season Sowing due to its Pusa Vrishti (IPC HT2) Genotype Background.

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Carrot (*Daucus carota* L.; 2n= 2x=18) is important nutritious root crop. It is being grown all across the world on an area of 1.15 million ha area with production of 42.8 million tonnes (FAOSTAT, 2017). It has temperate (European) and tropical (Asiatic) types. In India, it is being grown on 86,200 ha area with a production of 1,379,031 MT (NHB Database 2017). Here, both tropical and temperate types are popular but tropical red carrot are predominant due to their suitability for juice, *halwa*, sweets and vegetable purposes especially in north India. However, productivity of carrot in India is around 33.5% lower than world average mainly due to lack of hybrids which are known for uniformity, earliness, high yield, and more percentage of marketable roots (Kalia *et al*. 2019). In carrot, the cytoplasmic male sterility (CMS) is being used commercially for hybrid breeding which is of two types *i.e*. petaloid (anthers turns to petals) and brown anther (shriveled brown anther). Although, both systems are in use for commercially hybrid breeding seed production but petaloid type is environmentally stable hence, widely used in hybrid breeding of carrot. Presently, the only hybrid available in tropical red carrot is Pusa Vasuda which is developed by use of petaloid CMS system and suitable for main season cultivation only. However, demand is also increasing for early season carrots and conversion of elite inbred lines of early season having heat tolerance with stable CMS was required for early season hybrid breeding. The CMS line IPC HT2A is an indigenously developed heat tolerant CMS line of tropical carrot. It has petaloid type sterile cytoplasm into the genetic background of an elite inbred line IPC HT2B which is suitable for early season July sowing in the north Indian plains because of heat tolerance. The IPC HT2 (fertile) has been converted to IPC HT2A (male sterile) by introgression of petaloid CMS system from 'IPC 122A', a natural mutant identified at Division of Vegetable Science, ICAR-IARI, New Delhi (Kalia *et al.,* 2019) and backcrossing with recurrent parent (i.e. IPC HT2) for nine generations (BC_9).

Morpho-agronomic characteristics: The CMS line IPC HT2A is the first CMS line of tropical heat tolerant red carrot developed indigenously. It is suitable for sowing during early crop season (*i.e*. July end to mid August) and roots are ready to harvest in a period of 90 – 95 days (Table 1). The height of flowering plants was 129.6 cm with profuse flowering umbels and seed setting. The floral traits *i.e*. petal size, petal colour, petaloid (anther converted petals) colour and size and nectaries showed normal development (Fig. 1A-B; 2A-B). It produces red colour, medium long roots with self-core character. The average root length was observed to be 21.5 cm, root diameter 32.3 mm, core diameter 7.86 mm and root weight 100 g (Fig. 3A-B). The marketable root yield was observed to be 15.0 t/ha which was significantly low than its maintainer line IPC HT2B (27.5 t/ha) (Table 1). The bolting (elongation of flower stalk) occurs during January-February month and produce abundant seeds during March-April month in plains of India. The CMS line showed potential in hybrid breeding of early season carrot hybrid with tolerance to heat stress hence, can be used in commercial hybrid breeding programme.

The 'IPC HT-2B' is a promising genotype of early season tropical carrot with heat tolerance trait. It is suitable for sowing in July end to August first fortnight in north Indian plains. It has been already released as 'Pusa Vrishti' for commercial cultivation. It gets ready for harvesting in

Table 1: Important horticultural traits and seed yield of CMS line IPC HT-2A line as compared to the fertile maintainer line IPC HT2B

Traits	*IPC HT-2A*	*IPC HT 2B*
Maturity traits		
Growing season	Early season	Early season
Heat tolerance	Yes	Yes
Sowing period	July end to August first fortnight	July end to August first fortnight
Harvesting	October end to November first fortnight	October end to November first fortnight
Plant and root traits		
Plant height (cm)	78	85.2
Gross plant weight (cm)	185	215.0
Root colour	Red	Red
Root core colour	Red	Red
Root length (cm)	21.5	20.4
Root diameter (mm)	32.3	37.9
Core diameter (mm)	7.86	7.14
Root weight (g)	100	150
Root yield (t/ha)	150	275
Floral traits		
Petal colour	White	Light green
Petal length (cm)	0.99	0.44
Petaloid colour	Light purple	-
Petaloid length (cm)	1.67	-
Petaloid width (cm)	0.62	-
Petaloid shape	Spoon	-

90-95 days during last week of October to first fortnight of November. Plants are medium vigorous, semi-erect, medium in spread and leaves are green. It produces red root with self core colour (Table 1).

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57. BR 161 (IC0637585; INGR21057), a Cauliflower (*Brassica oleracea* var. *botrytis*) Germplasm Resistant to Black Rot Disease (*Xanthomonas campestris pv*. *campestris* race 1). Carries a Novel Single Dominant Gene Xca1bo for Black Rot Resistance Located on Chromosome 3 and Flanked by DNA Markers

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Cauliflower (*Brassica oleracea* var. *botrytis* L.) is one of the most important and widely grown *Brassica* vegetables in India. Among the diseases, black rot is a wide spread bacterial disease caused by *Xanthomonas campestris* pv. *campestris* (*Xcc*) (Pammel) Dowson. It is the most devastating disease of cauliflower worldwide including India (Singh and Dhar, 2011; Saha *et al.,* 2014). The line 'BR 161' is resistant to black rot disease caused by *Xcc* race 1. It was developed from progeny selection of a cross of S. No. 15 (susceptible genotype) and MGS-2-3 (resistant) by Division of Vegetable Science, ICAR-IARI, New Delhi, India The line carries a novel single dominant resistant gene *Xca1bo* on chromosome 3 and flanked by DNA markers RAPD 04_{833} and ISSR 11_{635} (Saha *et al.,* 2014).

Morpho-agronomic characteristics: The resistant line BR 161 belongs to mid-late maturity group with erect growth habit and medium in height (48–50 cm). The leaves are light green, medium in size with weak puckering habit. The curds are open, loose and creamy with an average weight of 401.05 g. The reaction of the plant at adult stage showed resistant reaction with plant disease index of 0-0.4 even at 60 days after inoculation (DAI) (Table 1) (Saha *et al.,* 2012).

Associated characters and cultivation practices: The curd of the line BR 161 become mature in the month of December end to mid- January requiring 12-16°C temperature for curd initiation and development. The crop gets ready to harvest in 75-80 days after transplanting in its normal growing season. The flowers of 'BR 161' are yellow and stalk length is medium and flowering occurs during February end to mid-March. The line can be a useful source for transferring the resistant gene in commercially susceptible variety (s) or to develop hybrid (s).

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Table 1: Response of BR 161 and commercial cauliflower varieties to black rot disease in four different season/environment after artificial inoculation with black rot pathogen (Xcc race 1)

Genotype/lines	*PDI at 60 days after inoculation Environment 1/season 1 (a)*	*PDI at 60 days after inoculation Environment 2/season 2 (b)*	*PDI at 60 days after inoculation Environment 3/season 3 (c)*	*PDI at 60 days after inoculation Environment 4/season 4 (d)*	*Disease reaction**
BR 161**	0.2	0.1	0.4	0.0	Resistant
Pusa Himjyoti	3.9	4.0	4.0	4.0	Highly susceptible
Pusa Sharad	3.4	3.9	3.8	4.0	Highly susceptible

*Based on PDI score developed by Thakur *et al.* (2003), 0-1: Resistant; 1-2: Moderately resistant; 2-3 Susceptible; 3-4: Highly susceptible.

58. DSG-7 (IC0588957) (IC0588957; INGR21058), a Sponge Gourd (*Luffa cylindrica*) Germplasm Highly Resistant to Tomato Leaf Curl New Delhi Virus. Good combiner and Gives Higher Heterosis for Yield & other Desirable Traits. Resistance is Governed by Single Dominant Gene.

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Sponge gourd is a popular low cost vegetable grown throughout India. Recently *Tomato Leaf Curl New Delhi Virus*, (*ToLCNDV*: genus *Begomovirus*, family Geminiviridae), the causal virus of tomato leaf curl has been reported to be associated with sponge gourd and causing a yield loss up to 100 % in north Indian plains during *kharif* season under epidemic condition (Sohrab *et al.,* 2003). The diseased plant is characterized by yellow spots appearing on newly emerging leaves, followed by a mosaic appearance and upward curling of the upper leaves. Incases of severe attack, the leaves of the plant are small and distorted and misshapen fruits are produced. The virus is transmitted through sap as well as whitefly (*Bemisia tabaci* Hemiptera-Aleyrodidae). The genotype DSG-7 was screened under natural epidemic condition and found to be completely resistant to *Tomato leaf curl New Delhi virus*, during rainy season which is conducive for white fly multiplication and the spread of diseases. The result was also confirmed through challenge inoculation with purified strain of the virus under insect proof green house at Virology Unit, Division of Plant Pathology, IARI, New Delhi.

DSG-7 is developed by selection from segregating material collected from Moradabad district of Uttar Pradesh. It is a monoecious trailing or climbing annual vine with stem and tendrils. The leaves are medium green, reniform, six lobed, nearly glabrous, non-hairy and smooth with long petioles. Stem is angular. Inflorescence is clustered, racemose, flowers unisexual, male flower large in number in cluster, yellow and showy with long peduncle. Female flower is solitary on short and round peduncle and yellow in colour. Fruits elongated(15-20 cm), straight, light green with thin skin and without stripes, average fruit weight 110g, flesh tender, suitable for spring-summer and *Kharif* season. It is ready for first harvesting in 45-50 days during *kharif* season and 50-55 days in spring summer season. Average fruit yield is 16 t/ha. Highly resistant to *Tomato leaf curl New Delhi virus* during *kharif* season which is conducive for white fly multiplication and the spread of diseases (Table 1 to 5).

Table 1: Screening of DSG-7 under natural epidemic condition during kharif season 2008-2010

Genotype	2008		2009		2010	
	Yield (t/ha)	Vulnerability Index & Category	Yield (t/ha)	Vulnerability Index & Category	Yield (t/ha)	Vulnerability Index & Category
DSG-7	13.95	8.67 (HR)	14.56	4.15 (HR)	14.05	6.67 (HR)
CHSG-1	1.65	100.00 (HS)	2.16	98.48 (HS)	2.15	97.50 (HS)
CHSG-2	2.01	99.33 (HS)	2.25	96.86 (HS)	2.34	95.25 (HS)
PSG-9	1.84	99.33 (HS)	2.39	95.10 (HS)	2.03	97.55 (HS)
KG-3/134 (IC 284787)	1.92	98.00 (HS)	1.85	99.05 (HS)	2.07	95.88 (HS)

HS: Highly susceptible; HR: Highly Resistant

Table 2: Screening of DSG-7 for resistance to *Tomato leaf curl New Delhi virus* through challenge inoculation (*Bemisia tabaci*) under greenhouse condition during 2008

Genotype	*Source*	*Vulnerability Index*	*Category*
DSG-7	IARI, New Delhi	6.00	Highly Resistant
CHSG-1	HARP, Ranchi	100.00	Highly susceptible
CHSG-2	HARP, Ranchi	100.00	Highly susceptible
PSG-9	PAU, Ludhiana	99.33	Highly susceptible
KG-3/134 (IC 284787)	NBPGR, New Delhi	98.67	Highly susceptible

Table 3: Screening of DSG-7 under natural epidemic condition during *kharif* season 2011-2013

Genotype	2011		2012		2013	
	Yield(t/ha)	Vulnerability Index & Category	Yield(t/ha)	Vulnerability Index & Category	Yield (t/ha)	Vulnerability Index & Category
DSG-7	14.30	8.90 (HR)	14.75	6.30 (HR)	15.00	6.85 (HR)
CHSG-1	1.90	100.00 (HS)	2.28	99.33 (HS)	2.35	98.48 (HS)
CHSG-2	2.15	98.00 (HS)	2.50	100.00 (HS)	2.10	96.25 (HS)
PSG-9	2.00	96.86 (HS)	2.45	97.30 (HS)	2.20	98.55 (HS)
KG-3/134 (IC 284787)	1.98	98.48 (HS)	1.90	99.15 (HS)	2.00	96.80 (HS)

HS: Highly susceptible; HR: Highly Resistant

Table 4: Screening of DSG-7 under natural epidemic condition during *kharif* season 2014-2016

Genotype	2014		2015		2016	
	Yield(t/ha)	Vulnerability Index & Category	Yield(t/ha)	Vulnerability Index & Category	Yield (t/ha)	Vulnerability Index & Category
DSG-7	15.20	7.50 (HR)	14.60	8.75 (HR)	14.85	7.20 (HR)
CHSG-1	2.10	99.33 (HS)	2.40	97.25 (HS)	2.05	100.00 (HS)
CHSG-2	2.25	99.33 (HS)	2.30	98.50 (HS)	2.50	98.48 (HS)
PSG-9	1.75	97.50 (HS)	2.04	97.10 (HS)	1.98	95.90 (HS)
KG-3/134 (IC 284787)	2.00	98.00 (HS)	1.95	98.60 (HS)	1.85	96.75 (HS)

HS: Highly susceptible; HR: Highly Resistant

Table 5: Screening of DSG-7 under natural epidemic condition during *kharif* season 2017-2019

Genotype	2017		2018		2019		Averageyield (t/ha)
	Yield(t/ha)	VulnerabilityIndex & Category	Yield(t/ha)	VulnerabilityIndex & Category	Yield(t/ha)	VulnerabilityIndex & Category	
DSG-7	14.72	3.80 (HR)	17.30	3.30 (HR)	16.40	3.30 (HR)	16.14
DSG-6	11.23	4.30 (HR)	16.90	4.10 (HR)	12.70	4.30 (HR)	
Pusa Supriya (check)	5.89	89.20 (HS)	4.20	89.30 (HS)	4.80	89.20 (HS)	
Kalyanpur Hari Chikni(check)	4.45	94.30 (HS)	4.65	84.90 (HS)	4.10	94.30 (HS)	

HS: Highly susceptible; HR: Highly Resistant

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59. DPMFWR-30 (IC0637586; INGR21059), a Fasciation Plant type Pea (*Pisum sativum*) Germplasm with. Synchronized Flowering and Pod Formation. Putative Mutant Synthesised from Azad P-1.

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Genotype	Days to flowering	Days to first picking	Pod length (cm)	Pod width (cm)	Seeds/ pod	Shelling (%)	Plant height (cm)	Pods/ plant	Average pod weight (g)	Pod yield/ plant (g)
DPPMFWR-30	96.33	141.33	8.95	1.69	5.53	45.50	61.80	10.23	3.75	37.73
Azad P-1 (c)	91.33	143.67	9.59	1.82	6.27	47.57	92.20	19.08	4.04	76.94
Palam Priya (c)	88.00	132.67	8.64	1.61	6.27	45.73	70.82	14.43	3.38	48.76

For processing industry, it is expected to harvest peas once only but it exacts a compromise of both yield and quality. At harvest stage, the pods on the plant are not matured concurrently and are of variable size and tenderness. Despite the customary attempt to select a harvest date consistent with maximum returns of prime quality pea, some of the pods are outside the limits of optimum quality either overmature or too immature. There are two sources of variation that contribute to the overall range of maturity experienced in the field. The first, interplant variation involves relative differences in maturity among neighbouring plants which are associated with cultural practices and local environmental conditions. The second one is intraplane variation, involves progressive maturity on the plant.

The garden pea is characterized by a compound racemose inflorescence. The main shoot proliferates unlimitedly during whole vegetation period and produces frondose leaves subtending short bractless axillary racemes usually of one or two flowers. The commercial varieties of pea are characterized by the production of inflorescences in successive leaf axils. Each succeeding inflorescence being less mature than the preceding ones. Frequently, both inflated pods and unopened flowers may be observed on the same plant. This variation is subject to genetic control. Fasciation is associated with genetic mutation (Lerner, 2007) and is significant for uniform maturity and mechanical harvesting. Breeding programmes established based on the variability induced by mutagenic treatment are commonly used for improvement of the most productive and well-adapted varieties (Kalapchieva and Tomlekova 2016).

Morpho-agronomic characteristics: Induced mutations have played a significant role in meeting challenges related to world food and nutritional security by way of mutant germplasm enhancement and their utilization for the development of new mutant varieties. Different morphological putative mutants were synthesised. The fascinated mutant was obtained from Azad P-1 variety treated with EMS @ 0.3%. The fasciation in pea give the plant a witches-broom appearance based on arrangement and order of both foliar and floral leaves (Marx and Hagedorn 1962) which is accompanied with a progressively dilated, twisted stem axis. The distinctive characteristic of fascinated individuals is having shorter shoots compared to control cultivars due to shortening of upper internodes that led to appearance of flowers and pods from a pseudo umbel/false umbel. The most desirable fasciated plants would be the one that have similarity to that of normal pea plant except for the position of the pods. It is the concentrated pod set that is attractive from the viewpoint of uniform maturity since the inflorescences usually are borne over a relatively short period of time. The line was evaluated in 2011-12 and in subsequent years. Its yield is comparatively low from the check varieties but has synchronized maturity. It is important to introgressed this trait of interest in different varieties to synthesized genotypes with synchronized maturity vis-à-vis pod characteristics as per consumers' preference and high yield.

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60. DGRMB 5 (IC0637587; INGR21060), a Groundnut (*Arachis hypogaea*) Germplasm Tolerant to Salinity. CAM (Crassulacean Acid Metabolism) Variant.

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The groundnut cultivated in India (area: 4.92 mha; production: 10 MT; productivity: 2065 kg/ha) is susceptible to both drought- and salinity- stress. Thus, efforts are being made to develop groundnut varieties tolerant to drought- and or salinity- stress following both conventional breeding and transgenic approaches, but with limited success. Therefore, transferring entire genetic machineries of CAM (Crassulacean Acid Metabolism; a water saving mechanism) pathways of desert succulents into C_3 plants, is considered an option for imparting drought-tolerance (Davis *et al*. 2015). Moreover, facultative CAM is also reported to impart salinity tolerance in *Mesembryanthemum crystallinum* (Winter and Holtum 2014). However, salinity- tolerant cultivars through CAM transition are yet to be identified in any field crops of agricultural importance.

The variants were selected from groundnut cultivar TG 37A by imposing drought (no water after emergence till harvest). Twelve such selections were evaluated for salinity- tolerance in addition to expression of all modules (carboxylation, decarboxylation, mesophyll succulence, and invert stomatal behaviour) of facultative CAM and quantified (ap Rees *et al*. 1983; Merlo *et al*. 1993) in field during summer seasons for salinity. DGRMB 5 was evaluated for salinity tolerance for three seasons (upto av. 4.5 soil EC at harvest during summer of 2017, 2018 and 2019) at Junagadh and one season (*kharif* 2019) at 4.55 soil EC at the CCSRI, Mandvi, Bhuj, Gujarat.

DGRMB 5 is a Spanish bunch, salinity- tolerant facultative CAM-photosynthetic transited variant of TG37A, obtained through selection at the ICAR-Directorate of Groundnut Research, Junagadh, Gujarat. In addition, it has expressed all modules of facultative CAM under salinity-stress as a tool to impart tolerance. It differed genetically from TG 37A, TG 38, TAG 24, TG 51, TG 26 and among other variants on the basis of genomic and EST based SSR markers: three genomic (PM137, pGPseq18E7 and pPGPseq2G4) and four EST (DGR114, DGR289, DGR811 and DGR2474). It has moderate plant height, irregular branching with flower on main axis, and small dark green lanceolate leaves. It bears compound inflorescence with light yellow coloured standard petal and takes about 37 days after sowing for 50% flowering in salinity stress. It produced ~156 g of pod/m^2; ~32% of Harvest Index, ~65% shelling out-turn and ~37 g of HKM. In salinity condition, kernels of DGRMB 5 are having tan colour and mature in 98 days after sowing. DGRMB 5 can be cultivated directly as a salinity- tolerant (upto 4.5 soil EC at harvest) genotype or as a donor for imparting salinity- tolerance through CAM-photosynthetic transition in other genotypes. Salinity- tolerance through facultative CAM- transition is the first report in any agricultural crop.

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61. DGRMB 19 (IC0637588; INGR21061), a Groundnut (*Arachis hypogaea*) Germplasm Tolerant to Salinity.

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Even through in India, groundnut (*Arachis hypogaea* L.) is cultivated in about 4.9 mha with production of around 10.0 MT with productivity of 2065 kg/ha, it is susceptible to both drought- and salinity- stress. Hence, efforts are being made to develop groundnut varieties tolerant to drought- and or salinity- stress, but with limited success employing both conventional and transgenic approaches. Therefore, transferring entire genetic machineries of CAM (Crassulacean Acid Metabolism) pathways of desert succulents into C_3 plants, is considered an option for imparting drought-tolerance (Davis *et al*. 2015). Moreover, facultative CAM is also reported to impart salinity tolerance in *Mesembryanthemum crystallinum* (Winter and Holtum 2014). However, salinity- tolerant cultivars through CAM transition are yet to be identified in field crops of agricultural importance.

The variants were selected from TG 37A by imposing drought (no water after emergence till harvest). Selections were also characterised for salinity- tolerance. In addition, they were characterised for expression of all modules (carboxylation, decarboxylation, mesophyll succulence, and invert stomatal behaviour) of facultative CAM and quantified (ap Rees *et al*. 1983; Merlo *et al*. 1993) in field during summer seasons. DGRMB19 was evaluated for three seasons for salinity tolerance (upto av. 4.5 soil EC at harvest during summer of 2017, 2018 and 2019) at Junagadh and one season (*kharif* 2019 at soil EC 4.55) at the CCSRI, Mandvi, Bhuj.

DGRMB 19 is a Spanish bunch, salinity- tolerant facultative CAM-photosynthetic transited variant, selected from TG 37A, at the ICAR-Directorate of Groundnut Research, Junagadh, Gujarat. In addition, it has expressed all modules of facultative CAM under salinity stress as a tool to tolerance. It differed genetically from TG 37A, TG 38, TAG 24, TG 51, and TG 26 on the basis of genomic (one: PM137) and EST (two: DGR114 and DGR811) based SSR markers. It has moderate plant height, irregular branching with flower on main axis and small dark green oblong-lanceolate leaves. It bears compound inflorescence with dark yellow coloured standard petal and takes about 38 days after sowing for 50% flowering in salinity stress. It produced ~151 g of pod/m^2; ~31% of Harvest Index; ~64% shelling out-turn; and ~36 g of 100-kernel weight. In salinity- condition, kernels of DGRMB 19 are having light tan in colour and matures in 100 days after sowing. DGRMB 19 can be cultivated directly as a salinity- tolerant (upto av. 4.5 soil EC at harvest) genotype or as a donor for imparting salinity- tolerance through CAM transition in other genotypes. This is a unique source of salinity- tolerance through CAM-photosynthetic transition.

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62. DRMRQ1-16-27 (IC00637589; INGR21062), an Indian mustard (*Brassica juncea*) Germplasm with High Antioxidants (Phenol and Tocopherol). Low Antinutritional Component (Phytic Acid). Double Low (<2% Erucic Acid in Oil and <30 µmoles Glucosinolate/G Defatted Seed Meal).

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The strain (DRMRQ1-16-27) is a double low Indian mustard line possessing high level of antioxidants (phenol content; 5.16% and tocopherol content; 196.93mg/100g seed meal) with low level of anti-nutritional components (phytic acid content; 1.78% and glucosinolate content; <13.74 µmoles/g of defatted seed meal, erucic acid; <2%) both in oil and seed meal. The strain namely, DRMRQ1-16-27 was selected as single plant selection following pedigree breeding method from the cross EC564648 x (NUDHYJ-3 x PCR-7). The strain (DRMRQ1-16-27) evaluated in the year 2018-19 at DRMR along with checks both morphologically in the field and biochemically. It was found to have low erucic acid content (<2% in oil) comparable to low erucic quality check (PM21), and also low glucosinolate content (<30µmoles/g of defatted seed meal) comparable to double low quality check (PDZ1 and RLC3). The strain (DRMRQ1-16-27) was further analyzed biochemically for quality traits including erucic acid, glucosinolate, beta carotene, antioxidants, tocopherol, phenol and phytic acid in the year 2019-20 at DRMR (Table 1) DRMRQ1-16-27 was also evaluated in biochemistry trials of AICRP-RM programme 2018-19 at six independent centers namely Bharatpur, Kanpur, Kangra, Pantnagar, Hisar and Ludhiana for antioxidant properties (phenol content and tocopherol content) and anti-nutritional factors (phytic acid and glucosinolate). The strain, DRMRQ1-16-27 showed highest phenol content (5.16%) and tocopherol content (196.93mg/100g seed meal) among 22 tested entries along with quality check, PDZ1 (phenol content (4.26%) and tocopherol content (162.39mg/100g seed meal). The strain, DRMRQ1-16-27 showed lowest phytic acid content (1.78%) and glucosinolate content (<13.74 µmoles/g of defatted seed meal) among 22 tested entries along with quality check, PDZ1 (phytic acid content (2.61%) and glucosinolate content (<21.11 µmoles/g of defatted seed meal).

The strain, DRMRQ1-16-27 have been registered as a germplasm, because of having high level of antioxidants and low level of anti-nutritional compound in oil and seed meal. The strain can act also as a check in AICRP-RM biochemistry trials and donor for the quality traits.

Table 1: Comparative data of quality traits of strain (DRMRQ1-16-27) and checks

Genotypes/Traits	*Erucic Acid (%)*	*Glucosinolate (µmoles/g)*	*Beta carotene (ppm)*	*Antioxidant (mg/g AAE)*	*Total phenol (%)*	*Tocopherol (mg/100g)*	*Phytic acid (%)*
DRMRQ1-16-27	1.9	19.3	3.98	38.85	6.58	197.52	1.62
DRMRQ 4-7-23	1.5	15.9	2.74	35.35	5.48	182.50	2.16
PDZ1 (Double low quality check)	1.65	22.6	2.77	29.35	4.45	162.98	2.85
NRCHB 101 (Non quality check)	39.38	136.7	3.26	47.35	3.59	147.58	3.36

63. DRMRIJ 12-40 (IC0637590; INGR21063), an Indian mustard (*Brassica juncea*) Germplasm Resistant to White Rust Disease. Presence of Two Different Genes Conferring Resistance against White Rust. Good Agronomic Base.

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White rust caused by *Albugo candida* (Pers. ex Lev.) Kuntze is one of the most devastating diseases of Crucifers and causes severe losses in Indian mustard (*Brassica juncea*). Genetic studies have revealed dominance of resistance over susceptibility. Resistance to white rust has been shown to be governed by a single dominant gene.

DRMRIJ 12-40 is an inbred line derived from a cross between Zem 2 (exotic germplasm)and JGM 1-11 followed by individual plant selection. Cross was attempted during 2004-05 between Zem 2 and JGM 1-11. F_1 generation was raised at Bharatpur during 2005-06 and F_2 generation was raised at IARI Regional Station Wellington during 2006. Homozygous single plants were selected from homogenous resistant lines. F_3-F_4 generations were raised at Bharatpur and Wellington, respectively. Subsequent generations were raised at Bharatpur. Single plants were selfed and advanced from F_6 (2008-09) to F_8 (2010-11) generation. In 2011 -12 promising resistant line was named as DRMRIJ 12-40 and later on maintained through selfing. DRMRIJ 12-40 was inducted to AICRP-RM during 2015-16 and had been evaluated continuously for four years during 2015-16. 2016-17, 2017-18 and 2018-19 White rust reaction at leaves was recorded at two different stages *viz*., 75 and 100 days, while staghead formation was recorded at floweringstage. Candidate strain DRMRIJ 12 - 40 expressed resistant reaction against white rust at 75 days stage which was at par with resistant check BIO YSR during two years of testing at Hisar. Mean

Disease index of DRMRIJ 12-40 was 0.0 in comparison to 34.1 of susceptible check Rohini. Disease reaction against white rust on leaves at 100 days stage was recorded at five locations *viz*., Hisar, Kangra, Kanpur, Pantnagar and Morena, which included three hot spots (Kangra, Pantnagar and Morena) (Table 1). On the basis of mean disease index over all five locations for four years, candidate strain DRMRIJ 12-40 expressed 2.45 % which was better than the resistant check BIO YSR (8.41%) and susceptible check Rohini (34.0%). Observations on staghead formation were recorded at Morena and on the basis of mean disease index over three years, DRMRIJ 12-40 had 0.0 % disease incidence in comparison to resistant check, BIO YSR (9.9%) and susceptible check Rohini (14.2%). Resistant reaction against white rust was confirmed with already reported IP markers and the candidate strain was found to possess both the WR resistance loci (Fig. 1). Hence, on the basis of disease reaction at five locations over four years and confirmation of resistance with molecular markers, candidate strain DRMRIJ 12-40 was found resistant against white rust.

Agronomic characterization of DRMRIJ 12-40: Strain DRMRIJ 12-40 was characterized for agronomic traits *viz*., days to flower initiation (52 days), plant height (205 cm), length of main raceme (73 cm), 1000-seed weight (4.1 g), siliquae length (5.5 cm).

Table 1: Mean disease index of candidate strain DRMRIJ 12-40 and check genotypes against white rust pathogen

S. No.	*Location*	*White rust (% WR severity)*								
		Disease reaction at 75 days			*Disease reaction at 100days*			*Staghead formation*		
		DRMR IJ 12-40	*Bio YSR (Res. Check)*	*Rohini (Sus. Check)*	*DRMR IJ 12-40*	*Bio YSR (Res. Check)*	*Rohini (Sus. Check)*	*DRM RIJ 12-40*	*Bio YSR (Res. Check)*	*Rohini (Sus. Check)*
									k)	
1	Hisar	0.0	0.0	34.15	2.2	0	34.8			
2	Kangra				1.1	14.2	44.8			
3	Kanpur				0	0	31.7			
4	Pantnagar				5.5	9.4	29.0			
5	Morena				0.5	8.7	31.2	0.0	9.9	14.2
Mean		0.0	0.0	34.15	2.45	8.41	34.0		9.9	14.2

64. RG-3060 (IC0449033; INGR21064), a Castor (*Ricinus communis*) Germplasm with Resistance to Leaf Hopper

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Castor (*Ricinus communis* L.) is an important industrial oilseed crop. India is the top castor oil producing country. Castor crop suffers from several disease and insect attacks. Leafhopper *Empoasca flavescens* Fabr. (Cicadellidae: Hemiptera) is one of the major insect pests of castor causing yield loss up to 89% (Lakshminarayana and Duraimurugan, 2014). Cultivation of resistant cultivar is the best leafhopper controlling measure. For breeding a resistant cultivar, availability of resistance donor is a prerequisite. Diverse source of resistance is required for sustaining high yields in castor crop. Intensive search for leafhopper resistance was taken up at the ICAR-Indian Institute of Oilseeds Research, Hyderabad, India. This has led to identification of leafhopper resistant castor accession, RG-3060. It was developed through mass selection from a heterogeneous and heterozygous population of a wild collection collected from Morgrdh-1, Anjar (Taluque), Kutch, Gujarat (Anjani, 2012). RG-3060 was screened against leafhopper using infester-row method at three locations along with susceptible (DCH-177) and resistant (DCH- 519) checks for three years. It has consistently exhibited resistance against leafhopper at all locations in all years of screening (Table 1).

Morpho-agronomic characteristics: RG-3060 has green stem with triple bloom, and green, spiny non-dehiscent capsules. It had 16-17 stem nodes, 30.7 g 100-seed weight and 48% oil content. RG-3060 flowers in 55-60 days and matures in 120-125 days.

Associated characters and utility: RG-3060 has also showed resistance (14-15% wilt incidence) against *Fusarium wilt* (*F. oxysporum* fsp.*ricini*) in wilt sick plots at two locations, while the susceptible check had 94-98% wilt incidence. RG-3060 is diverse from previously identified resistant sources as it is derived from a genetically diverse source. It would serve as a diverse source of leafhopper resistance in resistance breeding as well to tag/identify leafhopper resistant candidate gene.

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Table 1: Reaction of RG-3060 against leafhopper at multiolocations in different years

Genotype	Year of screening	Palem		Yethapur		IIOR, Hyderabad		Reference
		LH no.	HPB (0-4 scale)	LH no.	HPB (0-4 scale)	LH no.	HPB (0-4 scale)	
RG-3060	2013-14	20.4	1.0	1.9	0.0	18.3	1.0	AICRP-Castor Annual Report- 2013-14, page No.205,206
DCH-177 (SC)		37.4	4.0	9.3	2.0	152.4	4.0	
DCH-519 (RC)		15.0	1.0	4.6	0.0	25.5	1.0	
RG-3060	2014-15	13.6	0.0	6.0	1.0	10.8	1.0	AICRP-Castor Annual Report- 2014-15, page No.179,187
DCH-177 (SC)		31.8	4.0	22.3	4.0	84.3	4.0	
DCH-519 (RC)		11.3	0.0	2.7	0.0	12.5	1.0	
RG-3060	2015-16	12.1	1	1.7	0.0	10.0	1.0	AICRP-Castor Annual Report- 2015-16, page No.200,201
DCH-177 (SC)		61.1	3.0	38.7	3.0	54.9	4.0	
DCH-519 (RC)		22.9	1.0	9.0	0.0	16.0	1.0	

SC: susceptible check; RC: resistant check; LH no.: no. of leafhoppers/3 leaves/plant; HPB: hopper burn

65. HOSuS-1 (IC0637591; INGR21065), a Sunflower (*Helianthus annuus*) Germplasm with High Oil Content (41%).

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Sunflower (*Helianthus annuus* L.) is native to North America and contains 52 species (67 total taxa) (Kane *et al*. 2013), occupying prime position in Indian economy. In India sunflower is introduced in 1969 as an oilseed crop, prior to which it was used as an ornamental plant. It is mainly grown for its oil which is used for culinary purpose in the preparation of *vanaspati* and in the manufacture of soaps and cosmetics. Till date a total of 29 hybrids were released in sunflower suitable for different agro-climatic situations in India (Sujatha *et al*. 2019). Development of high oil content parental lines and hybrids are the major priority in India. In view of this and great prospect of cultivation of this crop successfully in various region of India, it is necessary to develop high oil yielding varieties/hybrids for different locations. HOSuS-1 is a selection from segregating progenies of the germplasm accession GP4-1424 of cultivated sunflower. This newly developed genetic stock will be very useful in developing high oil content and high oil yielding hybrids in sunflower.

Morpho-agronomic characteristics: Newly developed line HOSuS-1 was promising for oil content recording >40% consistently (Anonymous, 2018-19). The crop was raised in augmented block design along with checks and oil content was analysed through NMR during the year 2015, 2018, 2019 and 2020, respectively at ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad and confirmed through Soxhlet. The average oil content of this line was 41.32% compared to high oil content check RHA-6D-1 (37.9%). The plants were unbranched, medium in maturity (83 days), medium in plant height (105 cm) with slender stems. Leaves and stems were smooth and non-pubescent. Leaves were large and green with triangular shape. Medium blistering was present on leaves without petiole pigmentation. The stem pigmentation was absent. The ray florets were many in number with elongated shape. The ray floret colour was yellow. The disc floret colour was orange without pigmentation. The head attitude of the line was half-turned down with flat shape and small size (11.4 cm). The bract shape of the genotype was elongated without pigmentation. Seed base colour was black with ovoid elongated shape. Average seed yield of the line was 24.0 g/plant with test weight of 3.9g and volume weight 44.0 g. Average oil content of the line was 41.32% (Table 1).

Table 1: Oil content data of HOSuS-1 through NMR and Soxhlet methods

Method	*HOSuS-1*	*RHA 6D-1/DRSH-1 (Check)*
NMR*	41.32	35.54
Soxhlet	41.91	37.75

*Mean of 4 years

Morpho-agronomic characteristics of HOSuS-1

Characteristics	*Description*
Plant height (cm)	105.0
Head diameter (cm)	11.4
Days to flowering	53
Days to maturity	83
Seed colour	Black
Pollen colour	Yellow
100 seed weight (g)	3.9
Volume weight (g/100 ml)	44.0
Average oil content (%)	41.32
Leaf blistering	Medium
Leaf petiole pigmentation	Absent

Associated characters and cultivation practices: This genetic stock is medium maturing and is recommended for utilization in heterosis breeding programme for development of high oil yielding hybrids.

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66. AAC-1 (IC00625184; INGR21066), a China aster (*Callistephus chinensis*) Germplasm with Resistance to Alternaria Leaf Spot Disease. High Yielding. Branching Habit and Late Flowering Type.

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China aster is one of the most important flower crops grown in Karnataka afterrose, chrysanthemum and marigold and which is grown commercially for cut flowers, loose flowers and also in garden display and decoration purpose. The pure line AAC-1 is an open pollinated seedling selection from germplasm maintained at Department of Floriculture and Landscape Architecture (FLA), KRC College of Horticulture, Arabhavi. The unique characteristic of this variety is resistant to *Alternaria* leaf spot. Which was screened under both natural and artificial disease conditions.

Morpho-agronomic characteristics: Flowers of this pure line (AAC-1) are brick red in colour, flower diameter is 5.5-6.0 cm and flower weigh 4.50 g, plant height is 55 cm, stalk length of 30 cm and takes about 138 days to flower from seed sowing. The plants produce about 50 flowers/plant.

Associated characters and cultivated practices: In Karnataka, it is mainly grown in districts *viz.*, around Bangalore, Belgaum, Chitradurga, Tumakur and Davanagere. It can be grown in all seasons of the year, for quality flower production winter and rainy seasons are best. For seed production winter season is best.

China aster can be planted in ridge and furrow system. The spacing of 30 x 30 cm and fertilizer dose of 90:120:60 kg NPK/ha is recommended (as per UHS, Bagalkot package of practice) for its cultivation. The identified pure line AAC-1 has spreading growth habit and more biomass production. This pure line responses good at spacing of 45 x 45 cm and fertilizerdose of 112.5: 150: 75 kg NPK/ha for higher flower production and also a micronutrient combination of ZnSO4

Morpho-agronomic description of China aster pure line AAC-1

Characters	*Pure line AAC-1*
Plant Height (cm)	56.09
Number of branches	16.77
Number of leaves	235.83
Leaf area/ plant (dm^2)	9858.67
Stem girth (cm)	1.82
Plant spread E-W(cm)	42.64
Plant spread N-S(cm)	37.65
Days taken for bud initiation	48.25
Days taken for first flowering	39.52
Duration of flowering (days)	37.73
1000 Seed weight (g)	2.14
Seed yield (g)/plant	5.54
Seed yield/ha (kg)	615.86
Number of flowers/plants	52.33
Individual flower weight/plant (g)	4.53
Flower yield/plant (g)	173.19
Flower yield per ha (t)	17.58
Flower diameter (cm)	5.07
Flower stalk length (cm)	24.18
Vase life (days)	7.20
Total Chlorophyll (mg/g)	1.27
Disease incidence (%) – *Alternaria* leaf spot	9.93

@ 0.4% + FeSO4 @ 0.4%+ Boron @ 0.1% as tested at the department of FLA, KRC College of Horticulture, Arabhavi.

Before planting FYM at 10 t/ha along with half dose of above recommended fertilizersare applied. After planting 20-30 days earthing up is done to support the plants. At the time ofearthing up remaining half dose of P and K and 25% of N are applied, remaining 25% N is topdressed after 60 days of planting.

The pest and disease management practices are followed as per UHS, Bagalkot packageof practices.

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Web site: www.uhsbagalkot.edu.in

67. SBI/2020/GU 07-2276/266 (IC0636676; INGR21067), a Sugarcane (*Saccharum* sp.) Germplasm High cane yield (89.66 t/ha) under drought condition. Lowest reduction for single cane weight under drought. High Nitrogen (77.92 kg of dry biomass/kg of nitrogen). Use Efficiency with Erianthus Base

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Sugarcane is an important C4 crop cultivated in the tropics and subtropics for production of both sugar and bioenergy. Among abiotic stresses, drought causes severe yield losses worldwide in sugarcane. The present day cultivars are interspecific derivatives *of Saccharum offiicnarum* and *S. spontaneum* and the wild species *Saccharum spontaneum* has been the donor for many important traits including drought tolerance in sugarcane. In recent years, *Erianthus* spp. has been identified as a valuable source for important agronomic traits such as early vigour, biomass production, and ratoonability, tolerance to biotic and abiotic stresses. The clone GU 07-2276 was developed by crossing two wild species *viz*., *Saccharum robustum* 'PIR 00-1188' and *Erianthus arundinaceus* "IK 76-91" and backcrossing the resultant F1 'GU 04 (50) RE-9' with CoH 70 during 2007 at ICAR-Sugarcane Breeding Institute, Coimbatore. GU 07-2276 has tall, erect, light purple, cylindrical cane with slight zig zag alignment, green leaves with green leaf sheath, medium oval bud without bud groove.

Twenty-seven interspecific hybrids (ISH) and intergeneric hybrids (IGH) with diverse genetic base were evaluated for their drought tolerant potential at four sugarcane research stations under AICRP (Sugarcane) *viz*., Karnal (Haryana), Faridkot (Punjab), Anakapalle (Andhra Pradesh), Padegaon (Maharashtra) during 2016-17 to identify climate resilient ISH and IGH genetic stocks for further use in sugarcane improvement programmes. The stress was initiated by withholding irrigation at formative phase ie 60DAP till 150DAP. The results showed that, for cane yield, the entry GU 07-2276 recorded the lowest reduction of -8.71% with a mean cane yield of 89.66 t/ha under drought. The entry also maintained higher relative water content and had shown only -2.27% reduction under drought compared to control. It also recorded the least reduction (-10.80%) for single cane weight compared to other entries under drought.

In another set of trials conducted during 2014-16, 32 pre-breeding genetic stocks with diverse genetic base were evaluated for Agronomic Nitrogen use efficiency (Good *et al*. 2004). The results showed that GU 07-2276 recorded higher dry biomass under N_0 (46.06 t/ha) and N_{100} (57.67 t/ha) condition and also recorded the higher AgNUE of 41.40 with *Erianthus arundinaceus* base. Based on the results, the genetic stock GU 07-2276 has been identified as potential donor for drought tolerance combined with nitrogen use efficiency.

Reference

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68. Co 13003 (IC0638608; INGR21068), a Sugarcane (*Saccharum* sp.) Germplasm High fibre (15.05%) in Cane Combining High Sucrose (19.77%) Content of Commercial Level.

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Sugarcane is one of the important C4 crops, cultivated in more than 100 countries and contributing formore than 80% global sugar production. Though sugar is the main product, sugarcane is emerging as an energy crop in several countries including India, to meet the needs of clean energy and electricity. Fibre content in the canes and sucrose content in the juice are the major contributors for the primary energy content of sugarcane. These two characters are hard to combine (Huang, *et al.* 2017) and many wide hybrids and interspecific hybrids record high fibre and very low sucrose content. A clone combining these two characters is a potential source to meet energy demands. Co 13003 is one such rare recombinant combining high fibre per cent and juice sucrose content. Co 13003 is an early maturing clone selected from the cross involving two proven parents Co 86011 x CoT 8201. This clone was identified at ICAR-Sugarcane Breeding Institute, Coimbatore in the Pre zonal varietal trials conducted during 2012-13. The clone was selected as an early maturing clone with high early sucrose content of 18.07% at 240 days and 21.41% at 300 days at Coimbatore. The clone also recorded a cane yield of 145 t/ha with a sugar yield of 21.83 t/ha and was superior to the standards. Based on its superior performance, Co 13003 was promoted to AICRP (Sugarcane) and it was tested in 18 locations in 34 trials over two years. The trials were conducted with sixteen entries and three standards (Co 86032, CoC 671 & CoSnk 05103) in 14 centers under AVT IP during 2018-19 and AVT IIP during 2019-20.

In AVT I plant, the clone Co 13003 recorded the highest mean fibre of 15.15% compared to 15.07% in the best standard, 13.51% in the standard and popular variety Co 86032 and 14.33% in the third standard CoC 6711. High fibre content of this clone was recorded at Kolhapur, Mandya and Padegaon. Its fibre in AVT Ratoon crop was 14.77%. The pooled analysis of two plant and ratoon also showed the superiority of Co 13003 for fibre % (15.00) compared to the checks Co 86032 (13.22%), CoC 671(13.87%), CoSnk 05103 (14.93%). Co 13003 recorded 19.17% sucrose in AVT I Plant, 20.25 % in AVT II Plant and 19.98% in AVT ratoon trial. In a pooled analysis of two plant and ratoon data, it showed a mean sucrose of 19.77% and emerged as the best clone combining high fibre and high sucrose content.

Co 13003 has erect, light purple, heavily waxed, thick, erect canes, narrow purple growth ring, small bud, purple leaf sheath base with few hard spines, closed canopy with pointed to tip droopy leaves. It is sparse flowering late during the flowering season at Coimbatore. The clone combined high fibre of 15.05% and sucrose of 19.77% and recorded 14.51 t/ha sugar yield and 103.09 t/ha cane yield in AVTtrials in the zone. Such a combination of high fibre with sugar yield component traits is very rare and beneficial when sugarcane is being looked upon as a food and energy crop yielding sugar, ethanol andelectricity.

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69. AHCM-22-1 (IC-0621779) (IC00621779; INGR21069), a Lasora (*Cordia myxa*) Germplasm Resistance to Tingid Bug *Dictyla cheriani* Drake.

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Lasora or gunda (*Cordia myxa*) is an important and underexploited perennial fruit plant of dry land. A wide range of genetic variability for horticultural attribute such as fruit size, shape and yield attributes is existed in seedling population of available in arid and semi arid region of Rajasthan. The plant is widely promoted as horticultural crop in particular to immature tender fruit for vegetable and pickle industries. The tingid bug, *Dictyla cheriani* is a major pest of lasorain India and its outbreaks cause substantial crop losses to growers. The lace bugs sucked the sap from newly emerging leaves and young branches, which led to the leaves turned yellow and suppression of growth of the tree through drying of leaves and young branches. The maximum incidence of tingid bug is usually observed in October in two different phenotypic characters (51.67% on bold & 76.67% on small seeded plants) and minimum was in January (11.67% on bold & 21.67% on small seeded plants). The number of this lace bug ranged between (0.5 to 8.8 on bold & 4.5 to 25.97 on small seeded plants) nymphs and adults per leaves (Haldhar and Singh, 2014). A good amount of lasora germplasm is collected and 22 are conserved in field repository at ICAR-CIAH in May–July 2001. During the year, 2011 to 2013, the maintained lasora was evaluated for agro morphological traits, fruit yield and insect-pests incidence. Based on seasonal and over the year study, the germplasm AHCM-22-1 exhibited resistance towards to tingid bug. It is also high yielding and elite for fruit quality components. Therefore, its ripen fruits of AHCM-22-1 was collected, seedling progeny generated and plated in Entomology Block for further study.

The significant differences were found in percentage leaf infestation and bug density per leaf among the tested

Table 1: Salient characteristics of AHCM-22-1 (IC-0621779)

Genotypes	Bug/ leaf			Bug infestation (%)			Resistance category
	2014-15	2015-16	Pooled	2014-15	2015-16	Pooled	
AHCM-22-1	3.96	4.40	4.18	12.01	12.43	12.22	R
Germplasm	Flavinoid content** (mg/g)	Tannins content** (mg/g)		Phenols Content**(mg/g)	Total alkaloids**(%)	Free AminoAcid (mg/g) **	
AHCM-22-1	5.43	22.38		18.44	0.43	0.87	
Germplasm	Leaf length (cm)	Leaf width (cm)		Leaf size	Leaf roughness	Leaf hairyness	
AHCM-22-1	14.62	12.88		Large	High rough	High hairy	

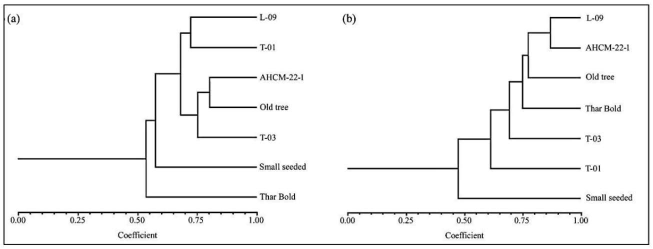

Figure 1: Phylogenetic tree construction using analysis of ScoT (a) and CBDP (b) markers

germplasm. Based on Kaiser Normalization method, the germplasm AHCM-22-1 was found resistant. The minimum bug density was observed in AHCM-22-1 (4.27 bugs/ leaf) followed by AHCM-25 (4.50 bugs/ leaf) and AHCM-34 (5.53 bugs/ leaf). The per cent leaf infestation was the highest in AHCM-32 (68.51 %) and the lowest in AHCM-22-1 (12.26 %) followed by AHCM-25 (14.25 %). The significant negative correlation was observed in AHCM-22-1 with percent bug infestation and total phenol, flavinoid and tanin content. The resistant germplasm AHCM-22-1 having leaf size (very large leaf), leaf roughness (high rough) and leaf hairyness (high hairy) and being high in resistant and low in susceptible germplasm accession. The germplasm AHCM-22-1 is tolerating drought, high temperature and fruit yield of 27.50 to 39.80 Kg per plant after 4 to 5 years of commercial harvesting. Therefore, identified tinged bug resistant line namely AHCM-22-1 was molecularly characterized using random functional molecular markers. To complete this study, 32 ScoT and 17 CBDP markers were analyzed for their polymorphism and informativeness in the 7 germplasm including AHCM-22-1 and 6 germplasm. Six germplasm including a *C. myxa* variety, Thar Bold were used to compare the molecular pattern with AHCM-22-1 line. As the result, it clearly demonstrated that the AMCM-22-1 line was distinct from other related and compared germplasm and makes a separategroup in phylogenetic analysis.

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70. AMMOL (IC0637592; INGR21070), an Apple (*Malus domestica*) Germplasm Better Fruit Size (higher (155g)). Early Maturity (114-117 days). Better Fruit Quality.

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Hybridization programme in indigenous apple cultivar "Ambri" was initiated to enhance the fruit quality parameters *viz* a *viz* early maturity. Hybridization of apple cultivar "Ambri" and early maturing Cultivar: Mollies Delicious" was done to obtain the desirable hybrid with better quality early maturing fruits.

Morpho-agronomic characteristics: Ammol is hybrid between Ambri and Mollies Delicious. Harvesting date is three weeks later than Mollies Delicious and forty days prior to Ambri i.e. in 4th week of August. Tree has moderate vigous with semi-spreading nature of growth habit suitable for high density plantation on clonal rootstocks.

Associated characters and cultivation practices: Fruit size is higher (155 g) than parents Ambri (140 g) and Red Delicious (145 g) with moderate acidity (0.23%). Anti-oxidative and free radical scavenging potential is significantly higher. DDPH activity of hybrid is 28. 1 µM AAE/g FW against Ambri (19.6 µM AAE/g FW) and Mollies Delicious (26.0 µM AAE/g FW) and FRAP activity is 220 µM FeSO4/100g FW in comparison to Ambri (179.4 µM $FeSO_4$/100g FW) and Mollies Delicious (102.1 µM $FeSO_4$/100g FW)

71. PRIDE (IC00638609; INGR21071), an Apple (*Malus domestica*) Hybrid with Scab Resistance . Fruit Quality (High TSS (18oB) and Higher firmness).

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Hybridization programme for development of scab resistant apple cultivars was initiated by introgression of scab resistant traits from apple cultivar "Prima" into commercial apple cultivar "Red Delicious". Hybridization of apple cultivar "Red Delicious" and scab resistant cultivar "Prima" was done to obtain the desirable hybrid with scab resistance trait.

Morpho-agronomic characteristics: PRIDE is hybrid between Prima and Red Delicious. Tree is having medium vigour with spreading branches. Stem vigour is medium with brown colour and twigs are medium to long with dark brown shade.

Associated characters and cultivation practices: Fruit is juicy, globose, medium size, has medium stalk cavity with small lobes, large overcolour, strong bloom of skin and graziness, fleshed stripped and mottled pattern of overcolour, rust free, flesh creamish in colour, high TSS with good firmness. Fruit size is moderate (130 g) with respect to parents Prima (120 g) and Red Delicious (145 g) with moderate acidity (0.30%). Fruits have higher TSS (18°B) than Prima (12.5 °B) and Red Delicious (14.3 °B). Firmness of fruits is also higher (65 RI) than Prima (60 RI) and Ambri (64.2 RI) which contributes is higher shelf life. Fruits have higher phytoanticipins having 160 mgGAE/100g FW phenols, 130 mg QE/100g FW flavanoids and 1.79 mg QE/100g FW flavanols. Anti-oxidative and free radical scavenging potential is moderate. DDPH activity of hybrid is 23.51 µM AAE/g FW against Prima (20 µM AAE/g FW) and Red Delicious (28.0 µM AAE/g FW) and FRAP activity is 158 µM $FeSO_4$/100g FW in comparison to Prima (183 µM $FeSO_4$/100g FW) and Red Delicious (106.4 µM $FeSO_4$/100g FW).

Specific trait: PRIDE is Scab Resistant as Prima

72. Arka Supreme (CHES-PA-III-1) (IC00612469; INGR21072), an Avocado (*Persea americana*) Germplasm High yield (about 370-400 kg/plant with average fruit weight of 367-428 g). Improved fruit quality. Regular bearing behaviour.

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Avocado is the most nutritive among fruits and is regarded as the most important contribution of the New World to human diet. Avocado is a nutrient dense and high oil content fruit. Avocados have the highest energy value (245 cal/100 g) of any fruit besides being a reservoir of several vitamins and minerals. The fruit has the highest fibre content of any fruit and is a source of antioxidants. The avocado (*Persea americana* Mill.) is also known as alligator pear and butter pear/butter fruit. It originated in Mexico and Central America, possibly from more than one wild species (Dreher and Davenport, 2013). The pulp is rich in proteins (up to 4%) and fat (up to 30%), but low in carbohydrates. Avocado production of the world was 6.4 million metric tons in 2018 (Anonymous, 2019). Mexico is the largest producer and exporter of Avocado in the world followed by Chile, Indonesia, United States, Dominican Republic, Colombia, Brazil, Peru *etc.,* while its production in Asia is limited. In India, it is cultivated on limited scale and in a scattered way in Tamil Nadu, Kerala, Maharashtra, and Karnataka in the south-central India and in the eastern Himalayan state

Table 1: Fruit yield and quality characteristics of avocado selections (*mean of three years*)

Parameters	*CHES-PA-III-1 (Arka Supreme)*	*CHES-PA-XIII-1*	*TKD-1*
Fruit yield (kg/tree)	254.7	209.8	198.5
Fruit weight (g)	389.4	472.4	289.3
No. of fruit/ tree	956.1	356.8	411.5
TSS (^{0}Brix)	8.1	7.3	8.3
Stone wt. (g)	170.8	192.7	122.3
Pulp %	56.1	51.8	62.6

Table 2: Biochemical parameters of avocado selections

Biochemical parameters	*CHES-PA-III-1 (Arka Supreme)*	*CHES-PA-XIII-1*	*TKD-1*
Moisture (%)	82.3	79.4	81.7
Carbohydrates (mg/g defatted dry wt.)	40.5	36.4	42.7
Protein (mg/g defatted dry wt.)	13.2	11.2	14.6
Fat (%)	20.0	16.8	23.8
Fibre (%)	0.45	0.48	0.41

of Sikkim (Gosh, 2000). During recent past its cultivation is gaining momentum as cash crop, owing to its high nutritional value, high market potential and less resource demanding nature of crop.

In India, avocado is not a commercial fruit crop. It was introduced from Sri Lanka in the early part of the 20th century. Avocados are grown scattered in southern tropical states like Tamil Nadu, Kerala, Karnataka (Coorg), and Maharashtra. Also popular in the northeastern Himalayan state of Sikkim on hill slopes at elevations if 800- 1600 meters (Gosh, 2000). The climate zone of avocados is from true tropical to warmer parts of the temperate zone. In Kodagu, avocado is grown as one of the mixed crops in coffee-based cropping system. Almost each house is maintaining few plants of avocado and lots of variability of Avocado is available in Coorg and adjoining areas (Tripathi *et al.,* 2014).

Varietal improvement in Avocado has so far been limited to selection of regular bearing and high yielding genotypes with improved fruit quality. The present study considering the emerging importance of the crop was therefore carried out with the objectives of identifying regular bearing and high yielding genotypes with higher nutritive value.

Avocado improvement work was started at ICAR – IIHR-Central Horticultural Experiment Station, Chettalli during 2000 with an objective to identify high yielding type with regular in bearing type. Extensive surveys were made in Southern tropical states like Tamil Nadu, Kerala, Karnataka (Coorg), and Northeastern Himalayan state of Sikkim for the identification of high yielding accession with regularity in bearing, as irregularity in bearing is major hindrance in avocado cultivation. The criteria adopted for selection of superior genotypes: regular bearer, higher yield, medium size fruits, soft and buttery pulp and higher fat percent. Passport data was recorded and in situ evaluation was carried out.

During the survey, out of 67 accessions, 17 accessions were evaluated for basic horticultural traits. The process resulted in identification of two superior accessions conforming to the criteria of selection outlined as above. Based on this, following selections made are detailed out and described here below:

CHESPA-III-1 (Arka Supreme)

It is a regular bearing and high yielding seedling selection from local collection with spreading type growth habit. A fully grown tree (16 year old) gives the fruit yield about 200-250 kg/plant with average fruit weight of 367-428 g. The fruits are oblong with 7.80 Brix TSS. The flowering behavior of this variety falls under Type "A" category. Total fat content is 20.0 %.

The different fruit parameters that were considered for evaluation of the accessions are listed in Table 1.

From above it may be observed that CHES-PA-III-1 (Arka Supreme) was found to be regular bearing and high yielding seedling selection from local collection with spreading type growth habit. The fruits are oblong, light green, pale yellow pulp with prominent lenticels on shoulders (Table 1 &2).

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73. SM/11-120 (IC0637593; INGR21073), a Potato (*Solanum tuberosum*) Germplasm Highly Resistant to Potato Cyst Nematode (*Globodera pallida* and *G. rostochiensis*). Highly Resistant to Late Blight (*Phytophthora infestans*) and Non Preference for White Fly. Performing Well Under Long Day Conditions

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Potato (*Solanum tuberosum* L.) is the 3rd important global food crop. It produces more food per unit of land in comparison to major crops, and its demand is growing continuously. In India too, potato has become a staple crop of masses and is grown in wide agro-ecologies (Pradel *et al.,* 2019; Sood *et al.,* 2020). Potato cultivation in diverse areas attract many biotic stresses which affect potato production in India. Major among them are late blight, viruses and potato cyst nematode (PCN) (Bhardwaj *et al.,* 2019). Development of new resistant varieties with higher productivity and other desirable traits is a continuous process. Host resistance, is cost effective, eco-friendly and easy to deploy strategy, which requires identified and known sources for resistance. Due to major focus on late blight and viruses resistance, breeding efforts have resulted in identification and successful deployment of resistance in newly developed varieties. Recently, PCN has emerged as a major problem in Northern hills in India and till date there is no highly resistance source for combating the disease. Moreover, white fly infestation transmits the viruses in potato tubers and affects health and quality of tubers.

Hybrid, SM/11-120 is a promising clone highly resistant to both the species of potato cyst nematode (*Globodera rostochiensis* and *Globodera pallida*), resistant to late blight disease (*Phytophthora infestans*) and showed resistance/non-preference to white fly. The hybrid was developed through biparental crossing between CP 2379 and Kufri Himalini. Kufri Himalini is a medium maturity adapted variety with good tuber attributes and is moderately resistant to late blight. CP 2379 is an advanced exotic line resistant to late blight and PVY. The clone was selected from the segregating population for late blight resistance under controlled conditions through artificial inoculation in year 2012. The clone was subsequently multiplied for tuber increase and evaluated for field resistance to late blight, potato cyst nematode, white fly and agronomic superiority. The clone is highly resistant to PCN, resistant to late blight, white fly and exhibited high yield with medium to late maturity. It produces round yellow pink tubers with medium deep eyes and light yellow flesh. The hybrid SM/11-120 did not observe even a single cyst of both the PCN species in the root balls during three years of evaluation under controlled conditions. The hybrid also showed least preference to white fly under choice assay. Besides, the hybrid is resistant to late blight and has shown agronomic superiority over best controls at Kufri. With these parameters, SM/11-120 is an exceptional hybrid/parental line suitable for PCN, late blight and white fly resistance breeding in developing new potato varieties.

In advanced generation yield trials, SM/11-120 consistently out yielded all the controls for total and marketable tuber yields at 120 days crop duration at Kufri. The hybrid out yielded the control variety, Kufri Girdhari by margin of 71.6%, Kufri Himalini by 68.75% and Kufri Jyoti by 238.5% for total tuber yield over last 4 years. During three years of evaluation under controlled conditions the hybrid observed highly resistant reaction to both *G. rostochiensis* and *G. pallida* and not even a single cyst of both the species of PCN was observed in root balls of the hybrid, while all other hybrids and control varieties were susceptible and highly susceptible to both the species (Table 1; Fig. 1). The hybrid possesses consistently high level of resistance against late blight over the years which was at par to best control Kufri Girdhari. The mean AUDPC for four years in SM/11-120 was 19.8 whereas best control variety, Kufri Girdhari recorded mean AUPDC of 18.4, which much lower than other control varieties *viz*., K. Jyoti (1654.2) and K. Himalini (789.7) (Table 2). The hybrid leaves also showed least preference to white fly under choice assay in comparison to control varieties and other hybrids.

Molecular markers data also supported its resistance to PCN as the hybrid showed resistant band for *H1* gene markers TG689 and 57R specific to *G. rostochiensis* and *Gpa2QTL* markers Gpa2-1 and Gpa2-2 specific to *G. pallida.* The hybrid also showed resistant band for late blight (cLET5E4_*R3*, *R1*-CosA) and PVY (YES3A and Ry_{adg}) resistant genes.

Table 1: PCN resistance of advanced hybrid, SM/11-120 under controlled conditions

Hybrids/ controls	*Globodera rostochiensis*				*Globodera pallida*			
	2018	2019	2020 (Kufri)	2020 (Shimla)	2018	2019	2020 (Kufri)	2020 (Shimla)
SM/11-120	HR	HR	HR	HR	HR	HR	HR	HR
K. Girdhari	S	HS	HS	HS	S	HS	HS	HS
K. Himalini	S	HS	S	HS	S	HS	S	HS
K. Jyoti	S	HS	HS	HS	S	HS	HS	HS

Table 2: Late blight resistance of advanced hybrid, SM/11-120 at Kufri

Hybrids/ controls	AUDPC				Average
	2017	2018	2019	2020	
SM/11-120	0	0	77.3	2	19.825
K. Girdhari	14.5	23.5	19.7	16	18.425
K. Himalini	543.3	265.63	1180	1170	789.7325
K. Jyoti	1609	994.38	2020	1993.33	1654.178

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74. MSH/14-129 (IC0637594; INGR21074), a Interspecific Somatic Hybrid of Potato (*Solanum tuberosum*) derived from [cv. Kufri Gaurav × somatic hybrid 'P2' (*S. tuberosum* + *S. pinnatisectum*)] with Wider Genetic Base. High Yield Combined with Moderate Late Blight Resistance.

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Inter-specific potato hybrid MSH/14-129 is a back-cross progeny of advanced stage clonal selection at seventh generation (BC_1-C_7). MSH/14-129 was developed by crossing between Kufri Gaurav and somatic hybrid 'P2'. The clone 'P2' an inter-specific somatic hybrid developed by protoplast fusion between *Solanum tuberosum* dihaploid 'C-13' and diploid wild potato species *S. pinnatisectum*. MSH/14-129 possesses wider genetic base into cultivated (*S. tuberosum*) from wild species (*S. pinnatisectum*) with high tuber yield (avg. 42.84 tonnes/hectare) and moderate resistance to late blight disease under the natural (hot-spot) field conditions at Kufri, Shimla. This shows successful utilization of somatic hybrid 'P2' in developing a promising advanced stage hybrid (MSH/14-129) for high yield combined with late blight resistance to be used as a parental line in potato breeding in future. Additionally, molecular profiling using SSR markers (STU: 174, 179, 182, 190, 200 bp; and STIKA: 152, 198, 201, 235, 242, 245 bp) were revealed for genetic fidelity purpose. A few DUS descriptors of MSH/14-129 are: white-green sprout, semi-compact plant foliage, medium plant height, green stem colour, open leaf structure, large leaf length, broad leaf width, no anthocyanin coulouration on flower bud, white flower corolla, small flower size, orange anther colour, normal anther cone, normal pistil, longer stylar length, light yellow tuber colour, smooth skin, oval shape, shallow eye depth and light yellow tuber flesh colour. This inter-specific potato hybrid with diverse genetic background, high yield and moderate resistance to late blight disease under hot-spot conditions has potential to employ in potato breeding programmes to widen the genetic base of the cultivated gene pool.

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75. MCD24 (IC0637595; INGR21075), a Diploid Wild Potato (*Solanum microdontum*) Highly Resistant to Late Blight Disease.

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The elite genetic stock MCD24 was developed at ICAR-Central Potato Research Institute, Shimla by Clonal Selection method from several clones regenerated from true potato seed (TPS) of wild species (*Solanum microdontum*, Accession no. PI218224). MCD24 is an important genetic material for fusion parent in somatic hybridization and parental line in diploid breeding programme for introgression of very high resistance to late blight trait with wider genetic base into cultivated potato and also basic research studies on diploid potato breeding. Since potato is native to Lima, Peru (South America) and under the routine germplasm procurement programme of the institute. Our finding shows successful utilization of clonal selection method in development of elite genetic stock MCD24 for high resistance to late blight over four seasons under controlled conditions by challenge inoculation. DNA fingerprinting of MCD24 revealed SSR alleles (STU: 171, 178, 182, 184, 187, 190, 197 bp, and STIIKA: 188, 192, 214, 218, 230, 234 bp) for genetic fidelity. A few DUS descriptors of MCD24 are: red-purple light sprout, compact plant foliage, small plant height, green stem colour, intermediate leaf structure, small leaf length, narrow leaf width, oval leaflet shape, white flower corolla, small flower corolla size, yellow anther colour, normal anther cone, normal pistil, longer stylar length, late maturity, white cream tuber skin colour, smooth skin type, ovoid tuber shape, shallow eye depth and white tuber flesh colour. This diploid wild species MCD24 with diverse genetic background having very high resistance to late blight disease has potential to widen the gene pool of the cultivated potato.

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76. IC-629872 (IC0629872; INGR21076), a Betle Leaf (*Piper betle*) Germplasm with Dark Green Deep Concave Leaves with Wavy Margins and Low Eugenol (27.57%) Content.

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Betelvine (*Piper betle* L.) leaves is used directly for chewing as raw which also carries medicinal plant where its leaves are used for remedial purpose. It is perennial aromatic plant and belongs to family Piperaceace. Leaves bear property like ant diabetic, antiulcer, antitumor, cardiotonic, antioxidant etc. It is also rich in potassium, phosphorous, calcium, protein, fiber, starch, eugenol etc. Essential oil is extracted from the leaves had a fragrance and is used as an industrial raw material for manufacturing food additives, perfume, medicine etc. It is being commercial cultivated in West Bengal, Assam, Andhra Pradesh, Bihar, Tamil Nadu, Karnataka, Kerala, Madhya Pradesh, Utter Pradesh, Maharashtra, Odisha and small part of Chhattisgarh in India. Demand of this crop is increasing both in national and international market. At IGKV, Raipur (C.G) the strain IC629872 is selection from land races developed from single plant selection, purification and multiplication of landrace. IC629872 is a dark green leaf colour, deep concave shape leaves, wavy margin in leaves, high protein and low eugenol (27.57%) content. It was compared with Bidhan Paan-1 developed by BCKV, Kalyani and is commercially grown by the farmers.

Table 1: Marketable leaf yield in numbers per plant

Structure	*Agroshed net*		*Poly tunnel*	
Entry	IC-629872	Bidhan Paan-1 (check)	IC-629872	Bidhan Paan-1 (check)
2017-18	75.92	81.92	73.04	77.28
2018-19	85.82	93.42	82.72	80.87
Mean	80.87	87.67	77.88	79.08

Table 2: Morphological description of betelvine strain IC-629872 in comparison with check variety Bidhan Paan-1

Morphological descriptor			
1.	Name of crop betelvine	IC-629872	Bidhan Paan-1 (Check)
2	Leaf color	Dark Green	Green
3	Internodes Color	Green	Green
4	Leaf Surface	Cariaceous	Cariaceous
5	Leaf Lamina Shape	Ovate Oblong	Ovate Oblong
6	Main Vein Let Number	7	7
7	Leaf Lamina Orientation Along Mid Rib	V Shaped	Flat
8	Leaf apex shape	Acute	Acute
9	Adventitious root production	Many	Many
10	Stem colour	Moderate Green	Moderate Green
11	Shelf life	17 days	17 days
Quantitative Traits:			
1	Leaf length (cm)	6.3	10.8
2	Petiole length(cm)	5.73	6.19
3	Leaf width (cm)	5.97	7.73
4	Leaf area (cm^2)	70.47	70.15
5	L/B ratio	1.75	1.30
6	Internodes length (cm)	8.10(more)	6.78(less)
7	Lamina length (cm)	10.41	10.05
8	Depth of sinus (cm)	1.13	1.08
9	Width of lobe (cm)	2.98	3.87
10	Ratio of depth of sinus & with of lobe	1.38	0.21
11	Leaf thickness (cm)	0.313	0.380
12	Leaf weight (g)	99.20	106.56
13	Specific leaf weight (mg/cm2)	5.21	4.80
14	Leaf area index	6.52	6.05
15	R-value	0.92	1.23
16	Leaf yield (g)	85.82	98.72
Qualitative traits:			
1	N(g/100g)	3.58	3.48
2	P(mg/100g)	745	991
3	K(mg/100g)	30.7	39.5
4	Ca(mg/100g)	380	396
5	Protein(g/100g)	2.23	2.17
6	Fiber(g/100g)	2.61	2.02
7	Starch(g/100g)	4.39	4.36
8	Chlorophyll(mg/g)	2.3	2.23
9	Moisture content	3.23	5.11
10	Oil (ml/500g leaves)	0.5-0.8	0.5-0.8
11	Eugenol content %	27.57	49.31

Morph agronomic characterization: IC-629872 collection from selection has dark green leaf colour, V-shaped leaf lamina orientation along mid rib whereas green colour leaf and flat leaf lamina orientation along mid rib of the check. Leaf length is 6.3cm, petiole length is 5.73cm, leaf width is 5.97cm, eugenol content is 27.57% which is less than Bidhan Paan-1 (check) for all the traits. IC629872 was found high for specific leaf weight (5.21mg/cm^2), leaf area index (6.52) and intermodal length (8.10cm), protein content (2.23g/100g) as compare to check.

MLT Data

The candidate strain (IC629872) was studied for its genetic diversity using molecular marker (ISSR and DAMD) which indicate that the strain is genetically diverse from check.

Associated characters and cultivation practices: Betelvine is cultivated in Protected structure in C.G. Deep ploughing is done during early summer. After ploughing upper soil is left exposed for one to two month to reduce soil borne pathogens. During onset of monsoon two to three ploughing with harrow is done. After that 500kg vermicompost in 500sm area is mixed in soil. The raised bed 45cm above surface is prepared to facilitate drainage from the field.

Cuttings with one or two nodes along with attached leaves are used as a propagating material. Established cutting can also be used for planting. Before planting furrows are made. In the furrow ridges are constructed. In the ridges two rows of budded vine with mother leaf is planted at 30cm plant to plant spacing and row to row spacing 45cm. For 500 sq.m 4000 planting material is sufficient. Before planting cutting are dipped in 1% of Bavistin and dried for 10-15 minute and the basal region along with node are dipped in 0.5% rootex (GA-3) for high germination percentage. Dibbling method is used for planting. Whole is made with help of stick or khurpi so that without damaging internodes below the bud point is dipped in soil. Hole is completely packed with help of thumb and finger. After that for fast sprouting the plant is covered with straw. The field is to be irrigated twice a day with help of water cane /drip/ sprinkler for twenty days and after that straw is removed carefully.

Fertilizers for 500 sq.m area is 100kg (19:19:19) in 12 split/ year along with foliar spray of 2% in 15 days interval.75kg oil cakes in four split in three month interval and vermicompost

500kg. During summer irrigation is given almost every day in new plant and 4-5 days interval in old plants. In winter season irrigation is reduced to fortnight interval. During rainy no irrigation is required unless there is long dry spell. Chemical spray to control pest should be avoided. Neem kernel oil 5% concentration is sprayed in field if there is infestation of mealy bug or leaf eating catterpiller. Wettable sulfur 0.5-1% is applied if there is mites. *T. viridii* 5-7g/lit of water two times in a month as basal application along with foliar application 3g/15lit which control most of the diseases. Drenching with 1% bordex mixture at 60 days interval. During November and June lowering of vines is carried to earthling the vine on soil surface before 30 cm to touches roof. Therefore, each vine is supported with help of nylon rope of 1mm thickness. Auxiliary branches are removed from main vine regularly. Harvesting of leaves starts after 7-8 month from the time of planting. In rainy season frequent harvesting is done but leaves are picked throughout the year when the leaves get mature from each plant 87 marketable leaves can be harvested.

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77. HV 2006-6 (IC00574228; INGR21077), a High Yielding Sun-Cured Chewing Tobacco (*Nicotiana tabacum*) Germplasm with Caterpillar Resistance.

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Chewing tobacco (*Nicotiana tabacum*) is one of the important commercial crops grown in Tamilnadu mainly for chewing purpose. In the chewing tobacco producing zone of Tamil Nadu tobacco, caterpillar *(Spodoptera litura)* is a major insect pest that causes serious economic loss to the growers. None of the varieties presently in cultivation in the zone is resistant to this pest. Hence, a caterpillar resistant cultivars line, HV.2000-6 was developed through through back cross breeding using Abirami, a sun cured chewing tobacco line as recurrent parent and DWFC as donor for caterpillar *(Spodoptera litura)* resistance (ICAR-CTRI 2006 & 2007). This line is morphologically akin to the caterpillar susceptible variety Abirami. The line shows its superiority in terms of resistance to tobacco caterpillar both under natural and artificial conditions (Table 1). It has an yield potential of about 3950 kg/ha as observed in various AINPT trials. Hence registered as a high yielding caterpillar resistant sun-cured chewing tobacco line.

Table 1: Reaction to Leaf eating caterpillar

Condition	*Year*	*HV.2000-6*	*Abirami*
Artificial	2000-01	100% resistant to first instars larvae.	Susceptible
	2001-02	100% resistant to first instars larvae.	Susceptible
	2002-03	100% resistant to first instars larvae.	Susceptible
Natural (% plants affected)	2003-04	-	48.0
	2004-05	1.2	64.8
	2005-06	1.6	56.8
	Mean	1.4	56.5

Morpho-agronomic characteristics: HV.2000-6 plants grows to a height of 1.4 m to 1.5 m under un-topped condition and 0.4 m to 0.6 m when topped. Plant are open in habit, leaves thick, shiny dark green, 75-80 cm long and 45-48 cm wide with good auricle development, prominent mid-rib acute tip and heavy puckering. Panicle is semi-open and branched. The days taken for seeding to transplanting is 45-50 days, transplanting-flowering 60-65 Days and seed to seed 155 – 165 days. Cured leaves have dark brown color, heavy bodied, elastic with whitish incrustations, sweet aroma and medium strength. HV 2000-6 recorded higher mean scores for various leaf quality characteristics by Trader's (62.2 out of 80) and Consumer's (59.6 out of 80) than control Abirami (57.5; 56.4, respectively).

Associated characters and cultivation practices: The recommended cultural practices for chewing tobacco can be adopted for rising HV.2000-6. The entry is susceptible to other pests and diseases and its reaction is comparable to control, Abirami.

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78. NLCR 6-10 (IC0634528; INGR21078), a FCV Tobacco (*Nicotiana tabacum*) somaclone with High Yielding Cured Leaf Having More Number of Longer and Broader Curable Leaves. Suitable for Irrigated Alfisols.

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Flue-cured Virginia (FCV) tobacco is the major exportable tobacco type grown in India. FCV tobacco grown in the irrigated alfisols of the Northern Light Soils (NLS) covering West Godavari district of Andhra Pradesh and Khammam district of Telangana is known for its premium leaf quality and is exported to several countries. In order to increase the yield level and export competitiveness of the tobacco of the area, NLCR 6-10, a high leaf yielding somaclone was developed from Kanchan explants at ICAR- Central Tobacco Research Institute Research Station, Jeelugumilli (ICAR-CTRI 2011, 2012, 2013, 2018, 2019a & 2019b). The line NLCR 6-10 produces a total of 35 leaves with about 31 good bodied ones suitable for harvesting and curing under NLS (Table 1) compared to 29 curable leaves in control, Kanchan (2009-12). The leaves of NLCR 6-10 are longer (up to 88 cm) and broader (up to 44 cm) than Kanchan (up to 77 cm long and 35 cm broad). The entry, NLCR 6-10 is high yielding than Kanchan and has a leaf yield potential of more than 3300 kg/ha (Table 2).

Table 1: Leaf characters of NLCR-6-10 under replicated (2009-12) and on-farm (topped condition) trials

Year	Village	No. of curable leaves		Leaf length (cm)		Leaf width (cm)	
		NLCR-6-10	Kanchan	NLCR-6-10	Kanchan	NLCR-6-10	Kanchan
	Replicated trial						
2009-10	CTRI RS, Jeelugumilli	32 (36)	31 (33)	51	52	58	22
2010-11	CTRI RS, Jeelugumilli	26 (30)	26 (29)	66	60	58	18
2011-12	CTRI RS, Jeelugumilli	34 (38)	30 (33)	64	63	31	19
	Mean	31 (35)	29 (32)	60	58	31	20
	On- Farm trials						
2016-17	Bandapuram	-	-	83	74	36	33
	Mangaparthidevepeta	-	-	85	80	41	36
	Muppinavarigudem	-	-	81	73	36	33
Mean		-	-	83	76	38	34
2017-18	Bandapuram	-	-	84	77	40	36
	Mangaparthidevepeta	-	-	88	83	44	38
	Muppinavarigudem	-	-	83	75	37	34
Mean		-	-	85	78	40	36

*Figures in the parenthesis are total leaves

Table 2: Leaf yields of NLCR-6-10 under different trials (2009-2019)

Trial	Year	No. of trials	Green leaf			Cured leaf			Grade Index		
			NLCR-6-10	Kanchan	CD 5%	NLCR-6-10	Kanchan	CD 5%	NLCR-6-10	Kanchan	CD 5%
RYT	2009-10 to 2011-12	3	13847*(13)	12190	1026	2237* (16)	1927	177	1376* (31)	1053	118
IVT (JML)	2013-14	1	13153* (39)	9458	1711	2257* (34)	1689	312	1532* (46)	1049	212
AVT (JML)	2014-15 to 2015-16	2	22314* (41)	15815	1070	3309* (39)	2373	182	2179 * (55)	1410	142
Bulk trial (JML)	2015-16 to 2018-19	4	19780 (48)	13371	-	3270 (47)	2227	-	1957 (66)	1177	-
On-farm trial	2016-17 to 2018-19	13	-	-	-	2568 (20)	2132	-	-	-	-

Note: RYT: Replicated trail; IVT: Initial Varietal Trial; JML: Jeelugumilli; AVT: Advanced Varietal Trial; * Significantly superior over Kanchan

Hence, recommended for registration as high cured leaf yielding FCV tobacco somaclone with more number of longer and broader leaves suitable for irrigated alfisols.

Morpho-agronomic characteristics: The leaves of NLCR 6-10 are dark green coloured, strongly puckered, broad elliptic and strongly recurved with strongly pointed tip. The cured leaf yield potential of FCJ-11 is 3981 kg/ha in AVT-1 (2014-15) at CTRI RS, Jeelugumilli, which is the highest among the FCV cultivars. Cured leaf of NLCR 6-10 is bright lemon to orange in colour with good aroma.

Associated characters and cultivation practices: Under field condition, NLCR 6-10 recorded slightly lower incidence of pests (*Spodoptera*, budworm and aphids) and mostly similar reaction to major diseases compared to control, Kanchan. The chemical quality parameters of NLCR 6-10 were within the permissible range and are comparable with control, Kanchan.

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79. F6-2-2 (IC0638885; INGR21079), a Tobacco (*Nicotiana tabacum*) Germplasm High seed yielding chewing tobacco.

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Tobacco is a commercial crop grown in India, mainly, for its traditional uses *viz*., smoking, chewing, etc. However, it can also be exploited for the production of seed oil as tobacco plant is a prolific producer of tiny seed containing ~ 35% oil. This oil is mainly used in paints, varnishes, lubricants and soap industries. The studies conducted at ICAR-CTRI, Rajahmundry indicated that tobacco oil can be used for edible purpose as its nutritional quality is comparable to sunflower and ground nut oils and is free from tobacco related harmful substances. As a part of the drive to exploit tobacco for edible oil production, a high seed yielding chewing tobacco line, F6-2-2 was developed at ICAR-CTRI Research Station, Vedasandur (ICAR-CTRI, 2017, 2018, 2019a and 2019b). The lines was developed through pedigree method of breeding from a cross between A 145 (a high seed tielding bidi entry) and Bhagyalakshmi (a chewing tobacco entry). F6-2-2 found to record higher seed yield than control varieties during 2015-19 (Table 1). The seed yield of this line ranged from 750-1600 kg/ha with the mean yield of 1257 kg/ha compared to 599 kg/ha in control, Abirami and 766 kg/ha in Bhaghyalakshmi. F6-2-2 yielded more than double the seed yield of control, Abirami and 64 % higher than Bhagyalakshmi. Higher seed yield in F6-2-2 may be due to higher number of capsules per plant (303) than controls Bhagyalakshmi (90) and Abirami (137). Hence, this line is registered as high seed yielding chewing tobacco line.

Table 1: Seed yield (kg/ha) of F6-2-2 and controls (2015-19)

Year	*F6-2-2*	*Abirami*	*Bhagyalakshmi*
2015-16	1512	800	1208
2016-17	1600	582	500
2017-18	750	460	634
2018-19	1167	552	723
Mean	1257	599	766

Morpho-agronomic characteristics: The plants of F6-2-2 are conical in shape, open in habit, leaves are lanceolate dark green in colour, 25 in number. During 2016-19, F6-2-2 yielded up to 3400 kg/ha cured leaf yield under topped condition. The inflorescence is medium, flowers are pink in colour, seed capsules are medium in shape and seeds are brown in colour.

Associated characters and cultivated practices: The recommended cultural practices for chewing tobacco can be adopted for rising F6-2-2 with a spacing of 75 cm x 60 cm. It reaction to pests and diseases is comparable to controls, Bhagyalakshmi and Abirami.

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80. JS-117 (IC0625211; INGR21080), a Flue-Cured Virginia Tobacco (*Nicotiana tabacum*) Germplasm with Low smoke tar delivery

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Tar is the partially combusted particulate matter produced by the burning of tobacco in the act of smoking. The smoke tar content in Flue-cured Virginia (FCV) tobacco range from 22-38 mg/cigarette (33-55 mg/g dry tobacco). The tar content of tobacco is associated with some of the harmful effects of tobacco use. In view of this, ICAR- Central Tobacco Research Institute Research Station, Jeelugumilli bred a low tar delivering Flue-cured Virginia (FCV) line, JS-117. The lines developed was through pedigree method of breeding involving the high yielding and popular FCV tobacco cultivar, Kanchan and low tar di-haploid line, D-1 (Sarala *et al.,* 2012). It delivers 12% less tar per gram tobacco used or 11% less tar/cigarette compared to control, Kanchan (Table 1 & 2; ICAR-CTRI 2014 & 2015). Hence, JS-117 registratered as low tar delivering FCV tobacco line.

Morpho-agronomic characteristics: JS-117 is a green cast line with semi erect habit and short internodes. It grows to a height of around 1.17 m. Plant shape resembles the ruling variety, Kanchan. The line gives more than 24 curable leaves. The leaves are long (65-72 cm) and slightly wider (24-34 cm) than Kanchan variety. Cured leaf is deep lemon to orange in colour, open grained, medium to thick bodied, semi-flavourful, rich in oil and fluffy. The line has a yield potential of about 2500 kg/ha. The physical and chemical characteristics of the variety, JS-117 are comparable with control, Kanchan and are in acceptable range.

In the station replicated trials (2003-2004 to 2005-2006), JS-117 recorded significantly higher leaf yields (18%) in cured leaf yield (2167 kg/ha) over Kanchan. In the IVT (2006-07) and AVT (2007-09) the line recorded a cured leaf yield of 2335 kg/ha and 2140 kg/ha (Pooled), respectively. In the station bulk plot trials conducted at ICAR-CTRI RS, Jeelugumilli (2009-10 to 2010-11), JS-117 recorded 15% superiority cured leaf yield over check, Kanchan. The line proved its superiority in on-farm trials (2011-12 and 2012-13) at four locations with an average of 21% increase in cured leaf yield (2565 kg/ha) over the control, Kanchan. In the agronomic trial (2012-14), a nitrogen dose of 130 kg N/ha and topping at 26 leaves were found to be optimum for realizing the yield potential of JS-117.

Associated characters and cultivated practices: JS-117 recorded lower natural incidence of Brown spot, *Fusarium* wilt, TMV and *Orobanche* compared to Kanchan. The reaction of JS-117 to other major pests and diseases is on par with Kanchan.

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Table 1: Data on Smoke tar deliveries

Smoke tar (mg/cigarette)			Smoke tar (mg/g dry tobacco)		
Year	JS-117	Check variety, Kanchan	Year	JS-117	Check variety, Kanchan
2005-06	20.92(13)*	23.96	2005-06	41.89(3)*	42.97
2007-08	19.46 (12)	22.11	2007-08 ('X' position)	31.19 (20)	38.88
2008-09	19.27 (14)	22.40	2007-08 ('L' position)	40.72 10)	45.28
2011-12	21.20 (07)	22.88	2011-12	38.97 (9)	42.89
2012-13	22.08 (08)	24.10	2012-13	37.60 (18)	46.0
Mean	20.59 (11)	23.09	Mean	37.07 (12)	43.20

*Figures in the parenthesis are % reduction in tar delivered over control, Kanchan

81. Jayalakshmi (IC0637597; INGR21081), a Flue Cured Virginia Tobacco (*Nicotiana tabacum*) Germplasm with White flower and White (cream colour) seed

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Table 1: Flower and seed colour characteristics

	Flower Colour				Seed Colour			
Entry	2016-17	2017-18	2018-19	2019-2020	2016-17	2017-18	2018-19	2019-2020
Jayalakshmi	White	White	White	White	White	White	White	White
A-145 (C)	Pink	Pink	Pink	Pink	Brown	Brown	Brown	Brown
Siri (C)	Pink	Pink	Pink	Pink	Brown	Brown	Brown	Brown

Flue-cured Virginia (FCV) tobacco is the major exportable tobacco type grown in India. FCV tobacco grown in India. In general, FCV (*Nicotiana tabaccum*) lines have pink flowers and produce brown seed. However, in the FCV tobacco germplasm, white flower and white seed (cream colour) producing entry, Jayalakshmi was identified . This is a line collected from the agricultural fields of East Godavari district, AP and is being maintained at the genebank of ICAR-CTRI, Rajahmundry. This line found to consistently give white flower and white seed (ICAR-CTRI, 2013, 2019a and 2019b).

This line being used in the development of a mapping population through crossing with A-145 an entry with pink flowers and brown seed in order to produce higher white seed yielding tobacco genotypes and to understand genes involved in seed and oil yield. Oil extraction from white colour seed results in clear seed oil and requires lesser processing compared to the oil extracted from brown seed. This assumes significance for exploring tobacco seed oil for edible purpose.

Morpho-agronomic characteristics: Jayalakshmi plants are conicle in shape with semi-erect plant habit. Leaves are sessile, moderately acute, medium pointed, broad elliptic, medium to dark green, with medium blistering, medium wavy margins and undulations. Inflorescence loose and spherical in shape. Flowers are white in colour and produce white/cream colour seed.

Associated characters and cultivated Practices: Jayalakshmi (ws) recorded higher seed oil content (39%) than A-145 (37%) (ICAR-CTRI, 2013). The standard cultural practices recommended for FCV tobacco can be adopted in raising the entry.

References

ICAR-CTRI (2013) ANNUAL REPORT 2012-13. ICAR-Central Tobacco Research Institute, Rajahmundry, 11 p

ICAR-CTRI (2019a) ANNUAL REPORT 2018-19. ICAR-Central Tobacco Research Institute, Rajahmundry, 30 p

ICAR-CTRI (2019b) ANNUAL REPORT 2019. ICAR-Central Tobacco Research Institute, Rajahmundry, 28 p

82. 1/135 (IC0637598; INGR21082), a Tobacco (*Nicotiana tabacum*) Germplasm with High Solanesol (3.43 %).

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Tobacco is mainly grown for its traditional uses *viz.* Smoking, chewing, snuff, Hookah *etc*. Tobacco can also be exploited for its alternative uses in the form of extraction of important native phytochemicals *viz*., solanesol, nicotine, organic acids, leaf protein etc. Solanesol is an important secondary metabolite available in tobacco having pharmaceutical importance in controlling cardiovascular diseases, aging etc. While carrying out research in the direction of alternative uses of tobacco at ICAR- Central Tobacco Research Institute, Rajahmundry, line 1/135 was developed from a cross between a high solanesol line, HDBRG and a low solanesol line, BY53 (Sarala *et al*., 2018). When the population of pure lines developed from the above cross was tested for solanesol, the line, 1/135 recorded higher solanesol than the high solanesol yielding line, HDBRG most of the years during 2014-17 and 2019-2020 as shown below. The line recorded a mean of 3.43 % with 73% mean increase over HDBRG during this period.

Associated characters and cultivation practices: The reaction of the line to major pests and diseases of tobacco under natural conditions is on par with HDBRG.

References

Sarala K, K Prabhakara Rao, C Chandrasekhararao, D Damodar Reddy and K. Bagyalakshmi (2018) Phenotyping tobacco recombinant inbred lines for solanesol. *Intl J Chem Stud* **6:** 3643-3650.

ICAR-CTRI (2019a) ANNUAL REPORT 2018-19. ICAR-Central Tobacco Research Institute, Rajahmundry, 30 p

Entry	Solanesol %				Mean
	2014-15	2015-16	2016-17	2019-2020	
1/135	4.9 (96)	3.6 (57)	2.8 (100)	2.4 (41)	3.43 (73)
HDBRG	2.5	2.3	1.4	1.7	2.00
By-53	1.4	1.7	0.6	o.70	1.23

*% improvement over high solanesol line, HDBRG

Morpho-agronomic characteristics

Parameter	HDBRG	1/135
Plant Shape	Cylindrical	Conical
Plant Height (cm)	145	135
Plant Habit	Semi Erect	Semi Erect
Plant Internodal Length (cm)	3	4.5
Plant Number of Leaves	28	33
Leaf Type	Sessile	Sessile

Parameter	*HDBRG*	*1/135*
leaf angle of insertion	Moderately Acute	Moderately Acute
leaf length (cm)	53	33
Leaf Width (cm)	20	18
Leaf Midrib	Thin	Medium
Leaf veins thickness & Angle	Medium/ModeratelyAcute	Medium/ModeratelyAcute
Leaf Blade Shape	Narrow Elliptic	Broad Elliptical
Leaf Tip Shape	Strongly Pointed	Strongly Pointed
Leaf Blistering of Blade	Weak	Weak
Leaf Undulation of Margin	Weak	Weak
Leaf Development of Auricles	Medium	Medium
Leaf Colour of Blade	Medium Green	Green
Leaf Colour of Midrib	Green	Green
Time of 50%Flowering	70 Days	114 Days
Inflorescence Shape	Spherical	Spherical
Inflorescence compactness	Medium	Medium
Inflorescence Position Relative to Upper Leaves	Above	Above
Flower Colour	Light Pink	Pink
development of stamens	Full	Full
Fruit form	Intermediate	Ovate
Testa colour	Light Brown	Light Brown

83. V-4914 (IC0634529; INGR21083), a Flue-cured Virginia Tobacco (*Nicotiana tabacum*) Germplasm with High Yield and Resistance to Tobacco Mosaic Virus

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Tobacco Mosaic Virus (TMV) is one of the major diseases in tobacco causing yield and quality losses. In order to stabilise the yield levels of Flue-cured Virginia (FCV) tobacco grown in Southern Light Soil (SLS) areas of Prakasam and Nellore districts, Andhra Pradesh, an attempt made to develop TMV resistant lines. V-4914 (FCR 15) a high yielding (24500 kg/ha), TMV resistant light cast FCV tobacco cultivar suitable for moisture stress prone was developed by hybridization (*N. tabacum, cv.* Siri *X N. tabacum, cv.* VT 1158) followed by pedigree selection after artificial inoculation in each generation (ICAR-CTRI, 2010, 2011, 2012, 2013 and 2019). The line V-4914 recorded resistance reaction to TMV under both artificial as well as natural conditions during 2015-19 (Table 1). Hence, registered as high yielding TMV resistant FCV tobacco cultivar.

Morpho-agronomic characteristics: V-4914 plant has semi erect habit, height 210 cm; Plant width at 5th leaf

Table 1: Reaction to TMV disease

S. No.	Year	V-4914	Control, Siri
Under artificial inoculation			
1	2015-16	R (0)	S (100)
2	2016-17	R (0)	S (100)
3	2017-18	R (0)	S(100)
4	2018-19	R (0)	S(100)
Natural Condition			
5	2016-17	R (0)	S (30)

Note: Figures in the parenthesis are % plants infected with TMV

position is about 80 cm as against 78 cm in Siri. Stem light green to cream coloured, internode short to medium (5 cm on an average). Leaf lamina is moderately long broad with good puckering and acute to acuminate tip. Leaf is light green cast in nature, sessile with medium auricle development. The average leaf length of 5th, 10th and 20th leaf are 56 cm, 58.4 cm and 29.5 cm respectively and the width is 29.5 cm, 30.4 cm and 14.5 cm respectively. The plant produces a total of 24-30 leaves with 22-27 economic leaves. During 2016-18, under 10 different AINPT trials, V-4914 (tested with the code FCR -15) recorded up to 48% increase in cured leaf over control, Siri at SLS areas of AP. The line found to have a yield potential of 2400 kg/ha.

Associated characters and cultivation practices: The recommended cultural practices for FCV tobacco grown under SLS conditions can be adopted for rising V-4914. Average weight of 100 cured leaves of V-4914 is about 510 grams against 470 g in Siri. The cured leaf is lemon yellow to orange in colour. Cured leaf is medium bodied, oily with good ripeness characteristics. The reaction to major pest and other diseases is similar to control, Siri.

References

ICAR-CTRI (2010) ANNUAL REPORT 2009-10. ICAR-Central Tobacco Research Institute, Rajahmundry, 29p

ICAR-CTRI (2011) ANNUAL REPORT 2010-11. ICAR-Central Tobacco Research Institute, Rajahmundry, 30p

ICAR-CTRI (2012) ANNUAL REPORT 2011-12. ICAR-Central Tobacco Research Institute, Rajahmundry, 23p

ICAR-CTRI (2013) ANNUAL REPORT 2012-13. ICAR-Central Tobacco Research Institute, Rajahmundry, 18-19p

ICAR-CTRI (2019) ANNUAL REPORT 2019. ICAR-Central Tobacco Research Institute, Rajahmundry, 2p

84. BSR-1 (IC0634526; INGR21084), a Chewing Tobacco (*Nicotiana tabacum*) Germplasm with Resistance to Black Shank (*Phytopthora parasitica*)

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Black shank (*Phytopthora parasitica*) disease is a serious problem in chewing tobacco cultivated in the coastal belt of Tamil Nadu. An effort made at the CTRI RS, Vedasandur to incorporate black shank resistance into the existing pure line variety VR-2 without affecting yield, physical and chewing quality attributes. VR-2 was crossed with Black shank resistant donor, Beinhart 1000-1 and the resultant hybrid was back crossed to VR-2. Back crossing continued for four generations while selecting the plants resembling VR-2 and possessing black shank resistance. The stabilised entry, BSR-1 (mentioned as BC5S1 in CTRI Annual Reports) found to consistently perform well in the Research station as well as in the black shank sick fields in Vedaranyam areas of coastal chewing belt. In the endemic areas, BSR-1 recorded resistance reaction to black shank disease under both artificial and sickfield conditions (Table 1) compared to controls, VR-2 and Kaviri. Hence, this line is registered as black shank resistant chewing tobacco line.

Table 1: Reaction of BSR-1 to black shank disease under inoculated and sick fields at Coastal chewing belt of Tamil Nadu (Hot spot area)

Condition	Year	BSR-1	VR-2	Kaviri
Artificial	2006-07	Resistant	Susceptible	Susceptible
	2007-08	Resistant	Susceptible	Susceptible
	2008-09	Resistant	Susceptible	Susceptible
Sick fields (% incidence)	2006-07	Nil	60.5	12.8
	2007-08	Nil	56.0	13.0
	2008-09	Nil-	45.3	13.3
	Mean	Nil	50.6	13.0

Morpho-agronomic characteristics: BSR-1 plants are open with dark-green, medium broad ovate leaves with prominent auricle and moderate puckering. Internodes are medium and stem girth moderate. BSR-1 recorded a mean yieldof 2624 to 3687 kg/ha in different trials with 42% and 17% higher mean yields, covering eight trials, than controls, VR-1 and Kaviri, respectively.

Associated characters and cultivation practices: The recommended cultural practices for chewing tobacco can be adopted for rising BSR-1. Chewing quality characteristics are rated superior by traders and consumers than recurrent parent, VR-2. BSR-1 is susceptible to other pests and diseases of tobacco and is comparable to controls, VR-2 and Kaviri. The farmers expressed satisfaction over raising BSR-1 as they could raise a healthy crop of tobacco without application of fungicide for black shank thus cutting down the cost on chemical fungicides thereby reducing production costs and increasing net returns besides being environment friendly.

References

ICAR-CTRI (2008) ANNUAL REPORT 2007-08. ICAR-Central Tobacco Research Institute, Rajahmundry, 21p

ICAR-CTRI (2009) ANNUAL REPORT 2008-09. ICAR-Central Tobacco Research Institute, Rajahmundry, 18-19 p

ICAR-CTRI (2010) ANNUAL REPORT 2009-10. ICAR-Central Tobacco Research Institute, Rajahmundry, 30-31 p

ICAR-CTRI (2015) ANNUAL REPORT 2014-15. ICAR-Central Tobacco Research Institute, Rajahmundry, 6 p

85. Cr-6017 (IC0636679; INGR21085), a Quality Tea (*Camellia sinensis*) Germplasm.

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The clone is selected from The Nilgiris, Tamilnadu. It is selected for its high-quality character for high grown orthodox tea. The genome of this plant has been sequenced under, "Tea genome re-sequencing project".

Morpho-agronomic characteristics: The clone is a diploid with medium sized leaves and dense crop shoots. Leaves are elliptic oblong in shape, young leaves are light green and are occasionally pigmented (pinkish tinge colour in young leaves).

Associated characters and cultivation practices: The clone is preferred for making high grown orthodox teas. It is a preferred scion clone for grafting on hardy root stock tea clones.

References

Mohanan M and VS Sharma (1981) Morphology and Systematics of some tea (Camellia spp.). Proceedings of PLACROSYM IV: 391-400.

Balasaravanan T, PK Pius and R Rajkumar (2002) Status of south Indian tea germplasm. *Newsletter UPASI Tea Research Foundation.***12**(2).

Biochemical characters

Biochemical parameters	*Quantity % (mg/g) **
Polyphenol	21.16
Amino acid	1.05
Catechin	15.44
Caffeine	2.60
Anthocyanin	0.03
Carotenoids	0.20
Theaflavin	1.09
Thearubigin	6.10
High polymer substance	7.63
Total liquor colour	3.33

*Data presented here is the average value of 4 consecutive years reading.

86. UPASI-9 (IC0636680; INGR21086), a Drought Tolerant Tea (*Camellia sinensis*) Germplasm.

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The clone is selected from the old seedling tea population in The Nilgiris, Tamilnadu. The clone is selected for its high yield and drought tolerance character. The genome of this plant has been sequenced under, "Tea genome re-sequencing project".

Morpho-agronomic characteristics: The Clone is a diploid with dense crop shoots and flushing throughout the year. The leaves are elliptic-oblong or obovate-oblong, young leaves are dark green in colour and the flush is fairly larger in size, narrow dark green in colour with medium internodal distance.

Associated characters and cultivation practices: The clone is preferred by all the growers for its high yield of 5000 kg made / ha /year. It severs as an excellent root stock for most of the scion. The quantum increase in yield was found to be greater when it is used as a root stock for grafting.

References

Venkataramani KS and VS Sharma (1975) Notes on the UPASI Tea clones approved by Tea Board and released for commercial planting. The hand book of tea culture. 1-3

Mohanan M and VS Sharma (1981) Morphology and Systematics of some tea (*Camellia* spp.). Proceedings of PLACROSYM IV: 391-400.

Morphological characters

Characters	*Quantification*
Leaf shape	Lanceolate
Total leaf length (cm)	14.3
Lamina length (cm)	13.8
Area of leaf in (mm^2)	4244
Lamina width (cm)	4.6
Ratio between Length and width of Lamina	0.33
Leaf venation	Sunken
Leaf margin	Serrate
Young shoot colour	Green
Individual shoot length (cm)	7.9
Individual shoot weight (g)	1.17
Internodal length (cm)	3.5
Internodal width (cm)	1.2
Stomatal conductance (mmol (H_20) m^{-2} S^{-1})	151
Transpiration rate (mmol (H_20) m^{-2} S^{-1})	2.07
Net photosynthetic rate ((Co_2) m^{-2} S^{-1})	3.5

*Data presented here is the average value of 4 consecutive years reading.

87. UPASI-3 (IC0636681; INGR21087), a Triploid Tea (*Camellia sinensis*) Germplasm.

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The clone is selected from an old seedling population in The Nilgiris, Tamilnadu. It is selected for its excellent quality characters of black tea. The genome of this plants has been sequenced under, “Tea genome re-sequencing project”.

Morpho-agronomic characteristics: The clone is a triploid with large leaves and succulent crop shoots. Leaves are large, often obovate or slightly obovate, elliptic in shape and bright green in colour. It is also a naturally occurring triploid which is rare in the tea gene pool that are primarily consists of diploid plants.

Associated characters and cultivation practices: This clone is one of the outstanding tea clones as it performs good at varying condition in varying elevation and climatic zone at different tea districts.

References

Mohanan M and VS Sharma (1981) Morphology and Systematics of some tea (*Camellia spp.*). Proceedings of *PLACROSYM IV:* 391-400.

Venkataramani KS and VS Sharma (1974) The Tea clone ‘Sundaram’, The hand book of tea culture. 1-3.

Biochemical characters

Biochemical parameters	Quantity % (mg/g) *
Polyphenol	23.22
Amino acid	1.87
Catechin	16.33
Caffeine	2.70
Anthocyanin	0.03
Carotenoids	0.22
Theaflavin	1.29
Thearubigin	8.13
High polymer substance	9.29
Total liquor colour	3.63
Chromosome number	3n=3(15) = 45

*Data presented here is the average value of 4 consecutive years reading.

88. ATK (IC0636684; INGR21088), a Tea (*Camellia sinensis*) Germplasm Drought Tolerance

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The clone is selected from old seedling tea population in the Nilgiris, Tamilnadu. The clone is selected for its drought tolerance character. The genome of these plants has been sequenced under, "Tea genome re-sequencing project".

Morpho-agronomic characteristics: This clone is a diploid with dense crop shoots, leaves are narrow elliptic-oblong in shape. Mature leaf is dark green in color whereas the young leaves contain a purple tinch.

Associated characters and cultivation practices: It is an easy rooting clone in the nursery and readily establishes in the field. The clone preferred for its drought tolerant character and is a suitable root stock clone.

Morphological character

Characters	*Quantification*
Leaf shape	Lanceolate
Total leaf length (cm)	15.2
Lamina length (cm)	14.5
Area of leaf in (mm^2)	4483
Lamina width (cm)	4.7
Ratio between Length and width of Lamina	0.32
Leaf venation	Sunken
Leaf margin	Serrate
Pigmentation in young shoot	Present
Young shoot colour	Mild pink
Individual shoot length (cm)	9.8
Individual shoot weight (g)	1.45
Internodal length (cm)	4.0
Internodal width (cm)	1.4
Stomatal conductance (mmol (H_2O) m^{-2} S^{-1})	113
Transpiration rate (mmol (H_2O) m^{-2} S^{-1})	1.95
Net photosynthetic rate ((Co_2) m^{-2} S^{-1})	3.2

*Data presented here is the average value of 4 consecutive years reading.

References

Spurgeon Cox and MA Subair (1999) Performance of the cultivar ATK-1 in Nilgiri-Wynaad. *Newsletter UPASI Tea Research Institute* **9(2)**:3-4.

Mohanan M and VS Sharma (1981) Morphology and Systematics of some tea (*Camellia Spp*) cultivars. Proceedings of *PLACROSYM IV*: 391-400.

89. TRI-2025 (IC0636685; INGR21089), a Tea (*Camellia sinensis*) Germplasm Drought Tolerance

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The clone is introduced from Sri Lanka during the 1970's. The clone is popular for its high yield and drought tolerant characters. The genome of these plants has been sequenced under, "Tea genome re-sequencing project".

Morpho-agronomic characteristics: This clone is a diploid with large leaves and grows vigorously throughout the year. Leaves are broadly elliptic or elliptic-oblong and glabrous. The young leaves are light green in colour.

Associated characters and cultivation practices: The clone is preferred for its drought tolerant character as well as for high yield. It is also a suitable root stock for grafting.

References

Morphology and Systematics of some tea (Camellia Spp) cultivars. Proceedings of *PLACROSYM IV:* 391-400.

Balasaravanan T, PK Pius and R Rajkumar (2002) Status of south Indian tea germplasm.
Newsletter UPASI Tea Research Foundation. **12**(2).

Sasidhar R and R Sanjay (2000) Incidence of collar canker in high range and Anaimallais.
Newsletter UPASI Tea Research Foundation **10** (1).

Morphological characters

Characters	*Quantification*
Leaf shape	Elliptic
Total leaf length (cm)	14.0
Lamina length (cm)	13.4
Area of leaf in (mm^2)	5391
Lamina width (cm)	6.0
Ratio between Length and width of Lamina	0.49
Leaf venation	Bullation
Leaf margin	Serrate
Tooth per centimetre	6
Young shoot colour	Green
Individual shoot length (cm)	11.6
Individual shoot weight (g)	1.57
Internodal length (cm)	4.1
Internodal width (cm)	1.5
Stomatal conductance (mmol (H_20) m^{-2} S^{-1})	122
Transpiration rate (mmol (H_20) m^{-2} S^{-1})	1.86
Net photosynthetic rate ((Co_2) m^{-2} S^{-1})	2.9

*Data presented here is the average value of 4 consecutive years reading.

90. IPC 11A Orange & IPC 11B Orange (IC0635038 & IC0635039; INGR21090), Is The First Orange Colour Main Season Tropical Carrot Carrot (*Daucus carota*) and its CMS Line Developed Indigenously. Roots are of Acceptable Size and Suitable for Main Season Sowing I.E. from Mid-September Onward in North Indian Plains with Petaloid Type Sterility.

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Carrot (*Daucus carota* L.; 2n= 2x=18) is an important vegetable crop being grown worldwide on 1.15 million ha area and production is 42.8 million tonnes (FAOSTAT, 2017). Orange colour carrot is rich in β-carotene, an improvement carotenoid which take care of night blindness. In India, orange carrot is preferred for their high level of uniformity in roots, better storage life, unique taste, and nutritional value. Originally, the orange carrots are temperate (European) type and needs vernalization for flowering and seed production. Hence, most part of the seeds of orange carrot is being imported in country which contributes significantly to foreign seed exchange value. Although, Pusa Nayanjyoti, a cytoplasmic male sterility (CMS) based hybrid was developed by IARI Regional Station, Katrain for main season cultivation but vernalization requirement and limited seed supply limited its spread. Hence, it was essential to develop CMS lines of tropical orange roots (non-vernalization requirement) for establishmentof hybrid seed production system in plains. The IPC 11A Orange is an indigenously developed CMS line of tropical carrot which has orange roots. It is developed by a naturally occurring mutant having 'petaloid' type sterile cytoplasm in Pusa Meghali identified at Division of Vegetable Science, ICAR-IARI, New Delhi. Its maintainer 'IPC 11B Orange' was also searched in the same population having orange self core coloured roots. This CMS line has potential in development of indigenous hybrid seed industry in orange carrot for benefit of local farmers and to improve balance sheet of foreign exchange for vegetable seeds.

Morpho-agronomic characteristics of CMS line IPC 11A Orange

The IPC 11A Orange is the first CMS line of tropical carrot having orange coloured self-core roots developed indigenously. It is suitable for sowing during main crop season (*i.e.* September to October) and roots are ready to harvest in a period of 90 – 95 days (Table 1). The height of flowering plants was 134.2 cm with profuse flowering and seed setting. The floral traits *i.e.* petal size, petal colour, petaloid (anther converted petals) colour and size and nectaries showed normal development (Fig. 1A-B; 2A-B). It produces orange colour, medium long roots with self-core character. Average root length of IPC 11A Orange was observed to be 21.5 cm, root diameter 34.3 mm, core diameter 11.68 mm and root weight (Fig. 3A-B). The marketable root yield was observed to be 27.4 t/ha which was higher than its maintainer line IPC 11A Orange (23.5 t/ha) (Table 1). The bolting (elongation of flower stalk) occurs during February – March months and produce abundant seeds during April month in plains of India. The CMS line showed potential in hybrid combination, hence, has potential in commercial hybrid breeding of indigenous tropical hybrids.

IPC 11B Orange: male fertile maintainer line of CMS line IPC 11A Orange

The 'IPC 11B Orange' is an elite genotype of main season tropical carrot. It is suitable for sowing in September to October in plains of north India. It matures during December to January months after 90-95 days of sowing. Plants are medium vigorous, semi-erect, medium in spread and leaves are green. It produces orange root with self core colour (Table 1).

References

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Kalia P, M Mangal, S Singh, C Chugh, M Mishra and S Chaudhary (2019) Morphological and molecular changes on cytoplasmic male sterility (CMS) introgression in Asiatic carrot (*Daucus carota* L.). *Planta* https://doi.org/10.1007/s00425-019-03185-4.

Table 1: Important horticultural traits and seed yield of CMS line IPC 11A Orange line as compared to the fertile maintainer line IPC 11B Orange

Traits	IPC 11A Orange	IPC 11B Orange
Maturity traits		
Growing season	Main season	Main season
Sowing period	September – October	September – October
Harvesting	December - January	December - January
Plant and root traits		
Plant height (cm)	85.0	88.0
Gross plant weight (cm)	185	215.0
Root colour	Orange	Orange
Root core colour	Orange	Orange
Root length (cm)	21.5	20.1
Root diameter (mm)	34.3	30.5
Core diameter (mm)	11.68	8.49
Root weight (g)	183.0	156.7
Root yield (t/ha)	27.4	23.5
Floral traits		
Petal colour	White	Green
Petal length (cm)	0.75	0.97
Petaloid colour Light purple		-
Petaloid length (cm)	1.21	-
Petaloid width (cm)	0.77	-
Petaloid shape	Spoon	-
Nectary development	Prominent	Prominent