Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXXth meeting held on October 21st, 2019 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 71 germplasm lines out of 79 proposals considered. 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. Kamini (IC599610) (IC0599610; INGR19033), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stress

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Till date the most studied rice germplasm for salinity stress is ‘Pokkali’ accessions from coastal saline areas of Kerala. A *Saltol*-QTL for salinity tolerance at seedling stage was identified from Pokkali and introgressed in high yielding background. But many other salt-tolerant cultivars besides Pokkali are grown along India’s eastern coast, especially in Odisha and West Bengal which may serve as sources of new QTLs for salinity tolerance. In West Bengal, Sundarbans (22° N, 89° E; 0–10 m above the mean sea level), covering parts of India and Bangladesh, is the largest single block of tidal halophytic mangrove forests in the world, where people mostly depend on rain-fed paddy cultivation. Even today they continue to grow traditional rice varieties because of their stable yield potential in coastal saline areas. However, these areas are increasingly vulnerable to frequent cyclones, high tidal waves, and erratic rainfall, which prompted rice growers and researchers to cultivate and conserve indigenous salt-tolerant lines. Kamini is one of such landraces which was collected from salt affected field at Gosaba block of South 24 Parganas (Sundarbans). In repeated control evaluation it was found tolerant to moderately tolerant (SES score-3-5) to salinity at vegetative stage under salinity stress (12 dSm-1).

Morpho-agronomic characteristics: This germplasm has intermediate early seedling vigour. In coleoptiles, anthocyanin colouration is absent. Basal leaf sheath colour is green. Leaf blade colour is pale green. Leaf is glabrous. It is highly photosensitive (days to 50% flowering is 133.5). It is tall (125 cm) and having low tillering ability (7.5). It has long (26 cm), horizontal and well exserted panicle. It has small bold grain with grain length-breadth ration of 2.52 and 13.4 g test weight (Table 1). Grain yield is around 2.5 t/ha under moderate (6 dSm^{-1}) salinity stress condition.

Associated characters and cultivation practices: ‘Kamini’ (AC 44118) was found tolerant to salinity stress (EC 12 d Sm^{-1}) at seedling stage. Its tolerance was associated with low ratio of Na/K (0.25) in shoot (Singh and Sarkar 2014; CRRI 2012; Chattopadhyay *et al.* 2014). Performance index (PI), which gives quantitative information on current state of plant’s ability to photosynthesis under stress was used to evaluate some salinity tolerant germplasm of rice including Kamini. The ‘salinity factor index’ (SFI) based on the salinity-induced changes in the PI during the stress and relative PI (PI $_{salinity}$/PI $_{control}$) were calculated. The genotypes were rated based on the SFI. The value of SFI was found positive only in Kamini. This was 0-0.5 in some Pokkali accessions and FL 478. This indicated that Kamini (AC 44118) might have better salinity tolerance ability than the genotype we are currently using a salt-tolerant donors (CRRI 2013; Singh and Sarkar 2014). *Saltol*-QTL derived from a Pokkali accession is a major QTL responsible for

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Compiled and edited by: Anjali Kak and Veena Gupta, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012 salinity tolerance at seedling stage. In our study, Kamini (AC44118) showed substantial allelic dissimilarity with FL 478 (a derivative line from Pokkali) in the *Saltol*-QTL region, indicating its allelic mismatch with Pokkali in the *Saltol* QTL region (NICRA 2012; Chattopadhyay *et al.* 2018). All these observations indicate the scope for identification of additional QTLs other than the *Saltol* from Kamini (AC 44118) for salinity tolerance in rice.

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2. Talmugur (AC 43228) (IC0596460; INGR19034), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stress at Vegetative Stage

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‘Pokkali’ rice from coastal saline areas of Kerala is the most studied germplasm for salinity tolerance in rice. A *Saltol*-QTL for salinity tolerance at seedling stage was identified from one of the accessions of Pokkali and introgressed in high yielding rice background. But many other salt-tolerant cultivars, besides Pokkali, are grown along India’s eastern coast, especially in Odisha and West Bengal which is found to serve as sources of new QTLs for salinity tolerance. In West Bengal, Sunderbans (22° N, 89° E; 0–10 m above the average mean sea level), covering parts of India and Bangladesh, is the largest single block of tidal halophytic mangrove forests in the world, where people mostly depend on rain-fed paddy cultivation. Even today people of this region continue to grow traditional low-yielding rice varieties because of stable grain yield. However, these areas are increasingly vulnerable to frequent cyclones, erratic rainfall and high tidal waves which compel rice growers to cultivate and conserve indigenous salt-tolerant lines. Talmugur is one of such landraces which was collected from salt affected rice fields at Mathurapur block of South 24 Parganas (Sunderbans). In repeated evaluation under control condition with salinity stress of EC= 12 dSm^{-1}, it was found to possess complete to moderately salinity stress tolerance (SES score- 3-5) at vegetative stage.

Morpho-agronomic characteristics: This landrace has early seedling vigour . In coleoptiles, anthocyanin colouration is absent. Basal leaf sheath colour is green. Leaf blade colour is pale green. Leaf is pubescent. It is photosensitive (days to 50% flowering is 122), tall (135.5 cm) and having low tillering ability (5). It has horizontal and well exserted panicle (23.48 cm). It has small bold grain with grain length-breadth ratio of 2.26 and test weight of 24.3 g (Table 1). Grain yield is around 2.5 t/ ha under moderate (6 dSm-1) salinity stress condition.

Associated characters and cultivation practices: ‘Talmugur’ (AC 43228) was found tolerant (SES score – 3-5) to salinity stress (EC 12 d Sm^{-1}) at seedling stage under control condition. Its tolerance was associated with low ratio of Na/K (0.25) in shoot (Research Highlights,

Table1. Minimal Descriptors for characterization and evaluation of rice germplasm, Talmugur (AC 43228; IC0596460)

Characteristics	*Kharif* 2017	*Kharif* 2018	Mean value
Early plant vigour	Tall	Tall	Tall
Coleoptile: Anthocyanin colouration	Absent	Absent	Absent
Basal leaf sheath colour	Green	Green	Green
Leaf blade colour	Pale green	Pale green	Pale green
Leaf pubescence	Pubescent	Pubescent	Pubescent
Leaf length (cm)	50.3	46.0	48.15
Leaf width (cm)	1.36	1.4	1.38
Days to 50 % flowering	121 (photosensitive)	123 (photosensitive)	122 (photosensitive)
Panicle exsertion	Well exserted	Well exserted	Well exserted
Stigma colour	Yellow	Yellow	Yellow
Apiculus colour	Purple	Purple	Purple
Number of effective tillers	5	5	5
Plant height (cm)	132	139	135.5
Panicle height (cm)	22.96	24.0	23.48
Panicle type	Horizontal	Horizontal	Horizontal
Awning	Absent	Absent	Absent
Days to maturity	151	153	152
Seed coat colour (kernel colour)	Brown	Brown	Brown
Grain length breadth ratio	2.16	2.36	2.26rtgh
100 grain weight (g)	2.55	2.3	2.43
Hull colour (husk colour)	Black	Black	Black
Threshability	Easy	Easy	Easy
Aroma	Absent	Absent	Absent
Grain yield per plant (g)	30.0	28.5	29.3
Abiotic Stress Note	Tolerant to moderately tolerant (SES Score = 3-5) to salinity stress at seedling stage	Tolerant to moderately tolerant (SES Score = 3-5) to salinity stress at seedling stage	Tolerant to moderately tolerant (SES Score = 3-5) to salinity stress at seedling stage

NICRA 2010-12; CRRI 2012; Chattopadhyay *et al.*, 2013; Chattopadhyay *et al.*, 2018). The experiment was repeated for four years (2011, 2012, 2017, 2018) taking susceptible check IR 29. *Saltol*-QTL derived from a Pokkali accession is a major QTL responsible for salinity tolerance at seedling stage. The UPGMA dendrogram and principal component analysis depicted that most of the salinity tolerant germplasm including 'Talmugur' from the 'Sunderbans' area were genetically closer to each other. Among the tested genotypes, Talmugur showed the highest allelic dissimilarity with FL 478 (a derivative line from Pokkali with *Saltol* introgression), indicating its highest allelic mismatch with Pokkali in the *Saltol* – QTL region (Chattopadhyay *et al.*, 2013). These observations indicate the scope for identification of additional QTLs other than the *Saltol* from Talmugur for salt tolerance at early vegetative stage in rice. In addition to that this germplasm was found to have anaerobic germination ability along with salinity tolerance (NICRA2010-12).

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3. Chettivirippu (AC 39394) (IC0413613; INGR19035), a Rice (*Oryza sativa*) Germplasm Tolerant to Salinity Stress both at Seedling and Reproductive Stage

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Rice is grown in the coastal saline areas of Kerala, sometimes at below sea level under Pokkali and Kaipad systems of cultivation. Pokkali refers to a system of rice cultivation which is characterized by prolonged partial flooding, and farmers practicing rice cultivation with shrimp farming. Virippu refers to rice crop growing under 'Pokkali' system in the autumn season. The rice germplasm and pure line selection from the traditional cultivars and landraces in this region are found to have single or multiple abiotic stress tolerance genes. Earlier *Saltol*-QTL for salinity stress tolerance at seedling stage was identified from one of the accessions of Pokkali and was introgressed into high yielding rice background. But researchers are still searching for donors for the reproductive stage salinity tolerance which can introduce QTLs for substantial reduction in yield penalty under salinity stress. This accession of Chettivirippu (IC 413613, AC39394) was collected from the village-Thirumalabhagom, Dist. Alappuzha in Kerala. In repeated evaluation under control condition with salinity stress, EC= 12 dSm-1, it was found tolerant (SES score- 3) to salinity at early vegetative stage. Most importantly it was also found moderately tolerant (<50% yield reduction) to salinity stress at reproductive stage.

Morpho-agronomic characteristics: This germplasm has intermediate seedling vigour. In coleoptiles, anthocyanin colouration is absent. Basal leaf sheath colour is green. Leaf blade colour is medium green. Leaf is pubescent. It is medium duration (days to 50% flowering is 101), tall (140 cm) and having medium tillering ability (8.5). It has medium, semi-erect and well exserted panicle (23.5cm).It has medium bold grain with grain length-breadth ratio of 2.96 and test weight of 27.5 g (Table 1). The grain yield is around 2.5 t/ha under moderate (6 dSm-1) salinity stress condition.

Table 1. Minimal Descriptors for characterization and evaluation of rice germplasm, Chettivirippu (AC 39394; IC 413613)

Characteristics	*Kharif* 2017	*Kharif* 2018	Mean value
Early plant vigour	Intermediate	Intermediate	Intermediate
Coleoptile: Anthocyanin colouration	Absent	Absent	Absent
Basal leaf sheath colour	Green	Green	Green
Leaf blade colour	Medium green	Medium green	Medium green
Leaf Pubescence	Pubescent	Pubescent	Pubescent
Leaf length (cm)	63.2	60.5	61.85
Leaf width (cm)	1.02	1.03	1.03
Days to 50 % flowering	100	102	101
Panicle exsertion	Well exserted	Well exserted	Well exserted
Stigma colour	White	White	White
Apiculus colour	Straw	Straw	Straw
Number of effective tillers	8	9	8.5
Plant height (cm)	139.0	140.0	139.5
Panicle length (cm)	23.0	24.0	23.5
Panicle type	Semi-erect	Semi-erect	Semi-erect
Awning	Short partially awned	Short partially awned	Short partially awned
Days to maturity	132.0	134.0	133.0
Seed coat colour (kernel colour)	Light brown	Light brown	Light brown
Grain length breadth ratio	2.92	3.0	2.96
100 grain weight (g)	2.6	2.9	2.75
Hull colour (husk colour)	Brown	Brown	Brown

Table 1 Contd.

Characteristics	*Kharif* 2017	*Kharif* 2018	Mean value
Threshability	Easy	Easy	Easy
Aroma	Absent	Absent	Absent
Grain yield per plant (g)	30.7	31.9	31.3
Abiotic Note	Tolerant to salinity stress (12 dSm^{-1}) at seedling stage and moderately tolerant to salinity (8 dSm^{-1}) at reproductive stage	Tolerant to salinity stress (12 dSm^{-1}) at seedling stage and moderately tolerant to salinity (8 dSm^{-1}) at reproductive stage	Tolerant to salinity stress (12 dSm^{-1}) at seedling stage and moderately tolerant to salinity (8 dSm^{-1}) at reproductive stage

Associated characters and cultivation practices: Chettivirippu (AC39394) was found tolerant (SES score = 3) to salinity stress (EC 12 dSm^{-1}) at seedling stage. Its tolerance was associated with low ratio of Na-K (0.20) in shoot (CRRI Annual report 2011-12; NICRA, 2012; Nath *et al.*, 2013). The findings related to AC 39394 have been validated by repeating the experiment in *kharif* 2017 and *kharif* 2018. Chettivirippu (AC39394) was found moderately tolerant to salinity stress at flowering stage (NICRA, 2012; Chattopadhyay *et al*, 2013) with yield reduction much below 50%. This germplasm is detected as a unique germplasm which posses tolerance to salinity stress at both seedling stage and at reproductive stage. This germplasm is being utilized in breeding for tolerance to both seedling and reproductive stage.

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4. RP5972-13-1-6-67-129-266 (IC0632071; INGR19036), a Rice (*Oryza sativa*) Germplasm Tolerant to Low Soil Phosphorous Condition in the Background of MTU1010 with about 95.2% Background Recovery of the Recurrent Parent Genome and Yields More than MTU1010

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MTU1010 (also popularly called as Cotton Dora Sannalu), is a high yielding, short duration, elite mega-variety of rice cultivated across the country but does not perform well in soils which are low in available Phosphorus (for e.g. upland rice). In order to improve MTU1010 for its tolerance to low soil phosphorus (P), marker assisted back cross breeding (MABB) approach was deployed to transfer *Pup1*, a major QTL/gene associated with tolerance to low soil P from Swarna, a high yielding, long duration variety. In screening studies carried out earlier in a low soil P plot of ICAR-Indian Institute of Rice Research (ICAR-IIRR), Hyderabad, MTU1010 was observed to be highly sensitive to low soil P levels, while Swarna showed high level of tolerance. A cross was made between Swarna and MTU1010 during Kharif 2012 and the heterozygous F_1s (identified using parental polymorphic SSR marker, RM206) were backcrossed with MTU1010 to generate a total of 253 BC_1F_1s. They were then screened using the gene-specific markers for *Pup1*, viz., K46-1 (a dominant functional PCR-based marker) and K20-2 (a co-dominant PCR-based marker, which is closely

Table-1. Agro morphological traits of RP5972-13-1-6-67-129-266 MTU1010 NIL both in Normal and Low soil P.

Traits	MTU1010 parental line growing in Normal soil P (32ppm)	MTU1010- NIL (RP5972-13-1-6-67-129-266) growing in Normal soil P (32ppm)	MTU1010 parental line growing in Low soil P (3-5 ppm)	MTU1010- NIL (RP5972-13-1-6-67-129-266) growing in Low soil P (3-5 ppm)
Plant height (Including panicles) (cm)	91.77±0.43	101.37±0.09	69.33±0.59	81.10±0.29
Number of productive tillers (No.s)	15±0.33	20±0.33	4±0.33	8±0.67
Panicle length (cm)	21.40±0.06	24.13±0.54	15.57±0.41	23.17±0.20
Root length (cm)	29.12±0.69	31.70±0.64	18.10±0.15	32.97±0.23
Root volume (cc)	68.57±1.13	71.53±0.55	14.53±0.61	30.60±1.04
Grain yield per plant (gm)	30.60±0.53	36.73±0.27	4.16±0.07	18.03±0.18

linked to *Pup1* locus) to identify the BC_1F_1 plants (n = 129), which are heterozygous for *Pup1*. Such plants were then screened with a set of parental polymorphic SSR markers to identify a single positive BC_1F_1 plant possessing maximum introgression of the recurrent parent genome (~ 82 % recovery). This plant was then crossed with MTU1010 to generate BC_2F_1s. The process of marker-assisted backcrossing as explained above was repeated in BC_2F_1 generation, wherein a single *Pup1* positive plant possessing maximum recovery of the recurrent parent genome (i.e. MTU1010 genome) was identified (possessing 95.2% recovery) and selfed to generate BC_2F_2s. Plants homozygous for *Pup1* were identified at BC_2F_2 generation (n = 32) with the help of the gene-specific co-dominant marker, K20-2 and reconfirmed with the dominant functional marker K46-1 and they were further advanced through selfing till BC_2F_7 generation by adopting pedigree method of breeding. Phenotypic screening of ten selected BC_2F_7 lines of MTU1010 possessing *Pup1*was carried in the Low soil-P plot and normal plot of ICAR-IIRR, Hyderabad during *Kharif* 2015. One of the near-isogenic lines, RP5972-13-1-6-67-129-266 showed similar or significantly better performance in the both low-P and normal soil-P in comparison with MTU1010 in terms of several growth and yield related parameters (Table-1; Figure-1). This line can be cultivated by MTU1010 farmers in areas where there is low soil P and also where the soil P levels are normal, thus reducing the application of P fertilizers by 25-30 %. Further, the breeding line can also be used as a promising donor for quick transfer for *Pup1* into other rice varieties.

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5. IC121865 (IC0121865; INGR19037), Rice (*Oryza sativa*) Germplasm Resistant to Blast Disease

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Rice blast is the most devastating fungal disease of rice caused by *Magnaporthe oryzae* that occurs all over world. It routinely causes 10–30% yield losses, and in severe cases can result in complete losses in major rice-production areas (Zhao *et al*., 2018). *M. oryzae* can infect most parts of the plant, but infections of the panicle neck node or the panicle are the most damaging phases of the disease with reports of the disease occurring in more than 85 countries. When *M. oryzae* infects rice and produces symptoms of neck rot or panicle blast, normal panicle and seed development is inhibited (Devi *et al*., 2015). Due to the severity of disease, genetics of plant pathogen interaction has been studied thoroughly and several blast resistance genes have been identified, characterized and deployed in breeding. But due to high pathogen plasticity in the field, identification of new sources of blast resistance may be of immense importance to pathologists and breeders for further exploration of pathogen resistance mechanism in the crop and as a trait donor in the breeding program.

htrhUnder CRP-agrobiodiversity, 1,214 accessions of rice germplasm were screened for resistance to blast disease during *Kharif* 2016 at four AICRIP Centres i.e., VPKAS, Almora, TNAU, Coimbatore, CRURRS, Hazaribagh and IIRR Hyderabad. Germplasm was evaluated under field conditions at Almora and Hazaribagh and under controlled conditions at other locations. Location Severity Index ranged from 5.6 to 7.0 in different locations. Thirteen accessions (IC245865, IC246277, IC246403, IC246274, IC454167, IC121865, IC199562, IC218270, IC245927, IC246012, IC246228, IC246273 and IC246659) were found resistant across the locations. All the resistant accessions are indigenous and were collected from Punjab, Rajasthan and Andhra Pradesh.

The accession IC121865 collected from Rajasthan was found resistant to rice blast. Identified material can be used as donor for blast resistance in breeding program.

Screening of Rice germplasm under CRP- Agrobiodiversity project during *Kharif* 2016*

Accession Id	Location	Field/Controlled	Location Severity Index	Susceptibility Index	Promising Index
IC121865	VPKAS, Almora	Field	6.4	3.5	100
	TNAU, Coimbatore	Controlled	5.6		
	CRURRS, Hazaribagh	Field/Controlled	5.7		
	IIRR, Hyderabad	Controlled	7.0		

*Based on ICAR-IIRR AICRIP Annual Progress Report 2016, Vol 2, Plant Pathology

6. IC0199562 (IC0199562; INGR19038), Rice (*Oryza sativa*) Germplasm Resistant to Blast Disease

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Rice blast is the most devastating fungal disease of rice caused by *Magnaporthe oryzae* that occurs all over world. It routinely causes 10–30% yield losses, and in severe cases can result in complete losses in major rice-production areas (Zhao *et al*., 2018). *M. oryzae* can infect most parts of the plant, but infections of the panicle neck node or the panicle are the most damaging phases of the disease with reports of the disease occurring in more than 85 countries. When *M. oryzae* infects rice and produces symptoms of neck rot or panicle blast, normal panicle and seed development is inhibited (Devi *et al*., 2015). Due to the severity of disease, genetics of plant pathogen interaction has been studied thoroughly and several blast resistance genes have been identified, characterized and deployed in breeding. But due to high pathogen plasticity in the field, identification of new sources of blast resistance may be of immense importance to pathologists and breeders for further exploration of pathogen resistance mechanism in the crop and as a trait donor in the breeding program.

Under CRP-agrobiodiversity, 1,214 accessions of rice germplasm were screened for resistance to blast disease during *Kharif* 2016 at four AICRIP Centres i.e., VPKAS, Almora, TNAU, Coimbatore, CRURRS, Hazaribagh and IIRR Hyderabad. Germplasm was evaluated under field conditions at Almora and Hazaribagh and under controlled conditions at other locations. Location Severity Index ranged from 5.6 to 7.0 in different locations. Thirteen accessions (IC245865, IC246277, IC246403, IC246274, IC454167, IC121865, IC199562, IC218270, IC245927, IC246012, IC246228, IC246273 and IC246659) were found resistant across the locations. All the resistant accessions are indigenous and were collected from Punjab, Rajasthan and Andhra Pradesh.

The accession IC199562 collected from Rajasthan was found resistant to rice blast. Identified material can be used as donor for blast resistance in breeding program.

Screening of Rice germplasm IC199562 under CRP- Agrobiodiversity project during *Kharif* 2016*

Location	Field/Controlled	Location Severity Index	Susceptibility Index	Promising Index
VPKAS, Almora	Field	6.4	3.5	100
TNAU, Coimbatore	Controlled	5.6		
CRURRS, Hazaribagh	Field/Controlled	5.7		
IIRR, Hyderabad	Controlled	7.0		

*Based on ICAR-IIRR AICRIP Annual Progress Report 2016, Vol2, Plant Pathology

7. NH219 (RP Bio 5477-NH219) (IC0632074; INGR19039), a Rice (*Oryza sativa*) Mutant with Higher Yield than Nagina22 in Normal and High Temperature Conditions. Dark Green Leaves, Drought Tolerant

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Mutants are valuable resources for genetic variations in crop improvement. Nagina 22 (N22) is an early maturing drought and heat tolerant *aus* variety. NH219 is Ethyl Methane Sulphonate (EMS) induced mutant of variety Nagina 22 The mutant was developed as part of a DBT funded project "Characterization and use of EMS induced mutants of rice variety N22 for yield, drought and phosphorus use efficiency" at IIRR. The mutant was identified in M3 generation as one of the four dark green leaf (*dgl*) mutants which survived under prolonged drought and high temperature stress in *rabi* season upto tillering stage in DRR (now IIRR) field conditions tested for two years 2011, 2012. Histochemical staining showed that there was negligible ROS accumulation in cut leaves of NH219 heat treated at 40C for 72h compared to N22 (Panigrahy *et al.*, 2011). Later, heat tolerance was evaluated in lab conditions at seed germination and seedling growth stage at 30C and 40C and NH219 was better than N22 in heat tolerance parameters such as %germination, chlorophyll stability, leaf senescence index and the ability to keep dry weight same at 30C and 40C. (Prasanth *et al* 2012). When field evaluated in DRR, the yield decrease under heat stress was 33% in N22 but only 23% in NH219. Under severe heat conditions in heat tunnel in summer (*Rabi* 2014) N22 and NH219 were the only lines which set seed. N22 gave 2.30g/plant and NH219 gave 2.92g/plant out of several lines tested. NH219 was also tested in multi-location trials conducted by AICRIP Physiology in 2016 at 7 locations with uniform facility for field testing for heat tolerance (Hyderabad, Pantnagar, Pattambi, Rewa, Maruteru, Titabar and Chinsurah) keeping Gontra Bidhan3as National Check. NH219 gave mean yield of 385g/m2 in heat conditions with only 13.09% decrease over normal. Gontra Bidhan3 gave 460g/m2 in heat conditions with 25.2% decrease over yield in normal conditions. In multilocation trials too NH219 showed 13% decrease in yield under heat conditions at par with National Check Gontra Bidhan3 in 2016. NH219 is also tolerant to low Phosphorus in soil, has high Photothermic Index and radiation use efficiency based on AICRIP report 2013. It has dark green leaves and a high SPAD value of 39-40 compared to 30 of N22.

Process of development of NH219: M1 seeds of Nagina22 (N22) were provided to IIRR as part of the DBT Network Project on Characterization of EMS induced N22 mutants of rice to screen and characterize for several agronomic traits. M1 seeds were grown in normal conditions and M2 seed collected from each M1 plant. M2 and M3 were tested in normal and stress (drought and heat) conditions. Seeds harvested from normal conditions were used each year for screening under stress. These mutants are now in M13 and were advanced from panicle to seed mutant wise each season. Mutant line NH219 is a stable elite genetic stock for tolerance to high temperature as it shows less yield decrease in heat. It gives higher yield than N22 under normal or heat conditions.NH219 has darker seed and apiculus than N22. It has dark green leaves and panicle is well exserted with long peduncle.

8. NH162 (RP Bio 5477-NH162) (IC0632599; INGR19040), a Rice (*Oryza sativa*) Germplasm Tolerant to Drought, with Higher Yield than Nagina22 in Normal, Drought and Aerobic Conditions. Functionally Stay Green with Dark Green Leaves, Drought Tolerant, Higher Yielder in Aerobic Condition. Seed Hull Dark and Seed Type Slender

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Mutants are valuable resources for genetic variations in crop improvement. Nagina 22 (N22) is an early maturing drought and heat tolerant *aus* variety. NH162 is Ethyl Methane Sulphonate (EMS) induced mutant of variety N22. The mutant was developed as part of a DBT funded project "Characterization and use of EMS induced mutants of rice variety N22 for yield, drought and phosphorus use efficiency" at IIRR from 2007-2012. The mutant was identified in M3 generation as one of the four dark green leaf (*dgl*) mutants which survived under prolonged drought and high temperature stress in *rabi* season upto tillering stage in DRR (now IIRR) field conditions tested for two years 2011, 2012 . Later drought tolerance was evaluated in field condition during 2010 and 2011. Grain yield was 2-fold higher than N22 under normal, water limited conditions in field. NH162 is the stable mutants and high yielding mutant under both normal and water limited conditions. Histochemical staining showed that there was negligible ROS accumulation in cut leaves of NH162 heat treated. The mutant was stay green, dwarf, with higher tiller number, stem thickness, late duration with higher grain yield when compared with N22 under normal condition. The grains of NH162 has darker than N22. When field evaluated in DRR, the yield decrease under water limited condition was 42% in N22 but only 25% in NH162. During the dark induced senescence with cytokinin 6-benzyl adenine (BA), N22 showed rapid reduction in the Chl a/b ratio, chlorophyll content than NH162 where with and without 6BA treatment the chlorophyll content of NH 162 is not significantly different. Chl analysis revealed that Chl a/b ratios and Fv/Fm values were maintained during dark induced senescence (DIS) in N22-H-*dgl*162 [RPBio5477-NH162] and BA-treated N22 leaves. The non-denaturing green gel analysis was performed to study the effect of senescence and BA on stability of chlorophyll complexes. In the untreated leaves at 0 h, three distinct major bands representing the RC–LHC complex, the LHCs, and free pigments were observed. In the untreated N22 leaves, the complexes were drastically reduced by 72 h of DIS and degraded by 96 h of DIS, whereas all the bands remained intact in NH162 and BA-treated N22 leaves after 96 h of dark induced senescence. The mutant NH162 along with N22 were tested for drought tolerance at seeding stage. In N22 plants, leaf rolling appeared on the fifth day after withholding water, and the leaves became wilted on the eighth day, whereas in NH162, leaf rolling appeared on tenth day and wilted on the 14 day. On the 8th day for N22 and 14th day for NH162 recovery of plants was attempted by rewatering, and the recovery time was recorded on 24 hours after rewatering. NH162 plants recovered in 16-20 hours of rewatering, N22 plants recovered after 2 days of rewatering . Apart from these traits, NH162 is a loss of function mutant under very low P condition. Nine SSR markers RM260, RM206, RM215, RM224, RM242, RM252, RM205, RM1920, RM1 had polymorphism between N22 and NH162.

NH162 was also tested in multi-location trails conducted by AICRIP aerobic condition in 2016 and 2017 at 16 locations and 57 entries along with three checks. The grain yield was ranged from 1506 to 6330 kg/ha. NH162 performed better than hybrid (IIRRH 111-2 and best check CRR Dhan 21 in most of the locations. The mean panicle no/m^2 is 314. This mutant was performed well over checks in zone III (CTK, BBN, BKG, SBR, PTN, BI, JH, UP). In the year 2017 the variety was tested again in AVT-1 in Zone 3 it was ranked 3 among the 20 entries and 3 checks with grain yield of 5200 kg/ha NH162 is resistant to sheath rot and bacterial leaf blight. NH162 scored 1 in GDL location for brown spot, 1 for sheath rot location MTU, 1 for bacterial leaf blight in PNT and NWG. It has dark green leaves and a high SPAD value of 39-42 when compared to 28 of N22 in dry bed condition.

Process of development of NH162: M1 seeds of Nagina22 (N22) were provided to IIRR as part of the DBT Network Project on Characterization of EMS induced N22 mutants of rice to screen and characterize for several agronomic traits. M1 seeds were grown in normal conditions and M2 seed collected from each M1 plant. M2 and M3 were tested in normal and stress (drought and heat) conditions. Seeds harvested from normal conditions were used each year for screening under stress. These mutants are now in M13 and were advanced from panicle to seed each season. Mutant line NH162 is a stable elite genetic stock for tolerance to water limited condition and also for high temperature (unpublished data for high temperature) as it shows 16% and 36% less yield decrease in both drought and heat. It gives higher yield than N22 under normal or drought conditions. NH162 has dark green leaves, higher tiller number, more stem thickness. The panicle length (range 16-20) and number of grains are almost double (range140-160) in the mutant.

9. RP Bio 4918-230S (IC0632075; INGR19041), a Rice (*Oryza sativa*) Germplasm with Resistance to Brown Planthopper (BPH) *Nilaparvata lugens*. Possesses High Resistance at Vegetative and Reproductive Stages

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Rice is the principal food crop in India and is grown in an area of ~ 44 Million hectares and with a production of ~100 Million metric tonnes. Rice production is limited by various biotic and abiotic stresses of which insects are estimated to cause 21-30% yield loss. Among the insect pests, rice brown planthopper (BPH) *Nilaparvata lugens* (Stal) (Delphacidae: Hemiptera) is very serious pest which causes severe yield losses upto 100% under severe hopper burn situations.

The large scale cultivation of dwarf, early maturing, photoperiod insensitive, high tillering and high yielding rice cultivars coupled with the increased use of nitrogenous fertilizers had become congenial for brown planthopper infestation in farmers' fields. All growth stages of rice plant right from seedling to maturity stage are affected. Nymphs and adults stay at the base of the plant and damage the crop by sucking phloem sap which results in yellowing of leaves, reduced tillers and plant height, unfilled grains and death of the plant. Damage is more severe in reproductive stage of crop wherein round yellow patches appear in the field which later turns brownish due to drying of plants called as hopper burn. The patches of infestation may spread in the entire field, coalesce together and in severe cases complete destruction of crop occurs.

Since1970's several devastating BPH epidemics have been reported and now outbreaks of brown planthopper have become common and severe. Many insecticides are suggested for the control of this pest, but application of these chemicals interrupts the natural balance of rice ecosystem. Cultivation of resistant varieties is the better and environmentally safe substitute. Hence, breeding programme for development of BPH resistant varieties with different modes of host plant resistance (such as antixenosis, antibiosis and tolerance) is extremely important.

More than 30 genes and QTLs have been identified from cultivated and wild species introgression lines. Most of the genes for BPH resistance identified so far are against biotypes 1,2 and 3 and only few are resistant against biotype 4, which could be one of the reason for their ineffectiveness against BPH biotype which is most destructive and is distributed over the Indian sub-continent. Many of the donors which showed stable resistance across the biotypes have one or two major genes along with QTLs associated with resistance. Hence, it is important to identify new donors, novel genes/major QTLs effective against BPH biotype4 to pyramid them for stable resistance. The genes from wild rices are reported to be robust and stable.

The wild species of *Oryza* representing AA, BB, CC, BBCC, CCDD, EE, FF, GG and HHJJ genomes are a rich reservoir of useful genes resistant to major biotic and abiotic stresses, more adapted to adverse and changing environmental conditions. The genetic variability for some of these stresses is restricted in the cultivated rice germplasm. Moreover, changes in insect biotypes are an enduring threat to increased rice production. There is thus a critical need to broaden the rice gene pool by introgressing genes for such traits from diverse sources. Therefore, it is important to discover these valuable genes hidden in wild rice species and use them in breeding programmes to develop resistant varieties. However, low crossability and limited recombination between chromosomes of cultivated and wild species limit the transfer of such genes. In addition, genes from wild rices are often linked with genes governing undesirable traits. So, development of advance back cross introgression lines is very essential, for selective transfer of only preferable genes and to avoid linkage drag. Creation of introgression lines using cultivated rice as recipient and wild rice as the donor is the most durable approach to explore primitive and broad genetic resources in rice breeding.

Most of the genes identified are based on the reaction at seedling stage but the maximum crop damage occurs at tillering and reproductive stage in farmer's field. Hence, it is necessary to know the effectiveness of donors/genes against BPH at later plant growth stages. Therefore, the present attempt was made to identifydonors for BPH resistance from introgression lines derived from *O.nivara* at seedling stage and also at maximum tillering and reproductive stage.

Process of development of RP Bio 4918-230S. With this background a set of backcross intogression lines were developed from one cross viz., Swarna/*O. nivara* (*accession no.* IRGC 81848 S) following single seed descent method. Swarna is a popular commercial variety susceptible to brown planthopper; *O. nivara* (*accession no.* IRGC 81848S) is a wild rice accession with AA genome. A backcross strategy was followed to develop the line RP Bio 4918-230S. A single plant of *O. nivara* (*accession no.* IRGC 81848 S) was used as a male parent and crossed to Swarna to generate F1 plants. These F1 plants derived from the cross between Swarna and *O. nivara* (IRGC 81848) were backcrossed to Swarna to produce BC1F1 plants. These BC1F1 plants were again backcrossed to Swarna to develop the BC2F1 generation. These BC2F1 were selfed till five generations to produce BC_2F_6 backcross introgression lines (BILs). 250 number of BILs were selected which were more like Swarna phenotypically and were screened for BPH resistance in the greenhouse and field conditions, out of which RP Bio 4918-230S and five more BILs were found resistant to BPH.

Phenotyping for Brown Planthopper Resistance: 250 number of BC_2F_6 backcross introgression lines (BILs) were screened for brown planthopper resistance by adopting mass screening test under controlled greenhouse conditions at Indian Institute of Rice Research. The method involved infestation of 12 day old young seedlings of the BILs grown in screening trays with BPH nymphs along with resistant (Ptb 33) and susceptible checks (TN1). When more than 90 per cent of TN1 plants were killed, the BILs were scored for the damage reaction, based on a 0-9 scale of Standard Evaluation System (SES). Out of the 250 number of BILs from Swarna/*O. nivara* screened, six BILs were found to be resistant and RP Bio 4918-230S was one of the BILs with brown planthopper resistance with a damage score of 1.8. Swarna and the susceptible check (TN1) recorded a damage score of 9, the resistant check PTB 33 recorded a damage score of 1.2 (Jhansi lakshmi *et al*., 2010) Fig 2 (a,b,c). The RP Bio 4918-230S was screened along with germplasm accessions in 2012 in DRR greenhouse and was found to be resistant with a damage score of 1.0 (Akanksha *et al*., 2017).

This BIL RP Bio 4918-230S was screened for brown planthopper resistance in the multilocation testing in 2010 in planthopper screening nursery (PHS) and performed better and promising in 6 out of 13 tests/locations and recorded damage score of <5 in two locations (total 8 viz., DRR, Coimbatore, Mandya, Raipur, Ludhiana, Madurai and Gangavathi out of 13 locations) (Table 1).The susceptible check TN1 recorded a damage score of 9 and the resistant check PTB 33 recorded a DS of 1-5 (Ref: Screening nurseries 2010 AICRIP DRR and Progress report 2010 AICRIP DRR, DRR Annual report 2010-11). In 2011, RP Bio 4918-230S was retested in planthopper screening nursery (PHS) and was found promising in four locations viz., DRR, Coimbatore, Madurai and Raipur (Ref: Screening nurseries 2011 AICRIP DRR and Progress report 2011 AICRIP DRR, DRR Annual report 2011-12). In 2012, RP Bio 4918-230S was retested in Multiple Resistance Screening Trial (MRST) and was found promising in four locations viz., Cuttack, Ludhiana and Raipur (Ref: Screening nurseries 2012 AICRIP DRR and Progress report 2012 AICRIP DRR, DRR Annual report 2012-13). In DRR, RP Bio 4918-230S was evaluated in 2012 in the field for planthopper reaction under hopperburn conditions and was found to be resistant in the tillering and reproductive stage (DRR Annual report 2012-13). The resistant check PTB 33 was resistant and susceptible check TN1 was completely susceptible with a damage score of 9. In APRRI-RARS Maruteru, the introgression line RP Bio 4918-230S was evaluated in 2014 in the field under natural infestation and it was found to be resistant.

Simultaneously RP Bio 4918-230S was evaluated for agronomic traits and quality traits and physiological parameters. It is a semi dwarf, mid duration culture (140 days) possessing medium grains. Quality wise it recorded medium head rice recovery (HRR) of 45% and intermediate amylose content (Table 2).

It has high photosynthetic efficiency (P_N)23.1 µmol CO_2 m^{-1} s^{-1}, Chlorophyll a 3.48 (mg/g), Chlorophyll b 1.26 (mg/g), total Chlorophyll 4.86 (mg/g) and Carotinoids 0.96 (mg/g) compared to the parents Swarna and *O. nivara* (Table 3) (Haritha *et al*., 2019).

It has given an yield advantage of 5.8% in zone 7 and an yield advantage of 9% over hybrid check PA 6444 in AICRIP IVT late trials (unpublished report).

This line could be used as elite genetic stock for resistance to brown planthopper (BPH), Nilaparvata lugens. It has resistance in seedling, vegetative and reproductive stages. It could be involved as donor parent in hybridization program for developing resistant varieties for brown planthopper**.**

Table 1. Reaction of RP Bio 4918-230S to BPH under natural and artificial infestation during 2009- 2014

Year/ location		2009	2010 PHS	2011 PHS	2012 MRST	2012	2014											
		DRR	DRR	CBT	MND	RPR	LDN	MDR	GGV	DRR	CBT	MDR	RPR	CTC	LDN	RPR	DRR	MTU
Greenhouse	RP Bio 4918-230S	1.8	4.5	5	1	1	1.6			5.2	3	3	0.3	1.0	1.2	0.6		
	PTB 33	1.4	1.7	5	1	1.3	1.5			1.7	5	4	0					
	TN1	9	9	9	9	9	9			9	7	8	9	9	7.7	9		
	Swarna	9																
Field	RP Bio 4918-230S				10%hb			0 DS	0/HILL								1	1
	PTB 33				5%hb			3 DS	25/ HILL								1.6	
	TN1				80%hb			9	34/ HILL								9	

DRR: Directorate of Rice Research, CBT: Coimbatore, MND: Mandya, RPR: Raipur, LDN: Ludhiana, MDR: Madurai, CTC Cuttack, MTU: Maruteru and GGV: Gangavathi

Table 2. Morphological characters of RP Bio 4918-230S and Swarna

Name of the variety	:	RP bio 4918-230S	Swarna
Plant height	:	81.42	101.27
Plant type	:	short	semidwarf
No. of tillers /plant	:	15.83	11.6
Days to 50% flowering	:	109.2	119.2
Seed to seed duration	:	139.15	148.15
Panicle type	:	Compact	Compact
No. of panicles /plant		13.17	10.64
Panicle exsertion	:	Well exserted	Well exserted
Panicle weight		2.03	2.65
Awning	:	present	absent
Yield/plant (g)		16.53	18.57
1000 grain weight	:	18.6g	15.1g
Kernel length	:	7.43	6.3mm
Kernel breadth	:	2.58	2.1mm
L/B ratio	:	2.88	3
Grain type	:	Medium	Medium
Kernel appearance	:	Grain chalkiness absent	Very occasionally chalky

Name of the variety	:	RP bio 4918-230S	Swarna
Hulling recovery		75.6%	73.9%
Milling recovery	:	65.3%	68.6%
Head rice recovery (HRR)	:	44.9%	56.3%
Alkali spreading value (ASV)	:	4	5
Amylose content (AC)	:	25.5%	26.54%
Gel consistency	:	31 mm	43 mm
Yield potential		5.45t/ha	5.5-6.0 t/ha

Table 3. Physiological characters of RP Bio 4918-230S and Swarna

Name of the variety	:	**RP bio 4918-230S**	**Swarna**
Photosynthetic efficiency (P_N) µmol CO_2 m^{-1} s^{-1}	:	23.1	14.58
Chlorophyll a (mg/g)	:	3.48	3.24
Chlorophyll b (mg/g)	:	1.26	1.06
Total Chlorophyll (mg/g)	:	4.86	4.3
Carotinoids (mg/g)	:	0.96	0.91

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10. BH 1146 (IC0415843; INGR19042), a Wheat (*Triticum aestivum*) Germplasm Tolerant to Waterlogging and Resistant to Spot Blotch

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Bread wheat (*Triticum aestivum L.*) genotype BH 1146 (Fronteira/Mentana//Ponta Grossa1) was selected and identified following method of breeding as selection from introduction. In a series of field experiments conducted under normal and waterlogged soils during four years (2012-2016), the proposed genotype (BH 1146) was rated as highly tolerant for waterlogged soil conditions. The genotype was identified based on stress tolerance index and lowest percent reduction under water logged conditions as compared to normal conditions (Table 1

& 2). Therefore, BH 1146 will be a potential source to be used as a donor to incorporate genes which will be suitable for higher production and productivity even under heavy rainfall and prolonged water stagnant situations. It is important to mention that the incidence of spot blotch disease of wheat is very high under such wet conditions which also affects the yield as well as grain quality.

Table 1. Selection indices (WL tolerance) and salient agro-morphological features of BH 1146.

Parameters	BH 1146	DBW 88 (best check among top 15 entries)
Stress tolerance index (STI)	0.778	0.746
Harmonic mean (HM)	893	850
Geometric mean productivity (GMP)	896	878
Mean relative performance (MRP)	2.58	2.45
Yield stability index (YSI)	0.837	0.602
Reduction percent	16.3	39.8

Table 2. Performance of BH 1146 and other wheat genotypes under non-waterlogged (NWL) and waterlogged (WL) conditions (unpublished data).

Genotype	Plant height		Days to maturity		Tillers/meter		100 grain weight		Grain yield/plot	
	NWL	WL	NWL	WL	NWL	WL	NWL	WL	NWL	WL
BH 1146	130	120	146	152	121	54	36	31	321	191
DBW 39	98	82	143	149	97	22	36	16	391	104
HD 2967	86	73	141	149	118	22	34	12	360	106
DBW 14	69	61	144	149	35	23	36	23	305	107
DBW 17	83	82	141	147	123	22	33	20	298	145
HD 2009	85	79	142	148	95	22	32	20	309	137
KRL 3-4 (C)	121	108	142	149	196	23	39	31	224	117

Table 3. Reaction of BH 1146 and Sonalika against spot blotch disease across different locations/environments and years

Location/ Environment	Crop season	BH 1146 (Proposed genotype)	Sonalika (Susceptible check)
Coochbehar	2012-13	24	89
	2013-14	13	89
Kalyani	2012-13	24	89
	2013-14	24	89
Karnal	2012-13	13	79
	2013-14	13	79
Poly house (artificial epiphytotics)	2012-13	35	99
	2013-14	24	99

Coincidently, the proposed genotype has also been found as highly resistant to spot blotch disease across locations and years. The recombinant inbred lines (RILs) were developed cross Sonalika (susceptible) /BH 1146 (resistant) and were evaluated along with parents for spot blotch resistance at natural hot spot locations viz; Cooch behar and Kalyani (West Bengal) as well as under field and artificial epiphytotics conditions in poly house for two years. The phenotyping results revealed that BH 1146 possesses high degree of tolerance against spot blotch (Table 3).

The data presented in above two tables clearly established superiority of BH 1146 over susceptible checks and test entries for both the highlighted traits (Waterlogging and spot blotch) and thus proposed for registration as genetic stock. In view of the above merits, BH 1146 could be prospective genotype to be utilized as a donor parent for improving tolerance to waterlogging along with spot blotch resistance for the area spread over 11 million ha of area across northern India.

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11. RWP 2014-18 (IC0630581; INGR19043), a Short Duration Wheat (*Triticum aestivum*) Germplasm with High 1000-grain weight

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Delay in wheat sowing in NHZ and NWPZ results in poor tillering and crop growth is generally slow due to low temperature. High temperature during grain filling stage also affects grain yield. For ameliorating these problems, the short duration varieties having plasticity for sowing period, resistance to yellow rust and tolerance to terminal heat stress are required.

RWP 2014-18 was from a cross DBW22/DBW30 through modified pedigree method of breeding. It was evaluated for three years (2015-16, 2016-17 and 2017-18) in Short Duration Screening Nursery (SDSN) of AICW&BIP. Under late sown conditions of NHZ, RWP2014-18 showed consistently superior yield performance over all the checks varieties.

RWP 2014-18 had significantly higher yield compared to all the checks with three year average mean yield of 330 g/plot compared all the checks viz. WR 544 (238 g/plot), HD2932 (227 g/plot), Sonalika, (227 g/plot), and NIAW34 (260g/plot).RWP 2014-18 is early flowering and early maturing genotype with days to heading of 110 which is at par with checks and matures in 152 days after sowing on an average n NHZ. It also has high grains per spike (av. 46) very high 1000 grain weight of 50g under late sown condition.

Table 1. Mean performance of RWP2014-18 in SDSN identified for earliness and high yield in NHZ during three years of evaluation (2015-16, 2016-17 and 2017-18)

Trait	Genotype	Checks			
	RWP 2014-18	Sonalika	WR544	HD2932	NIAW34
Mean Yield (g/plot)	330	227	238	227	260
Heading days	110	107	106	111	109
Maturity days	152	154	152	155	154
Grains/spike	46	37	44		
1000 gr. wt.	50	46	43	46	44

12. IC0529962 (IC0529962; INGR19044), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Spot Blotch (*Bipolaris sorokinina*). Stability for Grain Yield Performance

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Spot blotch disease leads to significant yield losses ranging from 18 to 50% in warm and humid regions of the world comprising Eastern India, Bangladesh, Terai region of Nepal, Latin America, China and Africa (Saari 1998; Singh *et al*., 2007; Gurung *et al*., 2014). Besides, losses in grain yield, leaf blight causes seed discoloration, shriveled seeds and loss in seed viability. In order to reduce the yield loss, development of wheat varieties with spot blotch resistance is priority of wheat breeders and therefore search of novel donor for spot blotch resistance is urgently required.

Under CRP-agrobiodiversity, one thousand four hundred and eighty-three spring wheat germplasm (*Triticum aestivum* L.) lines comprising Indian as well as exotic lines were screened for resistance to spot blotch disease during winter 2014-15 at hot spot locations *i.e.*, Banaras Hindu University, Varanasi and Uttar Banga Krishi Vishwavidyalaya, Cooch Behar. Severity of the disease at different stages beginning from tillering to dough stage was recorded. Twenty-eight accessions were resistant or highly resistant at both locations. These 28 accessions were validated during the winter season (2015-2016). These germplasms were also evaluated at four environments for agronomic traits. Out of 28 accessions, seven (IC564121, IC529684, IC443669, IC443652, IC529962, IC548325 and EC178071-331) were highly resistant across the locations and over the years of study (Kumari *et al*., 2018) and also confirmed under controlled condition during year 2017-18 at Division of Plant Pathology, IARI, New Delhi. These accessions comprised one exotic and six indigenous accessions belonging to Uttarakhand and Haryana. These lines can be deployed for identification of resistance gene and genomics study and also may be used in the breeding germplasm. Out of these, the accession IC529962 had at par mean yield as best check and had wider adaptability across the locations hence can be expedited for direct cultivation or for the development of high yielding and disease resistant cultivars.

Table 1. Spot blotch resistant germplasm with their disease reaction, maturity and yield

Accessions	Name/Source	Grain Yield (g/m row length)	Thousand Grain Weight (g)	Days to Maturity	Mean AUDPC value	DS (High)	DS (Av.)	Category
IC564121	Lal mundiya/ Pauri, Uttarakhand	91.90±7.18	25.78±1.75	122	362±13	23	13	HR
IC529684	VWFW-2299/Almora, Uttarakhand	117.90±11.44	28.30±1.62	127	79±17	23	12	HR
IC443669	PHR-1025/Karnal, Haryana	177.51±12.65	39.81±0.66	119	88±19	23	12	HR
IC443652	HUW-549/Karnal, Haryana	121.23±4.18	39.75±0.71	117	77±16	24	13	HR
IC529962	Almora, Uttarakhand	105.13±6.05	25.78±1.71	121	92±20	12	12	HR
IC548325	Shimla, Himachal Pradesh	161.97±19.06	37.62±0.60	109	174±42	23	12	HR
EC178071-331	Mexico	104.06±8.29	32.73±1.23	114	325±19	24	13	HR
Sonalika	Susceptible check	70±5.46	36.87±1.49	123	2630±22	69	59	S
DBW39	Resistant check	114±6.69	37±1.34	125	583±12	35	24	R

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13. IC0529684 (IC0529684; INGR19045), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Spot Blotch (*Bipolaris sorokinina*)

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Spot blotch disease leads to significant yield losses ranging from 18 to 50% in warm and humid regions of the world such as Eastern India, Bangladesh, the Terai of Nepal, Latin America, China and Africa (Saari 1998; Singh *et al*., 2007; Gurung *et al*., 2014). Besides, losses in grain yield, leaf blight causes seed discoloration, shrivelled seeds and loss in seed viability. In order to minimize the yield loss and attain yield stability, development of spot blotch resistant wheat variety is priority of wheat breeders and therefore search of novel donor for spot blotch resistance is urgently required.

Under CRP-agrobiodiversity, one thousand four hundred and eighty-three spring wheat germplasm (*Triticum aestivum* L.) lines comprising Indian as well as exotic lines were screened for resistance to spot blotch disease during *Rabi* season 2014-15 at hot spot locations *i.e.*, Banaras Hindu University, Varanasi and Uttar Banga Krishi Vishwavidyalaya, Cooch Behar. Severity of the disease at different stages beginning from tillering to dough stage was recorded. Twenty-eight accessions were resistant or highly resistant at both locations. These 28 accessions were validated during the next *Rabi* season (2015-16). These germplasm were also evaluated at four environments for agronomic traits. Out of 28 accessions, seven (IC564121, IC529684, IC443669, IC443652, IC529962, IC548325 and EC178071-331) were highly resistant across the locations and over the years of study(Kumari *et al*., 2018) and also confirmed under controlled condition during year 2017-18 at Division of Plant Pathology, IARI, New Delhi. These accessions comprised one exotic and six indigenous accessions belonging to Uttarakhand and Haryana. These lines can be deployed for identification of resistance gene and genomics study and also in the breeding germplasm. Out of these, the accession IC529684had at par mean yield as best check and can be used for direct cultivation or for the development of high yielding and disease resistant cultivars.

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Table 1. Spot blotch resistant germplasm with their disease reaction, maturity and yield

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IC564121	Lal mundiya/ Pauri, Uttarakhand	91.90±7.18	25.78±1.75	122	362±13	23	13	HR
IC529684	VWFW-2299/ Almora, Uttarakhand	117.90±11.44	28.30±1.62	127	79±17	23	12	HR
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IC443652	HUW-549/Karnal, Haryana	121.23±4.18	39.75±0.71	117	77±16	24	13	HR
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IC548325	Shimla, Himachal Pradesh	161.97±19.06	37.62±0.60	109	174±42	23	12	HR
EC178071-331	Mexico	104.06±8.29	32.73±1.23	114	325±19	24	13	HR
Sonalika	Susceptible check	70±5.46	36.87±1.49	123	2630±22	69	59	S
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Singh G, DP Singh, R Chatrath, BS Tyagi, GP Singh, SK Singh, J Shoran (2007a) Combating *Helminthosporium* leaf blight in wheat through resistance breeding. *Indian Journal of Genetics and Breeding*.**67**(3): 293-296.

14. IC290150 (IC0290150; INGR19046), a Wheat (*Triticum aestivum*) Germplasm Resistant to Stem Rust, Leaf Rust and Stripe Rust Pathotypes Prevalent in Indian Condition. Based on Linked Marker Analysis Germplasm has Combination of Different Leaf Rust, Stem Rust, Stripe Rust and Spot Blotch Resistance Genes *Lr*46+, *L*r67+, *Yr*5, *Yr*15, *Yr*36, *Yr*48, *Sr*13, *Sr*24/*Lr*24, QSb.bhu-2B

S Kumar[1], S Archak[1], RK Tyagi[1], J Kumar[2], VK Vikas[3], AK Sharma[4], J Kumari[1], S\R Jacob[1], R Parimalan[1], AK Singh[1], KC Bansal[1], Ashok Kumar[1], M Sivasamy[3], P Jayaprakash[3], SC Bhardwaj[5], MS Saharan[6], R Gogoi[6], K Singh[1] and GP Singh[4]

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A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of rust and spot blotch resistance.Genebank accessions comprising three species of wheat–*Triticum aestivum, T. durum* and *T. dicoccum* were screened sequentially at multiple disease hotspots, during the 2011-14 crop seasons, carrying only resistant accessions to the next step of evaluation. Wheat accessions which were found to be resistant in the field were then assayed for seedling resistance and profiled using molecular markers. In the primary evaluation, 19,460 accessions were screened at Wellington (TamilNadu), a hotspot for stem and leaf rusts. We identified 4925 accessions to be resistant and these were further evaluated at Gurdaspur (Punjab) a hotspot for stripe rust and Cooch Behar (West Bengal), a hot spot for spot blotch. A second round evaluation identified 498 accessions potentially resistant to multiple rusts and 868accessions resistant to spot blotch. Evaluation of rust resistant accessions for seedling resistance against seven virulent pathotypes of three rusts under artificial epiphytotic conditions identified 137 accessions with multiple disease resistance. Molecular analysis to identify different combinations of genetic loci imparting resistance to leaf rust, stem rust, stripe rust and spot blotch using linked molecular markers, identified 45 wheat accessions containing resistance genes against all three rusts as well as a QTL for spot blotch resistance. Among identified 45 germplasm lines, germplasm line IC290150 which showed the presence of resistance genes for stem rust, leaf rust and stripe rust and spot blotch *Lr46+, Lr67+, Yr5, Yr15, Yr36, Yr48, Sr13, Sr24/Lr24, QSb.bhu-2B* 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.

The evaluation detail for the genebank accessions during years 2011-14 is being presented in the diagram mentioned below. In addition, this germplasm line was also found resistant to all three rusts under NBPGR multi-location evaluation programme conducted during 2004-2009 as per Sharma *et al*., 2012.

15. DCMS 1A & 1B (IC0630582 & IC0630583; INGR19047), a New CMS (A) line of Wheat(*Triticum aestivum*) in PBW 343 Background with Diversified CMS Source (CMS1A) 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 proposed genetic stock DCMS1A was developed using MTSA 2A based CMS line CMS1A (MTSA 2A/BCN) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 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 was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set (Virmani *et al*., 1997).

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 4 consecutive crop seasons of 2014-15, 2015-16, 2016-17 and 2017-18. 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 (Virmani *et al*., 1997; Aruna *et al*., 2013). 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 1A (Table1).

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 1A was ranged from 95-100 days with mean of 98 days whereas average plant height was 95 cm with range of 91-100 cm. Compared to this, the maintainer line DCMS 1B (PBW343) showed average days to heading of 98 days and plant height of 96 cm which is in tune to CMS line. The results indicated improvement in spike length and spikelet number per spike in DCMS 1A as compared to the maintainer line. The maturity days was more in the DCMS 1A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

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

Year	DCMS1A (CMS-A line)						DCMS 1B (PBW 343: Maintainer-B line)				
	Male sterility(%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2014-15	100	100	93	12	23	148	100	96	10	19	148
2015-16	100	99	94	11	23	144	100	96	10	23	138
2016-17	100	95	100	11	21	143	95	101	11	19	139
2017-18	100	96	91	12	23	136	95	92	10	19	136
Mean	100	98	95	11	23	143	98	96	10	20	140

Table 2. Performance of DCMS 1A and its maintainer DCMS 1B for morphological traits

Traits	DCMS 1A	DCMS 1B (PBW 343)
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

In addition, few 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 343 (Table.2).

It may be concluded that the proposed genetic stock DCMS 1A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity

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16. DCMS 2A & 2B (IC0630584 & IC0630585; INGR19048), a New CMS (A) line of Wheat (*Triticum aestivum*) in PBW 343 Background with Diversified CMS Source (CMS 10A) 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 proposed genetic stock DCMS 2A was developed using CHUAN 18A based CMS line CMS10A (CHUAN 18A/CHUAN 18B//7*KAUZ/HEVO) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated.

:HTable 1. Performance of DCMS 2A and its maintainer for quantitative traits

Year	DCMS2A (CMS- A line)						DCMS 2B (PBW 343: Maintainer- B line)				
	Male sterility(%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2014-15	100	100	90	12	21	148	100	96	12	19	147
2015-16	100	101	91	9	21	143	100	97	10	23	138
2016-17	100	95	101	13	23	143	95	102	11	19	139
2017-18	100	97	88	10	21	136	95	87	9	19	137
Mean	100	98	93	11	22	143	98	96	11	20	140

In every generation, five spikes of recipient population was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

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 4 consecutive crop seasons of 2014-15, 2015-16, 2016-17and 2017-18. 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 2A (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 2A was ranged from 95-101 days with mean of 98 days whereas average plant height was 93 cm with range of 88-101 cm. Compared to this, the maintainer line DCMS 2B showed average days to heading of 98 days and plant height of 96 cm which is in tune to CMS line. The results indicated improvement in spikelet number per spike in DCMS 2A as compared to the maintainer line. The maturity days was more in the DCMS 2A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

In addition, few 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 343(Table 2).

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

Traits	DCMS 2A&2B
Coleoptile colour	Absent
Growth habit	Semi erect
Foliage colour	Green
Spike colour	white
Spike shape	Tapering
Awn colour	White
Grain colour	Amber

It may be concluded that the proposed genetic stock DCMS 2A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

17. DCMS 4A & 4B (IC0630586 & IC0630587; INGR19049), a New CMS (A) Line of Wheat (*Triticum aestivum*) 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 proposed genetic stock DCMS 4A was developed using CHUAN 18A based CMS line CMS12A (CHUAN18A/CHUAN18B/3/7*SERI/NKT//2*KAUZ) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 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 was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

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 crop seasons 2013-14, 2014-15, 2015-16, 2016-17 and 2017-18. 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 4A (Table 1).

Table.1. Performance of DCMS 4A and its maintainer for quantitative traits

Year	DCMS 4A (CMS- A line)						DCMS 4B (PBW 343: Maintainer- B line)				
	Male sterility (%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2013-14	100	101	91	-	-	-	99	95	-	-	-
2014-15	100	100	100	12	21	148	100	98	11	19	147
2015-16	100	101	101	12	25	142	100	99	10	23	138
2016-17	100	95	92	12	21	142	95	96	11	19	139
2017-18	100	97	96	12	21	138	96	93	11	23	136
Mean	100	99	96	12	22	143	98	96	11	21	140

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 4A was ranged from 95-

101 days with mean of 99 days whereas average plant height was 96 cm with range of 91-101 cm. Compared to this, the maintainer line DCMS 4B showed average days to heading of 98 days and plant height of 96 cm which is in tune to CMS line DCMS 4A. The maturity days was more in the DCMS 4A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

In addition, few 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 343 (Table 2).

Table 2. Performance of DCMS 4A and its maintainer DCMS 4B for morphological traits

Traits	DCMS 4A &4B
Coleoptile colour	Absent
Growth habit	Semi erect
Foliage colour	Green
Spike colour	White
Spike shape	Tapering
Awn colour	White
Grain colour	Amber

It may be concluded that the proposed genetic stock DCMS 4A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

18. DCMS 5A & 5B (IC0630588 & IC0630589; INGR19050), a New CMS (A) line of Wheat (*Triticum aestivum*) 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 proposed genetic stock DCMS 5A was developed using CHUAN 18A based CMS line CMS13A (CHUAN 18A/CHUAN 18B//7*CMH80A542/CNO79) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 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 was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

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 crop seasons 2013-14, 2014-15, 2015-16, 2016-17 and 2017-18. 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 5A (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 5A was ranged from 95-104 days with mean of 99 days whereas average plant height was 98 cm with range of 96-102 cm. Compared to this, the maintainer line DCMS 5B showed average days to heading of 100 days and plant height of 99 cm which is in tune to CMS line DCMS 5A. The results indicated improvement in spike length and spikelet number per spike in DCMS 5A as compared to the maintainer line. The maturity days was more in the DCMS 5A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

Table 1. Performance of DCMS 5A and its maintainer for quantitative traits

Year	DCMS 5A (CMS- A line)						DCMS 5B (PBW 343: Maintainer- B line)				
	Male sterility(%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2013-14	100	104	96	-	-	-	106	101	-	-	-
2014-15	100	102	97	12	21	151	100	100	11	19	148
2015-16	100	101	98	11	23	143	104	101	8	19	138
2016-17	100	95	97	11	21	144	95	98	11	23	139
2017-18	100	95	102	14	25	138	95	97	9	19	139
Mean	100	99	98	12	23	144	100	99	10	20	141

Table 2. Performance of DCMS 5A and its maintainer DCMS 5B for morphological traits

Traits	DCMS 5A	DCMS 5B (PBW 343)
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

In addition, few 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 343(Table.2).

It may be concluded that the proposed genetic stock DCMS 5A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

19. DCMS 6A & 6B (IC0630590 & IC0630591; INGR19051), a New CMS Line of Wheat (*Triticum aestivum*) in PBW 343 Background along with maintainer 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 proposed genetic stock DCMS 6A was developed using CHUAN 18A based CMS line CMS17A (CHUAN18A/3/7*KAUZ*2/MNV//KAUZ) as female parent in first cross with Indian advanced variety PBW 343 as male parent. PBW 343 was a mega variety for north western plains zone as well as north eastern plains zone for timely sown irrigated. After initial cross, 8 generations of backcrosses were made with PBW 343 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 was bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seedset.

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 4 consecutive crop seasons of 2013-14, 2014-15, 2015-16 and 2016-17. 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 6A (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 6A was ranged from 95-104 days with mean of 99 days whereas average plant height was 96 cm with range of 94-98 cm. Compared to this, the maintainer line DCMS 6B showed average days to heading of 100 days and plant height of 99 cm which is in tune to CMS line DCMS 6A. The results indicated improvement in spikelet number per spike in DCMS 6A as compared to the maintainer line. The maturity days was more in the DCMS 6A which is beneficial to get good grain development in the CMS line as well as seed set while attempting hybrid combinations.

Table 1. Performance of DCMS 6A and its maintainer for quantitative traits

	DCMS 6A (CMS- A line)						DCMS 6B (PBW 343: Maintainer- B line)				
Year	Male sterility (%)	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity	Days to heading	Plant height	Spike length (cm)	Spikelet number	Days to maturity
2013-14	100	104	96	-	-	-	106	101	-	-	-
2014-15	100	102	97	12	21	151	100	100	11	19	148
2015-16	100	101	98	11	23	143	104	101	8	19	138
2016-17	100	95	97	11	21	144	95	98	11	23	139
2017-18	100	95	94	11	21	137	95	95	10	19	137
Mean	100	99	96	11	22	144	100	99	10	20	141

Table 2. Performance of DCMS 6A and its maintainer DCMS 6B for morphological trait

Traits	DCMS 6A& DCMS 6B
Coleoptile colour	Absent
Growth habit	Semi erect
Foliage colour	Green
Spike colour	White
Spike shape	Tapering
Awn colour	White
Grain colour	Amber

In addition, few 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 343(Table.2).

It may be concluded that the proposed genetic stock DCMS 6A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

20. QLD112 (IC0632081; INGR19052), a Wheat(*Triticum aestivum*) Germplasm with Soft Grain

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

QLD112 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing 36th IBWSN364/36th IBWSN172//VL908 (Pedigree: BABAX/LR42//BABAX/5/ BOW//BUC/BUL/3/WEAVER/4/STAR/6/ VL908). The genotype was evaluated at 4 centers in Quality Component and Wheat Biofortification Nursery (QCWBN) during 2018-19. QLD112 was found to be superior with 15 grain hardness index to all the testing genotypes and best soft grain check variety HS490 (30: grain hardness index) (Table 1). QLD112 recorded the lowest grain hardness index in all the tested centers compared to the best check variety (HS490) for low grain index. QLD112 recorded lowest grain hardness index of 16, 15, 15 and 15, respectively at Delhi, Kanpur, Vijapur, and Pune centres. Whereas, the check variety HS490 recorded 27, 24, 33, and 37, respectively at Delhi, Kanpur, Vijapur, and Pune centres. QLD112 was 100% superior over check variety HS490. Low grain hardness index is very important factor to obtain high spread factor of biscuit and better biscuit quality. Thus, QLD112 would be a potential source to be utilized in future breeding programs to develop bread wheat varieties suitable for better biscuit making.

Table1. Grain hardness index of QLD112 during 2018-19 as compared to the best available soft grain check variety HS490

Zone	Location	Proposed Genotype	Best Check Variety
		QLD84	HS490
NWPZ	Delhi	16	27
NEPZ	Kanpur	15	24
CZ	Vijapur	15	33
PZ	Pune	15	37
Mean (National)		15	30
% Superiority of QLD 112 over best Soft grain check variety			100%

21. QLD102 (IC0632082; INGR19053), a Wheat (*Triticum aestivum*) Germplasm with High Sedimentation Value

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Sedimentation value measures the strength of gluten and determines the wheat for specific utility. Weak, medium and strong gluten as measured by low, medium and high sedimentation value are best suited for biscuit, chapatti and bread making, respectively.

QLD102 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing 36thIBWSN172/PBW502/3/PBW533//H9811/WH542 (Pedigree: BOW//BUC/BUL/3/ WEAVER/4/STAR/5/PBW502/6/PBW533//H9811/WH542). The genotype was evaluated at 15 centers in Quality Component Screening Nursery (QCSN) during 2017-18. QLD102 was found to be superior with67.2 sedimentation value to the best check variety UP2672 (63.2) and all other check varieties C306 (46.4), HS490 (44.5), and NIAW1415 (49.7) (Table 1). QLD102 recorded high sedimentation value compare to all the tested check varieties at all the centers. QLD102 was 6.4%, 44.8%, 51.0%, and 35.3%

Table1. Grain hardness index of QLD102 during 2017-18 as compared to the check varieties UP2672, C306, HS490, and NIAW1415

Zone	Location	Proposed Genotype	Best Check	Other check varieties		
		QLD102	UP2672	C306	HS490	NIAW1415
NWPZ	Ludhiana	68.8	67.2	46.0	40.7	50.0
	Durgapura	69.7	64.8	43.3	51.1	51.7
	Delhi	69.7	63.1	44.7	43.9	54.8
	Pantnagar	67.2	62.7	42.7	41.3	46.8
	Karnal	70.1	70.1	46.2	45.8	53.5
	Hisar	54.1	57.4	42.5	39.7	44.9
NEPZ	Kanpur	71.3	64.0	46.4	47.8	51.5
	Sabour	56.6	57.4	45.1	40.5	47.8
CZ	Junagadh	69.7	64.2	57.0	47.2	49.0
	Vijapur	66.5	67.0	51.0	46.0	47.0
	Indore	66.8	65.6	46.4	42.7	50.7
	Powarkheda	70.5	58.8	45.4	44.2	47.4
PZ	Pune	71.3	60.1	45.4	38.0	48.0
	Dharwad	66.0	60.7	47.6	56.0	53.5
	Niphad	70.1	65	46.8	42.7	48.6
	Mean	67.2	63.2	46.4	44.5	49.7
% Superiority of QLD 102 over check varieties			6.4%	44.8%	51.0%	35.3%

superior over the check varieties UP2672, C306, HS490, and NIAW1415, respectively. Sedimentation value is being used as a screening tool in wheat quality breeding programs globally to develop product specific wheat cultivars.

Thus, QLD102 would be a potential source to be utilized in future breeding programs to develop product specific wheat varieties.

22. IIWBR Phy 1 (IC0632600; INGR19054), a Wheat (*Triticum aestivum*) Germplasm with High phytase Level in the Background of PBW 502. Low Phytic Acid

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Though, it contains significant amount of essential nutrients such as proteins, minerals and vitamins; bioavailability of minerals to human beings is reduced because of presence of anti-nutritional factors such as phytic acid in wheat grains. Degradation of phytic acid by phytase enzyme present in the food can lead to enhanced bioavailability of Fe and Zn. Though, our earlier study reported 3.4 fold differences in phytase level among wheat varieties developed in India (284 FTU/Kg to 962 FTU/Kg with the mean value of 516 FTU/Kg) (Ram *et al* 2011), there was further need to expend diversity in phytase and phytic acid levels. Therefore, in the present investigation, mutant lines were generated using EMS mutagenesis in the background of wheat variety PBW 502 grown in North Western plains Zone in India and evaluated for phytase levels using microlevel tests developed in our laboratory.

Mutant lines were developed by treating PBW 502 seeds (around 3000) with 0.75% Ethyl Methyl Sulphonate overnight and followed by sowing in the field during 2008-09. The M1 seeds were sown during 2009-10 and more than 1000 plants were generated. 800 lines were advanced into higher generations using single seed descent method and evaluated for phytase levels during 2014-15, 2015-16, 2016-2017 and 2017-18. Mutant lines exhibited phytase levels ranging from 261 to 2578 with the average value of 1273

Table 1. Characteristics of PBW 502 and Mutant line (IIWBR Phy1) for Phytase levels (Average of 4 years data).

	Phytase level (FTU/Kg)	Phytic acid (%)	Yield
PBW 502	720 FTU/Kg	1.32	56.3 Q/Hect
Mutant line (IIWBRPhy1)	2400 FTU/Kg	0.92	57.5 Q/Hect

FTU/kg while PBW 502 exhibited phytase activity 720 FTU/kg. Ten Mutant lines were identified for very high phytase levels (>2000 FTU/kg) and sound grain characteristics. One of the mutants had high phytase level (2400 FTU/kg) and also high yield and good grain characteristics suitable for use in breeding. In addition it has low phytic acid content (Table 1). Since phytase levels is a trait which is mainly governed by genetics and less influenced by the environment (Ram *et al*; 2011), the genotype developed can be used in crossing programme for enhancing phytase levels for improving bioavailability of micronutrients to human beings.

23. IC113045/ F-13/ (IC0113045; INGR19055), an Early maturing, Extra Dwarf Barley (*Hordeum vulgare*) Germplasm in Six-Rowed Hulled Genetic Background

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Barley (*H. vulgare* L; 2n=14) is one of the oldest cultivated cereal and has been grown in India since ancient times. Barley is an important feed and fodder crop, besides it provides essential raw material for malting and brewing industries. Presently, it is the fourth most important cereal crop worldwide after maize, rice and wheat in terms of production. In India, it is cultivated on residual moisture by resource poor farmers under low input conditions and about 44% area under barley cultivation is rain-fed. Therefore, identification of trait specific accessions through evaluation of germplasm collections is a pre-requisite to diversify the parental material for sustained and continued increase in yield and quality of this crop. In this context, 4968 accessions of barley germplasm from National Gene Bank were characterised for agro-morphological traits at ICAR-NBPGR during the year 2016-17 and the trait specific accessions were validated in subsequent years (2017-19). Accession IC113045, exhibited dwarf plant habit in six-rowed and hulled genetic background with average plant height of 44.39 cm compared to recent check varieties of NWPZ namely BH959 (94.84 cm) and BH902 (110.04 cm) (Table 1). Dwarf plant height is highly desirable as barley is a lodging prone crop. In addition, it also showed early maturity in 117 days compared to checks BH902 (130 days) and BH959 (128 days). Early types are essential in most barley producing areas in India as rain-fed barley production needs early maturing varieties to escape drought and terminal heat in late March and early April. Average days to spike emergence and 100-grain weight for IC113045 were 56 and 3.34 g, respectively. The grains are hulled and white in colour.

Table 1. Year wise data of plant height in barley accession IC113045

Year	Field evaluation Location	Plant Height (cm)		
		IC113045	Check var.1 (BH959)	Check var. 2 (BH902)
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	45.96	91.54	106.83
2017-18	ICAR-NBPGR, New Delhi	41.33	90.30	105.80
2017-18	ICAR-NBPGR farm, Issapur, New Delhi	42.95	103.22	119.29
2018-19	ICAR-NBPGR farm, Issapur, New Delhi	47.33	94.32	108.25
Mean		44.39**	94.84	110.04

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

24. IC0113052 (IC0113052; INGR19056), a Long spiked with more number of grains/spike Barley (*Hordeum vulgare*) Germplasm in Two-Rowed and Hulless Genetic Background

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Once regarded as poor man's food and fodder cereal, barley has gained importance again owing to its increased use in multigrain blends, health tonics, malting and brewing industries. The new challenges for production in the era of climate change envisage involvement of diverse germplasm for further exploitation in breeding. In this context, 4968 accessions of barley germplasm from National Gene Bank were characterised for agro-morphological traits at ICAR-NBPGR during the year 2016-17 and the trait specific accessions were validated in subsequent years (2017-19). Accession IC113052, a two-rowed barley germplasm exhibited long spikes with average spike length of 13.74 cm compared to recent two-rowed check variety DWRB101 (7.82 cm) (Table 1). In addition, grains/spike, an important yield contributing trait were higher in IC113052 (32.44) compared to check DWRB101 (26.93), while plant height was lower (87.57 cm) which is desirable as barley is a lodging prone crop. Average days to spike emergence and maturity for IC113052 were 88 and 122, respectively. The grains are hulless and white in colour. Being hulless, this germplasm accession can be explored for consumption as food grain.

Table 1. Year wise data of spike length in barley accession IC113052

Year	Field Evaluation Location	Spike length (cm)	
		IC113052	Check var. (DWRB101)
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	13.23	8.00
2017-18	ICAR-NBPGR farm, IARI, New Delhi	13.50	7.46
2017-18	ICAR-NBPGR farm, Issapur, New Delhi	13.80	7.97
2018-19	ICAR-NBPGR farm, Issapur, New Delhi	14.44	7.83
Mean		13.74**	7.82

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

25. EC667420 (EC667420; INGR19057) an Early Maturing Hooded Barley (*Hordeum vulgare*) Germplasm in Six-Rowed Hulled Genetic Background

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Barley (*H. vulgare* L; 2n=14) is an important feed and fodder crop in India. In India, it is cultivated on residual moisture by resource poor farmers under rain-fed conditions. Hence, breeding for early maturity is a main breeding target. In this context, *a*ccession EC667420, a six-rowed barley germplasm was recorded showing early maturity with average 117.50 days to attain maturity compared to check variety BH902 (131.25 days) (Table 1). Early types are essential in most barley producing areas in India as rain-fed barley production needs early maturing varieties to escape drought and terminal heat in late March and early April. Furthermore, the awn type was recorded as sessile hoods in this accession. The hooded trait is desirable for fodder purpose barley as absence of awns allow more palatability and lip smacking in animals while the injurious awn reduces the feed value of straw for livestock (Takahashi, 1955; Yuo *et al.*, 2012). In addition, spike length was more in

Table 1. Year wise data of days to attain physiological maturity (DPM) in barley accession EC667420

Year	Field evaluation Location	DPM (days)	
		EC667420	Check var. (BH902)
2014-15	ICAR-NBPGR farm, Issapur, New Delhi	120	128
2015-16	ICAR-NBPGR farm, Issapur, New Delhi	115	132
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	114	136
2017-18	ICAR-NBPGR farm, IARI, New Delhi	121	129
Mean		117.50**	131.25

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

EC667420 (11.27 cm) compared to check BH902 (8.22 cm).Average days to spike emergence and 100-grain weight for EC667420 were 85.5 and 4.38 g, respectively. The grains are hulled and white in colour.

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26. EC492301 (EC492301; INGR19058) a Barley (*Hordeum vulgare*) Germplasm with Awnless Spikes

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The accession EC492301 has been identified for awnless spikes, which is a rare trait in barley as inflorescences are usually characterized by stiff bristles/awns in this crop. Under agricultural conditions, the long and stiff awn has persisted as a nuisance to farmers because they hinder manual harvesting and storage. More importantly, the injurious awn reduces the feed value of straw for livestock (Takahashi, 1955; Yuo *et al*., 2012). Thus awnless trait is desirable for fodder purpose barley as absence of awns allow more palatability and lip smacking in animals. Awnless forms (*lks1) reported as natural mutants in Himalayas are largely unknown, however* several natural mutant alleles of *lks2* (The short awn 2) represented as short awned or awnleted are present in the East Asian barley gene pool, including India, Nepal, China, Korea, and Japan (Yuo *et al*., 2012). During domestication and subsequent varietal differentiation, selection efforts were done to reduce awn length however, despite such selection pressure; most barley has retained rather long awns. Hence, the awnless trait has breeding value to develop awnless varieties. The close linkage between the genes V (awned) and Lk (awnless) is the main reason behind the scarcity of awnless forms reported in barley and mainly awned varieties are grown for production purpose (Tsvetkov and Tsvetkov, 2007). The molecular basis of awn elongation in grasses is still unclear. Barley provides excellent materials for such studies because many major genes subject to simple Mendelian inheritance are known to affect awn length in this species (Lundqvist and Franckowiack, 2003). In this perspective, the awnless forms possess potential to study the underlying genetic base of this rare trait. Moreover, EC492301 is the only accession characterised with awnless spikes among the entire assembly of germplasm (~8000 acc.) conserved at National Gene Bank. Regarding other agro-botanic features of EC492310, it is a six-rowed barley exhibiting prostrate growth habit. The spike length was recorded to be 6.57 cm, plant height was 105.82 cm. Average days to spike emergence, and days to attain physiological maturity were 107 and 141, respectively. The grains are hulled and white in colour.

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27. IC542197 (IC542197; INGR19059), an Early Maturing Barley (*Hordeum vulgare*) Germplasm in Two-Rowed and Huskless Genetic Background

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Early types are essential in most barley producing areas in India to escape drought and terminal heat. In this regard, barley germplasm accession IC542197 was identified showing early maturity in 109 days in two-rowed and hulless genetic background compared to two-rowed cultivar DWRB101 (129 days) and hulless variety BHS352 (125 days) used as checks (Table 1). The hulless grain trait in two-rowed barley is scarce as mostly hulless grain type is associated with six-rowed spike structure. In addition, hulless barley is an important food crop in the high altitude regions of J&K (cold desert of Leh-Ladakh), hilly Uttrakhand and Himachal Pradesh, where it is consumed by local people in the form of *sattu* as well as for the preparation of local beverage. Mainly hulless barley is grown and consumed for food purpose as absence of hulls require little or no processing after harvesting and can be rolled or ground into flour directly. In addition to early maturity, the hundred grain weight, an important yield contributing trait was higher (4.99 g) for IC542197 in comparison to checks, BHS352 (3.01 g) and DWRB101 (4.82 g).Average spike length and plant height for IC542197 was 9.48 cm and 104.60 cm, respectively. The grains are white in colour.

Table 1. Year wise data of days to attain physiological maturity (DPM) in barley accession IC542197

Year	Field Evaluation Location	DPM (days)		
		IC542197	Check var.1 (BHS352)	Check var. 2 (DWRB101)
2016-17	ICAR-NBPGR farm, Issapur, New Delhi	104	125	129
2017-18	ICAR-NBPGR farm, IARI, New Delhi	110	120	123
2017-18	ICAR-NBPGR farm, Issapur, New Delhi	108	127	130
2018-19	ICAR-NBPGR farm, Issapur, New Delhi	113	124	128
Mean		109**	124	128

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

28. S 614-13/SPV2263 (IC0632083; INGR19060), a Sorghum (*Sorghum bicolor*) Germplasm Resistant to Anthracanose and IVDMD 56%

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Forage quality is an important selection criterion in fodder crops especially in case of forage sorghum and IVDMD% is one of the most important quality components in forage sorghum. The genotype S 614-13 was developed by pedigree selection method from HJ 513 (Non sweet forage sorghum variety) x IS 2389-1 p29-1-3-4 and was selfed up to F6 generation. This germplasm is tall having 260 cm plant height, sweet, 9.5% TSS with good foliage and 56 % IVDMD (Table: 1).This genotype has high IVDMD and shows resistance against anthracnose (Table: 2) and other foliar diseases. This has also shown promise for shoot fly resistance and has moderate multiple leaf disease resistance. The genotype S 614-13 with a combination of improved quality traits and multiple foliar disease resistance may be of interest to forage sorghum breeder aiming at improving IVDMD of forage sorghum along with foliar disease resistance especially anthracnose.

Table 1. Performance of S 614-13 for IVDMD % in AICRP Trials

	IVDMD%				
Year of Testing	Proposed Genotype	Check I	Check II	CD@ 5%	% increase over best check
	SPV 2263 (S 614-13)	CSV21F	HC 308		
2013-14	56.0	52.0	52.0	4.0	7.69 %

Table 2. Performance of S 614-13 for anthracnose in AICRP Trials

	Anthracnose resistance				
Year of Testing	Proposed Genotype	Resistant Check I	Resistant Check (Local) II	CD@ 5%	% increase over check
	SPV 2263 (S 614-13)	Pant Chari-5	Local Check		
2013-14	3.0	4.7	4.1	1.3	36% less disease attack as compared to resistant check over the locations

29. IG 96-401 (EC397366; INGR19061), a Buffel grass (*Cenchrus ciliaris*) Germplasm Rich in sugar (more than 7%). Suitable for Ensiling (Silage Preparation) and Prostrate Growth Habit.

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Buffel grass *(Cenchrus ciliaris)* is a potential grass for pasture plantation due to ease of establishment and forage production in harsh environments (Cox *et al*., 1988) and occupies the major component of *Dichanthium–Cenchrus–Lasiurus* grass cover of India (Dabadghao and Shankarnarayan, 1973).Active growth of *C. ciliaris* occurs mainly during monsoon months which results in surplus availability of green fodder. These surplus green fodder need to be conserved for feeding livestock during lean periods. But low sugar content (2-4%) is the main limitation for ensiling tropical grasses as a minimum of 7-8% of sugar is required for bacteria to initiate the ensiling process (McDonald *et al*., 1991).

A total 108 accessions of *Cenchrus* were evaluated for water soluble carbohydrates (WSC) content and biomass production potential for two consecutive years at ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi. After two years evaluation 14 accessions (IG99-124, IG97-379, IG-97-377, IG97-403, IG96-358, IG96-87, IG97-75, IG97-378, IG96-401, IG96-414, IG96-3108, IG96-96, IG96-89 and IG96-50) having WSC>7%were selected and further tested for ensiling. Selected accessions were further multiplied and the silage was prepared from IG96-96, IG96-358, IG96-50, IG96-401, IG96-403 and natural *Cenchrus*. The silage prepared from IG 96-401was of good quality (Table 1)as evident from their pH (4.06) and lactic acid values (0.95% fresh basis). Growth habit of IG96-401 is prostrate with medium plant height (82.3cm) and days to 50% flowering (68 days), tillers number per plant were about 79.2 and leaf colour were normal green.

These findings confirm that good quality silage can be prepared from *Cenchrus ciliaris* selected genotype IG96-401 having adequate sugar to initiate ensiling. The IG96-401 may be further propagated in grazing lands and common areas to produce silage from post monsoon growth for ensuring quality fodder in lean periods for sustainable livestock production.

Table 1. Sugar contents and silage quality of *C. ciliaris* genotype IG96-401*

Parameters	IG96-401
Sugar %	1st cut 7.7 2nd cut 7.2
DM%	33.88
pH	4.06
Lactic acid % (Fresh basis)	0.95
Lactic acid % (Dry matter basis)	2.81
NH3- N g/Kg (Fresh basis)	0.39
NH3- N/Kg (Dry matter basis)	1.16
Total -N g/Kg (Fresh basis)	1.68
TN g/kg (Dry matter basis)	4.95
NH3- N % Total nitrogen	23.65

*Values are mean of 4-5 observations

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30. IG 96-50 (IC0630758; INGR19062), a Buffel grass (*Cenchrus ciliaris*) Germplasm with High Water Soluble Carbohydrate. Good for Silage Preparation. Leaf Colour Pale-Low Chlorophyll Content

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Cenchrus ciliar ensiling. For large scale silage production selected lines were multiplied and the silage was prepared from IG96-96, IG96-358, IG96-50, IG96-401, IG96-403 and natural *Cenchrus*. The silage prepared from IG 96-50 was of good quality (Table 1) as evident from their pH (4.61) and lactic acid values (0.47 % fresh basis). Growth habit of IG96-50 is semiprostrate with tall plant height (116 cm) and late days to 50% flowering (90 days), tillers numbers per plant were low (about 27) and unique pale leaf colour.

These findings confirm that good quality silage can be prepared from *Cenchrus ciliaris* selected genotype IG96-50 having adequate sugar to initiate ensiling. The IG96-50may be further propagated in grazing lands and common areas to produce silage from post monsoon growth for ensuring quality fodder in lean periods for sustainable livestock production.

Table 1. Sugar contents, fodder yield and ensiling properties of *C ciliaris* genotype IG96-50*

Parameters	IG 96-50
Sugar %	1st cut 8.4 2nd cut 7.3
GFY (t/ha)	96.8
DMY (t/ha)	23.3
DM%	27.37
pH	4.61
Lactic acid % (Fresh basis)	0.47
Lactic acid % (Dry matter basis)	1.71
NH3- N g/Kg (Fresh basis)	0.50
NH3- N/Kg (Dry matter basis)	1.83
Total -N g/Kg (Fresh basis)	1.76
TN g/kg (Dry matter basis)	6.43
NH3- N % Total nitrogen	28.77

* Values are mean of 4-5 observations

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31. IG 96-96 (IC0630759; INGR19063), a Buffel grass (*Cenchrus ciliaris*) Germplasm with High Water Soluble Carbohydrate. Good for Silage Preparation.

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Cenchrus ciliaris is a potential grass for pasture plantation due to ease of establishment and forage production in harsh environments (Cox *et al*., 1988) and occupies the major component of *Dichanthium–Cenchrus–Lasiurus* grass cover of India (Dabadghao and Shankarnarayan, 1973). Active growth of *C. ciliaris* occurs mainly during monsoon months which results in surplus availability of fodder. These surplus monsoon grasses need to be conserved for feeding livestock during lean periods. Woolford (1984) mentioned that good quality grass silage can be obtained by ensiling grass that contains WSC ranged from 60 to 80 g kg-1 DM.

Total 108 lines of *Cenchrus* were evaluated for water soluble carbohydrate (WSC) content and fodder yield production for two consecutive years at ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi. After two years evaluation 14 accessions (IG99-124, IG97-379, IG-97-377, IG97-403, IG96-358, IG96-87, IG97-75, IG97-378, IG96-401, IG96-414, IG96-3108, IG96-96, IG96-89 and IG96-50) having more than 7% WSC were selected. Selected accessions were further multiplied for ensiling with natural *Cenchrus*. The silage prepared from IG96-96 was of good quality (Table 1) as evident from their pH (4.97) and lactic acid value (0.35 % fresh basis). Growth habit of IG96-96 is erect with short plant height (42.8cm) and early days to 50% flowering (55 days), tillers number per plant were about 65 and leaf colour was dark green.

Table 1. Sugar contents, fodder yield and ensiling properties of *C. ciliaris* genotype IG96-96*

Parameters	IG 96-96
Sugar %	1st cut 9.79 2nd cut 8.08
GFY (t/ha)	91.3
DMY (t/ha)	18.2
DM%	25.80
pH	4.97
Lactic acid % (Fresh basis)	0.35
Lactic acid % (Dry matter basis)	1.37
NH_3-N g/Kg (Fresh basis)	0.71
NH_3-N/Kg (Dry matter basis)	2.74
Total-N g/Kg (Fresh basis)	2.00
TN g/kg (Dry matter basis)	7.75
NH_3-N % Total nitrogen	35.42

*Values are mean of 4-5 observations

These findings confirm that good quality silage can be prepared from *Cenchrus ciliaris* selected genotype IG96-96 having adequate sugar to initiate ensiling. The IG96-96 may be further propagated in grazing lands and common areas to produce silage from post monsoon growth for ensuring quality fodder in lean periods for sustainable livestock production.

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32. SM2254-8 (IC0632070; INGR19064), an Intergeneric (Sorghum x Maize cross) Forage Sorghum (*Sorghum bicolor*) with Low HCN. High IVDMD

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Crop improvement in sorghum has reached a plateau in realizing yield gains and further improvement requires introduction of variation through other methods like wide hybridization. Distant hybridization between incompatible species introduces *de novo* variation that can be used in crop improvement programs (Wang *et al.*, 2009). An attempt was made at the ICAR-Indian Institute of Millets Research, Hyderabad, to cross the superior genotypes from sorghum with maize parental lines through pollen treatment. There was wide phenotypic variation in F_2 generation derived from the two crosses (DSR, 2010, 2013). The variants were advanced through selection for specific traits and evaluated in the field trials. Forage segregates from the above were studied with an objective to determine their performance for forage traits *vis* a *vis* standard checks as well as to determine the association of the traits with forage yield. One of the promising forage lines is SM2254-8, having low HCN and high digestibility. This line is derived from the pollination of sorghum parental line, the 126A, pollinated with the maize line, the CM208.

Morpho-agronomic characteristics: The proposed genotype, SM2254-8, is a forage pre-breeding material. The plants are tall, have multiple tillers. Panicles are loose and long. It has low HCN content and high *in vitro* dry matter digestibility (Table 1). HCN content (54.1 ppm) is lower as compared to 71.3 ppm in SSG59-3 and 60.6 ppm in CSV21F and higher *in vitro* dry matter digestibility (IVDMD) 57.0% against checks SSG59-3 (53.0%) CSV21F (52.3%). It is on par with checks for rest of the traits such as green fodder yield of 527.0 q/ha compared to checks (SSG59-3 571.3q/ha, and CSV22F 576.0q/ha), total soluble sugars 4.5% compared to checks (5.0 and 4.5) (Visarada *et al.*, 2017).

Associated characters and cultivation practices: Low Low HCN content and high in vitro dry matter digestibility are the important traits for the improvement of forage sorghum hybrid parents and varieties. Forage traits were tested across two locations, Pantnagar and Hisar in India and the genotype, SM2254-8, is found promising for low HCN and high IVDMD. SM2254-8 is a novel source for genetic variability developed through wide hybridization of sorghum and maize. This genetic stock is a unique material as the cross between Sorghum and Maize has been accomplished for the first time in the inter-generic breeding.

Table 1. Forage yield, quality and phenological traits of sorghum-maize intergeneric derivative, 2254-8

Trait	Test genotype	Check 1	Check 2
	2254-8	SSG59-3	CSV21F
GFY 2 cuts (q/ha)	527.0	571.3	576.0
DFY 2 cuts (q/ha)	111.7	128.3	139.7
TSS (%)	4.5	5.0	4.5
HCN (ppm)	54.1	71.3	60.6
Protein (%)	8.3	8.7	8.3
IVDMD(%)	57.0	53.0	52.3
Early vigour (score 1-4)	4.00	3.75	3.25
Plant height (cm)	201	194	210
No. of leaves/plant	21.9	17.5	18.2
No of tillers	3.65	3.83	2.25
Leaf length (cm)	81.5	80.0	85.9
Leaf breadth (cm)	5.15	4.15	5.85
Leaf stem ratio	0.38	0.40	0.35
Stem girth (cm)	5.33	4.53	6.65
GFY= green fodder yield			
DFY= dry fodder yield			

TSS= total soluble sugars
Entries- 16; Checks- 2; Locations: 2

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33. EC724523 (EC724523; INGR19065), a Cowpea (*Vigna unguiculata*) Germplasm Resistant to Root-Knot Nematode (*Meloidogyne incognita*)

NK Gautam*, Z Khan, BH Gawade, SC Dubey, N Singh, Babu Ram, A Kumar and K Tripathi

And

34. EC723686 (EC723686; INGR19066), a Cowpea (*Vigna unguiculata*) Germplasm Resistant to Root-Knot Nematode (*Meloidogyne incognita*)

NK Gautam*, Z Khan, Bharat H Gawade, SC Dubey, N Singh, Babu Ram, A Kumar and K Tripathi

And

35. EC725122; TVu-9544 (EC725122; INGR19067), a Cowpea (*Vigna unguiculata*) Germplasm Resistant to Root Knot Nematode (*Meloidogyne incognita)*

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Root-knot nematodes, constitute a major group of plant-parasitic nematodes affecting crop production substantially. *Meloidogyne incognita* is an important constraint in the production of leguminous crops including cowpea in tropical and subtropical regions of the world (Sikora *et al*., 2005). Its infection leads to development of root galls, which impede normal uptake of water and nutrients. Root gall formation suppresses rhizobium nodulation and hampers nitrogen fixation in leguminous crops. Intensive root galling often results in permanent wilting, premature defoliation, and eventually plant death in cowpea. The nematode-resistant cultivars are an eco-friendly and economically feasible means for the management of root-knot nematodes. Therefore, 350 accessions of cowpea were screened at ICAR-NBPGR, New Delhi during the years 2013 to 2015 to identify the source of resistance to *M. incognita*. Preliminary screening was conducted in pots filled with nematode infected soil containing 3 second stage juveniles (J2) per gram of soil. After 45 days of sowing, plants were uprooted, root galls per plant root system were counted and a gall index (GI) of 0-5 was assigned as 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5=>100 galls per root system (Taylor and Sasser, 1978). Host responses of cowpea germplasm were determined using gall index (GI) and designated as immune (GI= 0.0), resistant (GI ≤ 2.0) and susceptible (GI>2.0) (Sasser *et al.,* 1984). Selection was made for those accessions showing <10 root galls during preliminary screening and were rescreened by artificial inoculation under net house conditions to confirm their resistance consistency. Based on the number of root galls induced by *M. incognita*, three selected accessions (EC0723686, EC0724523, EC0725122) were found resistant with <10 root galls per root system. Nematodes penetration into roots were decreased in resistant accessions as compared to susceptible accessions. Similarly, egg-mass formation was also reduced in the resistant accessions and were observed smaller in size with fewer eggs (Khan *et al*., 2018). In conclusion, the drastic reduction in nematode penetration into the roots, reduction in gall formation, and lower number of egg masses suggest that resistance may be both pre-infectional as well as post-infectional in resistant cowpea accessions. These resistant accessions may be useful in cowpea plant breeding programs for nematode management.

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36. IC559673 (IC0559673; INGR19068), a Lentil (*Lens culinaris*) Germplasm Resistant to Root-Knot Nematode

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Root-knot nematodes (*Meloidogyne* spp.) are one of the most widespread and damaging agricultural pests in the world causing an estimated US $100 billion loss/ year worldwide (Oka *et al*., 2000). *Meloidogyne incognita* is one of the major limiting factors affecting plant growth and yield of lentil crop (Sharma *et al*., 2005; Khan *et al*., 2017). Management of root-knot nematodes, using resistant cultivars is considered as one of the best alternatives, which is eco-friendly as well as economically feasible. However, very little information is available on screening of lentil germplasm to root-knot nematodes. Therefore, present experiments were conducted to evaluate and identify resistant source in lentil germplasm. Evaluation of 300 accessions of lentil germplasm was done at ICAR-NBPGR, New Delhi during the years 2014 and 2015 for nematode resistance. Preliminary screening was conducted in pots filled with nematode infected soil containing two second stage juveniles (J2) per gram of soil. After 45 days of sowing, plants were uprooted, root galls per plant root system were counted and gall index (GI) of 0-5 was assigned as 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5=>100 galls per root system. Host responses of lentil germplasm accessions were determined using gall index (GI) and designated as immune (GI= 0.0), resistant (GI $\leq$ 2.0) and susceptible (GI>2.0) using standard procedure (Sasser *et al*., 1984). Those accessions showing <10 root galls in preliminary screening were selected for rescreening by artificial inoculation under net house conditions. Based on number of root galls, two accessions, IC559673 and IC559890 were found consistent in resistance reaction, as <10 galls per root system were observed (Khan *et al*., 2017; Fig. 1). Nematodes penetration occurred into roots of both resistant and susceptible accessions, but penetration rate was significantly lower in resistant accessions as compared to the susceptible accession (IC560206). Very few, smaller and distorted nematode egg masses were formed in the resistant lentil accessions, suggesting that the nematodes penetrating the resistant plant roots were further inhibited in their growth and development. Variations in nematode penetration into roots, root gall formation and egg mass formation in the resistant accessions could be due to their genetic differences for nematode resistance.

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37. IC208329 (IC0208329; INGR19069), a Lentil (*Lens culinaris*) Germplasm with High Protein Content (27.4 %-28.5%)

NK Gautam*[1], R Bhardwaj[1], S Yadav[2], N Singh[1], K Tripathi[1], P Suneja[1], B Ram[1] and A Kumar[1]

and

38. IC208326 (IC0208326; INGR19070), a Lentil (*Lens culinaris*) Germplasm with High Protein Content (27.4-28.06 %)

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Malnutrition problem is basically of protein deficiency among children of developing countries (Amjad *et al.*, 2006). Hence, there is a need to identify high protein and amino acids rich lines either for direct consumption or for breeding programme. Plant genetic resources possess genetic variability for different agronomical and nutritional traits (Kumar *et. al.*, 2016). Selection of superior germplasm and bio-fortification of crop varieties is an option to combat the problem of protein malnutrition. Lentil is an inexpensive, sustainable and affordable source of vegetable protein that is mostly consumed as dry seeds. Protein quality is determined on the basis of amino acids composition more importantly the essential amino acids (EAAs) which can not be synthesized by human beings and therefore, EAAs are key parameters in food quality assessment. In lentil sulphur containing methionine is a major limiting amino acid followed by aromatic amino acids (Longwah *et. al.*, 2017). The experimental material consisting of five hundred seventy germplasm was grown at NBPGR experimental farm for five years (2000-01, 2001-02, 2013-14, 2014-15, 2015-16) under standard agronomic package of practices to identify and select promising germplasm especially rich in protein and amino acids. Protein content was estimated by Kjeldahl nitrogen multiplied by factor 6.25 as per AOAC method number 2001.11. Amino acids profiling was done using waters Aceq-tag kit on waters HPLC system equipped with fluorescent detector. Two germplasm accessions, IC208326 and IC208329 were found superior for high protein content, 27.4-28.5% with 1.5-2.0 times higher content of total aromatic amino acids and methionine (Table 1). In conclusion identified lines having higher percentage of protein and rich in amino acids methionine, arginine and tyrosine etc. can be used directly for consumption as well as for improvement of lentil cultivars with value added products after purification of proteins or amino acids.

Table 1. Total protein content and amino acids profile of selected lentil accessions

Year	Accessions	IC201700	IC208329	IC208326	IC208351	Precoz
2015-16	Protein (%)	25.2 ± 0.56	28.5 ± 0.39	27.6 ± 0.54	23.7 ± 0.36	21.3 ±0.24
2014-15		26.3 ± 0.38	28.4 ± 0.62	27.7 ± 0.76	25.5 ± 0.18	23.3 ±0.18
2013-14		25.9 ± 0.34	28.6 ± 0.06	28.06 ± 0.14	25.6 ± 0.63	22.8 ±0.16
2001-02		26.2 ± 0.43	27.4 ± 0.53	27.7 ± 0.37	25.2 ± 0.56	21.4 ±0.21
2000-01		26.0 ± 0.64	27.5 ± 0.44	27.4 ±0.48	24.3 ± 0.18	22.6 ±0.17
Amino acids (g/100 g protein) 2015-16	Serine	4.99 ± 0.38	6.28 ± 0.33	6.34 ± 0.30	5.39 ± 0.02	5.56 ±0.12
	Histidine	6.67 ± 0.78	9.15 ± 0.35	7.08 ± 0.07	1.21 ± 0.94	2.20 ±0.09
	Proline	4.85 ± 0.25	4.64 ± 0.05	4.99 ± 0.33	4.48 ± 0.18	5.22 ±0.08
	Tyrosine	4.86 ± 0.82	7.15 ±0.41	6.97 ± 0.44	2.71 ± 0.09	2.93 ±0.23
	Methionine	1.16 ± 0.13	2.23 ± 0.17	1.5 ± 0.05	1.59 ± 0.01	1.01 ±0.18
	Lysine	7.21 ± 0.42	5.81 ± 0.45	7.11 ± 0.61	9.59 ± 0.38	6.47 ±0.32
	Leucine	6.98 ± 0.15	7.17 ± 0.03	7.23 ± 0.06	5.89 ± 0.29	7.72 ±0.13
	Phenylalanine	7.02 ± 0.49	7.28 ± 0.30	7.55 ± 0.29	3.84 ± 0.48	5.32 ±0.21

Each column contains mean and S.D. of mean

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39. IC0559890 (IC559890; INGR19071), a Lentil (*Lens culinaris*) Germplasm Resistant to Root-Knot Nematode (*Meloidogyne incognita)*

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The root-knot nematode, *Meloidogyne incognita* is one of the major limiting factors affecting plant growth and yield of lentil crop. For the management of root-knot nematodes, use of resistant cultivars is considered as one of the best alternatives, which are eco-friendly as well as economically feasible. Resistant cultivars can also be employed as a component of integrated nematode management along with other strategies. Through screening experimentation, two accessions of lentil, IC-559673 and IC-559890 are identified as a resistant to *M. incognita*. Evaluation of 300 accessions of lentil was done at ICAR-NBPGR, New Delhi during year 2014 and 2015. Preliminary screening was conducted in pots filled with nematode infected soil, containing two infective stage juveniles (J2) per gram of soil. After 45 days of sowing, plants were uprooted, root galls per plant root system were counted and a gall index (GI) of 0-5 was assigned as 0=no gall, 1=1-2, 2=3-10, 3=11-30, 4= 31-100, 5=>100 galls per root system. Host responses of lentil germplasm were determined using GI to be designated as Immune (I) when GI= 0.0, resistant (R) GI $\leq$ 2.0 and susceptible (S) >2.0 to each accession (Taylor and Sasser 1978). Those accessions showing <10 root galls were rescreened using artificial inoculation strategy under controlled conditions for confirmation of resistance consistency. Two accessions, IC559673 and IC559890 were consistent in resistance reaction (<10 galls per root) and hence selected for registration (Khan *et al*., 2017).

The reduced nematode penetration into roots and reproduction revealed negative effect of lentil resistant accessions on nematode. Nematode penetrations occurred in both the resistant accessions, but significantly lowered compared to the susceptible lentil accession (IC560206). Very few smaller and distorted nematode egg masses formed in the resistant lentil accessions, suggesting that the nematodes penetrating the resistant plant roots were further inhibited in their growth and development (Table 1). Variations in nematode penetration into roots, root gall formation and egg mass formation in the resistant accessions may reflect their genetic differences related to the nematode resistance, and their planting could provide a useful tool to manage root-knot nematodes in lentil crop.

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Table 1. Host status of lentil accessions for resistance to *Meloidogyne incognita* and response of resistant/susceptible accessions to nematode penetration and egg mass formation

Accession number	Number of galls per rootsystem (mean±SD)[a]	Percent reduction over control accession	Gall index	Host status	Nematode penetration rate (%) at DAI[b]				No. of egg masses per root after 45 DAI (mean±SD)[a]
					2 DAI	4 DAI	7 DAI	14 DAI	
IC559890	7.0±2.23	94.11	2	Resistant	2.86	5.3	5.78	5.22	2.8±1.92
IC559673	4.2±1.78	96.47	2	Resistant	1.86	5.86	6.56	6.2	1.6±0.54
IC560206 (Control)	119±14.66	0	5	Susceptible	5.76	14.38	17.38	19.62	194.2±15.22

[a]Means and standard deviations are of five replications, [b]DAI- days after inoculation.

40. IC0317520 (IC317520; INGR19072), a Lentil (*Lens culinaris*) Germplasm with Extended Funiculus for Fast Water Uptake

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A unique seed morphotype of lentil (*Lens culinaris* Medik.) with extended funiculus was identified during mega germplasm characterization programme at ICAR-NBPGR, New Delhi undertaken during *Rabi* 2017–2018. Based on comparative study with selected accessions for seed morphology, nutritional traits and physiology, this accession was identified with very distinct and prominent funiculus on the seed coat and higher rate of water uptake. It was a first report of seed morphotype in lentil with extended funiculus. All the accessions selected for imbibition behaviour study were of the same moisture content. Imbibition curves clearly indicated that water absorption and weight gain of the seeds were highest in atypical accession as compared to normal cultivars used in the study. When imbibed seeds were used for germination, it showed 100% germination. Funicle was remain intact with seed in 1-month old seedlings that indicate uniqueness of atypical accession in holding funicle as fixed character. IC145263 showed a range of water uptake from 0.1614 to 0.2609 in an interval of 12 h, IC145281 showed a gradual increase from 0.2107 to 0.3634 in 7 h and then became static with 0.37 values. Highest water uptake was observed in seeds with completely intact funicle as compared to seeds with completely covered funiculus and completely removed funiculus. In later even after 12 h imbibition there was no water uptake and after 36 h, only 30–40% seeds were imbibed which may be due to absorbtion through the seed testa surface or micropylar region. This indicated that funiculus may be facilitating trapping of water flow between embryo and testa and control water uptake in the atypical accession. For trait stability this unique accession was evaluated under multi-location trial at NBPGR, New Delhi, NBPGR, RS, Ranchi and Bhowali in *rabi* 2018-19 and this unique trait was expressed across the locations.

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41. IC0120963 (IC120963; INGR19073), Extra Early Maturing (53 days) Moth Bean (*Vigna aconitifolia*) Germplasm

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Moth bean also known as matki, math, dew bean {*Vigna aconitfolia* (Jack.) Marechal} has been known for high degree of adaptation in hot- arid climatic situation due to its inbuilt capacity for its tolerance to drought and high temperature. In view of generating the more productive and adaptive varieties for harsh and hostile climatic conditions the shortening of maturity period was remained desirable trait to be identified in germplasm of mothbean. The all released varieties of mothbean have been grouped in late maturity (>75 days), medium maturity (65-75days and early maturity (60-65 days) based on their maturity period. The released variety FMO-96 variety maturing in 58-59 days (Manga *et al.*, 2015) otherwise none of the accessions or released varieties matures earlier than

60 days. Mothbean germplasm characterization and evaluation has been a continued programme at NBPGR Regional Station, Jodhpur. During 2012 an accession IC 120963was identified to be matured uniformly in 53 days. It takes 30-32 days in flowering uniformly. The early maturity of this accession has been verified during subsequent years till 2016. This is the first accession of mothbean that has been reported from NBPGR Regional Station, Jodhpur that matures in 53 days.

Associated characters and cultivated practices: Being early in maturity (53days) mothbean accession IC 120963 escapes drought, generally recurring at later stage of the crop. Late maturing varieties (>75 days) as a rule generally suffer from the terminal drought and diseases. Consequently, these varieties have virtually wiped out from the cultivation map of this crop. This extra early maturing accession of mothbean is capable to yield better and withstood in the scorching heat and depleting soil moisture. Extra early maturing varieties due to short growing seasons, usually successfully escape drought and sometimes devastating diseases like (Yellow Mosaic Virus) and Cercospora leaf spot in mothbean. Such varieties are however, more suited to hot-arid climatic conditions like western Rajasthan. Where rainfall generally too low (200-250 mm) and temperature is high during growth period of the crop. Extra early maturing varieties of mothbean have high yield potential d (6-8 q/ha) and have increased harvest index up to 35% (Kumar, 2002). Thus this identified early maturing accession can be used in breeding programme of mothbean to shorten the crop duration.

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42. IC039289 (IC039289; INGR19074), an Early Maturing (50 days) Germplasm of Mung Bean (*Vigna radiata*)

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Mung bean (green gram) or mung (*Vigna radiate L. Wilczek*) known for high degree of adaptation in rain fed arid situation due to tolerance to drought and high temperature is one of the major pulses grown in Rajasthan and other parts of the country. The short duration varieties are more suited in harsher climatic conditions as they mature before the onset of harsher climatic conditions. The germplasm of any crop species is the best source to identify early maturing (short duration) genotypes to be used in the breeding programme to shorten the length of crop duration. Regional Station of NBPGR, at Jodhpur has collected and conserved 2745 accessions of mung bean which are being characterized and evaluated and multiplied at its research farm. During characterization and evaluation study of mung bean germplasm in 2013 to 2016 at ICAR-NBPGR Regional station Jodhpur in an augmented block and randomized block designs during summer and *kharif* seasons the mung bean germplasm accession IC-39289 matured in just 50 days. It took 28 to 30 days in flowering uniformly and matured uniformly in another 20-22 days. This is the earliest maturing accession reported by NBPGR Regional Station, Jodhpur till date.

Associated characters and cultivated practices: Being early in maturity (50 days) mung bean accession IC-39289 escapes drought, generally recurring at later stage of the crop. Late maturing varieties as a rule generally suffer from the terminal drought and diseases. Consequently, these varieties are virtually wiped out from the cultivation map of this crop. This extra early maturing accession of mung bean is capable to yield better and withstand the scorching heat and depleting soil moisture. Extra early maturing varieties due to short growing seasons usually could evade drought problems and escaped devastating diseases like (Yellow Mosaic Virus) and Cercospora leaf spot successfully. An average yield of IC 39829 accession is recorded about 14.5 q/ha and it produces bold shiny seeds with seed weight of 6.34g per 100 seeds.

43. P-637 (IC0241565; INGR19075), a Post Emergence Herbicide (Metribuzin) Tolerant Pea (*Pisum sativum*) Germplasm

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Field pea (*Pisum sativum L.*) is an important cool season legume crop of the world and is a rich source of protein (21.1-32.9%), carbohydrate, minerals and vitamins which are good for human and livestock consumption and health (Parihar *et al*., 2016). The productivity of this crop is affected by several biotic and abiotic factors. Among these factors, weeds can cause > 75 percent reduction in crop yield (Tripathi *et al*., 2001; Singh *et al*. 2016). Weeds have competition to the crops for nutrient, water, sunlight, space and also harbour many insect-pest and diseases (Gaur *et al.* 2013), subsequently, the performance of crop in term of the yield is drastically reduced. Presently, pre-emergence herbicide (pendimethalin) and manual weeding at 30-35 days after sowing is recommended in pea. However, manual weeding is proving difficult because of labour scarcity at critical time of weeding and increasing cost. Therefore, to control the later flush of weeds, use of post-emergence herbicides becomes important. But, no post-emergence herbicide is available for controlling broad-leaved weeds like *Medicago denticulala, Vicia sativa, Convolvulus arvensis, Chenopodium album, Phalaris minor* and others. Therefore, an effective and efficient weed management is essential to achieve potential yield (Nath *et al*., 2017). Field pea is a poor competitor to weeds owing to its slow initial growth and wider plant spacing that provide congenial environment for weeds to grow. Besides, its succulent plant type also do not allow second manual weeding as it can cause damage to the crop. Therefore, herbicide tolerance cultivars may offer larger elasticity for use of post-emergence herbicides and are immediately required by the *P. sativum* growing farmers. An attempt has been made at ICAR-IIPR, Kanpur, Uttar Pradesh to identify the genotypes with resistance to the post-emergence herbicide metribuzin in Field pea. Metribuzin (4-Amino-6-tert-butyl-3-methylsufanyl-1, 2, 4-triazin-5-one) is a potential broad-spectrum herbicide used in soybean and wheat crops. It inhibits the photosystem-II pathway, which demonstrates adverse effect on the fully developed leaves and subsequently on plant growth. Thus far no report is available on herbicide tolerance in *P. sativum*. Also, till date no systematic study was conducted to see the efficacy of this post-emergence herbicide in fieldpea. In present investigation total 822 genotypes were examined for their sensitivity under preliminary screening against metribuzin at 0.5 kg ai/ha during the winter season of 2015-16 at ICAR-IIPR, Kanpur. Of the tested genotypes, a set of eighty five promising genotypes were re-evaluated with same dose during the winter season of 2016-17 with visual phyto-toxicity score. Based on two years screening (2015-16 & 2016-17), a set of fifteen genotypes was made comprising of tolerant, moderately tolerant, sensitive and highly sensitive genotypes. These genotypes were examined in larger plot for resistance against popular post-emergence herbicide metribuzin 500 g a.i./ha during winter season of 2017-18. The plants were observed for herbicide phyto-toxicity on three different stages i.e. 15 days after herbicide application (DAHA), 30 DAHA and 60 DAHA. Based on scoring for the visual appearance and phyto-toxicity on plants, a genotype ‘P-637’ was found tolerant. This genotype has constantly registered tolerance for metribuzin 500 g a.i./ha during three years of screening. Hence, this genotype can be utilized as a potential donor in future fieldpea breeding programme towards development of herbicide (metribuzin) tolerant varieties and in other basic studies.

Morpho-agronomic characteristics: The genotype (P-637) is medium tall type (70-75 cm) and leafy type.It has red colour flowers, pigmented pods and yellow green (tan colour) dimpled seeds. It flowered and matured in 64 days and 125 days respectively. The 100-seed weight is 16.0-17.0 gm and pod length is 4-5cm. The average yield of the genotype (P-637) is 14-15 qt/ha.

Associated characters and cultivation practices: This genotype has anthocyanin on stem and leaves of plants. Its leaves total chlorophyll and carotenoids content is 2.302 (mg/g fresh weight) and 0.143 (mg/g fresh weight), respectively. The chlorophyll a content (1.909 mg/g fresh weight) and chlorophyll b content is (0.39 mg/g fresh weight). This genotype also has powdery mildew resistance. It can be grown on different type of soil; however, a well drained soil is essential to achieve good yield potential of this genotype. The field should be prepared well by two to three ploughings. The seeds treatment should be done with fungicide like Thirum/ Captan/Carbendazim @ 3.0 g/kg seed $_{+}$ rhizobium culture @ 1 packet/10 kg + Trichoderma @ 4.0 g/kg at 4-5 days before sowing. The optimum sowing time is second fortnight of October with 100 kg/ha seed rate. At the time of field preparation 40 kg N, 40-60 kg $P_2O_{5:}$20-30 kg K_2O: 20 kg S: 15 kg $ZnSO_4$ should be applied as basal application. First irrigation should be given at 45 days and second, if needed, at pod filling stage. This genotype has good worth as a donor in future fieldpea breeding programme towards development of herbicide (metribuzin) tolerant varieties and in other basic studies.

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44. AL 1747 (IC0632084; INGR19076), a Pigeon Pea (*Cajanus cajan*) Germplasm Moderately Resistant to Pod Borer. Indeterminate Growth Habit. Early Maturing (130-140 days)

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Development of pigeonpea cultivars with resistance to pod borer has a considerable potential in pest management. The genetic stock, AL 1747, is moderately resistant to pigeonpea pod borers, *Helicoverpa armigera* and *Maruca vitrata*. It has indeterminate growth habit and belongs to early maturity group (130-140 days). It has been developed at Punjab Agricultural University, Ludhiana (Punjab) from a cross *Cajanus scarabaeoides* ICPW 213 (wild species) × AL 201 (cultivated variety) using backcross method followed by pedigree selection.

Morpho-agronomic characteristics: AL 1747 was evaluated under field conditions against pod borer in advance stage screening (multilocation) research trials at National level (2010-2013) at five different locations of India. The per cent pod damage in AL 1747 was 11.88% as compared to 13.25, 14.37 and 30.51% in local checks PAU 881, AL 201 and infester, respectively. At Ludhiana, AL 1747 recorded significantly lowest cumulative pod damage (12.11%) due to both borers (*M. vitrata* and *H. armigera*), whereas, susceptible infester recorded significantly higher cumulative pod damage of 29.97 per cent (Taggar *et al.*, 2015). On the basis of its performance, AL 1747 was recommended as a donor in the early maturity group as per the Proceedings and Recommendations of AICRP Pigeonpea Entomology, at Annual Group Meet of AICRP Pigeonpea held at MPKV, Rahuri, 2014 (Anonymous 2014).

Associated characters and cultivated practices: Under field conditions, AL 1747 registered significantly lower number of *Maruca* webs per plant and a lower percentage of pod damage as compared to other test genotypes evaluated under field conditions (Wubneh and Taggar 2016a).

Mechanism of resistance: Under artificial infestation, larval weight gain, per cent pupation and mean pupal weights were significantly lower when the *M. vitrata* larvae were fed on flowers of AL 1747, thus confirming antibiosis as a mechanism of resistance against the pod borer. Nutritional indices such as efficiency of conversion of ingested food (ECI), efficiency of conversion of digested food into body matter (ECD) and relative growth rate (RGR) for pod borer, *M. vitrata* were significantly lower in AL 1747 (Wubneh and Taggar, 2018).

Bases of resistance: Biochemical analysis of AL 1747 revealed a higher activity of polyphenol oxidase, diamine oxidase, polyamine oxidase and tyrosine ammonia lyase in pod wall infested with *H. armigera* (3.2, 2.9, 5.7 and 3.7 fold, respectively). Besides, higher status of ascorbate oxidase in both uninfested and infested developing seeds of AL 1747 was also observed earlier (Kaur *et al*., 2015). The condensed tannins were higher in developing seeds and pod wall after *H. armigera* herbivory (2.5 and 5.6 fold, respectively) in AL 1747 (Kaur *et al*., 2014). Studies conducted on biophysical basis of resistance to pod borer revealed that AL 1747 possessed significantly higher non-glandular trichome density on leaves and pods (Wubneh and Taggar, 2016b).

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45. VRPM-901-5 (IC0630592; INGR19077), a Pea (*Pisum sativum*) Germplasm Capable of Producing 3-5 Pods/Peduncle at Multiple Flowering Nodes (Multi-Podded Genotype)

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The inflorescence trait, number of flowers per peduncle/node is among one of the major yield attributes that has played a significant role in genetic improvement of legumes through various breeding programmes. Multi-flower is the condition when plant bears more than 2 flowers on a single flowering node/peduncle, alternatively referred to as many-flowered raceme or multi-podded phenotype. In garden peas, with very limited variation, single or double pod bearing habit is most common feature of present day cultivars. However as reported in pea and other legumes, development of three or more pods per node, while maintaining the pod size over one and two, appears an attractive option to increase the yield (Devi *et al*., 2018). The newly bred ‘VRPM-901-5’ is a mid-season pea genotype capable of producing 3-5 flowers/pods at multiple flowering nodes (Fig. 1). This genotype was developed by using single plant selection approach from a cross ‘VL-8 × PC-531’ made during 2011-12 at ICAR-Indian Institute of Vegetable Research, Varanasi located at 82°52′37″

E and 25°18′21″ N at an elevation of 83 m above the mean sea level.

Morpho-agronomic characteristics: 'VRPM-901-5' is a mid-season genotype that requires 50 days for days to first flowering and first picking can be done in 75-80 days after sowing. The first multi-flowering node appears on average 21st node. Pods are 7.5-9 cm in length and light green in colour. The yield of a cultivar is dependent on the number of flowers produced and percentage conversion of these flowers to pods. VRPM–901–5, appeared most promising for pod yield per plant (208g) and were significantly superior to the double-podded cultivars PC–531 (120g) and VL-8 (126g) as well to the single podded genotype NO-17 (60g) over study period of four years. (Table 1). The higher yield potential of VRPM–901–5 could be attributed to the formation of more number of flowers (48-52) and pods per plant (32-48) in the multi-podded line than in the double or single-podded lines. Further, this line was also having longer flowering duration and flowering starts from 7th week after sowing and continue up to 16th week after sowing (Devi *et al*., 2018). Our study also showed that VRPM-901-5 produced a significantly higher number of flowers than the double podded cultivars because of higher number of reproductive nodes per plant (Devi *et al.*, 2018).

Associated characters and cultivation practices: VRPM-905-1 is susceptible to powdery mildew; however, disease can be escape if sowing is done between last week of October to first week of November. Further, this genotype is tolerant to leaf minor and aphids under field condition. The optimum temperature for seed germination is about 22±2°C.Due to its prolific branching and longer plant height, a wider spacing of 40×10 cm is recommended than normal spacing of 30×10 cm. Standard cultivation practises can be adopted to raise a healthy crop.

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Table 1. Mean performance of 'VRPM-901-5' genotypes compared with triple, double and single podded cultivars through Tukey-Kramer's HSD test (pooled over years).

Years	Genotypes	MNFP/N	DTF	AFMFN	TFP	BPP	PDL	PD	PL	PW	PPP	APW	SPP	PH	YPP
Pooled over the years	VRPM-901-5	5	50.6b	21.1a	52.5a	2.3a	6.9b	0.23a	8.2b	1.06c	40.5a	5.7bc	5.1b	121.0b	208.0a
	VRP-500	3	49.3b	16.1b	33.9b	1.9bc	5.7c	0.23a	7.6b	1.38b	29.1b	6.0b	7.0a	80.3c	152.7b
	PC-531*	2	50.1b	0.0c	23.3c	1.6cd	8.3a	0.20b	9.3a	1.65a	19.6c	7.3a	7.0a	64.3d	120.5b
	VL-8*	2	69.3a	0.0c	35.9b	1.2d	5.6c	0.20b	6.2c	1.15c	29.0b	5.2c	6.7a	115.3b	126.9b
	NO-17*	1	50.0b	0.0c	25.5c	2.2ab	6.2c	0.20b	6.2c	1.12c	19.2c	3.3d	5.0b	163.8a	60.5c
	LSD (5%)		0.94	0.47	2.22	0.14	0.21	0.01	0.27	0.05	2.33	0.25	0.23	4.27	11.8
	R2		92.51	98.6	79.76	61.3	79.8	49.4	77.2	84.6	67.9	82.7	73.16	92.17	74.4

Values followed by the same letter in each column are not significantly different by Tukey-Kramer's HSD test

($p < 0.05$);MNFP/N=Maximum number of flower produced/node; DFF: Days to first flowering; AFMFN: Appearance of first multi-flowering node (No); TFP: Total number of flower produced; BPP: No. of primary branches per plant; PDL: Peduncle length (cm); PDD: Peduncle diameter (cm);PL: Pod length (cm); PW: Pod width (cm); PPP: No. of pods per plant; APW: Average pod weight (g); SPP: No of seeds per pod PH: Plant height (cm) and YPP: Yield per plant (g); *Multi-flowering nodes were not present in the double podded cultivar PC–531,VL–8 and single podded genotype No17.

46. BR-2 (IC0632605; INGR19078), a Medium Maturity Group Cauliflower (*Brassica oleracea*) Resistant to Downy Mildew with Resistance Governed by Single Dominant PPa3 Gene.

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Cauliflower is an important vegetable crop across the world. In India, it is being grown on 0.45 million ha area with annual production of 8.4 million tonnes (NHB Database, 2017). Downy mildew [*Hyaloperonospora parasitica* (Pers.: Fr) Fr. Constantinescu and Fatehi formerly *Peronospora parasitica*] is major disease of cauliflower which causes heavy toll to mid group of Indian cauliflower during November – December months. It also affects seed crop of early group cauliflower. Although, chemical control is effective but their use is of consumer health concerns. Hence, resistant varieties offers a more practical and long-term solution for effective control of downy mildew disease.

The 'BR-2' has strong resistance to downy mildew pathogen while this pathogen devastates the susceptible genotype 'PHJ'. Percent disease incidence (PDI) of the genotype was observed to be 6.5 % under artificial inoculation condition (Table 1) (Singh *et al*., 2013). Over the years, it maintained resistance level which indicates about durable resistance in BR-2. A single dominant gene *Ppa3* is responsible for downy mildew resistance in 'BR-2' and it has been mapped with three molecular markers $OPC14_{1186}$, $OPE14_{1881}$, and $ISSR23_{1103}$. Among them, $OPC14_{1186}$ was located 22.3 cM from *Ppa3* gene (on top-arm end) while $OPE14_{1881}$ and $ISSR23_{1103}$ flanked the geneat 10.6 cM and 26.4 cM, respectively on other side of the gene on linkage map (Singh *et al*., 2012).

Agro-morphological traits: The cauliflower genotype 'BR-2' is one of the BR-series progenies derived from a cross (S. No. 15×MGS-2-3) between two mid-late maturity group genotypes (Sharma *et al*., 1972). It has medium vigorous semi-erect plants with bluish green leaves. Plant stem is of medium length and plant spread is broad. Leaves are long and have prominent mid-rib, broad lobes and medium puckering on margins. Curds are very compact, cream white and medium in size and average curd weight is 710.5 g. It is mid-late group genotype (16-20 °C temperature for curd initiation) and attains curd maturity during December end to mid January. The crop becomes ready to harvest in 80-85 days after transplanting in its normal growing season. The flower colour of 'BR-2' is yellow, stalk length is medium and flowering occurs during February end to mid-March. The self-incompatibility is weak hence it produces seeds profusely. A single dominant gene *Ppa3* control of downy mildew resistance in 'BR-2' can be explored in hybrid breeding and to empower commercial susceptible varieties.

Table 1. Response of 'BR-2' and commercial cauliflower varieties to downy mildew

Genotype	Maturity group	Horticultural traits	Disease score (1-5 scale)*	PDI (%) through artificial inoculation	Disease reaction	Curd weight in well managed crop (g)
BR-2	Mid-late	Cream white, compact, solid curds	0.0-1.0	6.5	Resistant	710.5
Pusa Himjyoti 'PHJ'	Mid-late	White, compact curds	3.0-4.0	77.0-89.3	Highly susceptible	645.5
Pusa Sharad	Mid-early	White, compact granular curds	3.0-4.0	70.5-87.5	Highly susceptible	725.2

*On disease scale of 0 – 5; PDI = Percent disease incidence

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47. AHW/BR-5 (IC0627526) (IC0627526; INGR19079), a Watermelon (*Citrullus lanatus*) Germplasm with Stable Andromonoecious Sex Form

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Watermelon [*Citrullus lanatus* (Thunb.) Matsam. & Nakai] is an important crop belonging to Cucurbitaceae family with (2n=2x=22). Watermelon act as a coolant, thirst-quencher, detoxifier, diuretic, febrifuge, and, according to some natural healers, an aphrodisiac. The fruits of watermelon are fleshy, juicy and sweet. Mostly eaten fresh, provide a delicious and refreshing dessert in hot weather. The major nutritional components of the fruit are carbohydrates (6.4 g/ 100g), vitamin A (590 IU) and lycopene (4100 µg/ 100g), an anti-carcinogenic compound found in red flesh of watermelon which is beneficial in prevention of heart attacks and certain types of cancer. It is a rich in iron content among all members of cucurbitaceous crops. The rind is rich in citrulline, an amino acid that contributes to the removal of ammonia from the body and wound healing. Watermelon is native to Tropical Africa chiefly the Kalahari Desert (the current nations of Namibia and Botswana) where wild forms are still found (De Candolle, 1882). Whitaker and Davis (1962) also describe the existence of a secondary diversification centre in India. Watermelon is thought to have been domesticated in Africa at least 4000 years ago and now grown worldwide, particularly in regions with long, hot summers (Robertson, 2004).

A wide range of genetic variability has been observed in quantitative and qualitative traits of watermelon (Choudhary *et al.*, 2016). Watermelon is mainly monoecious (staminate and pistillate flowers borne on the same plant separately) in sex expression however, andromonoeciuos (staminate and perfect flowers borne on the same plant) sex form is also found rarely. Identified an andromonoecious plant from segeregating population and homogenized through repeated inbreeding. The developed material (AHW/BR-5; IC-0627526) possess unique trait *i.e.* stable andromonoecious sex form and able to set fruits under net house conditions without pollinators and produced viable seeds. AHW/BR-5produced round, red fleshed fruits having light green rind devoid of stripes in 80-85 days after sowing weighing 2.08-2.78 kg with 10.80-11.74% TSS and 1.38-1.92 cm thick rind.

Table 1. Salient characteristics of AHW/BR-5 (IC-0627526)

Trait	Description
Days taken to produce 50% pistillate flowers after sowing	45-50
Node number at which first female flower appeared	9-12
Days to first fruit harvest after sowing	80-85
Fruit weight (kg)	2.08-2.78
Fruit diameter (cm)	14.68-17.80
Rind thickness (cm)	1.38-1.92
TSS (%)	10.80-11.74
Sex form	Andromonoecious
Leaf shape	Pentalobate
Fruit shape	Round
Rind colour	Light green devoid of stripes
Flesh colour	Red

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48. NRCGCS-602 (HOS-130 or HOP_IL_130) (IC0630593; INGR19080), a Groundnut (*Arachis hypogaea*) Germplasm with High Oleic Acid (80%) Content

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Edible oil with higher oleic acid content reduces riskin cardio-vascular disease (CVD), while higher linoleic acid increases tumerogenesis and CVD. High oleic to linoleic acid ratio enhance oxidative stability of the oil. In normal groundnut oleic acid content ranges from 35% to 50%, while oleic to linoleic acid ratio ranges from 0.5 to 3.0. The groundnut germplasm, NRCGCS 602 with 81% oleic acid content and oleic to linoleic acid ratio of 30 has been developed through marker assisted breeding in ICAR-Directorate of Groundnut Research, Junagadh for the first time in India. The NRCGCS 602 is an advance breeding line developed from a cross between ICGV 06100×Sunoleic 95R. The ICGV 06100 is a high oil content (55%) breeding line developed by ICRISAT, Hyderabad, while the Sunoleic 95R is a high oleic acid content (80%) breeding developed by Florida Agricultural Research station, USA. ICGV 06100 was crossed with Sunoleic 95Rto introgress ahFAD2A and ahFAD2B mutant alleles, which enhance the oleic acid content in groundnut, from Sunoleic 95R to ICGV 06100. Allele-specific polymorphic chain reaction (AS-PCR) markers were deployed to select plants with ahFAD2A and ahFAD2B mutant alleles in F_1 and F_2 generations. While cleave damplified polymorphic sequence (CAPS) markers were used to select homozygous plants forahFAD2A and ahFAD2B mutant alleles in F_2 generation. NRCGCS 602 was selected in early generation (F_2) using AS-PCR and CAPS markers. The selected line was further advanced to F_7 generation for seed enhancement and biochemical analysis. Kernels harvested in *kharif* 2015, *kharif* 2016, Summer 2017 and *kharif* 2017 seasons were used in biochemical analysis. Biochemical analysis of NRCGCS 602over four seasons confirmed as high oleic as well as high oil content line. NRCGCS 602 has semi spreading growth habit with 30-35 cm height; light green leaves; average 4-5 primary branches. It produces 50%flowering in 25 days after sowing (DAS) and matures in ll5-120 DAS during rainy season. The genotype produces an average pod yield of 296 g per square metre with 7l% shelling outturn. Pods are medium in length having moderate reticulation, beak and constriction. Pods are mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 33 g and contain 55% oil. The genotype has 81% oleic acid content and 2.6% linoleicacid content with an oleic to linoleic ratio of 30. This will be a potential donor for high oleicas well as high oil content in groundnut.

49. NRCGCS-605 (HOS-145 or HOS-IL_MAS_145) (IC0630594; INGR19081), a Groundnut (*Arachis hypogaea*) Germplasm with High Oleic Acid (80%) Content

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Edible oil with higher oleic acid content reduces risk in cardio-vascular disease (CVD) while higher linoleic acid increases tumerogenesis and CVD. High oleic to linoleic acid ratio enhance oxidative stability of the oil. In normal groundnut oleic acid content ranges from 35% to 50%, while oleic to linoleic acid ratio ranges from 0.5 to 3.0. The groundnut germplasm, NRCGCS 605 with 81% oleic acid content and oleic to linoleic acid ratio of 30 has been developed through marker assisted breeding in ICAR-Directorate of Groundnut Research, Junagadh for the first time in India. NRCGCS 605 is an advance breeding line developed from a cross between ICGV 06100×Sunoleic 95R. ICGV 06100 is a high oil content (55%) breeding line developed by ICRISAT while Sunoleic 95R is a high oleic acid content (80%) breeding line developed by Florida Agricultural Research station, USA. ICGV 06100 was crossed with Sunoleic 95R to introgress *ahFAD2A* and *ahFAD2B* mutant alleles, which enhance the oleic acid content in groundnut, from Sunoleic 95R to ICGV 06100. Allele-specific polymorphic chain reaction (AS-PCR) markers were deployed to select plants with *ahFAD2A* and *ahFAD2B* mutant alleles in F_1 and F_2 generations. While cleaved amplified polymorphic sequence (CAPS) markers were used to select homogygous plants for *ahFAD2A* and *ahFAD2B* mutant alleles in F_2 generation. NRCGCS 605 was selected in early generation (F_2) using AS-PCR and CAPS markers. The selected line was further advanced to F_7 generation for seed enhancement and biochemical analysis. Kernels harvested in *kharif* 2015, *kharif* 2016, Summer 2017 and *kharif* 2017 seasons were used in biochemical analysis. Biochemical analysis of NRCGCS 605 over four seasons confirmed as high oleic as well as high oil content line. NRCGCS 605 has semi spreading growth habit with 25-30 cm height; light green leaves; average 4-5 primary branches. It produces 50% flowering in 25 days after sowing (DAS) and matures in 115-120 DAS during rainy season. The genotype produces an average pod yield of 286 g per square metre with 67% shelling outturn. Pods are medium in length having moderate reticulation, beak and constriction. Pods are mostly two seeded with rose colour kernels. Kernels are medium in size with hundred kernel mass of 33 g and contain 55% oil. The genotype has 81% oleic acid content and 2 % linoleic acid content with an oleic to linoleic ratio of 30. This will be a potential donor for high oleic as well as high oil content in groundnut.

50. CS 52-SPS-1-2012 (IC0630607; INGR19082), an Indian mustard (*Brassica juncea*) Germplasm with High Tolerance to Salinity (ECe 14-15 dS/m) and Alkalinity (pH 9.4-9.5). High 1000- Seed Weight (8.0-9.0g). High Photosynthetic Efficiency under Salinity Stress

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Indian mustard [*Brassica juncea* (L.) Czern and Coss] is an important oil-seed crop in the world and is grown in more than 50 countries across the globe, which often experiences saline stress as it is grown extensively in the arid and semi-arid regions of the world. Globally, 932.2 million hectare area is affected with salinity and sodicity stresses (Metternicht and Zinck, 2003), out of which, an area of nearly 6.73 million hectare is affected by these stresses in India (Singh *et al.*, 2014). Salinity stresses contribute to yield losses and this low economic yield is related to the crop's susceptibility. There is a greater need to improve crop plants for salinity tolerance. Hence, it becomes necessary to develop salt tolerant genotypes in Indian mustard. One of the approaches is the characterization of the available germplasm for identification of tolerant accession that provides an initial germplasm base/donor for breeding salt-tolerant crops.

At ICAR-Central Soil Salinity Research Institute (ICAR-CSSRI), Karnal, we have identified a mutant from CS 54 (Salt tolerant variety released by CVRC in 2005) population and maintained its genetic purity by individual plant selection method in salt affected soils for high seed yield and tolerance to soil salinity conditions. This genotype also was characterized for its photosynthetic efficiency using portable infrared gas analyzer [LI-6400XT, Li-COR, USA).

Morpho-agronomic characteristics: On the basis of 2014 to 2016 evaluation trials conducted for saline (Soil Salinity ECe 15 dS/m; Irrigation water salinity EC_{iw} 9-18 dS/m) and alkalinity (pH 9.4-9.5) conditions under field and pot house at ICAR-CSSRI, Karnal, the CS 52-SPS-1-2012 seed yield of 2.2 t/ha which was 22% and 46% higher than yields of two checks i.e. CS 54 and Kranti, respectively. It also provided 5% higher oil yield than Kranti and CS 54. This strain matures, on an average, in 122 days and takes 52 days to flower. The strain attains the height of approximately 166 cm and produces high number of primary branches (6), secondary branches (11), main shoot length (78) and 1000 seed weight (8.0-9.0g) (Table 1).

Table 1. Performance (yield contributing traits, adaptation traits, quality traits), tolerance to salinity/ alkalinity stress and biochemical evaluation data of CS 52-SPS-1-2012 under salt stress (ECe 10-14 dS/m and pH 9.4-9.5)

Name of Genotype	Year of reporting	Yield contributing traits under salt stress (ECe 10-14 dS/m and pH 9.4-9.5)							
		Plant height (cm)	No. of primary branches	No. of secondary branches	Main shoot length (cm)	No. of pods on main shoot length	No. of Seed/ pod	1000 Seed weight (g)	Yield (t/ha)
Kranti	2014	199	5	13	84	55	15	5.0	1.4
	2015	200	5	11	80	45	15	5.0	1.50
	2016	209	5	11	75	45	14	5.0	1.67
Mean		202.7	5.0	11.7	79.7	48.3	14.7	5.0	1.5
CS 54	2014	180	5	12	85	50	14	5.4	1.7
	2015	184	5	12	82	50	15	5.5	1.75
	2016	194	5	11	77	50	14	5.5	2.05
Mean		186.0	5.0	11.7	81.3	50.0	14.3	5.5	1.8
CS 52-SPS-1-2012	2014	164	5	10	76	48	14	9.0	2.1
	2015	165	6	12	80	50	15	9.1	2.15
	2016	170	6	12	80	55	15	8.9	2.38
Mean		166.3	5.7	11.3	78.7	51.0	14.7	9.0	2.2
Name of Genotype	Year of reporting	Quality traits under salt stress (ECe 10-14 dS/m and pH 9.4-9.5)							
		Oil (%)	Protein (%)	Erucic acid (%)		Crude fiber (%)			
Kranti	2014	39.0	19.8	45.6		10.5			
	2015	37.2	18.8	46.3		11.0			
	2016	38.2	18.2	46.0		11.2			
Mean		38.1	18.9	46.0		10.9			
CS 54	2014	37.6	19.9	48.3		10.1			
	2015	38.6	19.8	49.6		11.5			
	2016	39.0	19.0	49.0		11.0			
Mean		38.4	19.6	49.0		10.9			
CS 52-SPS-1-2012	2014	39.9	20.1	35.7		9.9			
	2015	39.8	20.2	34.6		9.5			
	2016	39.9	20.0	33.8		9.6			
Mean		39.9	20.1	34.7		9.7			

Associated characters: The net photosynthesis, stomatal conductance, water use efficiency and transpiration rate decreased substantially in the mustard at higher salinity (EC_{iw} 15 dS m^{-1}) as compared to control (Singh *et al*., 2019). The lowest reduction at 15 dS m^{-1} in photosynthesis rate (55.85%); stomatal conductance (33.33%); transpiration rate (48.19%) was recorded in CS 52-SPS-1-2012 while other genotypes surpasses more than 50% reduction in photosynthetic traits. Further, CS 52-SPS-1-2012 also showed least reduction in the instantaneous water use efficiency (14.80%) and CO_2 assimilation rate (26.74%) as compared to control. Looking to its high 1000 seed weight, better oil parameters and high photosynthetic efficiency under high salt stress condition CS 52-SPS-1-2012 is being proposed for registration as a national genetic stock/ donor for the development of salt tolerant mustard genotypes to affected soils and water conditions.

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51. DRMR10-40 (IC0632085; INGR19083), an Indian Mustard (*Brassica juncea*) Germplasm with Drought Tolerance

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DRMR 10-40 was derived from base population developed by intermating of DRMR 06-1942, DRMR 06-1946, NDYR 8, NDYR 10 and Rohini. The base population was grown for successive years for promising selections. During 2012-13 one genotype namely DRMR 10-40 was isolated and found promising under moisture stress conditions. The genotype was tested under AICRP-RM plant physiological trials during 2014-15 and 2015-16 at 5-7 locations (AICRP Rapeseed-Mustard, 2015 and 2016). Pooled summary over the years and locations indicate that proposed genotype has shown less reduction in RWC, SPAD, seeds/silique, 1000 seed weight and seed yield as compared to drought tolerant checks. The drought susceptibility index (DSI) value of the proposed genotype was lowest as compared to checks (Table 1). This indicates drought tolerant characteristics of the DRMR 10-40 and promising genotype can be utilized in breeding programme aimed at developing high yielding drought tolerant varieties.

Morpho-agronomic characteristics: Morphological traits of the DRMR 10-40 is as follows: Plant Height (cm),164; Days to maturity, 135; Primary branches/ plant (no.), 4.9; Secondary branches/plant (no.), 5.1; Main shoot length (cm), 75.5; Siliquae/plant (no.), 157; Siliqua length (cm), 3.7; Seeds/siliqua (no.), 14.1; 1000 seed weight (g), 5.4; Oil content (%), 41.9; Seed yield/ plant (g), 15.8.

Table 1. Pooled summary of physiological parameters (Drought tolerance) for proposed genetic stock DRMR 10-40 and checks in physiological trials during 2014-15 to 2015-16

Parameter (s)	No. of locations	DRMR 10-40	Check varieties		
			RB 50	Kranti	RH 406
Relative water content (Reduction %)	5	**8.1**	8.5	10.6	13.6
SPAD values (Reduction %)	5	**3.9**	5.5	3.6	10.5
Seeds/siliqua (Reduction %)	5	**5.5**	6.7	10.3	7.3
Seed yield (Reduction %)	7	**18.3**	18.1	18.7	18.5
Drought susceptibility Index (DSI)	7	**0.63**	0.69	0.70	0.74

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52. DRMR 2059 (IC0520764; INGR19084), an Indian Mustard (*Brassica juncea*) Germplasm with High temperature Tolerance at Seedling Stage. High Temperature Tolerance at Terminal Heat Stress

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DRMR 2059 (IC 520764; JBT-41/92) is an indigenous germplasm of Indian mustard (*Brassica juncea* L.) collected from Deoghar, Jharkhand. The DRMR 2059 was tested for physio-biochemical parameters and found superior over checks (BPR-543-2, BPR-543-4, Urvashi) in terms of percent increase in RWC (Bud stage, 0.97%; Pod stage, 5.94%) and CSI (pod stage, 2.53%) (DRMR Annual Report 2016-17). During screening for high temperature tolerance (seedling stage), DRMR 2059 recorded significantly superior seed yield/plant (19.5g/plant) over the best check BPR541-4 (16.9g/plant) (DRMR Annual Report, 2017-18). During 2018-19 DRMR 2059 was evaluated for high temperature tolerance at seedling stage both under laboratory and field conditions at 4 locations (Hisar, Kanpur, Ludhiana, Mumbai) along with checks under plant physiological traits (AICRP-RM, 2019). Seedling mortality ≤20% and DW/10 seedlings ≥ 40mg were used parameter for rating genotypes tolerant under controlled conditions and field conditions. Average seedling mortality (%) of DRMR 2059 under controlled conditions over four locations was 17.3% and DW/10 seedlings over four locations was 51.4 mg (Table 1). For field conditions genotype was tested at three locations (Dholi, Kanpur, Ludhiana). Based on mean of three locations for seedling mortality (17.5%) and DW/10 seedlings (6.0 g) DRMR 2059 rated tolerant to high temperature at seedling stress(Table 1). Field evaluation of DRMR 2059 over 4 locations (Dholi, Hisar, Kanpur and Ludhiana)showed yield reduction≤20% and HSI≥0.6 hence considered highly tolerant to terminal heat stress with relatively lesser depression in membrane stability, seed weight and seeds/siliqua (Table 1). Thus, DRMR 2059 possesses high temperature tolerance at seedling stage and terminal heat stress. This line can be used as a donor in mustard hybridization programme.

Morpho-agronomic characteristics: Morphological traits of the DRMR 2059 is as follows: Plant Height (cm),183; Days to maturity, 136;Primary branches/plant (no.), 6.4; Secondary branches/ plant (no.), 11.7; Main shoot length (cm), 81.7; Siliquae/plant (no.), 322; Siliqua length (cm), 5.6; Seeds/ siliqua (no.), 16.7; 1000 seed weight (g), 5.7; Oil content (%), 40.97; Seed yield/plant (g), 25.56.

Table 1. Pooled data of DRMR 2059 over locations (Four locations) during 2018-19 under AICRP-RM trials for different parameters

Genotypes	Controlled condition		Field condition		Genotypes	Membrane stability reduction (%)	Seed yield reduction (%)	HSI
	Seedling mortality (%)	DW/10 seedlings (mg)	Seedling mortality (%)	DW/10 seedlings (g)				
DRMR 2059	17.3	51.4	17.5	6.0	DRMR 2059	11.31	16	0.777
RGN 73 (ZC)	52.8	43.7	34.2	6.3	NRCHB 101 (ZC)	19.02	31.1	1.08
PM25 (NC)	23	49.3	19.8	5.5	PM-26 (ZC)	14.24	24.9	0.944
JD 6 (ZC)	30.2	41.1	33.1	3.8	JD 6 (ZC)	13.33	26.7	1.016
Kranti (NC)	44.3	42	27.4	5.1	Kranti (NC)	16.88	21.2	1.115
RH 749 (ZC)	30.7	45.2	23.2	5.7	RH 749 (ZC)	15.6	21.9	0.913

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DRMR Annual Report (2016-17) ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur 321303 Rajasthan, page 28-29

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53. DRMR 4001 (IC0632086; INGR19085), an Indian Mustard (*Brassica juncea*) Germplasm for Drought Tolerance

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Indian mustard (*Brassica juncea* L.) is an important oilseed crop of India. It is major source of income especially for marginal and small farmers in rainfed areas of 7 states. This is mostly grown on light textured soils with conserved moisture from monsoon rains. The crop inevitably suffers from moisture stress (drought) during reproductive period when stored water becomes depleted. This leads to a heavy loss of seed yield during severe conditions. Therefore, it is highly needed to have some good sources of drought tolerance that will be utilized for development high-yielding drought-tolerant varieties. The genotype DRMR 4001 was derived from a cross between BEC 107 (*B. juncea*) × HC 2 (*B. carinata*) at DRMR, Bharatpur. This genotype was isolated as a pure line through pedigree selection and found promising under moisture stress conditions. The genotype was tested under AICRP-RM plant physiological trials during 2015-16 and 2016-17 at 4-7 locations. Pooled summary over the years and locations indicates that proposed genotype DRMR 4001 has less reduction RWC, SPAD, 1000-seed weight, seed yield and other important traits as compared to drought tolerant checks. The drought susceptibility index (DSI) value of proposed genotype was lowest as compared to checks (Table 1). This indicates drought tolerant characteristics of DRMR 4001 and the genotypes can be utilized in breeding programmes for development of high-yielding drought-tolerant varieties. Hence, this promising line needs protection through germplasm registration.

Table 1. Pooled summary of physiological parameters (Drought tolerance) for proposed genetic stock DRMR 4001 and checks in physiological trials during 2015-16 to 2016-17

Parameter	No. of locations	DRMR 4001	Check varieties		
			RH 406	RB 50	Kranti
Relative water content (Reduction %)	7	9.9	12.9	10.0	13.4
SPAD Values (Reduction %)	7	15.4	15.6	17.4	5.0
Seed yield (Reduction %)	7	23.3	23.1	25.6	25.0
1000 seed weight (Reduction %)	6	11.4	13.1	15.6	16.2
Drought Susceptibility Index (DSI)	7	0.77	0.81	0.94	0.81
Seeds/siliqua (Reduction %)	7	10.9	10.3	10.0	8.1
Harvest Index (Reduction %)	7	10.1	15.8	14.8	13.1
Oil content (Reduction %)	4	2.9	2.6	3.5	3.0
Biological yield (Reduction %)	7	17.7	14.2	19.0	19.5

54. DRMR 4005 (IC0632087; INGR19086), an Indian Mustard (*Brassica juncea*) Germplasm with Thermo Tolerance at Juvenile Stage Coupled with High Seed and Oil Yield

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Indian mustard (*Brassica juncea* L.) is an important oilseed crop of winter in India & plays a vital role in edible oil pool of the country. High temperature at juvenile stage (germination / seedling stages) is becoming a severe threat in major mustard growing states like Rajasthan and Haryana and badly affecting the production. An optimum temperature around 25°C is required for proper germination and seedling establishment in this crop. However, due to changing climatic conditions the temperatures during last many years crossed this limit in major mustard areas and soil temperature reaches up to 40-42°C affecting seed germination and plant stand in the field. This prevents early sowing, generally on conserved moistures recommended in many areas. Therefore, it is highly needed to have germplasm lines with heat tolerance at seedling stage and will be utilized in breeding programmes.

The genotype DRMR 4005 was derived from a cross between SEJ-2 × K 28 at DRMR, Bharatpur. It was isolated as a pure line through pedigree selection and found promising for thermo tolerance at seedling stage coupled with high seed & oil yield and suitable for early sown conditions. The genotype was tested under AICRP-RM plant physiological trials during 2017-18 and 2018-19 at 6 locations (environments) and plant breeding trials during 2016-17 and 2017-18 at 11locations. Pooled summary over the years and locations indicates that proposed genotype DRMR 4005 has less seedling mortality (<20%), high RWC

(%), SPAD values (chlorophyll), dry seedling weight along with high seed & oil yield as compared to heat tolerant (seedling stage) checks (Table 1). Proposed genotype DRMR 4005 has 8.39 to 18.19% higher oil yield and 8.47 to 17.49 % higher seed yield over the checks. This indicates thermo tolerant (at seedling stage) characteristics of DRMR 4005 and it can be utilized in breeding programmes for development of high-yielding thermo (heat) tolerant varieties with high seed and oil yield, as it has better yield traits. Hence, this promising line needs protection through germplasm registration.

Table 1. Pooled summary of physiological parameters (thermo tolerance) and performance for oil yield & contributing traits of proposed genetic stock DRMR 4005 and checks under AICRP-RM trials during 2016-17 to 2018-19.

Parameters	No. of locations	DRMR 4005	Check varieties			
			PM 25	JD 6	Kranti	PM 28*
Seedling mortality (%)	6	16.6	23.4	33.2	30.8	--
Dry weight (g) of 10 seedlings	6	7.8	8.6	7.6	5.5	--
SPAD values (Chlorophyll content)	6	40.8	40.1	35.3	37.9	--
Relative water content (%)	6	79.1	74.5	68.2	72.4	--
Seed yield (kg/ha)	11	2330	1983	2131	--	2148
Oil yield (kg/ha)	11	955	808	868		881
1000 Seed weight (g)	11	4.7	4.9	4.4	--	4.3
Oil content (%)	11	41.0	40.8	40.7	--	41.0
Days to maturity	11	131	124	133	--	127

***Latest Release check for early mustard in Zone II.**

55. IC0268345 (IC0268345; INGR19087), a Linseed (*Linum usitatissimum*) Germplasm with High Seed Oil Content (43.65%) and More Number of Primary Branches

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Linseed is one of the oldest domesticated crops in the world and is considered to be originated and domesticated in Indian sub-continent. Two distinct morphotypes namely seed-type and fibre/flax type are recognized in linseed. In India, it is grown as *rabi* oilseed crop mainly utilized for industrial purpose and as edible oil. Breeding for high oil content is one of the main objectives of linseed breeding. Wide diversity in linseed germplasm indicates a considerable potential for improving this crop for both agronomic and quality traits (Kaur *et al.*, 2017). A wide range of variation in oil content with mean of 38.3% was observed in Canadian collections of 2934 accessions of linseed from 72 countries (Diederichsen and Fu, 2008).In this perspective, one landrace accession IC0268345 from Dindori district of Madhya Pradesh was identified for high oil content up to 43.65% (Table 1) along with other desirable agronomic traits such as number of primary branches per plant, moderately

Table 1. Year wise data of oil content in linseed accession IC0268345

Year	Field evaluation location	Laboratory- Biochemical analysis	Oil Content (%)		
			IC0268345	Check var.1 (Rashmi)	Check var. 2 (RLC-76)
2014-15	ICAR-NBPGR, New Delhi	ICAR-NBPGR	41.78*	37.50	39.10
2015-16	ICAR-NBPGR, New Delhi	ICAR-NBPGR	42.45*	38.20	38.90
2016-17	ICAR-NBPGR, Issapur farm, New Delhi	Division of Biochemistry, ICAR-IARI	43.50	38.15	38.45
2017-18	ICAR-NBPGR, New Delhi	Division of Biochemistry, ICAR-IARI	43.65	37.35	38.30
Mean			42.85**	37.80	38.68

*adjusted pooled mean value is 42.7% for year 2014-15 and 2015-16 as mentioned in Kaur *et al.,* 2018.
**significantly superior at $P_{0.001.}$

high seed yield per plant. The identified accession can have potential utility in linseed breeding program for central India particularly Madhya Pradesh – the major linseed producing state in terms of area, production and productivity. In addition, the landrace (IC0268345) *per se* holds greater promise as perfect germplasm accession for participatory breeding which has implications on social welfare of resource poor farmers as well as conservation of genetic diversity *in situ*.

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56. NRC 142 (IC630595; INGR19088), a Lipoxygenase 2 Free Soybean (*Glycine max*) Germplasm. Free from Kunitz Trypsin Inhibitor

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Soybean was introduced in India with the expectation that the crop being one of the most economical sources of protein would combat rampant protein malnutrition among masses. Apart from the proteins, presence of several nutraceutical molecules reduces the risk of the onset of lifestyle diseases (Kumar *et al.*, 2010). However, soybean did not gain popularity as a protein source despite the declining per capita availability of pulses, the staple source of protein in Indian diet. Presence of anti-nutritional factor, namely, Kunitz trypsin inhibitor (KTI) and off-flavour generating lipoxygenases in soybean grains constrain their utilization in food uses. Kunitz trypsin inhibitor present in soybean seeds affects the digestibility of proteins and if left active in the soy products may cause pancreatic hypertrophy. Lipoxygenase is the off-flavour generating enzyme which exists in 3 isozymic forms, namely, lipoxygenase 1, lipoxygenase 2 and lipoxygenase 3 in soybean seed. These isozymes act upon polyunsaturated fatty acids, when the seeds are crushed to process soy food products, thereby releasing aldehyde and ketone compounds. Of these 3 isozymes, lipoxygenase 2 (Lox 2) is the principal contributor to the off-flavour. Though both KTI and lipoxygenase 2 are heat labile but the heat treatment incurs extra cost and affects the solubility of proteins. Genetic elimination of these two formidable undesirable components from soybean seeds is the dire need of soy food industry. ICAR-IISR has already developed and commercialized KTI free soybean genotypes, namely, NRC 101 and NRC 102. The institute has developed NRC 127, which is the first KTI free soybean variety released for farmers in Central zone. The institute has also developed and commercialized lipoxygenase 2 free soybean, namely, NRC109 to soy food industries. However, soy food industries are seeking soybean genotypes free from KTI as well as lipoxygenase 2.

To develop soybean genotype free from both KTI and lioxyegnase-2 for soy food industries, NRC 142 was developed from a triple cross JS 97-52 x PI 596540 x PI 542044, through marker assisted forward breeding. PI 542044 and PI 596540 were the donors for null alleles of KTI and lipoxygenase 2, respectively. Presence of null alleles of lipoxygenase-2 and KTI in the plants during advancement of generations of JS 97-52 × PI 596540 × PI 542044 were tested using null allele-specific primers of Lox2 designed by Shin *et al.* (2012), and that of KTI designed by Moraes *et al.* (2006) and deployed in development of KTI free lines (Kumar *et al.*, 2013). For this purpose, genomic DNA was extracted from the young leaves using the CTAB method and used as template for amplification using the null allele specific primers for lipoxygenase-2 and KTI. Presence of null allele of lipoxygenase-2 plants in each generation was validated by rapid assay in the seeds, according to Suda *et al.* (1995) and presence of null allele of KTI was validated by native PAGE. Template DNA isolated from NRC142, JS 97-52, PI 596540 and PI 542044were amplified with null allele specific primers of lipoxygenase 2 and KTI. Null Lox2 specific marker generated amplicons of 550 bp size in NRC142, similar to the donor parent PI 596540 but no amplicon in JS 97-52 and PI 542044, while null KTI specific marker generated amplicons of 420 bp in NRC142 similar to donor parent PI 542044, while no amplicon in JS 97-52 and PI 596540 The seed extracts of NRC142 along with its parents were subjected to native PAGE. A 21Kda band of KTI was observed in JS97-52, while it was absent in NRC142 and the donor of null allele PI 542044.The seed extracts of NRC142 along with its parents were also subjected SDS PAGE and rapid test for testing absence of lipoxygenase.

Morpho-agronomic characters: The plant of NRC142 bears white flowers in 40 days, attains height of 75 cm, and reaches harvest maturity in 98 days. The seeds are of light-yellow colour with black hilum, and weight of 100 mature seeds (10% moisture) is 14.4 g. The yield potential of this genotype is 3.2 tonnes/ha. The genotype would serve as excellent raw material for soy food industry, and more importantly, being high yielding with additional quality traits can fetch better prices to farmers. This is the first genotype developed in India, which is free from lipoxygenase 2 as well as Kunitz trypsin inhibitor.

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57. Dun-nun II-2-15/EC34101 (EC34101; INGR19089), a Photoinsensitive Soybean (*Glycine max*) Germplasm. Source of Recessive Photoperiodic Allele e3

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Soybean (*Glycine max* (L.) Merr.) is a photoperiod sensitive short-day plant and its different accessions starts flowering when the day length, which depends on latitudes, is less than their critical day length. Although soybean adapts to a very wide range of latitudes, its individual accessions adapt to a narrow latitudinal band. India lies in the latitudes between 6°-37° and latitude specific adaptation is observed in soybean accessions and varieties (Bhatia *et al*, 2003). At IISR, Indore, we have identified six photoinsensitive accessions. Soybean germplasm accession EC 34101 originally acquired from Hungary has been identified as photoperiod insensitive through screening of 2071 germplasm accessions under long day conditions created by extending day length with incandescent light (ILD) (Bhatia *et al*, 2008; Singh *et al*, 2008; Gupta *et al.*, 2017). EC 34101 flowered in same number of days to flower in ILD as in ambient day length showing no effect of photoperiod on flowering. EC 34101 has been characterized for genes underlying photoperiod insensitivity and maturity traits using allele specific markers, and its genotype has been determined as *E1E1E2E2e3e3E4E4*(Gupta *et al*, 2017). Polymorphic markers between six photoinsensitive accessions (MACS 330, EC 325097, EC 325118, EC 333897, EC 34101, EC 390977) and 25 varieties/accessions have been identified and diversity studies have placed MACS 330 in a separate cluster and EC 333897, EC 34101 and EC 325118 are grouped together (Gupta *et al*, 2014).

Characteristic botanical and morpho-agronomical features of EC 34101 are given in Table 1 and its consistent flowering response over latitudes, in comparison to photosensitive varieties Pb1, JS 335, JS 80-21 and Type 49, is shown in Figure 1.

Genotype EC 34101 is a useful germplasm source for breeding of photo-insensitivity, earliness and semi-determinate growth habit in soybean. These traits are desirable for development of soybean cultivars for growing in new areas across latitudes for wider adaptation and increasing cropping intensity of the crop. Identified allele specific markers would be useful for gene pyramiding for earliness and photo-insensitivity using marker assisted breeding.

Table 1. Salient characteristics/chief botanical and morpho-agronomical description of soybean genotype EC 34101

Trait	Value	Trait	Value
Hypocotyl pigment	Green	Early Plant Vigour	Good
Leaf color	Green	Leaf Shape	Intermediate
Number of leaflets	3	Stem determination	Semi-determinate
Flower Colour	White	Photoperiod sensitivity score	Photoinsensitive
Pubescence	Present	Pubescence color	Gray
Pubescence density	Normal	Pubescence type	Erect
Seed Colour	Yellow	Hilum colour	Brown
Number of primary branches	2.8	Days to flower	30 (30)*
Plant height	33.0 cm	Days to maturity	84 (82)*
Pod color at maturity	Tan	No. of seed/pod	2.0
100-seed weight	12.0	No. of nodes/plant	9.4
Number of pods/plant	36.4	Pod colour	Light Brown
Cotyledon colour	Yellow	Seed coat colour	Yellow
Seed Coat Pattern	Light hilum	Hilum Colour	Brown

*Value in parenthesis denotes flowering in extended day length conditions.

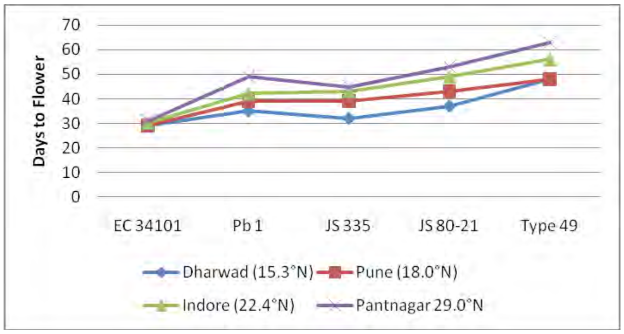

Fig. 1. Latitudinal consistency of photoinsensitive accession EC 34101 for days to flowering

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58. AGS 25 (EC150149; INGR19090), a Soybean (*Glycine max*) Germplasm with Source of Earliness

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Soybean (*Glycine max* (L.) Merr.) is a photoperiod sensitive short-day plant and its different accessions starts flowering when the day length (depends on latitudes) is less than their critical day length. Soybean genotypes grown at higher latitudes have high critical day length and are photoinsensitive as they can flower under very high day length. However, when soybean is grown near equator or where days are short or under short day conditions like delayed sowing due to late monsoon arrival, it flowers precociously without sufficient vegetative biomass to support good grain yield. For such conditions long juvenile trait is useful as it allows plant to remain in vegetative conditions even under extreme short day conditions. Commercial soybean cultivation in countries near equator (lower latitudes) became possible only after the identification of long juvenile trait (Hartwig, 1970). Delayed flowering in long juvenile lines results in the gain of more height, nodes, grain yield and other agronomic characters (Lawn, 2011a&b).Introduction of this trait has helped extend soybean cultivation in lower latitudes and made Brazil the second largest soybean producing country in the world (Gavioli, 2013).India lies in lower latitudes between 6°-35°N latitudes. Soybean is a rainfed crop in India and its sowing starts with the onset of monsoon. Under delayed monsoon conditions soybean sowing is undertaken in shorter day length condition which results in yield penalty due to early flowering. Although sources of long juvenility are known but performance of these resources is poor in Indian conditions. We have identified a novel long juvenile germplasm resource AGS 25 by screening of germplasm under delayed sowing conditions (ICAR-IISR annual reports 2010-11, 2011-12). This germplasm has been tested for adaptation in AICRP multi-location germplasm evaluation trials and it has shown the potential to delay flowering and gain high biomass in these locations (AICRPS annual report 2014-15 and 2015-16). This germplasm was hybridized with popular soybean varieties JS 93-05 and JS 95-60 and long juvenility trait was found to be governed by single recessive gene (ICAR-IISR annual report 2013-14). AGS 25 has been used in breeding programmes and many high yielding long juvenile advanced breeding lines have been developed and are under AICRPS trial (ICAR-IISR Indore annual report 2016-17 and AICRPS technical programme 2019-20). Recombinant inbred lines of JS 93-05 x AGS 25 and JS 95-60 x AGS 25 have been developed and used for QTL identification and gene responsible for long juvenility was identified on chromosome 16 where earlier reported long juvenile gene *e9* resides. A novel recessive allele of *E9* developed due to single nucleotide polymorphism has been identified and attributed for long juvenile response of AGS 25. Sequencing of AGS 25 at known photoperiodic loci identified its genotype as E1E1E2E2E3E3E4E4Dt1Dt1.

Characteristic botanical and morpho-agronomical features of AGS 25 are given in Table 1.

Genotype AGS 25 is a useful germplasm source for breeding for long juvenility and wider adaptation. These traits are desirable for development of soybean cultivars suitable for sowing under wider array of sowing dates and latitudes. Identified new allele has been converted to CAPS marker and would be helpful in breeding for long juvenility using marker assisted breeding.

Table 1. Salient characteristics/chief botanical and morpho-agronomical description of soybean genotype AGS 25

Trait	Value	Trait	Value
Hypocotyl pigment	Purple	Early Plant Vigour	Good
Leaf color	Light Green	Leaf Shape	Intermediate
Number of leaflets	3	Stem determination	Semi-determinate
Flower Colour	Purple	Photoperiod sensitivity score	Photosensitive
Pubescence	Present	Pubescence color	Tawny
Pubescence density	Normal	Pubescence type	Semi-appressed
Seed Colour	Yellow	Hilum colour	Brown
Plant height	91.4	Days to flower	64
100-seed weight	6.6	Days to maturity	106
Cotyledon colour	Yellow	Seed coat colour	Yellow
Seed Coat Pattern	Dark hilum	Strophile at hilum	Present
Surface lustre	Dull	Lodging score	Severe
Pod Colour	Light Brown	Primary branches/plant	6.2
Pods/plant	50.4	No. of nodes/ plant	18.4

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59. EC174527 (EC174527; INGR19091), a Basil (*Ocimum basilicum*) Germplasm with Essential Oil Rich in Linalool Content (~ 61.18 ± 4.41%) in Oil Isolated from Aerial Plant Parts

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The genus *Ocimum* L. (Lamiaceae) is an extremely versatile and largest group consisting of about 150 specieswhich are found in tropical and sub-tropical regions of Asia, Africa and South America. Most members of this genus are annual or perennial, highly aromatic, branched herbs or shrubs. *Ocimum basilicum* L. (Sweet basil) is one of the most important species which is planted as a popular culinary and medicinal herb. The basil essential oils are usually extracted from the leaves and flowering tops of basil plants. The plant shows great chemical and morphological variability because of the abundant cross pollination, inter-specific hybridization, polyploidy. The essential oils exhibited a wide and varying array of chemical compounds, depending on variations in chemotypes, leaf and flower colors, aroma and origin of the plants. There are significant differences in the chemical composition and amounts and kinds of aromatic components in the essential oils of basil depending on the species/variety and environmental conditions of the cultivation locations (Pushpangadan and Bradu, 1995). According to the chemical composition and geographical origin, *Ocimum* species were classified into three large groups: European type, Exotic or Reunion type and African type. Lawrence (1988) established four essential oil chemotypes (methyl chavicol, linalool, methyl eugenol and methyl cinnamate) and also numerous subtypes. The chemical composition of basil is highly variable depending largely on the source, and can vary by extraction method and with developmental stages (Verma *et al*., 2013). Variations in chemical composition of basil oil play an important role in evaluating their utilization and value for industrial applications (Raina *et al*., 2017 and 2018)

Ocimum species have been extensively used as spices, flavouring agents and as source of commercial essential oils. These are known for their diverse use in folk medicine for the treatment of various gastric and urinary diseases, insomnia, inflammation and constipation. The essential oil obtained from these species has found important application in perfumery, flavour and pharmaceutical and medicinal uses. *Ocimum* species are reported to have diverse biological activities like antibacterial, antimicrobial, antioxidant, antipyretic, insecticidal, antispasmodic. These volatile oils have been applied in perfumery, to inhibit growth of microorganisms, in food preservation and in aromatherapy.

The present exotic germplasm collection of *O. basilicum* EC174527 was imported from Germany in 1986. The germplasm was grown in Experimental Fields of ICAR-NBPGR, New Delhi for characterization and evaluation of agro-morphological and quality traits for four years. It was evaluated for the economically important quality trait of essential oil obtained from aerial parts of plant by hydrodistillation. Detailed chemical profiling of essential oil isolated from aerial plant parts of EC174527 by GC/MS exhibited linalool-rich chemotype was present in this collection. Validation of this value-rich superior accession of *Ocimum* germplasm was performed over consecutive four years for major aroma compound and identified trait-specific value-rich germplasm accessions EC174527 (linalool 61.18 ± 4.41%). Linalool is an important compound highly prized for its use in perfume and flavor industry. The essential oils of basil extracted from leaves and flowering tops are used in food flavours, dental and oral products, in fragrances and in traditional medicines. Essential oils derived from *O. basilicum* offers a bright future for perfumes and flavours industry.

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60. IC599290 (IC599290; INGR19092), a Velvet Bean (*Mucuna pruriens)* Germplasm with High L Dopa Content in Seeds (7.1% DWB)

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Mucuna pruriens (L.) DC *var. pruriens* Wilmot-Dear (family Fabaceae) is an important medicinal plant, which has long been used as a traditional medicine in India due to the presence of bioactive compound L-DOPA (L-3,4-dihydroxy phenylalanine) in seeds and serves as potential drug for the treatment of Parkinson's disease. The plant is commonly known as Kewanch or Kaunch in Hindi, Atmagupta in Sanskrit and Velvet bean in English. It is a twining annual legume, originally from Eastern India and Southern China and later widespread in other parts of the tropics including Central and South America. The genus *Mucuna* consists of about 120 – 130 species of annual and perennial legumes and about fifteen species are found in the lower hill slopes and plains of India. It is widely used in traditional Ayurvedic, Unani, and Homoeopathic system of Indian medicine for the management of male fertility, as neuro-protective, anti-snake venom/ scorpion stings and an aphrodisiac (Sathiyanarayanan & Arulmozhi 2007).

It is a constituent of more than 200 indigenous drug formulations. Active compound L-DOPA (L-3,4-dihydroxy phenylalanine), a non-protein amino acid is a precursor of the neurotransmitter dopamine and is being used in the treatment of Parkinson's disease a degenerative disease of the nervous system and is characterized by muscular rigidity difficulty with balance and walking, depressions and dementia. L-DOPA, a dopamine precursor, either alone or in combination with and aromatic amino acid decarboxylase inhibitor is the most effective drug for the treatment of this disease, since dopamine fails to pass through the blood brain barrier. Use of biological sources for production of L-DOPA, is always desirable and advantageous because the chemical synthesis results in racemic DL-mixture, which is inactive and further separation of enantiomerically pure L-dopa from this mixture, is very difficult and cumbersome. In addition, D-DOPA interferes with the activity of dopa decarboxylase, the enzyme involved in the production of dopamine in the brain. L-dopa isolated from *Mucuna* was found to be more effective than the synthetic product.

Keeping in view the increasing demand for herbal drugs, importance of this species and vast diversity of *Mucuna* germplasm available in Indian sub-continent, efforts were made to characterize diverse germplasm of *Mucuna pruriens* collected from wild habitats of Odisha located in Eastern coastal areas of India. A total of 34 accessions were collected, characterized and evaluated in respect of agro-morphological and economic traits at NBPGR Regional Station, Cuttack.

Agro-morphological characterization and chemical evaluation of *M. pruriens* germplasm resulted into identification of a value-rich genetic stock of *M. pruriens* IC599290(collector number RCM/GD/75)with high L-dopa content of 7.1 % on dry weight basis in seeds by HPTLC for four years 2013-2014 to 2016-2017 (Raina and Misra, 2018). This genotype was identified for high L-DOPA content in seeds against normal range of 2.2 to 5.3 reported in Indian conditions. This germplasm was collected from wild areas of Jajpur district in the coastal delta zone of Odisha. Pods contained 5 to 6 seeds, black, shining, glossy and 0.9 - 1.1 x 0.76 - 0.80 cm. This genetic stock can be used as a source for L-DOPA for commercial cultivation and exploitation for the pharmacological properties. It may be an affordable alternative for patients suffering from Parkinson's disease.

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61. CSIR-IHBT-CL-Y-1 (IC0623597; 19094), a Calla Lily (*Zantedeschia elliottiana*) with Trumpet Flower Shape. Bright Yellow Flower Colour and Stalk Length >40cm

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The parental genotypes of *Zantedeschia elliottiana* CSIR-IHBTCL-ZE-1 (light yellow coloured) and CSIR-IHBT-CL-ZE-2 (Red purple coloured) were crossed and variable colours of calla lilies were obtained in the progenies which were morphologically characterized for floral traits. The genotype CSIR-IHBT-CL-Y-1 has been selected for its unique cylindrical trumpet flower shape and attractive bright yellow colour. The genotype along with parents were evaluated for two years with respect to flower production potential and other agronomic attributes *viz*., flower stalk length, stalk diameter, leaf size and numbers, plant height, number of flowers per plant and number of shoots under field and protected conditions. The hybrid F_1 genotypes were morphologically characterized under field conditions with respect to floral traits and evaluated for agronomic performance over a period of two years and CSIR-IHBT-CL-Y-1was found superior to the parental lines. The genotype has been released as cultivar 'Him Sumukh' (CSIR-IHBT-CL-Y-1) by CSIR-Institute of Himalayan bioresource Technology, Palampur, having high vegetative propagation potential for commercial utilization.

62. HIM SHWETA (CSIR-IHBT-CL-W-1) (IC0623597; 19094), a Calla lily (*Zantedeschia elliottiana*) with White Flower Colour, Large Spathe and Stalk Length (>80cm)

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In *Zantedeschia aethiopica*, hybridization programme was undertaken using two parental genotypes CSIR-IHBT-CL-ZA-1 and CSIR-IHBT-CL-ZA-2. Variable floral shapes of calla lilies were obtained in the progenies which were evaluated for agronomic traits under protected and field conditions. The genotype CSIR-IHBT-CLW- 1 has been selected for desirable flower shape and white colour. The evaluation of selection along with parents was done for two years with respect to flower production and agronomic parameters viz. flower stalk length, stalk diameter, leaf size and numbers, plant height, number of flowers per plant and number of shoots and the selection was found promising compared to parental lines. The genotype has been released as cultivar 'Him Shweta' (CSIR-IHBT-CL-W-1) by CSIR-Institute of Himalayan Bioresource Technology, Palampur, having high vegetative propagation potential for commercial utilization.

63. CSIR-IHBT-Gr-13-1 (IC0623707; 19095), a Gerbera (*Gerbera jasmeonii*) with Double Flower Shape. Standard Size (>10cm Flower Diameter)

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Hybrid F_1 genotypes of gerbera were developed through controlled crossing program and mature seeds obtained from different cross combinations were used for the establishment of *in vitro* gerbera cultures. Seeds were cultured on MS basal medium and the developing micro-shoots from seeds were further cultured on MS media supplemented with different doses of growth regulators to achieve shoot proliferation. Of the different media, highest number of micro-shoots, number of leaves and leaf length were observed in MS medium supplemented with 1 mg/L BAP + 0.03mg/L IBA + 0.025 mg/L NAA which gave best proliferation among the gerbera genotypes. Half strength MS medium supplemented with 0.4 mg/L IBA was found best for *in vitro* rooting. Rooted plantlets were successfully hardened in trays filled with moist sand and transferred to sleeves for cultivation in soil. The hybrid F_1 genotypes were morphologically characterized under field conditions with respect to floral traits and evaluated for agronomic performance over a period of two years. Based on mean performance of hybrid gerbera genotypes compared to respective parents, gerbera genotype CSIR-IHBT-Gr-13-1was found promising having double flower shape of standard size (flower diameter of 10.5 cm) and is red in color. The genotype has been released as cultivar 'Him Gaurav' by CSIR-Institute of Himalayan bioresource Technology, Palampur, with high micro-propagation potential for commercial utilization.

64. CSIR-IHBT-Gr-24-6 (IC0623708; 19096), a Gerbera (*Gerbera jasmeonii*) with Semi Double Flower Shape. Standard Size (>10cm flower diameter). Yellow Orange Flower Colour

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Parental lines of gerbera were used controlled crossing program and mature seeds obtained from different cross combinations were used for the establishment of *in vitro* gerbera cultures. Seeds were cultured on MS basal medium and the developing micro-shoots from seeds were further cultured on MS media supplemented with different doses of growth regulators to achieve shoot proliferation. Of the different media, highest number of micro-shoots, number of leaves and leaf length were observed in MS medium supplemented with 1 mg/L BAP + 0.03mg/L IBA + 0.025 mg/L NAA which gave best proliferation among the gerbera genotypes. Half strength MS medium supplemented with 0.4 mg/L IBA was found best for *in vitro* rooting. Rooted plantlets were successfully hardened in trays filled with moist sand and transferred to sleeves for cultivation in soil. The hybrid F_1 genotypes were morphologically characterized under field conditions with respect to floral traits (Figure 1) and evaluated for agronomic performance over a period of two years. Based on mean performance of hybrid gerbera genotypes compared to respective parents, gerbera genotype CSIR-IHBT-Gr-24-6 was found promising having semi-double flower shape of standard size (flower diameter of 11.7 cm) and is yellow orange in color. The genotype has been released as cultivar 'Him Aabha' by CSIR-Institute of Himalayan bioresource Technology, Palampur, which also has high micro-propagation potential for commercial utilization.

65. IIHRV1 (IC0624189; INGR19097), a China Aster (*Callistephus chinensis*) Germplasm for Flower colour: NN155D, White group, Fan 4

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China aster is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for loose flower, cut flower, landscape, floral decoration, making garlands and *venis* (Rao *et al.*, 2012). The China aster germplasm IIHRV1 is derived from cultivar Arka Poornima through individual plant selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13^{o} 58' N Latitude, 78^{o}E Longitude and at an altitude of 890 meter above mean sea level), India. The germplasm IIHRV1 is unique for white flower colour (NN155D), semi-double flower form with pseudo ray florets.

Morpho-Agronomic Characteristics: The China aster germplasm IIHRV1has average plant height (54.50cm), number of branches per plant (9.75) and number of flowers per plant (20.00).

Associated characters and cultivation practices: The flowers of China aster germplasm IIHRV1 is white (White group, NN155D, Fan 4), semi-double flower type with 4-5 rows of pseudo ray florets. It has average flower head diameter (3.09cm), length of outer sepals (2.19cm), length of pseudo ray florets (0.66cm), breadth of pseudo ray florets (0.25cm), length of disc florets (0.61cm) and vase life (10.33days).

It grows best in open and well drained loamy soil with soil pH 6 to 7. A temperature of 20^{o} to 30^{o}C during day and 15^{o} to 17^{o}C during night with relative humidity of 50-60% is most suitable for its growth and flowering. Thirty days seedlings are transplanted at a spacing of 30 cm x 30 cm. Plants are pinched 35 to 40 days after transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra. The germplasm IIHRV1 is suitable for cut flower and floral decoration.

Table 1. Morpho-agronomic description of China aster germplasm IIHRV

Traits Description	Average value
Plant height (cm)	54.50
Number of branches per plant	9.75
Number of flowers per plant	20.00
Flower head diameter (cm)	3.09
Length of outer sepals (cm)	2.19
Length of ray florets (cm)	0.66
Breadth of ray florets (cm)	0.25
Length of disc florets (cm)	0.61
Vase life (days)	10.33
Flower colour as per RHS Colour Chart	White group, NN155D, Fan 4
Flower form	Semi-double
Utility	Cut flower and decoration

References

Rao TM, Rajiv Kumar and PB Gaddagimath (2012) China aster. *Extension Bulletin*. The Director. ICAR-IIHR, Bengaluru, pp 1-16.

66. IIHRV2 (IC0624190; INGR19098), a China Aster (*Callistephus chinensis*) with New Flower Form: Semi-double with Pseudo Ray Florets

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China aster is commercially important popular annual flowering plant belonging to the family Asteraceae. In India, it is grown traditionally for loose flower, cut flower, landscape, floral decoration, making garlands and *venis* (Rao *et al.*, 2012). The China aster germplasm IIHRV2 is derived from cultivar Arka Violet Cushion through individual plant selection and it was developed at ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka (13^{o} 58' N Latitude, 78^{o}E Longitude and at an altitude of 890 meter above mean sea level), India. The germplasm IIHRV2 is unique for violet flower colour (N81A), semi-double flower form with pseudo ray florets.

Morpho-agronomic characteristics: The China aster germplasm IIHRV2 has average plant height (64.50cm), number of branches per plant (12.00) and number of flowers per plant (32.00).

Associated characters and cultivation practices: The flowers of China aster germplasm IIHRV2 is violet colour (N81A, Purple Violet group, Fan 2), semi-double flower form with 4 to 5 rows of pseudo ray florets. It has average flower head diameter (2.79 cm), length of outer sepals (1.59cm), length of pseudo ray florets (0.55 cm), breadth of pseudo ray florets (0.21 cm), length of disc florets (0.48cm) and vase life (10.93 days).

It grows best in open and well drained loamy soil with soil pH 6 to 7. A temperature of 20^{o} to 30^{o}C during day and 15^{o} to 17^{o}C during night with relative humidity of 50-60% is most suitable for its growth and flowering. Thirty days seedlings are transplanted at a spacing of 30 cm × 30 cm. Plants are pinched 35 to 40 days after transplanting. The China aster is extensively grown in Karnataka, Tamil Nadu, West Bengal and Maharashtra. The germplasm IIHRV2 is suitable for cut flower and floral decoration.

Table 1. Morpho-agronomic description of China aster germplasm IIHRV2

Traits Description	Average value
Plant height (cm)	64.50
Number of branches per plant	12.00
Number of flowers per plant	32.00
Flower head diameter (cm)	2.79
Length of outer sepals (cm)	1.59
Length of ray florets (cm)	0.55
Breadth of ray florets (cm)	0.21
Length of disc florets (cm)	0.48
Vase life (days)	10.93
Flower colour as per RHS Colour Chart	N81A, Purple Violet group, Fan 2
Flower form	Semi-double
Utility	Cut flower and floral decoration

References

Rao T M, Rajiv Kumar and P B Gaddagimath (2012) China aster. *Extension Bulletin*. The Director. ICAR-IIHR, Bengaluru, pp 1-16.

67. IC0625848 (IC0625848; INGR19099), a Fruit Fly Resistant Ber (*Ziziphus mauritiana*) Germplasm

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Indian jujube (*Ziziphus mauritiana* L.) commonly known as ber, belongs to the family *Rhamnaceae*, is mainly distributed in the tropic zone of southern Asia, Australia, and Africa including Taiwan and China. The productivity and quality of ber fruits are adversely affected by a number of insect pests among them fruit fly (*Carpomiya vesuviana*) considered the most serious pest which can cause damage up to 80% of the crop under severe condition (Cherian and Sunderam, 1941). Although these insects can be controlled by applying insecticides on the crop (Gyi *et al.*, 2003), inbuilt genetic resistance offers better option to control the incidence of insects. In susceptible cultivars the infestation starts with the fruit setting. The adult female lays eggs singly by inserting its ovipositor in the young developing fruit. After 2 to 5 days the larvae hatch, start feeding on the pulp and make galleries in it. Generally, only one larva is found in one fruit. The excreta of the larva accumulate in the galleries, results in rotting of the fruit. Infested fruits become deformed and their growth becomes stunted. A large number of such fruits drop off. The larval stage lasts 9 to 12 days. Full grown (6 mm length) larva finds its way out by making a hole in the fruit skin and drops to the ground. The larva bores down to soil upto the depth of 2 to 12 cm where it pupates and occasionally pupation takes place within infested fruits (Bagdavadze *et al.*, 1977). The pupal period lasts about 2 weeks after which the adult fly (5 to 8 mm long and 3 mm broad) emerges. Pairing and oviposition occur during day light and at night, fly usually rests in the canopy and it completes two generations per year (Berdyeva, 1978).

At Jodhpur Regional Station of ICAR-NBPGR, the 80 live trees of wild, land races and cultivated varieties are being maintained in the field gene bank. Trait specific mean values of three replications over four years of some of the selected cultivars of ber have been recorded for fruit and seed characters. Data were recorded on infestation of fruit fly on the selected cultivars at the interval of 10 days in three trees during 2017-18 and 2018-19. In all cases, 10 randomly selected fruits were examined carefully for oviposition marks, occurrence of exit hole in the fruits and number of larva present inside fruit through peeling of fruits with knife to confirm the stone and fruit fly damage and percentage of infested fruits was calculated. TSS of these fruits was also calculated .It is evident that a large genetic variation is present among cultivars for fruit fly resistance. "*Tikdi*" the land race of ber that had been collected and planned by DP Chopra, Economic Botanist, at ICAR-NBPGR Regional Station, Jodhpur on 28-06-1968 had shown absolute resistance to fruit fly. It also appears from the concentration of TSS in the ber fruits is not having any impact on resistance or susceptibility for fruit fly.

The fruits of *Tikdi* rarely contain insect larva and their excreta. There was no visible oviposition marks or exit hole in its fruits over the growing period. In contrast all other accessions taken for study had fruit fly infestation. The grown plants of *Tikdi* are highly tolerant to drought and resistant to frost. Owing to these qualities it is used as a root stock for other commercial varieties of *ber*. Trees are vigorous with upright growth habit and have higher leaf fodder production potential.

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68. IC0625849 (IC0625849; INGR19100), a Stoneless Ber (*Ziziphus mauritiana*) Germplasm

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Indian jujube (*Ziziphus mauritiana* L.) commonly known as ber, belongs to the family *Rhamnaceae*, is mainly distributed in the tropic zone of southern Asia, Australia, and Africa including Taiwan and China (Pasternak *et al*., 2009). The ripen fruits of the plant are mostly consumed raw but sometimes they are stewed also (Morton, 1987). In ber fruits its pulp portion is soft and edible whereas stone portion is very hard and not edible. The 60-90% part of the fruit is made up of inedible stone in most of the popular ber varieties (Om Vir *et al.*, 2015). Pulp character is an important character of ber fruit if breeding is aimed for long storage life (Krishna *et al.* 2014). The pulp: stone ratio is an important character as it indicates towards the edible portion in the fruit (Saran *et al.*, 2006). Thus there is need for improvement of *Z. mauritiana* for its fruit quality. The choice of suitable cultivars is of paramount importance for its success. The twelve accessions of ber germplasm, maintained in the field gene bank of National Bureau of Plant Genetic Resources Regional Station Jodhpur were characterized and compared on the basis of fruits characters *viz.*, fruits, pulp and presence or absence of stone in the fruits. Accordingly, observations were recorded on ten fruits from each replication (with three replications) in each case for four years *i.e*. year 2014-15 to 2017-18. Observation on ripen fruits and stones were recorded when fruits had attained its full size and were ready for harvesting. The chief characteristic features of different ber accessions under study are presented in Table 1 to Table 4. A landrace IC0625849 was recorded with a unique trait *i.e.*, the stone part of the fruit of this landrace is merely absent and small, soft and shriveled edible seeds were present, thus this landrace is named as stoneless ber, whereas, in all other accessions the large sized stone is present. It is observed that 97-99 % part of the fruit of the IC0625849 is made up of edible fleshy pulp. While in other accessions only 10 to 40 % part of the fruit was made up of edible pulp and rest of the part (60-90 %) of the fruit is made up of stone that is inedible. The highest pulp: stone ratio was noted in IC0625849 and it was recorded as high as 100 per cent, while the least pulp: stone ratio was recorded in IC-0625848 among the studied germplasm. Complete absence of stone in stoneless ber could be useful in breeding programme for development of ber fruit cultivars with stoneless fruits.

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69. MSH/14-113 (IC0630606; INGR19101), an Interspecific Potato Hybrid [Interspecific Potato Somatic Hybrid P8 (*Solanum tuberosum* + *S. pinnatisectum*) × cv. Kufri Jyoti (*S. tuberosum*)]. with Diverse Genetic Base Very High Resistance to Potato Late Blight Disease. High Tuber Dry Matter Content

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Interspecific potato hybrid (MSH/14-113) is a back-cross progeny of advanced stage clonal selection (BC_1-C_5). MSH/14-113 was developed by crossing somatic hybrid clone 'P8' and potato cv. Kufri Jyoti. The parent 'P8' is an interspecific somatic hybrid and was produced by protoplast fusion between *Solanum tuberosum* dihaploid 'C-13' and wild potato species *S. pinnatisectum*. MSH/14-113 possesses wider genetic base from cultivated (*S. tuberosum*) and wild species (*S. pinnatisectum*). MSH/14-113 possesses very high resistance to late blight disease- the most devastating disease of potato, and also has high dry matter content- an important for processing trait. This shows successful exploitation of interspecific potato somatic hybrid 'P8' in developing a promising advanced stage interspecific potato hybrid (MSH/14-113) with high resistance to late blight and high dry matter content. Besides, SSR alleles (103 and 144 bp) were linked to the interspecific potato hybrid MSH/14-113 were identified for genetic fidelity, of which SSR allele 103 bp was introgressed into MSH/14-113 from the parent P8, having very high resistance to late blight. A few DUS descriptors of MSH/14-113 are: purple sprout, semi-compact plant foliage, tall plant height, green stem colour, open leaf structure, small leaf length, narrow leaf width, anthocyanin colouration is present on flower bud, white-purple flower corolla, small flower size, yellow anther colour, irregular anther cone, normal pistil, longer stylar length, white cream tuber colour, smooth skin, ovoid shape, shallow eye depth and white tuber flesh colour.This interspecific potato hybrid with diverse genetic background, having very high resistance to late blight disease and high tuber dry matter content has potential to employ in potato breeding programmes to widen the cultivated gene pool.

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70. Allohexaploid (H1) (IC0628060; INGR19102), an Allohexaploid (*Brassica juncea* + *Sinapis alba*) Germplasm resistant to *Alternaria brassiceae* and *Sclerotinia sclerotiorum*. Tolerant to temperature

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The Brassicas serve as important sources for vegetables, oilseeds and cultivated throughout the word. The crop suffers from biotic factors such as *Alternaria* blight caused by the *Alternaria Brassicae* and *Sclerotinia* stem rot caused by the *Sclerotinia sclerotiurum* are the major limiting factors along with the abiotic factors high temperature and drought. The yield reduction due to *Alternaria* blight up to 47% and severe conditions raised upto 70 percent (Kolte *et al.*, 1987 and Shukla, 2005). The *Alternaria* blight does not only causes reduction in seed yield but also adversely affects oil and meal quality. The resistance sources for these diseases are not available within cultivated gene pools. However the wild relative of Brassica, namely, *Sinapis alba,* has been reported to possess resistance to *A. brassicae* (Brun *et al.*, 1988; Conn *et al.*, 1988; Sharma *et al.*, 2002) and *Sclerotinia sclerotiorum* (Morrall and Dueck 1882, Li *et al.*, 2009). Therefore, with the aim of introgression of these valuable genes into cultivated Brassicas. We have developed somatic hybrid (H1) through PEG mediated protoplast fusion. The hypocotyl protoplast of *Brassica juncea* RLM-198 and mesophyll protoplast of *Sinapis alba* were isolated and fused as per previous standardized protocols (Kirti *et al.*, 1990). We have standardized the regeneration media and found very good regeneration frequency. The regenerated shoots were attained roots into half MS medium and acclimatized very well in the net house conditions. The hybridity was confirmed through morphological, molecular and cytological basis. The hybrid carried complete nuclear genomic constitution of the parent (amphidiploid *B. juncea* =AABB and diploid *S. alba*=SS). The hybrid acquired organelles (chloroplast and mitochondria) from *B. juncea*. The chromosomal constitution of the Allohexaploid Brassica (H1) was confirmed through mitotic counts and Genomic In situ Hybridization (GISH) by using the FITC labeled *S. alba* genome as a probe. The hybrid possessed total sixty chromosomes in their somatic cells. The Allohexaploid (H1) obtained thirty six chromosomes from *B. juncea* and twenty four chromosomes from *S. alba.* All the twenty four chromosomes of *S. alba* were hybridized with FITC labeled *S. alba* probes. The present somatic hybrid maintained meiotic pairing between the homologous chromosomes. Therefore, bivalent formation was maintained and monovalent/ multivalent formation was not evident.

Morpho-agronomic characteristics: The somatic hybrid was grown vigorously in net house as well as in field conditions. The plant attained the height approx 320 cm when sown in the last week of October. The prominent trichomes were found on the stems and leaves of the somatic hybrid. The pollen viability of the Allohexaploid Brassica (H1) was found more than 90% and very good female fertility. This is a first instance when somatic hybrid possessed very good male and female fertility. Due to normal meiosis, the hybrid is stable over the generations.

Associated characters and cultivation practices: The Allohexaploid (H1) was found resistant to *Alternaria* blight and *Sclerotinia* stem rot during the screening up to six seasons at four different environments along with hot spot conditions to the disease in four successive years. The present allohexaploid showed temperature tolerance up to 40°C during the flowering and seed setting stages. The normal meiosis and stability of the somatic hybrid proved the feasibility of the cultivated Brassicas at the hexaploid level. However, the cultivated Brassicas exist at the tetraploid level now but beyond this ploidy level, the fertile Brassicas are not reported so far. Therefore, this is a novel genetic resource for carrying high degree of resistance for two major diseases of oilseed brassicas such as *Alternaria* blight and *Sclerotinia* stem rot. Allohexaploid Brassica (H1) will be unique because of their crossable nature to all oilseed and vegetable Brassica. Thus, it would be used as genetic resource for resistance breeding and development of climate resilient varieties. The population derived from this somatic hybrid (H1) can be exploited for searching resistance genes of *Alternaria* blight and *Sclerotinia* stem rot.

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71. J.93-58 (IC0625993; INGR19103), a Potato (*Solanum tuberosum*) Germplasm with Better Water Use Efficiency than Popular Cultivars. High Yielder

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Improving water use efficiency is required in response to growing water scarcity. In India Potato is grown under diverse agro-climatic conditions. Many areas in India have limited water resources for irrigation. Keeping this in view a line J.93-58 was bred at Central Potato Research Station Jalandhar that can give comparatively higher yield at relatively lower water availability.

Morpho-agronomic characteristics: Tubers of J.93-58 are oblong shape, white skin, with shallow eye depth and cream flesh colour. The flower corolla colour is white. Foliage is compact and plant is medium tall. Leaflets are ovate lanceolate. Sprout colour is white-green. It is a high yielding with very good water use efficiency as it produce yield better than popular varieties at lower doses of water. J.93-58 was selected from amongst 100 genotypes, mainly advance breeding lines tested under water deficient and sufficient conditions. Evaluation for water use efficiency was done for 4 consecutive years during 2012-2016. The trial was laid out with three soil moisture regimes i.e. 0.20-0.25, 0.40-0.45 and 0.60-0.65 bars/atm soil moisture tension at 15 cm soil depth. The germplasm, J.93-58 performed well under various soil moisture regimes. The yield performances of J.93-58 at various soil moisture regimes were better than that of popular cultivars Kufri Pukhraj and Kufri Bahar. J.93-58 also had better water use efficiency than cultivars Kufri Pukhraj and Kufri Bahar (Table 1).

Associated characters and cultivation practices: This accession is medium maturing and susceptible to late blight and early blight diseases.

Table 1. Water Use Efficiency (q/mm) of advance hybrids/genotypes

Treatment	Water Use Efficiency (q/mm)				Mean
	2012-13	2013-14	2014-15	2015-16	
At wet regime (0.20-0.25 bars)					
J. 93-58	1.198	1.540	1.299	1.373	1.353
K. Bahar	1.132	1.355	1.184	1.105	1.194
K. Pukhraj	1.286	1.379	1.312	1.191	1.292
CD at 5%	0.079	0.077	0.096	0.067	0.048
At moist regime (0.40-0.45 bars)					
J. 93-58	1.319	1.763	1.520	1.434	1.509
K. Bahar	1.260	1.548	1.360	1.145	1.328
K. Pukhraj	1.489	1.678	1.434	1.287	1.472
CD at 5%	0.068	0.105	0.103	0.080	0.037
At semi-dry regime (0.60-0.65 bars)					
J. 93-58	1.609	2.106	1.766	1.641	1.780
K. Bahar	1.421	1.861	1.515	1.358	1.539
K. Pukhraj	1.555	1.981	1.690	1.479	1.676
CD at 5%	0.111	0.138	0.120	0.099	0.047