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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXVIIIth meeting held on June 2nd, 2018 at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 46 germplasm lines out of 54 proposals considered. The information on registered germplasm is published with the purpose to disseminate the informationto respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. RP Bio Patho-2 (IC0626002; INGR18001), Rice (*Oryza sativa)* with Broad-Spectrum Resistance for Leaf Blast (Pi-54) and Bacterial Blight (Xa21 & xa13). Present in the Elite Genetic Background of Improved Samba Mahsuri and 94.9% Recurrent Parent Genome Recovery. Moderate Resistance for Neck Blast, Sheath Blight, Sheath Rot and Brown Spot besides Blast Resistance.

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The Near isogenic line (NIL), RP Bio Patho-2 (RP Bio 5864 Patho-2-18-5) was developed at Indian Institute of Rice Research (ICAR-IIRR) by making a cross between Improved Samba Mahsuri as a recurrent parent with Tetep as a donor (*Pi-54*) through Marker assisted backcross breeding. This NIL contains two bacterial blight resistance genes *i.e.Xa21* and *xa13* from Improved Samba Mahsuri and one blast resistance gene *Pi-54* from Tetep.

Associated Characters and Cultivation Practices

Phenotyping for blast and bacterial blight resistance: RP Bio Patho-2 was screened for blast and bacterial blight resistance in Uniform blast nursery (artificial screening method) and leaf clip inoculation method (pot culture) respectively during the years 2009 & 2010. The result showed a mean resistance score of 1.0 for leaf blast and 1.0 for bacterial blight disease.

Phenotyping for multiple disease resistance in various screening nursery trials: RP Bio Patho-2was screened under donor screening nursery of AICRIP 2011 to 2016 in replication for multiple disease resistance. The result showed that the RP Bio Patho-2 has promising resistance for leaf blast with susceptibility index (SI) of 4.5, 3.4, 2.9, 3.3, 3.6 & 3.3 respectively. Further the line was screened under National Screening Nursery of AICRIP 2015 to 2016 in replication for multiple disease resistance.

The result showed that the RP Bio Patho-2 has promising resistance for leaf blast with susceptibility index (SI) of 2.8 & 3.0 and bacterial blight with susceptibility index (SI) of 3.7 & 3.6 during 2015 and 2016 respectively, whereas recurrent parent Improved Samba Mahsuri showed mean SI of 5.6 and 7.5 (for leaf blast), 3.0 and 3.0 (for BB) during 2015 and 2016 respectively.

The susceptible checks for leaf blast are HR-12 and TN_1 showed mean susceptibility index (SI) of 7.8, 8.5 and 5.0, 5.7 during 2015 & 2016 and susceptible checks for bacterial blight are TN1 and BPT5204 showed mean susceptibility index (SI) of 7.5, 8.3 and 6.0, 7.0 during 2015 and 2016 respectively. Based on various screening nursery trials conducted across country it is confirmed that NIL (RP Bio Patho-2) showed promising resistance against blast and bacterial blight diseases

Genotyping: The RP Bio Patho-2 has been checked for the presence of blast resistance gene (*Pi-54*) and bacterial blight resistance genes (*Xa21+xa13*) using linked markers Pi-54 MAS (*Pi-54*), pTA248 (*Xa21*) and xa13 promoter (*xa13*). Back ground selection with 118

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SSR markers revealed that, this line (RP Bio Patho-2) has 94.9 % recurrent parent genome recovery.

Morpho-agronomic characteristics: The Identified NIL (RP Bio Patho-2)was evaluated for their agronomic and grain quality traits as compared to the recurrent parent Improved Samba Mahsuri at the field farm Indian Institute of Rice Research (ICAR-IIRR), Hyderabad during *kharif* season with two replications. RP Bio Patho-2showed (13.5%) yield advantage over Improved Samba Mahsuri. The Identified NIL (RP Bio Patho-2) showed excellent blast and bacterial blight resistance, yet it is 10 days early maturing than Improved Samba Mahsuri and shorter than recurrent parent (Improved Samba Mahsuri).

This line could be used as elite genetic stock for resistance to rice blast and bacterial blight disease. It could be involved as donor parent for developing resistance varieties for rice blast and bacterial blight disease.

Important Agro-morphological Characteristics of RPBioPatho-2 & Improved Samba Mahsuri

Character	RPBioPatho-2 (NIL)	Improved Samba Mahsuri (RP)
Spad values	39.6	36.0
No.of tillers per plant	21	18
Plant height at maturity	80.0 cm	89
No.of panicles per plant	19	15
Time of heading	90 days (Medium duration)	110
Basal leaf sheath Color	Green	Green
Stem Length	Very short	Very short
Decorticated grain type	Medium Slender	Medium Slender
Decorticated grain color	White	White
Decorticated grain Aroma	Absent	Absent
Resistance genes	*Pi-54+Xa21+xa13*	*Xa21+xa13+xa5*
Resistance to	Rice blast isolate	Susceptible
Resistance to	Rice BB isolate	Resistant

2. RPBio4918-228S (IC0626001; INGR18002), Rice (*Oryza sativa)* Introgression Line Resistant to Brown Plant Hopper (BPH) *Nilaparvata lugens*. Possesses High Resistance in Vegetative and Reproductive Stages. Present in Background of Popular Commercial Variety Swarna (MTU 7029).

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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 turn 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.

Since 1970'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 area gainst 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 ismost 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 identify donors 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 RPBio 4918-228S: 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 81848 S) is a wild rice accession with AA genome. A backcross strategy was followed to develop the line RP Bio 4918-228S. 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 RPBio4918-228S 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 (TN1) checks. 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). The lines were screened for three seasons in the DRR greenhouse during 2009-2010. In the repeated screening in the greenhouse, out of the 250 BILs from Swarna/O. *nivara* screened, six BILs were found to be resistant and RP BIO 4918 228S was one of the BILs with brown plant hopper resistance with damage score of 1.2. 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). The RP bio 4918-228S was screened along with germplasm accessions in 2012 in DRR greenhouse and was found to be resistant with a damage score of 1.4 (Akanksha *et al.,* 2017).

Table 1. Reaction of RP Bio 4918-228S to BPH under natural and artificial infestation during 2009-2014

Year/located on		2009	2012 MRST								2013 MRST						2014 MRST					2012
		DRR	DRR	CBT	MTU	RPR	LDN	CTC	PNR	GGV	DRR	CBT	MND	LDN	GGV	PNR	DRR	LDN	CBT	MTU	GGV	DRR
Greenhouse	RP bio 4918-228S	1.2	2.3	3.0	5	0	1.1	1.0			3.4	5.0	3.0	1.3		1.7	2.5	3.2	5.0			1.4
	PTB 33	1.2									1.2	3	1.0	1.3		2.0	1.8		5.0			
	TN1	9	9	9	9	9	8	9			9	9	9	9		9	9	9	9			
	Swarna	9																				
Field	RP bio 4918-228S								4.8/ hill	1.0					3.0					3.0	1.0	
	PTB 33														0							
	TN1								5/hill	3.0					5					9.0	9.0	

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

Table 2. Morphological characters of RP Bio 4918-228S and Swarna

Name of the variety	:	RP bio 4918-228S	Swarna
Plant height	:	84.6	101.27
Plant type	:	dwarf	Semi-swarf
No. of tillers /plant	:	12	11.6
Days to 50% flowering	:	114	119.2
Seed to seed duration	:	145	148.15
Panicle type	:	compact	compact
No. of panicles /plant		11	10.64
Panicle exsertion	:	Well exserted	Well exserted
Panicle weight		2.4	2.65
Awning	:	present	absent
Yield/plant (g)		13.8	18.57
1000 grain weight	:	13.0 g	15.1 g
Kernel length	:	7.308333	6.3mm
Kernel breadth	:	2.116667	2.1mm
L/B ratio	:	3.46	3
Grain type	:	Medium slender	Medium
Kernel appearance	:	Very occasionally chalky	Very occasionally chalky
Milling recovery	:	63%	68.6%
Head rice recovery (HRR)	:	45%	56.3%
Alkali spreading value (ASV)	:	4	5
Amylose content (AC)	:	24.8	26.5
Gel consistency	:	24	43
Yield potential		4.6 t/ha	5.5-6.0 t/ha

This BIL RP Bio 4918-228S was screened in hotspot locations for brown planthopper resistance in the multilocation testing in 2012 in Multiple Resistant Screening Trial (MRST) and performed better and promising in 8 out of 8 tests/locations and recorded damage score of <3 in six locations and 5 in one location (total 8 *viz.,* DRR, Coimbatore, Cuttack, Raipur, Ludhiana, Maruteru, Pantnagar and Gangavathi). 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 2012 AICRIP DRR and Progress report 2012 AICRIP DRR). In 2013, RP Bio 4918-228S was retested in Multiple Resistant Screening Trial (MRST) and was found to be resistant and recorded a damage score of <3 at 4 locations viz., Pantnagar, Ludhiana, Mandya and Gangavathi and <5 in two locations *viz.,* DRR and Coimbatore. The susceptible check TN1 recorded a damage score of 9 (Ref: Screening nurseries Entomology Pathology AICRIP 2013, DRR AICRIP Progress report 2013, DRR Annual report 2013-14). In 2014, RP bio 4918-228S was retested in Multiple Resistance Screening Trial (MRST) and was found to be resistant in five locations viz., DRR, Maruteru and Gangavathi with a damage score of <3 and in Ludhiana and Coimbatore with a damage score of <5. The susceptible check TN1 recorded a damage score of 9 (Ref: DRR Screening nurseries 2014 AICRIP DRR and DRR AICRIP Progress report 2014, Proceedings of the 49th Annual Rice Research Group Meetings, 2014, Proceedings of the 50th Annual Rice Research Group Meetings, 2015, DRR Annual report 2014-15). In the 49th Annual Rice Research Entomology Group Meetings, 2014, RP Bio 4918- 228S was identified as resistant to brown planthopper and recommended for registration with NBPGR (Ref. Proceedings of the 49th Annual Rice Research Group Meetings, 2014). In the 50th Annual Rice Research Entomology Group Meetings, 2015, RP Bio 4918-228S was identified as resistant to brown planthopper (Ref. Proceedings of the 49th Annual Rice Research Group Meetings, 2014).

Simultaneously, RP Bio 4918-228S was evaluated for agronomic and quality traits. It is an intermediate, mid duration culture (145 days) possessing medium slender grains. Qualitywise, it recorded medium head rice recovery (HRR) of 45% and intermediate amylose content 24.8% (Table 2).

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

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3. NH686 (RP Bio 5477-NH686) (IC0626284; INGR18003), a Rice (*Oryza sativa*) Germplasm Tolerant to Low P Condition. Dark Green Leaves and Grain Yield Six fold more than N22 under Low P Condition. Early Duration, Broad Leaves and Medium Bold Grains.

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NH686 or SM686 is Ethyl Methane Sulphonate induced mutant of an upland rice cultivar Nagina 22 (N22). N22 is a well known early maturing, drought and heat tolerant aus variety giving yield of 12 to 15 g/plant. Mutants are valuable resources for causal gene discovery and use in crop improvement. The mutant was developed as a part of DBT funded project "Characterization and use of EMS induced mutants of rice variety N22 for yield, drought and phosphorus use efficiency" at ICAR-IIRR, Hyderabad. The M2 mutants were first screened along with wild type N22 and check varieties Rasi and Kasalath in low P field conditions (2Kg/ha P) and NH686 was identified as the best low-P tolerant mutant in terms of tiller number and grain yield. The grain yield of NH686 and N22 in normal soil is 23g and 14g per plant while in low P condition it was 7g and 1 g/plant respectively. Thus, NH686 is tolerant to low P condition showing 6 fold more grain yield than N22.

Table 1. AICRIP data of NH686

IET No. 23834 (RP Bio5477-NH686)				
			Concentration (ppm)	
Year	Number of locations	Grain yield (Kg/ha)	Zn	Fe
2013	12	3835	17.27	9.27
2014	14	3535	18.68	3.19
2015	19	3450	19.0	3.7

Table 2. Important agro-morphological characteristics of NH686

Characteristics	
Days to flowering (50%)	76
Plant height (cm)	70
Number of tillers	24
Plant type	Stay green
Flag leaf	Erect
Panicle	Well exerted
Stem thickness	Medium
Grain shape	Medium bold
Stem colour at nodes	Absent
Number of grains/ panicle	150
Spikelet fertility (%)	96
Yield / plant (g)	23

Apart from tolerance to low P condition, NH686 is tolerant to multiple abiotic stresses and also has high Zn concentration in polished rice as evaluated under AICRIP biofortification trial for 3 years (Table 1). The mutant is stable and breeding true as it was tested in normal (60Kg/ha) and low P (2Kg/ha) soil till M9 generation. NH686 has highest grain yield and per day productivity among mid early lines. Additionally, the mutant shows heat tolerance characteristics. The agro-morphological characteristics of NH686 evaluated under normal soil are shown in Table 2.

NH686 is a stable, elite rice genetic stock tolerant to low P condition in field. It can be used as a donor parent or as a check when screening for rice varieties with tolerance to low P.

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4. DBW-EMS 98 (IC0625990; INGR18004), a Wheat (*Triticum aestivum*) Chlorophyll Deficiency Mutant.

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Fast evolving field of functional genomics calls for use of effective tools and techniques for understanding the mechanisms underlying traits of importance. Study of functional basis of gene function through study of trait mutants is an effective tool in functional genomics. A mutant population of wheat cultivar DPW621-50 derived through 0.7 per cent Ethyl Methanesulfonate (EMS) treatment was screened for mutant phenotypes three stations of ICAR-IIWBR at Karnal, Hisar, Dalang Maidan during 2014-2016 (Table1).

Large numbers of altered phenotypes were observed along with variation for yield parameters. Lines showing stable altered phenotypes for various traits were isolated. Efforts are underway to study the genetics of these mutants. One of the mutants DBW-EMS98 is deficient in chlorophyll content at seedling stage and remained pale green throghout its life cycle compared to its wild type parent DPW 621-50. Physiological characterization of this mutant has showed that it consistently showed lower total chlorophyll content, Chlorophyll a&b,

NDVI, photosynthesis and lower stomatal conductance throughout its life cycle compared to its wild type parent DPW 621-50 (Table 2). Though the mutant has recovered greenness to some extent compared to seedling stage still the significant difference was seen between parent and mutant throughout its life cycle.

Table 1. Confirmation of mutant traits at three sites over two years

Year	Location	Line	Chlorophyll mutant
Year 1 (2014-15)	Karnal	EMS-98	Yes
	Hisar	EMS-98	Yes
	Dalang Maidan	EMS-98	Yes
Year 2 (2015-16)	Karnal	EMS-98	Yes
	Hisar	EMS-98	Yes
	Dalang Maidan	EMS-98	Yes

Thus, DBW-EMS98 is a stable mutant wheat line deficient in chlorophyll at seedling stage and will act as a valuable source in understanding functional basis of genes and pathways involved in chlorophyll synthesis and photosynthesis. This chlorophyll mutant may serve as an effective tool for functional genomics studies of wheat photosynthesis**.**

Table 2. Comparison of mutant and parent for different chlorophyll associated traits

Trait	DBW-EMS 98	DPW 621-50
Assimilation rate (µmol m^{-2} s^{-1})	8.3	26.5
Stomatal conductance (mmol m^{-2} s^{-1})	256.4	805.5
Chlorophyll Content Index	24.26	44.54
Total chlorophyll (mg g^{-1})	0.27	0.59
Chlorophyll a(mg g^{-1})	0.15	0.34
Chlorophyll b(mg g^{-1})	0.12	0.25
Normalized difference vegetation index (NDVI)	0.16	0.52

5. PHS 1108 (IC0624499; INGR18005), a Wheat (*Triticum aestivum*) Germplasm with High Protein Content, Bold Seeds and High Manganese Content.

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Indian wheat production brought food self-sufficiency ensuring the national food security. Now-a-days the quality of wheat grains and products is becoming important criteria for consumer's preferences. Wheat is recognized primarily as a source of energy and protein in human diets (Garvin *et al., 2006*). The micronutrients iron, zinc, copper and manganese (Pomeranz, *1988;* Doisy, *1973*) are important components of nutritional quality in wheat.

The proposed genotype PHS 1108, as source of high protein content with bold seeds, was developed from the cross CMH83.2517/GW190 following pedigree method. Parental line CMH83.2517was obtained from CIMMYT nursery INDV 96. PHS 1108 was contributed in NGSN and evaluated for three seasons (2011-12 to 2013-14) along with check varieties DBW 17, Sonalika and durum variety HI 8498 at more than 25 centres across the country. It was also evaluated for quality traits including nutritional quality parameters.

The results (Table 1) indicated 9.6% superiority of PHS 1108 for protein content over best check variety DBW 17. PHS 1108 has protein content of 14.8% ranging from 14.3-15.8% during three years of evaluation. This genotype also has high 1000-grain weight (55g) with range of 52-57g which indicated higher content of protein per unit grain weight. In addition, the manganese (Mn) content of 44.2 ppm (mg/kg) was 36.4% higher as compared to best check variety Sonalika. The manganese content in PHS 1108 is even higher than the earlier reports of manganese availability in wheat grains to the tune of 25.23+3.86 mg/kg (Bawiec *et al*., 2014; NDL, 2016). PHS 1108 also has longer spikes (12 cm) and early in heading (73 days) and maturity (123 days) as compared to all the check varieties.

PHS 1108 is a promising source for high protein content with bolder seeds (high 1000-grains wt.) which may be useful as donor in wheat improvement programmes. High manganese content in grains is an additional feature for nutritional improvement. PHS 1108

Table 1. Performance of PHS 1108 in National Genetic Stock Nursery

Traits	Year	Entry	Check varieties		
		PHS 1108	DBW 17	Sonalika	HI 8498 (d)
Protein content (%)	2011-12	14.3	12.5	12.2	12.6
	2012-13	15.8	14.6	14.4	14.6
	2013-14	14.4	13.3	13.5	12.9
	Mean	14.8	13.5	13.4	13.4
1000-grains weight (g)	2011-12	57	39	44	50
	2012-13	52	39	43	48
	2013-14	55	41	43	48
	Mean	55	40	43	49
Manganese (ppm)	2011-12	44.2	30.2	32.4	25.7
Zinc content (ppm)	2011-12	43.5	29.6	29.7	27.1
	2012-13	38.4	31.4	31.6	36.7
	2013-14	36.7	36.4	35.3	37.1
	Mean	39.5	32.5	32.2	33.6
Days to heading	2011-12	74	88	79	84
	2012-13	74	86	76	83
	2013-14	71	82	71	79
	Mean	73	85	75	82
Days to maturity	2011-12	123	128	125	128
	2012-13	124	130	127	129
	2013-14	123	128	123	127
	Mean	123	129	125	128
Spike length (cm)	2011-12	12	9	9	8
	2012-13	12	9	9	8
	2013-14	12	9	9	7
	Mean	12	9	9	8

would add further un-exploited genetic variability for yield components and mineral nutrient content.

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6. DBW 129 (IC0624497; INGR18006), a Wheat (*Triticum aestivum*) Germplasm with Multiple Disease and Pest Resistance (Stripe, Leaf & Leaf Blight, Karnal Bunt, Flag Smut, Powdery Mildew and Shoot Fly).

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The disease and pest resistance is crucial to realize high yield potential in any variety under commercial cultivation. This necessitates development of high yielding genotypes with resistance to most of the prevailing diseases. The efforts made under warmer area programme of the ICAR-IIWBR, Karnal has resulted in identification of germplasm line DBW 129 which showed promise for multiple diseases and pest resistance and is being proposed for registration as genetic stock.

The proposed genotype DBW 129 (PFAU/ Milan/5/ Chen/*Ae. squarrosa* (Taus)//BCN/3/VEE#7 / BOW/4/Pastor) was developed by pedigree method at IIWBR, Karnal. It was cross of 21st ESWYT-44 (PFAU/ MILAN) used as female parent and 34th IBWSN-295 (Chen/*Ae. squarrosa* (Taus) //BCN/3/VEE#7/BOW/4/ Pastor) as male parent. The germplasm line DBW 129 was initially contributed in NIVT-5A in 2012-13 for evaluation under restricted irrigation conditions (Anonymous, 2013a). Based on its yield superiority and disease resistance, it was promoted to Advance Varietal Trial of the NWPZ in 2013-14 (Anonymous, 2014a). During its testing for yield under coordinated trials, it was also evaluated for disease resistance under artificial epiphytotic conditions at multi-locations in the Plant Pathological Screening Nursery (PPSN) during 2012-13 and 2013-14. Thereafter, it was evaluated in Elite Plant Pathological Screening Nursery (EPPSN), Multiple Disease Screening Nursery (MDSN) and Multiple Pest Screening Nursery (MPSN) for disease and insect pest resistance. DBW 129 was found promising for multiple diseases and pest resistance in all these nurseries.

The PPSN was conducted at 13 locations for screening against stripe rust (10 locations) and leaf rust (8 locations) during 2012-13 to 2013-14 in which DBW 129 showed highly resistant reactions to stripe (ACI: 3.7) and leaf (ACI: 2.5) rusts (Anonymous, 2013b, 2014b). Based on its performance in PPSN (Table 1), it was promoted to EPPSN during 2014-15 conducted at 13 locations (Anonymous, 2015) in which it again showed highly resistant reactions (Table.1) to all three rusts (ACI of 3.1 to yellow rust, 0.0 to leaf rust and 3.1 to stem rust).

Table 1. Response of DBW 129 against rusts in PPSN & EPPSN

Genotypes	Rust diseases			
	Stripe (North)	Leaf (North)	Leaf (South)	Stem (South)
	HS (*ACI*)	HS (*ACI*)	HS (*ACI*)	HS (*ACI*)
PPSN (2012-13 & 2013-14)				
DBW 129	20S (3.7)	20S (2.5)	-	-
WH1080 (C)	40S (18.2)	30S (9.9)	-	-
HD 3043 (C)	60S (20.2)	20MS(5.0)	-	-
PBW 644 (C)	80S (37.3)	20S (4.4)	-	-
EPPSN (2014-15)				
DBW 129	5S (3.1)	tR(0.0)	tR (0.0)	5S (3.1)
Infector (C)	90S (75.0)	100S (63.3)	60S (41.3)	100S (55.0)
MDSN (2015-16)				
DBW 129	5S (1.0)	tR(0.0)	5MS (1.6)	5X (1.7)
PBW 343(C)	80S (43.0)	20S(13.3)	60S (34.6)	5S(3.0)
Raj 4015(C)	40S (18.0)	20S(6.6)	60S (20.3)	40S(30.0)
Sonalika(C)	100S (48.0)	60S (20.0)	80S (55.0)	30S (15.1)

HS- Highest score ; ACI- Average coefficient of infection

Further, it was evaluated in MDSN at 15 locations during 2015-16 for disease response against rusts, leaf blight, Karnal bunt, flag smut and powdery mildew (Anonymous, 2016). DBW129 showed highly resistant response to all the three rusts, leaf blight, Karnal bunt, powdery mildew and flag smut (Table 2). The screening of DBW 129 against different insect pests in MPSN during 2015-16 also showed resistance to shoot fly with very low incidence of 7.81% and falling in the resistant category (Anonymous, 2016).

In addition, this germplasm showed mean yield of 47.2q/ha with 2.4% superiority over check WH 1080 with yield potential of 67.4q/ha under limited irrigation conditions (Table.3).

DBW 129 is a promising source for resistance to multiple diseases and pests in wheat with high yield under restricted irrigation conditions. These features make it very useful for wheat improvement programmes. DBW 129 would add further un-exploited genetic variability for yield component and resistance to diseases and insect pests.

Table 2. Performance of DBW 129 in MDSN & MPSN (2015-16)

Genotypes	Diseases in MDSN				Insect-pests in MPSN	
	Leaf blight (dd)	Karnal Bunt (%)	Powdery mildew (0-9)	Flag smut (%)	Shoot fly incidence (%)	Brown wheat mite(No./cm^2)
	Av (HS)	HS	Av (HS)	Av (HS)	Av (HS)	Av (HS)
DBW 129	35 (57)	5.0	2 (4)	3.3 (10.0)	7.8 (15.4)	10.3 (10.6)
Checks						
Raj 4015 for LB	67 (78)	18.0	4 (6)	15.6(20.0)	-	-
PBW 343 for PM	34 (45)	21.0	6(9)	42.5(76.5)	-	-
Sonalika for SF	68 (79)	17.0	-	-	24.6 (66.7)	-
IWP 72 for BWM	-	-	-	-	-	19.0 (22.3)

Av- Average score; HS- Highest score

Table 3. Performance of DBW 129 for yield in coordinated trials (2012-13 to 2013-14)

Traits	Entry	Check Varieties		
	DBW 129	WH 1080	PBW 644	HD 3043
Mean Yield (q/ha)	47.2	46.1	45.7	45.2
Yield potential (q/ha)	67.4	59.3	57.5	61.8

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7. DBW 246 (IC0625998; INGR18007), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Yellow Rust.

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Yellow rust caused by *Puccinia striiformis* is one the important disease of the wheat crop grown in Northern India and the fungus causes significant yield losses to the wheat productivity in the region. The pathogen can cause 100% yield loss, but damage generally ranges from 10-70% in a single field depending upon the stage, duration and severity of infection during the growing season and susceptibility of the cultivar. Keeping pace with the varietal improvement for the rust resistance, the yellow rust pathogens evolve very fast into more virulent ones.A resistant cultivar becomes susceptible when a new pathotype evolves. During the year 2016, seven pathotypes were identified for the first time and designated as 46S117, 110S119, 238S119, 110S84, 110S247, 7S0 and 6S0 and they would change the resistance pattern of wheat cultivars in northern India.

Winter wheats act as source for biotic resistance in wheat. DBW 246 is a spring wheat line developed from winter x spring wheat hybridization (UP2556//ID13.1/MLT/3/Danphe) and it has been selected for yellow rust resistance during its course of development. In 2016-17 it was tested in the coordinated trials and the genotype showed resistance against yellow rust during the course of evaluation.

In the field reactions, the genotype showed resistance response at all the locations under artificial epipytotic conditions. (Table 1) The highest reaction was tR (ACI : 0.6) recorded at Malan centre while at rest of the locations it was free from the disease. The released cultivars DBW 88, WH 1105 and HD 2967 showed high susceptible reaction against the yellow rust. In Seedling Resistance Test (SRT) carried out at IIWBR-RS Flowerdale, Shimla, DBW246 has shown resistant reactions against all the stripe rust races including the recently identified virulent races viz., 238S119, 110S119, 110S84 and 110S247 (Table 2)

Apart from highly resistant to yellow rust, the agronomic features of DBW 246 like heading duration (91 days), maturity (138 days), plant height (95 cm) thousand grains weight (38 g), easy threshability and amber coloured grains makes it suitable to be used in future hybridization programmes. This line would be useful for bringing diversity in the breeding material for yellow rust resistance.

Table1. Yellow rust reactions of DBW 246 and cultivars at hot spots

Entry	Hisar	Jammu	P'nagar	Durgapura	Karnal	Ludhiana	Delhi	Gurdaspur	Malan	Khudwani	HS	ACI
DBW 246	0	0	0	0	0	0	0	0	tR	0	tR	0.6
DBW88 (C)	10S	40S	20S	60S	80S	60S	40S	40S	20S	10MR	80S	37.4
HD2967 (C)	60S	60S	20S	80S	60S	60S	60S	60S	20S	30S	80S	51.0
HD3086 (C)	tMR	5MS	tMS	0	tMR	10S	tR	10MS	5S	10MR	10S	3.3
WH 1105 (C)	10S	20S	20S	40S	60S	60S	30S	10S	tR	10MR	60S	25.4

Table 2. Seedling Resistant Test of genotypes against yellow rust pathotypes

Variety /Line	Pathotypes																		Gene	Remarks
	110S119	110S247	110S68	238S119	110S84	111S68	46S119	78S84	6S0	79S4	79S68	T	P	K	L	38A	7S0	31		
DBW 246	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	-	Resistant
DBW88 (C)	S	S	R	MS	R	R	R	R	R	R	R	R	R	R	R	R	R	R	*YrA*+	
HD2967 (C)	S	S	R	S	R	R	MS	R	R	R	R	S	S	S	MS	R	R	R	*Yr2*+	
HD3086 (C)	S	S	S	S	R	R	MS	R	R	R	R	S	S	S	R	R	R	R	*Yr2*+	
WH 1105 (C)	S	S	R	R	R	R	R	R	R	R	R	MS	R	R	R	R	R	R	*Yr2*+	

8. IC-0624570 (IC0624570; INGR18008), a Wheat (*Triticum aestivum*) Germplasm Resistant Spot Blotch and Early Maturing.

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Spot blotch caused by *Bipolaris sorokiniana* is a major disease of wheat in warm humid regions. Average losses caused by this disease is 16% and expected yield loss form 9 million hectare is estimated around 3 million tons annually. Spot blotch resistant germplasm are late maturing hence trapped under terminal heat. Developing early maturing spot blotch resistant genotypes facilitate wheat crop to escape terminal heat and spot blotch.

In 2000 at Banaras Hindu University, Varanasi two diverse wheat germplasm for spot blotch Sonalika (Susceptible) and Yangmai 6 (Resistant) were crossed for developing recombinant inbred lines. RILs were developed following single seed descend method in successive generations at BHU and Wellington, Tamilnadu. This RIL population (YS) was extensively used for QTL mapping (Kumar *et al.*, 2009, 2015). From this population YS#24 and YS#58 were identified in Sonalika background similar for most of the phenological traits except spot blotch resistance (Yusuf *et al.*, 2016). YS#24 was highly resistant and YS#58 was highly susceptible against spot blotch. These two lines (YS#24 and YS#58) were crossed in the 2010–11, utilizing off-season facility and following SSD method a new RIL population with 211 lines was developed.

These 211 RILs, 2 parents (YS#24, YS#58) and Sonalika as a susceptible check were planted in 7 environments i.e., during 2014-15 and 2015-16 at 3 locations viz., BHU, Varanasi, BISA, Samastipur and UBKV, Coochbehar W. B. and in 2016-17 only at BHU. On the basis of pooled data of 7 environments, line#94 (IC-0624570) was highly resistant against spot blotch. Mean of important traits over 7 environments are as AUDPC (280), early days to heading (66.5 days), early maturity (110 days), 1000-grain weight (35.78g) and plant height (90cm). This line was superior for all the mentioned traits over resistant parent (YS#24) as well as Sonalika.

This genotype is important genetic resource and may be used as a variety directly or as a parent in a crossing programme for developing genotypes with spot blotch resistance and early maturing in order to escape the terminal heat.

9. HTW (IC0625994; INGR18009), a Wheat (*Triticum aestivum*) Germplasm with Heat Tolerance.

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Heat stress is a major environmental stress limiting wheat productivity in most cereal growing areas of the world.The optimum temperature for wheat during anthesis and grain filling ranges from 12 to 22°C (Tewolde *et al.*, 2006). Exposure to temperatures above this range can significantly reduce grain yield. In many parts of the Asian subcontinent, due to the rice-wheat cropping system, crop damage due to heat stress under late planting conditions has become a significant factor limiting wheat yields. To sustain the wheat production and productivity, identification of heat tolerant genotypes and simultaneously transfer of tolerance into high yielding backgrounds is of utmost importance. The genotype HTW 9 was identified to be highly tolerant to heat stress based on multi-location and multiyear evaluation.

The heat tolerant genotype, HTW 9 was developed from the cross RAJ 3765/P11632 following a pedigree breeding approach. HTW 9 was evaluated for heat tolerance for two years under irrigated timely, irrigated late, rainfed timely and rainfed late sown field conditions at four locations viz. Akola, Dharwad, Karnal and Powarkheda under NICRA project. This genotype was found to be highly tolerant to heat stress (HSI -0.08) as compared to the identified heat and drought tolerant checks AKAW 2862-1(HSI 0.66), C 306 (HSI 0.64), C306-M 10 (HSI 1.10), HINDI 62 (HSI 1.25), HTW 11(HSI 1.61) and HTW 6 (HSI 0.80) under field conditions (Table 1). The genotype was found to be tolerant under late sown heat stress conditions at all the locations during both years. Location-wise and year wise data is given in Table 2.

Another experiment was also conducted simultaneously under temperature controlled conditions to confirm its tolerance to heat stress. This genotype along with all checks was planted under controlled conditions during 2016-17. The genotypes were planted under normal temperature conditions in one chamber and high temperature conditions in another chamber. The genotype HTW 9 was found to be tolerant to heat stress. The heat susceptibility index (HSI) value for HTW 9 was 0.77 as compared to the checks AKAW 2862-1(HSI 2.61), HINDI 62 (HSI 2.34), HTW 11(HSI 0.96) and HTW 6 (HSI 0.69) (Table 1).

Table 1. Heat susceptible index (HSI) of HTW 9 and checks (Pooled over 4 locations and 2 years)

Entry	Field conditions	Controlled Temperature conditions
HTW 9 (J31-24)	-0.08	-0.03
Checks (Registered Genetic stocks for heat tolerance)		
AKAW 2862-1	0.66	2.61
HINDI 62	1.25	2.34
HTW11	1.61	0.96
HTW 6	0.80	0.69

Table 2. Heat susceptible index (HSI) of HTW 9 and checks at 4 locations during 2015-16 and 2016-17

	Heat susceptible index (HSI)				
Genotype	Akola	Powarkheda	Karnal	Dharwad	Average
2015-16					
HTW 9 (J31-24)	0.34	-0.11	0.23	-0.58	-0.03
Checks (Registered Genetic stocks for heat tolerance)					
AKW2862-1	0.95	0.00	-0.18	0.91	0.42
HINDI 62	0.93	1.45	0.44	0.76	0.90
HTW11	0.90	1.08	0.61	0.64	0.81
HTW6	0.88	1.04	-0.66	-1.21	0.01
2016-17					
HTW 9 (J31-24)	-1.7	0.41	-0.03	0.81	-0.13
Checks (Registered Genetic stocks for heat tolerance)					
AKW2862-1	0.44	1.49	0.93	-0.76	0.52
HINDI 62	1.45	0.45	1.07	0.83	0.95
HTW11	0.57	0.66	0.82	0.84	0.72
HTW6	0.10	0.70	-0.76	0.66	0.17

The performance of HTW 9 under irrigated late sown conditions with respect to other desirable agronomic features namely: days to heading (71 days), days to maturity (113 days), plant height (111cm) and 1000 grain weight (42.6g) has also indicated its suitability to be used in crossing programmes (Table 3).

This genotype is found to be highly tolerant to heat stress conditions showing potential to be used as a donor for enhancing heat tolerance in wheat.

Table 3. Agronomic characteristics of the drought tolerant genotype, HTW 9 pooled over two years under field conditions

Genotypes	Days to Heading		Days to maturity		Plant Height (cm)		1000 grain weight (g)	
	*IR-TS	IR-LS	IR-TS	IR-LS	IR-TS	IR-LS	IR-TS	IR-LS
HTW 9	68	71	119	113	86	111	44.1	42.6
Checks (Registered Genetic stocks for heat tolerance)								
AKW2862-1	70	67	120	112	101	109	49.5	40.5
HINDI 62	87	72	129	112	99	99	36.4	35.0
HTW11	82	64	124	108	94	114	41.6	41.0
HTW6	84	64	127	108	103	92	38.8	40.4

*IR-TS- irrigated timely sown conditions; IR-LS- irrigated late sown conditions

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10. DBW 218 (IC0625997; INGR18010), a Wheat (*Triticum aestivum*) Germplasm with High Sedimentation Value and Grain Hardness.

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In order to meet the food nutritional demands of the future population, the breeding programmes need to focus on developing cultivars possessing high yield coupled with good quality characteristics. Wheat genotype, DBW218 was identified as a promising genotype possessing high sedimentation value, grain protein content and grain hardness along with acceptable yield.

The new wheat genotype DBW218 (PRL*PASTOR//PBW343*2/KUKUNA) was selected from an international nursery and was evaluated over years at ICAR-IIWBR, Karnal. This genotype was found promising and contributed to the special trial (very late sown) for testing under AICRPW&B.This genotype was evaluated at total nine locations including five locations (Delhi, Karnal, Hisar, Ludhiana and Gurdaspur) of North Western Plains Zone (NWPZ) and four locations (Faizabad, Kanpur, Pusa and Sabour) of North Eastern Plains Zone (NEPZ) along with the three checks (DBW71, WR544, DBW14) during 2015-16 for grain yield, disease resistance and quality traits and this followed as criterion for selecting genotypes for end productpurpose.

The key determinants for making good quality chapatti are sedimentation value (30-60 ml), grain protein content (11-13%) and grain hardness (40-75). Sedimentation value gives an idea of gluten strength. DBW218 showed high sedimentation value of 57ml pooled over both 9 locations coupled with desired level of protein content (12.7%) and grain hardness (76) as compared to the check varieties (Table 1).

Besides quality attributes, it also showed better performance for other desired agronomic characteristics over checks in nine locations indicating its wider adaptability. DBW 218 had high grain yield (32.7 q/ha) under very late sown conditions as compared to all three checks namely; DBW 71(32.5q/ha), WR544 (29.1 q/ha) and DBW14 (31.6q/ha). It also had a thousand grain weight of 33g (21- 42g), plant height 90cm (61-106 cm) and matures in about 101 days (79-114 days).

Therefore, DBW218 being high yielding genotype having exceptionally good for chapatti making traits (high sedimentation value, grain protein content and grain hardness). This promising genotype may be utilized as donor parent (quality, yield and short duration) in breeding programs to improve chapatti quality and thus would contribute significantly for food and nutritional security of the country.

Table 1. Mean performance of DBW 218 and checks for agronomic and quality traits pooled over NWPZ and NEPZ under AICW&BIP (2015-16)

Traits	Proposed genotype DBW 218		Check varieties					
			DBW 71		WR 544		DBW 14	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Quality traits								
Sedimentation Value	57.0	52-62	44.5	42-47	43.0	40-45	44.0	42-47
Grain Hardness	76.0	66-86	75.0	65-82	70.5	62-77	65.5	58-65
Protein Content (%)	12.7	10.8-15.4	12.9	11.3-15.1	13.7	11.7-15.5	13.1	11.8-15.5
Agronomic traits								
Grain Yield (q/ha)	32.7	22.2-45.8	32.5	24.4-41.5	29.1	25.8-35.2	31.6	23.8-42.9
1000 grain weight (g)	33.0	21-42	33.5	22-40	34.5	24-42	33.5	25-40
Plant height (cm)	90	61-106	80	64-94	88	58-105	76	58-85
Days to maturity	101	79-114	99	81-115	95	75-110	96	77-115

11. EC531185 (EC531185; INGR18011), aWheat (*Triticum aestivum*) Germplasm with Low DSI (Drought Susceptibility Index) <0.5 for 5-6 traits including yield/m2. High & Stable Grain/Spike under Irrigated and Non-Irrigated Conditions. Presence of Genes Associated with Various Drought Responsive Traits v*iz*., Thylakoid Membrane Stability (Fv/Fm), Grain Filling Duration (GYD), Grain Yield (GY) and Gene Maintaining Low Leaf Temperature under Drought Stress Condition.

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Drought is one of the most devastating phenomenon, which occurs in all the climatic regions leading to the great losses in agriculture. There are projections that drought events may intensify in future making farming exceedingly challenging for the farmers. Wheat (*Triticum aestivum* L.) is the major staple crop satisfying hunger globally. Wheat production may decline substantially in China, India and Russia due to climate variability (Knox *et al*., 2012). Yield losses due to drought depend on the growth stage and severity of stress (Daryanto *et al*., 2016). Breeding for drought tolerance using novel genetic resources is the most viable strategy to cope with the changing climatic conditions (Mwadzingeni *et al*., 2016). However, due to limited availability of resistance sources, progress in breeding drought tolerant cultivars is not satisfactory. Present study was conducted to identify drought tolerant wheat lines. In this study, field screening was done in multi-environment for four years followed by validation at molecular level to identify stable drought tolerant wheat genotypes. In field screening, based on ten quantitative traits including drought susceptibility index (DSI) under irrigated and non-irrigated conditions in two successive years, 44 wheat genotypes were selected from an initial set of 177 genotypes. These selected lines were further screened for two more years against drought stress. Stability analysis and AMMI biplot was also performed to analyze the performance of genotypes across the environment and years. Selected genotypes were further evaluated for the presence of six drought-linked molecular markers. Based on drought susceptibility index, other physiological parameters and molecular analysis, the genotypes namely, ET127225, ET127230, EC531185, ET127236, ET127267 and ET127269 were found drought tolerant. Among these germplasm lines, EC531185, a cultivar named Kanchan derived from cross UP 301 X C306 is being proposed to be registered as genetic stock for drought tolerance. It is a semi –dwarf variety with plant height 90-100 cm, number of tillers 6-7, panicle initiation 60-80 days, days to maturity 106-112, 45-55 grain per spike, white grain, 1000 grain weight 45-48 gram. It is an ideal genotype for genetic and physiological studies and a potential genetic resource for drought tolerance, which can be used in wheat improvement programme.

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12. EC339604 (EC339604; INGR18012), a Wheat (*Triticum aestivum*) Germplasm with Resistance to Prevailing Leaf Rust Pathotypes. Presence of Leaf Rust Resistance Genes viz., *Lr22a, Lr46+, Lr67+* and additionally Carries Stripe Rust Resistance Genes *Yr5, Yr15 and Yr48*.

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OP Gangwar[3], MS Saharan[4], Indoo Bhagat[5], Madhu Meeta[5], NS Bains[5], JB Sharma[6], Robin Gogoi[6] 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 (Tamil Nadu), a hotspot for stem and leaf rusts (Nagarajan & Joshi 1985). 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 hotspot for spot blotch. A second round evaluation identified 498 accessions potentially resistant to multiple rusts and 868 accessions 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, EC339604 which showed the presence of resistance genes for leaf and stripe rust diseases viz., *Lr22a,Lr46+,Lr67+,Yr5,Yr15* and *Yr48*is a promising multiple disease resistant germplasm and could be included in wheat improvement program as one of the parents for developing durable multiple rust resistant cultivars.

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13. IC252459(IC0252459; INGR18013), a Wheat (*Triticum aestivum*) for Resistant to Stripe Rust Pathotypes K (47S102), P (46S103), L (70S69), 13 (67S8), I (38S102), 46S119 & 78S84 Carries Stripe Rust Resistance Genes viz., *Yr5*, *Yr15* & *Yr48* additionally also carries Leaf Rust Resistance Genes *Lr46+*, *Lr50* & *Lr24/Sr24*.

Sundeep Kumar[1*], Sunil Archak[1], RK Tyagi[1], Jagdish Kumar[2], VK Vikas[2], AK Sharma[3], Jyoti Kumari[1], Sherry Rachel Jacob[1], Kalyani Srinivasan[1], J Radhamani[1], BS Phogat[1], R Parimalan[1], Amit Kumar Singh[1], Manas Bag[1], Anirban Roy[1], TV Prasad[1], M Datta[1], KC Bansal[1], M Sivasamy[2], P Jayaprakash[2], SC Bharadwaj[4], P Parsad[4], OP Gangwar[4], MS Saharan[3], Indoo Bhagat[5], Madhu Meeta[5], NS Bains[5], AK Chaudhary[6], BC Saha[6], PM Bhattacharya[6], JB Sharma[7], Robin Gogoi[7], Deep Shikha[8], SP Singh[9], SS Vaish[10], PC Mishra[11], BK Honrao[12], IK Kalappanavar[13], VA Solanki[14], GP Singh[3]

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14. IC564121 (IC0564121; INGR18014), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Spot Blotch.

Jyoti Kumari[1]*, Sundeep Kumar[1], Nidhi Singh[1], SS Vaish[2], Saikat Das[3], Arun Gupta[4], JC Rana[5], Amit Kumar Singh[1], Ruchi Bansal[1], Sherry R Jacob[1] and Ashok Kumar[1]
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Spot blotch disease leadsto significant yield losses ranging from 18 to 50% in warmer 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 reduce the loss and stabilize the yield, 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 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). 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. 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 breeding germplasm. The lines showing highly resistant reaction alongwith wider adaptability can be expedited for direct cultivation or for the development of high yielding and disease resistant cultivars.

The spot botch resistant accession IC564121, a landrace named as Lal Mundia was collected from Pauri district of Uttarakhand. It has red kernel colour, medium maturity and medium spike length (~8cm) and grains per spike (~50). This germplasm line can be used as a donor for spot blotch resistance in wheat breeding programme.

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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

15. IC443669 (IC0443669; INGR18015), a Wheat (*Triticum aestivum*) Germplasm Highly Resistant to Spot Blotch.

Jyoti Kumari[1,*], Sundeep Kumar[1], Nidhi Singh[1], SS Vaish[2], Saikat Das[3], Arun Gupta[4], JC Rana[5], Amit K Singh[1], Ruchi Bansal[1], Sherry R Jacob[1] and Ashok Kumar[1]
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DBW39	Resistant check	114±6.69	37±1.34	125	583±12	35	24	R
HD2967	Agronomic check	105.45±6.39	36.65±0.74	118	-	-	-	-

16. QLD 49 (IC0626288; INGR18016), a Wheat (*Triticum aestivum*) Germplasm with Soft Grain (Very Low Grain Hardness Index) Suitable for Biscuit Making.

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Soft grain textured wheat produces tender and larger biscuits. The key determinants of good biscuits are soft texture, low protein content and weak gluten. Biscuit industry is India's largest industry amongst food industries with an estimated production of 70,000 tonnes and cost of USD 3bn.

QLD 49 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing 37th IBWSN 72/5th IAT. The genotype was evaluated at 12 centers in Quality Component Screening Nursery (QCSN) for three consecutive years (2014-15 to 2016-17). QLD 49 was found to be superior with 20.0 grain hardness index over the years and locations to all the testing genotypes and soft grain check variety HS 490 (27: grain hardness index) (Table 1).

QLD 49 recorded the lowest grain hardness index in all the 12 tested centers compared to the best check variety (HS 490) for low grain index. QLD 49 recorded lowest grain hardness index of 17.0, 21.0 and 21.0, respectively during 2014-15, 2015-16 and 2016-17. Whereas, the check variety HS 490 tested in 2015-16. QLD 49 was 25.93% superior over check variety HS 490. Low grain hardness index is very important factor to obtain high spread factor of biscuit and even better biscuit quality.

Thus, QLD-49 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 QLD 49 at 12 locations during three years as compared to the best available check HS 490.

Zone	Location	QLD 49			HS 490 (Check)
		2014-15	2015-16	2016-17	2015-16
NHZ	Almora	23	14	19	24
NWPZ	Ludhiana	14	24	12	26
	Durgapura	13	21	13	33
	Delhi	17	20	21	27
	Pantnagar	10	21	26	29
	Karnal	9	26	23	29
NEPZ	Pusa	-	18	12	26
	Kanpur	18	20	-	21
CZ	Junagadh	18	23	22	25
	Vijapur	23	20	20	24
PZ	Pune	17	19	32	21
	Dharwad	30	24	30	37
Mean (National)		17	21	21	27
Three years mean		20			27
% Superiority of QLD 49 over best check variety HS 490		25.93%			

17. QLD 46 (IC0626289; INGR18017), a Wheat (*Triticum aestivum*) Germplasm with High Grain Protein Content.

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Grain protein is an important trait that determines the nutritional quality and baking properties of wheat. Protein is an essential component of cells and it supports muscle growth, immune and enzymatic reactions; protein-energy malnutrition causes marasmus and kwashiorkor.

QLD 46, a promising bread wheat genotype was developed at ICAR-Indian Institute of Wheat & Barley Research (ICAR-IIWBR), Karnal by crossing NL 655/OPAT85//NL836. The genotype was evaluated at 12 locations along with high protein check variety (UP 2672) during 2014-15, 2015-16 and 2016-17 under Quality Component Screening Nursery (QCSN). QLD 46 found to be superior with 14.42% protein content over the years and locations to all the testing genotypes and check variety UP 2672 (13.59%) (Table1).

QLD 46 recorded the high grain protein content in all the 12 tested centers compared to best check variety (UP 2672) for high grain protein content. QLD 46 was recorded high grain protein content of 13.18%, 15.19% and 14.90%, respectively during 2014-15, 2015-16 and 2016-17. The check variety UP 2672 recorded 12.67%, 14.39% and 13.72%, respectively during 2014-15, 2015-16 and 2016-17.

Thus, QLD 46 would be a potential source to be utilized in future breeding programs to improve grain protein content of bread wheat varieties.

Table 1. Grain protein content of QLD 46 and UP 2672 (C) at 12 locations during 2014-15, 2015-16 and 2016-17.

Zone	Location	QLD 46			UP 2672 (C)		
		2014-15	2015-16	2016-17	2014-15	2015-16	2016-17
NHZ	Almora	11.6	14.9	14.2	10.77	13.27	12.64
NWPZ	Ludhiana	13.6	14.7	14.76	13.10	12.73	13.26
	Durgapura	13.5	15.8	14.24	13.33	15.67	13.64
	Delhi	13.2	15.7	14.68	13.20	14.70	14.24
	Pantnagar	13.7	14.7	12.73	13.23	12.90	11.84
	Karnal	13.2	15.0	14.86	13.07	14.00	12.85
NEPZ	Pusa	-	15.6	14.37	-	15.10	13.91
	Kanpur	13.7	15.4	-	12.03	13.83	-
CZ	Junagadh	13.2	16.3	15.68	12.73	15.33	14.99
	Vijapur	13.1	14.8	15.43	12.30	14.63	13.89
PZ	Pune	13.0	14.3	14.93	13.27	14.80	15.00
	Dharwad	13.2	15.1	14.72	12.37	15.70	14.63
Mean (National)		13.18	15.19	14.90	12.67	14.39	13.72
Three years mean		14.42			13.59		

18. DDW 32 (IC0626290; INGR18018), a Wheat (*Triticum durum*) Germplasm with Loose Smut Resistance.

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Loose smut disease can cause losses as high as 25 percent or more in severe cases. In general, percent yield loss from loose smut is approximately equal to the percentage of affected wheat heads. A durum genotype, DDW 32, developed at ICAR-IIWBR, Karnal was found to be having significantly higher resistance against loose smut with better pasta quality. DDW 32 is an indigenous durum line with PDW245/WH896//WH896 parentage. The spikes of DDW 32 along with check varieties were inoculated during 2014-15 with local isolates of loose smut pathogen using Go-go method of inoculation and disease infections were recorded in 2015-16 at hot spot locations like Almora, Durgapura, Hisar, Karnal and Ludhiana ICAR-IIWBR Annual Report 2016-17; AICW&BIP, Progress Report, Vol. III (Crop Protection), 2016).

The percentage of tillers showing loose smut infection in different entries is presented in Table 1. The genotype DDW 32 showed immune type of reaction at all five tested locations. On the contrary, the susceptible check variety Sonalika (*aestivum*) showed higher infection levels ranging from 31.3 (Ludhiana) to 87.2 (Almora) with an average score of 61.3. In North Western Plains Zone, all the checks showed higher score of loose smut infection. The released durum varieties of Central Zone showed the loose smut score from 10.5 (HI 8498) - 60.1 (HD 4728). While, the durum varieties of peninsular zone showed the score from 4.7 (UAS 446) to 61.3 (MACS 3927). DDW32 was also evaluated for yield in NIVT 4 during 2013-14. It yielded 54.4 q/ha and had significant superiority over the best check PDW314 (50.7 q/ha) and was promoted in AVT 1st year of North western plain Zone 2014-15. In AVT it yielded 48.4 q/ha. In addition to having loose smut resistance DDW 32 also has superior pasta quality by having Sedimentation value (ml) of 44.

Table1. Percent infection of loose smut in DDW 32 and check varieties during 2015-16 crop season

Entry Name	Almora	Durgapura	Hisar	Karnal	Ludhiana	HS	Avg.
DDW32	0.0	0.0	0.0	0.0	0.0	0.0	0.0
North Western Plains zone (Checks / released varieties)							
PDW 233	0.0	0.0	37.1	0.0	0.0	37.1	7.4
PDW 291	0.0	0.0	40.3	0.0	0.0	40.3	8.1
PDW 314	52.2	0.0	50.3	0.0	0.0	52.2	20.5
Central Zone (Checks / released varieties)							
HD 4728	0.0	0.0	60.1	0.0	0.0	60.1	12.0
HI 8498	0.0	0.0	10.5	0.0	9.0	10.5	3.9
HI 8737	0.0	0.0	51.6	0.0	5.0	51.6	11.3
MPO 1215	0.0	0.0	27.1	5.1	19.2	27.1	10.3
Peninsular Zone (Checks / released varieties)							
MACS3927	13.3	0.0	61.3	0.0	0.0	61.3	14.9
AKDW2997-16	0.0	0.0	10.1	0.0	7.5	10.1	3.5
UAS428	12.9	0.0	21.3	0.0	5.7	21.3	8.0
UAS446	4.1	0.0	-	0.0	4.7	4.7	2.2
Sonalika (Susceptible check)	87.2	73.9	80.4	33.5	31.3	87.2	61.3

Table 2. Additional traits in DDW 32: Quality Parameters

Variety	Grain Appearance	Test Weight (Kg/hl)	Protein Content	Grain Hardness Index	Sedimentation value (ml)
DDW32	6.4	76.6	11.6	82	44
Varieties / Checks					
PDW233	6.8	78.5	12.3	92	37
PDW291	7.2	80.1	11.9	94	31
PDW314	6.8	79.9	12.0	86	38

Thus, DDW 32 would be a potential source to be utilized in future breeding programs to improve loose smut resistance.

DDW32 is resistant to loose smut at 5 locations of NWPZ and had ‘0’ reaction at all centres compared to check varieties having average infections ranging from 15% to 61% of spikes

DDW 32 was found resistant to loose smut against popular ruling varieties of all zones.

DDW 32 also has higher sedimentation value compared to check varieties

19. DWRB152 (IC-0624535) (IC0624535; INGR18019), a Barley (*Hordeum vulgare*) Germplasm Highly Resistant to Stripe Rust at Seedling and Adult Plant Stages.

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Stripe rust is one of the cereal devastating diseases and caused by the fungus *Puccinia striiformis* f. sp. *hordei* in barley. It is wide spread in different in northern upper and mid hills, foot hills, north western plains zone (NWPZ) and with medium to low incidences in north eastern plains zone (NEPZ). DWRB152 (DWRB73/ DWRB78) is a two row malt barley genotype, which is highly resistant to stripe rust at seedling and adult plant stages. DWRB152 was evaluated for disease reactions at multi-locations for consecutive two years *viz. rabi*, 2015-16 and 2016-17, under National Barley Disease Screening Nursery (NBDSN) and Elite Barley Disease Screening Nursery (EBDSN), respectively (Anonymous, 2016; Anonymous 2017). The genotype DWRB152 exhibited highly resistant response (0) for yellow rust under artificial disease epiphytotic conditions during both the years. Whereas, the two-rowed malt barley check DWRUB52 and six-rowed feed barley check BH902 exhibited susceptible yellow rust reactions (HS) of 15S and 40S, respectively (Table 1).

Table 1. Multi-location adult plant resistance (APR) for stripe rust reactions (*artificial inoculation*) of DWRB152and checks over two years

Year	Location	DWRB152	Checks		Registered stock DWRB137	Infector
			DWRUB52	BH902		
First Year (2015-16)	Bajaura	0	0	20S	0	100S
	Ludhiana	0	10S	10S	0	60S
	Durgapura	0	TMR	10MS	0	100S
	Karnal	0	0	5MR	0	60S
	Jammu	0	5S	10S	0	80S
	Almora	0	0	20S	0	80S
Second Year (2016-17)	Durgapura	0	5MS	30S	TS	100S
	Ludhiana	0	0	40S	0	60S
	Bajaura	0	15S	40S	0	100S
	Jammu	0	10MS	10S	5MS	80S
	Karnal	0	0	40S	0	100S
Two years HS		0	15S	40S	5MS	100S

In seedling resistance test (SRT), DWRB152 showed resistant reactions for prevalent barley stripe rust races viz. 57 and M consecutively for two years *i.e.rabi*, 2015-16 and 2016-17. DWRB152 exhibited resistant response to all the barley stripe rust races and depicted mix response to the races 24 and 6S0 during *rabi*, 2015-16 and 2016-17, respectively.Average days to heading, maturity and 1000 grain weight for DWRB152 were recorded as 77 days (65-81), 114 days (102-136) and 50 g (44-56), respectively in IVT-LS-MB-NWPZ coordinated trial, during *rabi*, 2015-16.

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20. DWRB190 (IC-0624536) (IC0624536; INGR18020), a Barley (*Hordeum vulgare*) Germplasm Resistant to Spot Blotch.

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Spot blotch (*Bipolaris sorokiniana*) is devastating disease in barley and broadly resistance for the disease is not available in released cultivars of north western and eastern plains in India. The genotypic resistance is always desirable and eco-friendly over chemical control to protect environment and to enhance profitability of small and marginal farmers. DWRB190 is six-row barley genotype, which showed moderately resistance reactions for spot blotch under coordinated evaluation (*artificial inoculation*) in initial barley disease screening nursery (IBDSN) during 2016-17 (Table 1). The genotype DWRB190 was selected from segregating exotic material (M104/TOCTE//OROSUS/PETUNIA1) for spot blotch resistance and other morphological characters at Karnal during *rabi*, 2014-15 to 2015-16. During *rabi*, 2016-17, the genotype was evaluated in IBDSN at the centres namely, Pantnagar, Varanasi, Kanpur and Faizabad and showed resistance for spot blotch (Anonymous, 2017). The details of DWRB190 with checks are as hereunder-

Table 1. Multi-location screening for spot blotch (artificial inoculations) of DWRB190 and checks

Year	Location	DWRB190 (BK1633)	Zonal Checks			Infector
			BH902 (NWPZ*)	HUB113 (NEPZ)	BH959 (CZ)	
(2016-17)	Pantnagar	35	67	78	99	79
	Varanasi	35	68	89	89	89
	Kanpur	24	36	36	79	89
	Faizabad	35	57	57	79	78

**NWPZ=north western plains zone, NEPZ=north eastern plains zone, CZ=central zone*

Average days to heading, maturity and 1000 grain weight for DWRB190 were observed as 88 days (84-90), 130 days (127-135) and 37 g (35-41), respectively.

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21. DWRB174 (IC0626008; INGR18021), a Barley (*Hordeum vulgare*) Germplasm with Extra Early Heading and Short Plant Height.

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The genotype DWRB174 is six-row early heading barley genotype coupled with higher grain yield, short plant height, which was selected (single plant selection) and purified from segregating exotic material (GIJA 121/CI 06248/4/APM/IB65//11012-2/3/API/CM67//DS/APRO/5/ATHS) for earliness, plant height and other morphological characters. DWRB174 has an extra early heading (54 days) coupled with desirable plant height (81-85 cm). The genotype was evaluated at Karnal and Hisar (Anonymous, 2017; Kumar *et al*., 2016) and heading details are presented in Table 1.

DWRB174 is six row feed barley genotype with desirable yield attributes, higher grain yield, short plant height than earlier registered genetic stock DWRB173 and can be directly utilized in rainfed breeding programmes with-out grain yield penalty. The botanical comparison and extra traits than DWRB173 are presented below in Table 2.

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Table 1. Heading days details of DWRB174 with check BH902 and earlier registered genetic stock DWRB173

Location	Year	DWRB174 (six-rowed awned)	BH902 (six-rowed check)	DWRB173 (two-row hooded)
Karnal	2015-16	55	89	55
Karnal	2016-17	54	91	54
Karnal	2017-18	54	89	54
Hisar	2015-16	54	87	53
Hisar	2016-17	54	88	-
	Mean	54	89	54

Table 2. Advantage of DWRB174 over DWRB173

Trait	DWRB174	DWRB173
Spike type	Six-row	Two-row
Awns type	Present	Hooded
Plant height (cm)	81-85	110-115
Grain yield (q/ha)	42-45	26-30
Grains/spike	55-75	22-27

22. IC568489 (IC0568489; INGR18022), Scented Sorghum (*Sorghum bicolor*) Germplasm.

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Sorghum [*Sorghum bicolor* (L.) Moench] is originated from North-East quadrant of Africa. India is secondary centre of diversity (Singh, 2002). The first FAO-IBP report on the survey of crop genetic resources in their centers of diversity spotted out in India and important among is the river valley of Madhya Pradesh (Singh, 1973). The first major effort on the collection of sorghum genetic diversity was made under the auspices of the Rockefeller Foundation and the Indian Council of Agricultural Research (ICAR); and a total of 16,138 collections were assembled by 1970 (Rockefeller Foundation, 1970).

The present exploration was to collect the traditional cultivars of sorghum especially the unexploited basmati (scented) jowar in the Bundelkhand regions of Madhya Pradesh. Prasada Rao (1979) reported the collection of Basmati jowar in the Chattarpur district of Madhya Pradesh. Scented sorghum with the local name “Basmati” was collected for the first time from Karri and Sarwa villages near Bijawar (Prasada Rao and Murthy, 1979). Its grains are dimpled, chalky white in colour with a characteristics aroma resembling that of Basmati rice. Five scented sorghum germplasm viz., IS 18674, IS 19907, IS 19908, IS 19910 and IS 19912 has been reported in the ICRISAT list of promising sorghum germplasm, which are the collections from Madhya Pradesh (Elangovan et. al. 2006).

Morpho-agronomic Characteristics: The basmati jowar plant is very tall in height, semi compact panicle, white caryopsis, which are very bold, straw glume with dark red colour at the basal part of the glume and grains with 75% coverage and belong to *durra guinea* race. The whole panicle gives aroma like basmati. Even the flowering panicles smelled like basmati. The results of the search were encouraging. The basmati (scented) jowar was not only re-collected from the first ever collection location but explored in two more locations viz. Katia (E 228) and Kerwan (E 254) villages of Chattarpur district. In the process of natural crossing, basmati jowar also has been collected in the name of *chatkul basmati* (E 213), *basmati sabet* (E 220), and *zunku basmati* (E 219) where the aroma was identified.

Associated Characters and Cultivation Practices: The collected basmati jowar was characterized through marker assisted selection (Rahul Zanan *et al*., 2016). Fragrance is one of the most important and valued quality characters in sorghum and other foods and attracts a premium price in local and global trade. The allele of the SbBADH2 gene in fragrant sorghum cultivar E228 was characterized. A 1441 bp deletion extending from exon 13 to 15 was found rather than a deletion from exon 12 to 15 as had been reported earlier. This allowed the development and validation of a new perfect PCR-based marker for identification of fragrant sorghum accessions in breeding. The concentration of 2-acetyl-1-pyrroline (2AP) in the grain of this cultivar was estimated to be 6.5 ± 0.4 ppb using headspace solid-phase microextraction (HSSPME) coupled with GC-MS. Flavor components of fragrant sorghum accession E228 (IC 568489) were analyzed and compared with the non-fragrant M35-1 cultivar. PCA analysis revealed that 2AP, benzothiazole, 2,3,5-trimethylpyridine, (1E)-1-ethylidene-1H-indene, cedrene, 2,4-bis(2-methyl-2propanyl)phenol, 2-hexyl-1-octanol, and 2-butyl-1octanol were among 25 compounds that were found in sorghum grain that may be contributing toward the aroma of fragrant sorghum. Proline and methylglyoxal contents were found to be higher in E228 than in M35-1, while SbBADH2 expression in E228 was half that in M35-1, suggesting a similar 2AP biosynthetic mechanism to that found in fragrant rice and soybean.

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23. *Corchorus aestuans* (WCIN179); KC/AK/DS-54 (IC0558459; INGR18023), a Jute (*Corchorus aestuans*) Germplasm Highly Resistant to Jute Hairy Caterpillar.

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The uniqueness and novelty of *C. aestuans* (accession WCIN-179) is confirmed on the basis of unique biochemical and VOC profile which makes it resistant against jute hairy caterpillar through multiple mechanisms *i.e.* antibiosis and non-preference recording least suitable for egg laying, biology and growth of insects. As *C. aestuans* is crossable with the cultivated species, *C. olitorius,* it is quite practical that this accession can further be used for insect resistance breeding program in jute.

Till date there is no source of resistance against hairy caterpillar which is a regular pest of jute. Occasionally its infestation becomes alarming due to outbreak in large area causing extensive damage to jute crop. India is harboring nine species (7 wild and 2 cultivated) of *Corchorus* namely, *C. aestuans, C. depressus, C. fascicularis, C. pseudo-olitorius, C. tridens, C. trilocularis, C. urticifolius, C. capsularis and C. olitorius* (Mahapatra *et al.,* 1998). Few accessions of wild species germplasm were evaluated to find out the source of resistance against this pest and the associated mechanism of resistance. Among these species, *C. aestuans* accession namely, WCIN-179 was found to be highly resistant to jute hairy caterpillar, *Spilosoma obliqua* during the four years of study at ICAR-Central Research Institute for Jute and Allied Fibres, Barrackpore, Kolkata and ICAR- Central Tuber Crops Research Institute, Regional station, Bhubaneswar. This accession was confirmed to be resistant as evidenced through the biology, feeding preference and oviposition behavior of *S. obliqua* recorded on *C. aestuans* (Accession: WCIN-179) as compared to other *Corchorus* species. The wild species (*C. aestuans* accession number,WCIN-179) showed resistance to hairy caterpillar and had recorded 71% less oviposition and 52% less preference for feeding by *S. obliqua* compared to cultivated variety, *C. olitorius* (cv. JRO-204).

The plants have cylindrical stem with red color with a plant height of 149 cm and basal stem diameter of 0.76 cm. The leaf posess green lamina with red margin and a cordate shape with yellow petal color. The color of the stigma is green; fruit (Pod color) is brown, cylindrical in shape with prominent horns on the fruits. Shattering behavior of fruit with Chocolate brown seed and 1000 seed test weight is 0.532 grams. Oviposition and feeding by *S. obliqua* on *C. aestuans* (WCIN-179) was also significantly less compared to other wild species. The larval growth on WCIN-179 was significantly impaired and the larvae failed to pupate and complete the life cycle. Normal growth of the immature stages on this accession *i.e.* WCIN-179 was heavily impaired compared to the other jute species (Gotyal *et al.,* 2013).

Biochemical studies revealed that the adverse effect on fecundity, feeding, biology recorded on WCIN-179 is imparted by the specific compositions and level of biochemical constituents which make it a unique and novel line of jute highly resistant to *S. obliqua* because of non-preference and antibiosis mechanism of resistance. The phenol content was also estimated in other wild and cultivated *Corchorus* species and it has been found that the phenol content of WCIN-179 was significantly higher than JRO-204 *(cv. C. olitorius)* and other two wild species *i.e., C. fascicularis and C. trilocularis*. Higher level of phenol generally has adverse effect on insect biology and causes pre-mature mortality. Such type of resistance is due to antibiosis mechanism. This accession number (WCIN-179) also contains significantly less protein and higher phenol over *C. olitorius* and other wild species which may be the cause of imparting the resistance to *S. obliqua* (Gotyal *et. al*., 2015). Besides this accession has very specific profile of volatile organic compounds (VOCs) because of which it is not preferred by the adults for egg laying and feeding as these compounds cause repellent effect on the insects. Other accessions of wild species have different set of VOC profile. The GC-MS analysis of VOCs from WCIN-179 indicated that *S. obliqua* repellent compounds, benzene-1 ethyl-3 methyl, dodecane and tridecane were eluted at 6.70, 12.13 and 14.17 min. respectively. Other jute species have different set of VOCs and not as unique as it is present in WCIN-179 that makes it resistant due to non-preference mechanism resulting in less preference for egg laying and feeding. The uniqueness and novelty of this accession of *C. aestuans* is confirmed on the basis of very unique biochemical and VOC profile which makes it resistant against hairy caterpillar through multiple mechanisms i.e. antibiosis and non-preference recording least suitable for egg laying, biology and growth of insects. As *C. aestuans* is crossable with the cultivated species, *C. olitorius* (Choudhary *et al.,* 2015), it is quite practical that this accession can further be used for insect resistance breeding program in *tossa* jute. The seeds of the accession (WCIN-179) obtained from the institute germplasm unit and multiplied in research farm of ICAR- Central Research Institute for Jute and Allied Fibres, Barrackpore.

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24. GGPS 7x-1 (IC0625987; INGR18024), Novel Cytotype (heptaploid) (2n=7x=56) Member of Ploidy Series in Guinea Grass (*Panicum maximum*).

and

25. GGPS 11x-1 (IC0625988; INGR18025), a Novel Cytotype (eleven-ploid) (2n=11x=88) Member of Ploidy Series in Guinea Grass (*Panicum maximum*).

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Polyploidy is an important feature of plant evolution as many agriculturally important crops are polyploids (Udall and Wendel 2006). Naturally available or artificially synthesized ploidy levels within taxa were used to understand features amenable to modification by ploidy changes. Ploidy modifications by enhancing or reducing the ploidy levels were achieved by chemical treatments (eg. colchicine, oryzalin), haploid cell and tissue culture (eg. anther and ovule culture), and utilizing genes interfering with cell divisions (Crismani *et al*., 2013). Recently, a Hybridization-supplemented Apomixis-components Partitioning Approach (HAPA) has been reported to successfully manipulate the ploidy without using any chemical treatment. This method relies on utilization of uncoupled apomixis components for enhancing or reducing the ploidy levels in apomictic crops (Kaushal *et al*., 2009).

Guinea grass (*Panicum maximum* Jacq.) is a high yielding perennial multicut forage grass, widely grown in tropical and sub-tropical countries. Tetraploid cytotypes (2n=4x=32) with obligate apomictic mode of reproduction are most predominant (Savidan 1980, Jain *et al.* 2003). We have identified eight pathways of seed development arising from recombination between the three apomixis components in this crop (Kaushal *et al.* 2008). These recombination events were utilized to generate a ploidy series represented by 3x, 4x, 5x, 6x, 8x and 9x cytotypes from a single 4x progenitor following HAPA (Kaushal *et al.,* 2009). Such exhaustive ploidy series offers advantages to study incremental effect of addition of monoploid genome for the traits of interest. The above members of ploidy series are already registered with PGRC (INGR 09039 – 09044). In present communication, we report further enrichment of this series with two new novel cytotypes viz., representing 7x and 11x ploidies. Including these two novel cytotypes, the ploidy series in guinea grass is most exhaustive with 8 different ploidy levels and represent worlds' largest ploidy series in a crop plant.

A facultative aposporous 8x (2n=64) plant (identity GGPS 8x-1) was used as a maternal parent alongwith a 6x paternal plant (identity 3/29/2) to generate plants with novel ploidies. The cross pollinated progeny was initially screened using flow cytometry to identify plants with desired ploidies. One plant each representing 7x (designated as GGPS 7x-1) and 11x (designated as GGPS 11x-1) were recovered and established from a total of 209 plants tested. These selected plants were subjected to detailed characterization including growth habit, cytology and reproductive behavior. We have used reproductive diversity of GGPS 8x-1 maternal plant in generating these ploidy levels. Origin of 7x plant is from fertilization between both reduced female and male gametes. Egg cell in sexual embryo-sac (ES) of facultative aposporous GGPS 8x-1 was expected to be 4x which when fertilized with male gamete (3x) from the 6x parent generated the 7x progeny through n+n hybridization (BII) pathway. The 11x plant would have a B_{III} origin, whereby the unreduced egg cell (8x) from an aposporous ES of GGPS 8x-1 got fertilized with reduced 3x male gamete from the 6x parent. Reproductive diversity in seed development arising from uncoupled apomixis components in guinea grass had been described (Kaushal *et al.,* 2008).

GGPS 7x-1: 7x cytotype (2n=56): This plant has originated GGPS 7x-1 contained 2n=56 chromosomes, showing $2_{I}+13.4_{II}+2.6_{III}+3.2_{IV}+0.6_{V}+0.6_{VI}$ as an average chromosome confirmation. Hexavalents were the largest chromosome association observed. About 48% chromosomes were involved in bivalent formation whereas 49% chromosomes were involved in trivalents or higher associations. The plant was male fertile with 68% pollen stainability, though variable sized pollens were of common occurrence. This plant was measured to have 3.2 pg sporophytic DNA content, matching with the chromosome numbers (DNA ploidy). It was facultative aposporous in mode of reproduction, exhibiting 72% aposporous ES (four nucleated Panicum type). Multiple ES were seen in 38% ovules of this plant. Well filled seeds could be obtained upon self-pollination of this plant.

GGPS 11x-1: 11x cytotype (2n=88): The plant GGPS 11x-1 had 2n=88 chromosomes with $3.75_{I}+15.25_{II}+3.75_{III}+4.75_{IV}+2.25_{V}+ 1.75_{VI}+0.25_{VII}$ average meiotic chromosome configuration, and 5 pg sporophytic DNA content. The plant was semi-sterile showing 57% pollen stainability and high variability in pollen size. The plant was obligate aposporous with high frequency of occurrence of multiple embryo-sacs (72%). In general, this plant exhibited larger size of gynoecium and ovary, and characterized with occurrence of trifid stigma (70% expressivity), a feature rarely reported in guinea grass. This plant was a shy seed setter upon self pollination.

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26. P. ori 6x-1 (IC0625989; INGR18026), a Novel Hexaploid (6x) Cytotype with 2n=54 Chromosomes of Pennisetum (*Pennisetum orientale*) Recovered through BIII Hybridization of a 4x (2n=36) Cytotype.

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Pennisetum L. Rich is one of the largest genera (tribe Paniceae) of Gramineae (Poaceae) family and encompasses several economically important crops species. *P. orientale* belongs to tertiary gene pool and is a valuable pasture grass with high palatability, nutritive value and drought tolerance. It is a tall rhizomatous, deep rooted and perennial grass known for its excellent soil binding qualities (Bor 1960). *P. orientale* has a basic chromosome number x=9 with tetraploid cytotypes (2n=4x=36) as most predominant forms. Other ploidy levels, such as 2x, 3x, 5x, and 6x are rarely reported (Jauhar 1981). Being apomictic in mode of reproduction, gene transfer through hybridization approach is difficult. However, owing to recent knowledge on uncoupled apomixis components, fertilization of unreduced egg cell with reduced pollen (known as 2n+n or B_{III} hybridization) (Rutihauser 1948) is one of the possible approaches to obtain gene transfer. Uncoupling of the apomixis components (apomeiosis, parthenogenesis and functional endosperm development) has been recently reported in several agamic species (reviewed in Ozias-Akins and van Dijk 2007).

Tetraploid accessions (2n=4x=36) of *P. orientale* are being maintained at Indian Grassland and Fodder Research Institute, Jhansi, Indiai. In one of our experiments on progeny analysis of apomictic crops, self-pollinated seeds from one of these tetraploid accessions (identity P. ori 4x-2) were collected and raised in the nursery. Fifty five germinated seedlings were tested for their ploidy levels, utilizing flow cytometric measurement of DNA contents. All the progenies were found to have 4x DNA-ploidy, except one off type plant which was confirmed to have a 6x ploidy level. This plant was separated from other siblings and was characterized for its morphological, cytological and reproductive traits, *vis-à-vis* its 4x progenitor (Kaushal *et al.* 2015).

The 6x plant (P. ori 6x-1) had 2n=54 chromosomes exhibiting 22.3_{II}+2.3_{IV} average chromosome configuration. The sporophytic DNA content was estimated as 4.25 pg that matched with the 6x ploidy level, as the tetraploid accession had 2n=36 chromosomes and 2.83 pg DNA content. P.ori 6x-1 was perennial in life cycle similar to its 4x parent, however, was less vigourous. Higher ploidy in *P. orientale* seemed not to affect perenniality but had modified some morphological, biochemical and reproductive attributes. Most of the metric traits were similar in both the plants except for less number of tillers and more compact spike in P. ori 6x-1 than 4x plant. Both of them were male fertile, though the 6x cytotype showed occurrence of sterile pollens (about 27%), however set seeds on self-pollination. Mode of reproduction, as estimated by embryo-sac (ES) studies was found to be apomictic (four nucleated aposporous ES) in both the cytotypes, though frequency of multiple ES was higher in 4x (90%) as compared to 6x (74%). In general, ES were observed to be larger in size in the 6x plant.

The recovery of 6x cytotype from a 4x maternal plant suggested the 2n+n (termed as B_{III}) hybridization pathway of its origin, through fertilization of an unreduced egg cell (2n) with reduced male gamete (n) in the 4x cytotype (Kaushal *et al.*, 2008) and had provided the first direct experimental evidence of uncoupling (partitioning) of apomixis components (viz. apomeiosis, parthenogenesis and functional endosperm development) in *P. orientale*.

In addition, these uncoupling events had also generated variability in an otherwise apomictic species. The system may be used to elucidate mechanisms of uncoupling events in *Pennisetum* genus in general, andin *P. orientale* in particular. Such material where the ploidy is raised by uncoupling events offer advantages to manipulate ploidy at will and also offer a system to study regulation of morphological, physiological, reproductive and molecular traits in response to or as modulated by the ploidy levels.

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27. IC11613 (IC011613; INGR18027), a Blackgram (*Vigna mungo*) Germplasm Resistant to Mungbean Yellow Mosaic Virus.

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Yellow mosaic disease (YMD) of blackgram is an important production constraint in India. Yellow mosaic disease of blackgram, mungbean, cowpea and soybean cause yield losses even upto 100% under severe conditions. YMD is caused by at least four different species of whitefly transmitted begomoviruses collectively called legume yellow mosaic viruses. Use of resistant varieties is the feasible, effective, economical, environment friendly and sustainable approach to alleviate occurrence of YMD in areas where it is major constraint to grain legume cultivation. Search for new resistant lines is a continuing process. No specific large scale systematic screening has been conducted in India to identify resistant source against yellow mosaic viruses by combining field screening, vector inoculation and agro-inoculation. 344 germplasm accessions were grown in augmented block design (ABD) during kharif 2010. Susceptible check Barabanki local was usedas infector line. The response of the virus was assumed based on percent disease incidence and disease severity. Germplasm accessions while showed resistance response in three consecutive years under natural disease pressure were subjected to further screening through artificial inoculation using viruliferous whiteflies. Germplasm accessions which showed resistance response after whitefly inoculation were further challenged by infectious virus clones through agro-inoculation with the infectious cloned DNA-a and DNA-B components of a new Delhi isolate of MYMV. The IC-11613 germplasm collected from Punjab was found as potential source of resistance to MYMV Along with the virus response the resistant germplasm i.e IC-11613 was also evaluated for agronomic traits viz., plant ht(32.8cm), branches/Plant (7.1), number of pods/plant (35.8) pod length (4.99), number of seeds/pod (5.7), 100 seed wt.(4.3g) and seed yield/plant (9.8g). IC-11613 germplasm was found superior in above morphological traits also in comparison to T-9 used as check. In the present investigation combined repeated field screening, whitefly transmission and agro-inoculation has shown that this particular accession is resistant to MYMV and hence it can be used for YMD resistant breeding programme or for cultivation after testing its adaptation to various zones and accepting quality traits.

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28. IC485638 (IC0485638; INGR18028), a Blackgram (*Vigna mungo*) Germplasm Resistant to Mungbean Yellow Mosaic Virus.

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Grain legumes are next to cereals due to their nutritional importance as food for human consumption. Yellow mosaic disease (YMD) mostly accounts for low harvest index of the present day blackgram cultivation. Although many resistant varieties of blackgram and mungbean have been developed using conventional breeding but durability of resistance does not hold good for a long time due to narrow genetic base of the cultivars as well as rapid emergence of new begomoviruses. Hence there is a need to book for new sources of resistance.A part of the germplasm collections of blackgram (344 accessions) was taken from The National Bank Gene and evaluated against yellow mosaic disease (YMD) and attempt was made to identity potential sources of resistance that could serve as valuable genetic resource for further disease resistance breeding programme. Field experiments were conducted on germplasm screening during the years Kharif 2010, 2011, 2012 at NBPGR experimental farm (28’ 64’ or 77’ 15 E) using barabanki local as highly susceptible check.Germplasm accessions which showed resistance under field conditions for three years were subjected to artificial inoculation using viruliferous white flies. Accessions which showed resistance were further tested for validation of resistance through agro-inoculation with the infectious cloned DNA- A and DNA-B components of a New Delhi isolate of MYMV. A germplasm collection IC 485638was found resistant to MYMV some morphological traits of agronomic importance were also recorded like plant height (30.8 cm), primary branches (7), pods/plant(23) pod length (3.8 cm) sub/pod5.7), 100 seed wt. (2.9 gm) seed yield /plant (6.5g). This germplasm can be used as one of the parents in YMD resistant breeding programme. After verifying its stability and wider adaptation it can be recommended for further cultivation and utilization.

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29. IC420405 (IC0420405; INGR18029), a Cucumber (*Cucumis sativus*) Germplasm with High Carotenoid Content. Orange Flesh Colour.

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The pulp colour of common cucumber (*Cucumis sativus* var *sativus*) is white to greenish with low carotenoid content. A unique accession namely IC420405, showing orange flesh (mesocarp and endocarp) colour and lemon yellow skin colour was identified in 2012 at NBPGR farm, New Delhi (Ranjan *et al*., 2013; Ranjan *et al*., 2015). Due to difficulty in adaptaion during initial years, the evaluation and regeneration of enough quantity of seeds were conducted during 2013 to 2017 at NBPGR farm and Vegetable Research farm, IARI, New Delhi. This unique accession was collected long back in 2004 from Mamit district of Mizoram. The carotenoid content is found as high as 27.5 µg/g as compared to 1.44-2.2 µg/g in the best check variety Pusa Uday at Delhi conditions and 29.2 µg/g as compared to 1.06 µg/g in check variety Pusa Uday at Varanasi conditions. The detailed morphological description is presented in Table 1. This unique genotype has also got some more distinct features. Unlike common cucumber, it has five carpels and delayed flowering with short day requirement. Interestingly, it has a tendency of parthenocarpy at high temperature and fasciation during low temperature resulting clustered flowers.

The mature fruit can be used in making vegetable recipe or as salad. It can be best utilized in mixed salad as the appealing orange colour makes the salad more attractive to the consumers with enhanced nutritional value. Hence, this unique line may be used directly or as a donor parent for developing carotenoid rich cucumber to combat with the problem of vitamin A deficiency prevalent in our country.

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Table 1. Morphological and biochemical characters of IC420405

Trait Description	IC420405	Check variety (Pusa Uday)
Vine length	2.5-3.5	2-2.5
Day length requirement	Short day	Day neutral
Parthenocarpy	Present (at high temperature)	absent
No. of carpel	5	3
Fruit length (cm)	17-24	20-22
Fruit skin colour at market stage	Creamish green	Creamish green
Fruit skin colour (mature stage)	Lemon yellow	Brown netted
Spine colour	White	Black
Spine density	Sparse	Medium
Flesh colour (mature stage)	orange	white
Number of seed per fruit	100	400-600
Shelf life (days)	7-14	6-7
TSS (ºB)	4.0-4.6	5.2-6.0
Ash (%)	0.56	0.34
Total Carotenoid (µg/g)	27.5-29.2	1.06-2.2

30. IC257296 (IC0257296; INGR18030), a Cucumber (*Cucumis sativus*) Germplasm with Two Female Flowers Per Node. Earliness. Small Fruit.

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Cucumber (*Cucumis sativus* L.), one of the important indigenous cucurbitaceous vegetables, is grown all around the world for fresh vegetable market as well as for processing industry. Cucumbers are generally monoecious, bearing separate staminate and pistillate flowers on a single plant. Generally, each leaf axil produces either a cluster of staminate flowers or one pistillate flower. However, evaluation of cucumber germplasm conducted during Spring and *Kharif* season of 2011-2013 and *Kharif* 2017 at NBPGR, New Delhi, has identified an unique accession, IC257296 having two female flower per node (on upper nodes i.e. after 7th node), rare and unique character with very small fruits. Besides this, it is very early in bearing with first female flower at 4th or 5th node. This accession was collected in 1999 from Khurda district of Orissa. This variant was selected and grown for four years at Delhi conditions. The morpho-agronomic characters are presented in Table 1. The number of fruits per vine is significantly higher as compared to check variety Pusa Uday. Thus, variety with two female flowers per node can produce more fruits than varieties with single female flower per node within a short period as reported earlier for pickling cucumbers in glasshouse (Nandgaonkar and Baker,1981; Hikosaka and Sugiyama, 2004) and common cucumber in open (Ranjan *et al*., 2015).

This unique accession of cucumber having small fruit in large numbers may be used for processing industry in place of long fruited type. Due to earliness and two female flowers/ node, this accession bears small tender fruits in succession, suitable for salad purpose. This accession offers an advantage to organic growers who aim to harvest large numbers of fruits before plants are severely damaged by pests and diseases. Moreover, due to its short vine length, the accession may also be suitable for growing in high density, kitchen gardens as well as for pot cultivation.

Table 1. Morpho-agronomic features of IC257296

Trait	Description (IC257296)	Check variety (Pusa Uday)
Plant growth habit	Short viny	Long viny
Node bearing first female flower	4.25	7.20
Fruit length (cm)	7.88	13.87
Fruit diameter (cm)	4.44	5.28
Seed cavity length (cm)	6.5	12.0
Diameter of seed cavity (cm)	3.55	3.42
Fruit colour	Green	Green
Number of fruits/plant	14.27	9.2
Sex type	monoecious	monoecious
Number of female flower/ node	02	01

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31. Allohexaploid (H2) (IC0626000; INGR18031), an Indian mustard (*Brassica juncea*) Germplasm with Heat Tolerance. Resistant to *Alternaria brassiceae.*

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Crop Brassicas are cultivated throughout the world and serve as important sources of vegetables, oilseed and spices. The blackspot disease caused by the fungus *Alternaria brassicae* is a major problem for which no source of resistance is available in cultivated Brassica germplasm. In particular, the losses in India due to black spot disease have been estimated between 35-47% under epidemic conditions (Kolte *et al*., 1987). The disease not only causes reduction in seed yield but also leads to lowering of oil and meal quality.Wild relatives of Brassica are rich reservoir of genes that are invaluable in improvement of cultivated species. *Sinapis alba* is a close relative of Brassica (Warwick and Black 1991) and is known to possess many desirable traits besides *Alternaria* resistance, tolerance to high temperature and drought (Primard 1988, Brown *et al*., 1997), resistance to shattering (Chandler *et al*., 2005; Wang *et al.,* 2007), beet cyst nematode (Lelivelt and Hoogendoorn, 1993) and club root (Lelivelt *et al.,* 1993). However, successful transfer of genes for blackspot resistance from wild species has not been achieved so far. We have developed somatic hybrid between *Brassica juncea and S. alba* through protoplast fusion with the ultimate goal of transferring genes for resistance to *Alternaria brassicae* and heat stress, the traits that are lacking in cultivated Brassica. Here we have reported vary high frequency of regeneration after protoplast fusion.

Morpho-agronomic Characteristics: Somatic hybrid shows mixed features of the parents. The hybrid show vigorous vegetative growth and attains more than 3.0 m height in contrast to its parent *S. alba* (2m) and *B. juncea* (1.57m). Days-to-flowering is intermediate (115-135 days) to parent (*S. alba*-166 days; *B. juncea*-145 days). Leaves of the hybrid are lobed with dentate margins and bear prominent trichomes on upper and lower surfaces. Stem is highly grooved, angular, thick and lacks wax, features similar to *S. alba*. Flowers are bright yellow and are larger than the parent. However hybrid bears fewer seeds per siliques as compared to *B. juncea* parent. The siliqua show characteristics beak as found in *S. alba.*

Associated characteristics and cultivation practices: Mitotic count of somatic hybrids reveals that hybrid (H2) carry 2n=60 chromosomes (Fig. 1C), a sum of the parental chromosomes of *B. juncea* (2n=36) and *S. alba* (2n=24). Hybrid shows mostly 30 bivalents at meiosis and even distribution of chromosomes at anaphase/telophas. Nuclear genome constitution of the hybrid is determined by using 10 SSR markers showed polymorphism between the parents. Hybrid shows the bands corresponding to the parents indicating the presence of nuclear genomes of both the parents. We use primers corresponding to the *orf108* upstream region and the *atpA* region to determine the mitochondrial genome constitution of hybrid. *S. alba* mitochondrial genome carries the male sterility inducing *orf108* upstream of the *atpA* gene (Kumar *et al*., 2012) which is also detect in somatic hybrid suggesting that the hybrid might carry recombinant mitochondrial genome. *In vitro* leaf assay and filed inoculation studies reveal that the hybrid is highly resistant to *A. brassicae* (1D). Besides, the hybrid set seeds at temperature of >38°C while the parents fail to produce seeds indicating that hybrid possess heat tolerance. These stable hybrids provide a reliable genetic resource for transfer of genes from *S. alba* into cultivated *Brassica* species.

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32. IC265495 (IC0265495; INGR18032), an Indian Mustard (*Brassica juncea*) Germplasm with White Rust Resistance (PDI = 0).

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White rust is a highly destructive disease of oilseed *Brassica*s; thus, it is essential to identify useful sources of host resistance in *B. juncea* as breeding and/or selection for resistance is the most cost-effective method of delivering control for farmers.The germplasm accession IC265495 collected from Aizwal, Mizoram was a part of2000 accessions of *B juncea* which were screened at three locations viz. Ludhiana, Pantnagar, Hissar during 2014-15 and 2015-16 crop season. This showed 0% disease severity with no infection at all the locations for two years. This was further evaluated under artificial inoculation in the pathological laboratory of Division of Plant Pathology, IARI, New Delhi against DELHI isolate of *A. candida* during 2016-17 as per the method described by Fox and Williams (1984). Observations for per cent incidence of white rust on leaves were recorded 20 days before the maturity of crop as per disease scoring scale adopted by Conn *et al.* (1990) and AICRIP R&M (2011). IC265495 showed resistant reaction (PDI = 0) under artificial inoculations indicating the presence of strong genetic mechanism in the expression of resistance. Apart from resistance to white rust, the mean performance of IC265495showed appreciably high values for different traits like days to maturity, silique length and 1000-seed weight. Thus it can be used for breeding Indian mustard varieties with resistance to white rust and high yield It is assumed that genetic stocks having high level of resistance and superior agronomic background may yield better progenies than those having poor agronomic performance while using them in breeding programmes.

Table 1. Mean of performance of IC265495 and National check- Kranti for various agronomic traits

Accessions	PB	DF	PH (cm)	DM	SMS	SL (cm)	SS	YP (g)	SWT (g)	OC (%)
IC265495	4.9	42.5	180.3	112.0	31.8	4.4	15.2	14.6	4.7	34.6
National Check (Kranti)	6.3	46.0	176.4	143.6	48.9	3.6	12.7	20.7	3.5	41.7

Primary branches/plant (PB), days to 50% flowering (DF), plant height, cm (PH), days to 80% maturity (DM), silique on main stem (SMS), silique length,cm (SL), seeds/silique (SS), yield/plant,g (YP), 1000-seed weight,g (SWT) and oil content, % (OC)

Table 2. Disease resistant reaction of Indian mustard accessions to white rust resistance over the locations

Score	Total no. of accessions			Promising accessions over the location	Resistant accessions under artificially inoculated controlled
	Ludhiana	Pantnagar	Hissar		
0	168	46	185	IC597932, IC267703, IC313380, IC20167, IC265495, EC657030, EC699003, EC766091, EC766133, EC766134, EC766136, EC766144, EC766145, EC766148, EC766152, EC766164, EC766191, EC766192, EC766193, EC766230, EC766232, EC766272, EC766311, EC766313, EC766315, EC766316, EC766402	IC 265495, IC313380, EC766091, EC766133, EC766134, EC766192, EC766230, EC766272

33. IC313380 (IC0313380; INGR18033), an Indian Mustard (*Brassica juncea*) Germplasm with White Rust Resistant (PDI = 0).

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White rust is a highly destructive disease of oilseed *Brassica*s; thus, it is essential to identify useful sources of host resistance in *B. juncea* as breeding and/or selection for resistance is the most cost-effective method of delivering control for farmers. The germplasm accessionIC313380 collected from Pithorgarh, Uttarakhand was a part of2000 accessions of *B juncea* which were screened at three locations viz. Ludhiana, Pantnagar, Hissar during 2014-15 and 2015-16 crop season. This showed 0% disease severity with no infection at all the locations for two years. This was further evaluated under artificial inoculation in the pathological laboratory of Division of Plant Pathology, IARI, New Delhi against DELHI isolate of *A. candida* during 2016-17 as per the method described by Fox and Williams (1984). Observations for per cent incidence of white rust on leaves were recorded 20 days before the maturity of crop as per disease scoring scale adopted by Conn *et al.* (1990) and AICRIP R&M (2011).

IC313380 showed resistant reaction (PDI = 0) under artificial inoculations indicating the presence of strong genetic mechanism in the expression of resistance. Apart from resistance to white rust, the mean performance of IC313380showed appreciably high values for various traits like days to flowering, silique on main stem, silique length, seeds per silique and oil content (Table 1). Thus it can be used for breeding Indian mustard varieties with resistance to white rust and high yield It is assumed that genetic stocks having high level of resistance and superior agronomic background may yield better progenies than those having poor agronomic performance while using them in breeding programmes.

Table 1. Mean of performance of IC313380 and National check-Kranti for various agronomic traits.

Accessions	PB	DF	PH (cm)	DM	SMS	SL (cm)	SS	YP (g)	SWT (g)	OC (%)
IC313380	4.6	40.0	181.0	136.0	52.6	4.2	17.2	12.0	2.1	41.5
National Check (Kranti)	6.3	46.0	176.4	143.6	48.9	3.6	12.7	20.7	3.5	41.7

Primary branches/plant (PB), days to 50% flowering (DF), plant height (PH), days to 80% maturity (DM), silique on main stem (SMS), silique length (SL), seeds/silique (SS), yield/plant (YP), 1000-seed weight (SWT) and oil content (OC)

34. IC0096539; NC-212 (IC0096539; INGR18034), a Linseed (*Linum usitatissimum*) Germplasm with Early Maturity.

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Linseed is an important multipurpose crop known for seed oil, stem fibre, paper, wax, nutraceutical and food processing industries. Indian sub-continent is a center of origin and domestication for this crop and this region is known to have high biological diversity of genus Linum (Fu, 2005). India is the sixth largest producer in the world with contribution to global linseed area and production 13% and 5.5%, respectively. Early maturity is one of the important breeding objectives for linseed as it protects crops from stresses such as disease, heat, drought, and frost (*Kaur et al., 2017)*. Short duration crop varieties are expected to prove boon to rain-fed farmers as it could give bonus income by growing linseed crop on residual moisture. In the above mentioned perspective, one landrace accession from Akola district of Maharashtra *viz.* IC0096539 was identified for early maturity (average 102 days). This accession is having semi-erect growth habit with funnel shaped, white colored flowers showing valvate aestivation. The stamen color is white while anthers are yellow. It produced medium sized lustrous brown seeds in non-dehiscent capsules. The oil content estimated was 40.36 %.

The identified accessions (IC0096539) is significantly early for flowering and maturity compared to early maturing released cultivar, RLC76 (Table 1).In addition, this accession is also early flowering and good for other agro-morphological traits such as large boll size with more number of seeds per boll and high thousand seed weight which are desirable agronomic traits. This accession has potential to be used in linseed breeding program for earliness/short duration which is an important breeding target in India owing to linseed cultivation in rain-fed and *utera* conditions. In addition this accession is expected to prove valuable genetic resource to unravel candidate genes/markers associated with flowering time and maturity to assist genomics/markers assisted breeding as well as to understand regulatory network involved there in.

Table1. Year-wise data of linseed accession IC0096539 and check variety RLC76 pertaining to different phenophases

Trait	Days to 50% flowering					Days to 95% flowering					Days to maturity				
Year	2014-15 (IARI farm)	2015-16 (IARI farm)	2016-17 (IARI farm)	2016-17 (Issapur farm)	**Mean**	2014-15 (IARI farm)	2015-16 (IARI farm)	2016-17 (IARI farm)	2016-17 (Issapur farm)	**Mean**	2014-15 (IARI farm)	2015-16 (IARI farm)	2016-17 (IARI farm)	2016-17 (Issapur farm)	**Mean**
IC0096539	60	58	57	59	**58****	77	70	71	78	**74****	103	102	102	99	**102****
RLC76	77	78	76	83	**79**	97	101	99	96	**98**	118	116	122	115	**118**

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

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35. LG 05817 (IC0627273; INGR18035), a Sugarcane (*Saccharum officinarum*) germplasm Moderately Resistant to 4 Pathotypes of Red Rot. 18.8 % Sucrose. Better Ratoonability.

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Red rot caused by *Colletotrichum falcatum,* is considered to be cancerous disease of sugarcane resulting in substantial economic loss to crop in Indian condition (Alexander and Vishwanathan, 1996). Many sugarcane varieties namely Co 213, Co 312, Co 419, Co 997, Co 1148, Co 62175, CoS 510, CoJ 64, CoS 767, CoC 671 and BO 54 succumbed to this disease after extensive cultivation. In sporadic incidences, the yield loss by red rot can be up to 30% in red rot prone area whereas cv CoJ 87 exhibited 100% incidence by red rot disease. Durable resistance in a plant is the kind of field resistance that remains effective for a long period while cultivars containing it are grown in diverse areas. It is also used as synonym of partial resistance or horizontal resistance/ or race non specific resistance. The name, although has no specific relation to its genetic control of resistance or degree of expression or its race-specificity. Sugarcane varieties such as CoC 671, Co 86032, Co 1148, CoJ 64, CoLk 8102, BO91 and CoS 767 are grown over large area and exhibit durable resistance but for race specific resistance only. Donors of durable resistance like commercial varieties BO 91 and CoLk 8102 grown in red rot prone area were used in breeding programme to develop two population of CoLk 8102 × ISH 176 and BO 91 × ISH 100.

LG 05817 is progeny of cross between CoLk 8102 (a susceptible and widely adapted variety of north east zone) and Interspecific hybrid ISH 176 (Co6806 × Khakai) (moderately resistant to Cf 08 and moderately susceptible to Cf 09). LG 05817 possesses moderately resistant (MR) reaction to four important red rot pathotypes of north west zone i.e. *Cf* 01, *Cf*08,*Cf* 09 and resistant (R) reaction to *Cf* 11 indicating durable resistance (Pandey *et al*., 2012, 2014, 2015; Anonymous, 2010). This clone showed horizontal resistance over past 10 years. It has cylindrical shape of inter node with greenish colour. This clone is characterized with more than 18.8 % sucrose and cane yield of > 88 t/ha. It has good ratoonabilty. It has good flowering at Coimbatore but do not flower in Lucknow condition. In Coimbatore climatic conditions, the clone shows 36% pollen fertility.

When it was used as recurrent parents with susceptible clone Co 62198, it produced high number of moderately resistant progeny indicating its high breeding value for this trait. High inheritance of the trait was attributed to cumulative effect of all four genes present in the clone. The clone is being constantly used as parent in breeding sugarcane clones for resistance against red rot. The most recent one is LG 05817 x LG 97050. The first cycle of recurrent selection of the cross has produced clones with desirable combination of resistance to red rot and high sucrose content.

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36. NBIHT-3 (IC0625991; INGR18036), an Opium poppy (*Papaver somniferum*) Pure Breeding Line Rich in Thebaine content >10%.

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Thebaine is one of the non-narcotic alkaloid among the diverse array of alkaloids in opium latex, which is extensively used in synthesis of pharmaceutical drugs (Fist *et al*., 2011). Though thebaine is not directly used in therapy but it is an important component for manufacturing of number of opiates. Nowadays, thebaine is industrially converted into a number of compounds like oxycodone, oxymorphone, buprenorphine, nalbuphine, naloxone, naltrexone and etorphine (Mishra *et al*., 2013). The international demand for specific alkaloids especially of thebaine has increased multifold in recent past due to its non-narcotic and non-addictive nature and ease in conversion for industrial preparation of morphine and codeine (Report of INCB, 2014). The global demand of thebaine increased from 2009 (241 tons) to 2013 (348 tons) but India's share is only 3 tons of the total global production of thebaine. Owing to such intense pharmacological application, production of thebaine in India is quite less in comparison to its demand. Although India is one of the largest producer of licit opium but has to import thebaine and its derivatives due to the lack of thebaine rich lines/varieties. Indigenous germplasm as well as developed varieties of opium poppy are primarily rich in morphine (9.20-20.86%) and narcotine (4.79-8.97%) in latex while content of codeine (1.69-2.48%), thebaine (1.78-2.80%) and papaverine (0.00-2.07%) remain substantially low. To trap this ever increasing global demand of thebaine, Govt. of India was keen for the development of thebaine rich opium poppy lines which could suffice the national and international demand. In this context, CSIR-National Botanical Research Institute, Lucknow for the first time developed a number of thebaine rich lines through rigorous selection from advance generations of interspecific population derived from cross between *Papaver somniferum* L. and *Papaver setigerum* DC (Shukla *et al*., 2015). The developed lines had thebaine content upto 15% in comparison to the existing indigenous varieties/lines having 1-2% thebaine content. A total of 11 high thebaine yielding lines developed through interspecific hybridization were evaluated along with two checks in randomized block design with three replications for eight years for thebaine content, other alkaloids, yield traits and other unique agronomic features at experimental field of Genetics and Plant Breeding Section, CSIR-National Botanical Research Institute, Lucknow. Standard cultural practices throughout crop season was followed which included pre sowing addition of farmyard manure at the rate of 10 t/ha (Approx.), 5–6 t/ha neem cake and 30, 50, 40 kg/ha N, P, and K respectively as basal dressing. 60 kg/ha N in two split after 30 and 60 days after sowing as top dressing and spray of the fungicide diethelene biscarbamate (Dithane M-45 0.2%) at 45, 60 and 90 days after sowing as per requirement was provided. The field was irrigated as and when required. Out of these, one most promising high thebaine pure breeding line NBIHT-3 (Thebaine content ~15.97%) was identified suitable for commercial cultivation based on overall performance in terms of seed, raw opium, other major alkaloids beside high content of thebaine and unique agronomic features (Tables 1 & 2). As per the calculations based on per hectare yield of each components of economic benefit (opium, seed and major alkaloids), the benefits from the cultivation of the developed thebaine rich line is at par or either higher than the cultivated varieties beside meeting national and international demand of thebaine.

Table 1. Economic features of developed high thebaine pure breeding line NBIHT-3 of opium poppy (Average over eight years)

Traits	Developed high thebaine pure breeding line	Checks	
	NBIHT-3	Madakini	BROP-1
Thebaine %	15.97	2.00	1.80
Morphine %	16.06	13.90	12.61
Codeine %	3.66	2.17	1.94
Narcotine %	0.33	9.70	11.27
Papaverine %	0.00	0.28	0.31
Opium yield (kg/ha)	30.36	39.68	38.37
Seed yield (q/ha)	11.39	12.12	12.35

Table 2. Morphological features of developed high thebaine pure breeding line NBIHT-3 of opium poppy (Average over three years)

Traits	Developed high thebaine pure breeding line	Checks	
	NBIHT-3	Madakini	BROP-1
Plant height (cm)	124.55	121.39	122.14
Peduncle length (cm)	23.35	24.38	23.87
Flower color	White	White	White
Leaves / plant	22.90	21.09	21.05
Branches / plant	2.95	3.19	3.06
Stem diameter (cm)	1.33	1.18	1.20
Capsule size (cm^2)	8.70	12.29	11.69

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37. Jor Lab L-9 (IC0625982; INGR18037), a Malabar Lemon Grass (*Cymbopogon khasianus*) Germplasm with High Essential Oil 0.80 %. Methyle Eugenol Rich>75%. High Herbage Yield 242.5 qtl/ha/year.

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Genus Cymbopogon is a valuable medicinal and aromatic grass of the world. The objective of the experiment was to identify methyl eugenol rich genotype of *Cymbopogon khasianus*. Methyl eugenol is widely used as a perfumery chemical as well as starting material for the synthesis of methyl dopa, an important hypertensive medicine (Kumaran *et al.,* 2013). Moreover it can also be used in confectionery, condiments, non-alcoholic beverages etc. In this experiment total 72 accessions of *Cymbopogon khasianus* were collected from different parts of North Eastern India and planted in complete randomized block design with three replications at experimental farm of CSIR-NEIST in the year of 2013.Morphological data recording and its oil constituents were analyzed during the year 2013-14 and 2014-15. On the basis of two years selection trial data a new and distinct methyl eugenol rich strain of *Cymbopogon khasianus* was identified and named as Jor Lab L-9. This new genotype was planted in multi-location trials in four different locations and found the results were stable and contented. The average oil yield was 0.8% which comprises of 74-75% methyl eugenol. Essential oil was extracted through hydro distillation method and the quantification was done by GC and GC/MS instrument (Lal *et al.,* 2016a; Baruah *et al.,* 2017; Dutta *et al.,* 2016., Dutta *et al.,* 2017; Lal *et al.,* 2018). In GC-MS analysis it was found that methyl eugenol was the major component of essential oil while geraniol, myrcene, elemicin, citral, linalool, geranyl acetate, methyl isoeugenol were the minor compounds. Till date none of the methyl eugenol rich germplasm of lemon grass is reported and we for the first time identified a novel methyl eugenol rich germplasm.

The oil yield % was significantly higher in the variety Jor Lab L-9 than the check variety Jor Lab L-2. The metyl eugenol content is significantly higher in the essential of identified germplasm (Table 1.). The higher oil yield is a desired character in *C. khasianus* as it is more economically beneficial. Plants of this variety are vegetatively propagated through slips and the plants are stable for commercial cultivation.

Our present study revealed that major portion of methyl eugenol in identified germplasm of *C. khasianus*, occupying 75% of the total essential oil. Methyl eugenol can be used commercially for various purposes like insect trapping. It can be used for further crop improvement

Table 1. Multilocation data of methyl eugenol rich germplasm (Jor Lab L-9) with check variety (Average of four locations)

Variety	Vegetative plant height (cm)	Flowering plant height (cm)	Herbage yield (tones/ ha/year	Oil %(w/w)	Methyl Eugenol (%) in the essential oil
Jor Lab L-9	111.75	239	27.50	0.82	75.13
Jor Lab L-2 (check variety)	121.75	160	22.7	0.44	4.78

Table 2. Essential oil analysis of *C. khasianus* genotype Jor Lab L-9

Chemical Compounds	Percentage of compound in the essential oil
Methyl Eugenol	74.94
Myrcene	4.2
Geraniol	4.9
Elemicin	3.1
Methyl isoeugenol	2.4
Geranyl acetate	1.6
Citral a	0.7
Citral b	0.3
Linalool	0.8
Unidentified	4.6

programme of lemon grass. For the first time a novel strain of methyl eugenol rich lemon grass identified through pure line plant breeding method is reported. This novel variety can be used for commercial cultivation by the farmers, agro industries and pharmaceuticals industries.

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38. Jor Lab K-1 (IC0625983; INGR18038), a Galanga (*Kaempferia galanga*) Germplasm with Higher Essential Oil Yield 2.31 %. Higher Rhizome Yield 6.75 tones/ha/year. Higher Dry Rhizome Recovery 27.50 %.

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Kaempferia galanga, known as Chandramula in Hindi is a rhizomatous herb of Zingiberaceae family cultivated mainly for its aroma and other medicinal importance. It is widely cultivated in tropics and subtropics of Asia including India, China, Bangladesh, Japan and Indonesia.In India it is grown in the states of Tamil Nadu, Kerala, Karnataka, North East states and West Bengal (Raina *et al.,* 2015). Essential oil of *Kaempferia galanga* rhizomes gives yellow colour oil on distillation with a yield of upto 2.5 percent. The oil is a complex mixture of volatile monoterpenes, oxygenated terpenes and sesquiterpenes as well as non–terpene hydrocarbons, ester, fatty acids and ketones (Amberkar *et al.,* 2011). *Kaempferia galanga* is famous for its medicinal uses due to presence of many important bioactive compounds like ethyl-p-methoxycinnamate which is a good constituent for antimicrobial and antineolplastic activity, ethyl cinnamate is used as vasorelaxant; luteolin and apigenin are good anti oxidant agents (Mustafa *et al.,* 2010). Some of these active compounds are used in the medicinal as well as perfumery industry that holds a great promise in ancient as well as modern era. The rhizomes also have a good nutritive value and are quite rich in protein and carbohydrate but low in fat (Hatano *et al.,* 1989; Jiang, 2013). In India the present price of dry rhizome is Rs 300 to 400 per kg and the price of essential oil is Rs

15000-17000 per litre which can be helpful for both farmers and enterpreneurs in increasing their earning (Lal *et al.*, 2017). Due to the limited improved varieties there is need of superior varieties of *Kampferia galanga* for high oil yield and rhizomes yield. Therefore, in this regard thirty-five germplasms were evaluated during the year 2013-14.After two years of evaluation of high oil and rhizome yielding genotype of *K. galanga* was identified and named "Jor Lab–K -1" (Fig 1) which was propagated through vegetative means using the rhizome as explant.This elite new genotype was evaluated in four different locations of North East India during the year, 2015 and 2016.

As per data from Table-1, the new variety Jor Lab K-1 contains higher oil yielding capacity of 2.37% with high rhizome yield of 7.156 tonnes/hectare compared to the check variety. One promising variety earlier released by the Kerala Agricultural University named"Rajani" was used as check variety.

The major chemical constituents identified in the rhizome of essential oil are ethyl trans-p-methoxycinnmate (31.12%),ethyl trans-cinnamate(14.3%),1,8-Cineol(10.57%), Delta -3- Carene (5.12%) and n- pentadecane (4.8%) which is responsible for its pharmacological properties.

Table 1. Quantitative and qualitative data of *Kaempferia galanga* (Jor Lab K-1) (Average of four locations)

Variety	Rhizome yield (tons/ ha)	No. of Mother Rhizomes	No.of Primary rhizomes	Dry rhizome recovery %	Oil % (w/w)	Days to maturity
Jor Lab K-1	7.156	5.62	12.25	28.50	2.37	273.75
Rajani(Check variety)	4.931	4.00	10.00	30.00	1.825	279.12

Cultivation of this high yielding germplasms will open new prospects for utilizing underutilized sloppy land.This will create avenues for employment of rural population in India. Cultivation of superior variety of *Kaempferia galanga* may give necessary boost to the pharmaceutical industry through higher value of essential oil which will lead to high income generation of the rural and entrepreneur development.

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39. Jor Lab L-10 (IC0625984; INGR18039), a Malabar Lemon grass (*Cymbopogon khasianus*) germplasm with High Elemicin content 70%. High Herbage yield 24.26 tones/ha/year.

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Cymbopogon Spreng is a genus belonging to family Poaceae. It is characterized by its different species having great variation in morphology and chemotypes (Bor 1960; Soenarko 1977). It is a valuable medicinal and aromatic grass comprising of 140 species all over the world out of which only 45 species are reported in India and tropical Asia (Dutta *et al.,* 2016; Lal *et al.,* 2016a, Dutta *et al.,* 2017). This medicinal and aromatic oil bearing grass plays an important role mainly in flavours, fragrances, cosmetics, soaps, perfumery, detergents and pharmaceuticals (Lal *et al.,* 2016b) throughout the world and also gives essential oil upon steam distillation (Lal *et al*., 2016a; Baruah *et al*., 2017, Lal *et al.,* 2018). It is a vegetatively propagated perennial crop basically found in Khasi and Naga Hills and some lower part of Assam of North East India. Elemicin is a natural organic compound which is known as phenylpropene (Villanueva *et al.*, 1993 and Leela *et al.,* 2008), also a constituent of oleoresin. In this experiment total forty eight accessions of *Cymbopogon khasianus* were collected from different parts of Meghalaya and planted in complete randomized block design with three replications at experimental farm of CSIR-NEIST in the year 2013.Morphological data recording and its oil constituents were analyzed during the year 2013-14 and 2014-15. On the basis of two years selection trial data a new and distinct elemicin rich strain of *Cymbopogon khasianus* was identified and named as Jor Lab L-10. This new genotype was planted in the year 2015-16 and 2016-17 in multi-location trials at four different locations and the results were found to be stable and contented.

Till date none of the elemicin rich germplasm of lemon grass is available in the public domain. So we have made an effort to identify high elemicin rich germplasm of lemon grass from the collected germplasm. Therefore, development and cultivation of the elemicin rich strain is very much beneficial to the farmers as well as pharmaceutical industries and net return will be higher as compared to the other lemon grass variants.

Table1. Average multi-locational evaluation of quantitative and qualitative data of Cymbopogon khasianus (Jor Lab L-10)

Variety	Vegetative Plant height (cm)	Flowering Plant Height (cm)	Herbage yield (tones/ha/year)	Oil %(w/w)	Elemicin %
Jor Lab L-10	98	201	24.26	0.40	70.35
RRLJ-021 (check variety)	118.85	159.23	22.33	0.44	25.56

As per data from Table-1, the new variety Jor Lab L-10 has average oil yield of 0.40 % which comprises of 70% elemicin content and 175% superior in the term of elemicin content from the check variety.

Table 2. GC-MS data of some of the identified components present in the essential oil of *Cymbopogon khasianus (*Jor Lab L-10)

Chemical Compound	Percentage of compounds in the essential oil
Elemicin	70.475
Cis-Asarone	8.235
β-ocimene	5.632
Methyl eugenol	3.145
Limonene	2.269
Germacrene-D	1.569
Neral acetate	1.241
Camphene	0.982
α-pinene	0.891
Geranyl acetate	0.720
Caryophyllene	0.490
Trans-β-farnesene	0.312
Unidentified	4.039

In GC and GC-MS analysis it was found that elemicin was the major component of essential oil while cis-asarone, β-ocimene, methyl eugenol, limonene, germacrene-D, transneral acetate, camphene, α- pinene, geranyl acetate, caryophyllene and trans-β-farnesene etc. were the minor compounds. Till date none of the elemicin rich (>70%) variety of lemon grass is reported and we first time identified a novel elemicin rich variety (Lal *et al.,* 2018).

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40. Jor Lab L-14 (IC0625985; INGR18040), a Malabar Lemon Grass (*Cymbopogon flexuosus*) Germplasm with High Essential Oil 1.25 %. High Herbage yield 28.32 tones/ha/year. Citral Content 76 %.

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A new and distinct high essential oil and high herbage yielding variety of lemongrass (*Cymbopogon flexuosus*) was developed named Jor Lab L-14. After evaluation of four locations with two year 2015-16 and 2016-17 the novel germplasm contains 1.25 per cent essential oil and 28.32 tonnes /ha/year herbage yield. This novel variety Jor Lab L-14 of lemongrass is developed through mutation breeding. This variety is propagated through vegetative means using the slips and is stable for commercial cultivation.Lemongrass (*Cymbopogon flexuosus* L.), family Poaceae is an aromatic grass species and is commonly known as 'East Indian Lemongrass'. It is a vegetatively (also, seed) propagated perennial, multicut crop in the tropics Lal *et al.*, 2016., Saikia *et al.,* 2015., Baruah *et al*., 2017, Lal *et al.,* 2018). The prefix 'Lemon' owes to its typical lemon-like odor, released from the leaves on maceration, which is mainly due to the presence of citral as a cyclic monoterpene. The lemongrass oil as such is widely used in perfumes, soaps and cosmetics to obtain typical lemon notes (Lal *et al.,* 2016a; Lal *et al.,* 2016b; Lal *et al.,* 2018. Besides, it's an important source of citral, which is used in perfumes and medicine (Saikia *et al.,* 2015). While citral forms a significant raw material for confectionery and beverages, it is the principal source of β-ionone which is extensively used for the synthesis of vitamin A and a number of chemicals including synthetic violet perfumes (Lal *et al.,* 2016). In future, thus generating new varieties with higher oil yield and citral content in lemongrass is of utmost necessity.

In the view of above demand it is necessary to evolve essential high essential oil yielding varieties for respective locations. Due to the limited improved varieties for high oil yield and herbage yield, its cultivation is not popular among farmers. Therefore, there is a need to develop superior varieties of lemongrass for high oil yield and herbage yield. In CSIR-NEIST farm there is more than 534 accessions of *Cymbopogon* species. As per record this germplasm banks is first position followed by Oddakali germplasm bank (Dutta *et al.,* 2017). We screened the genotypes based on high oil yielding and high herbage yield from Gamma mutant progenies and identified a high oil yielding and high herbage yielding genotype named as Jor Lab L-14. Then, these superior selected clones were evaluated in four locations (Jorhat Assam, Imphal Manipur, Pasighat Arunachal Pradesh and Lakhimijan Assam) where these were compared to all the checks and found stable and high essential oil yield.

As per data from Table 1 the tillers per plant for Jor lab L-14 was significantly higher than the checks. As well as the oil yield is higher than the both check varieties. The oil yield per kg/ha/ year was significantly higher in the variety Jor lab-14. The characters plant height and herbage yield/tons/ha/year are non significant difference between the elite line and checks. The higher oil yield is a desired character in lemon grass as it more economically beneficial. This elite clone Jor Lab L-14 maintained its superiority over all the checks for herb and oil yield. Plants of this variety are propagated through only vegetative means using the slips, and the plants are stable for commercial cultivation.

Morpho-agronomic characterises

Characters	Range
Plant height (cm)	124-139
Growth habit	Semi compact
No of tillers/plant	70-92
Herbage yield /Qt/ha/year	275 to 302
Oil content %	1.25
Citral %	76

Table 1. Average morphological and quality data of Jor lab L-14 lines with checks in four Locations (2016-17)

Variety	Plant height (cm)	Tillers/plant	Herbage yield/tones/ha	Oil % w/w	Oil yield/kg/ha/year	Citral %
Jor LabL-14	124-139	86	28.32	1.25	350.4	76
Jor Lab L-2	118-132	44	27.80	0.42	116.76	79
Krishana	102-126	58	26.90	0.89	239.41	80

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41. Jor Lab P-1 (Patchouli) (IC0625986; INGR18041), a Patchouli (*Pogostemon cablin*) Germplasm with High Essential Oil Yield and High Herbage Yield 3220 kg /year.

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Patchouli (*Pogostemon cablin* (Blanco) Benth) is a medicinal and aromatic plant which has natural essential oil that can be extracted by steam distillation from both fresh and dry leaves. It is a perennial aromatic herb/shrub, belonging to family Lamiaceae. Patchouli is native to Philippines 1 and other cultivating countries which include Indonesia, Malaysia, Thailand, West Africa, Brazil, China and India (Jadhav *et al.,* 2002). The Indian demand for patchouli oil is 220tones/annum and a major quantity of oil is imported (Kumar *et al.,* 2004). Patchaulol and α-patchoulene are the major components and many sesquinterpenes hydrocarbon such as α, β, γ-patchoulenes, α-bulnesene, α-guaiene and seychellene, cycloseychellene are the minor compounds of the essential oil (Donelian *et al*., 2009). The oil contains unique aroma and flavour, products made from its oil such as soaps; detergents, etc. have be-come successful commercial products in global business industries.It is also blended with sandal wood oil which is one of the finest attars widely used for scenting soaps, perfumes, body lotions, after shave lotion, detergents and cosmetics. In aromatherapy, it is used to calm nerves, control appetite and relieve depression and stress. It also possesses insecticidal, antibacterial and antifungal properties (Swamyand *et al*., 2015). At present, the most important concern with commercial cultivation of *P. cablin* is availability of a cultivar that can produce high oil yielding along with high patchouli alcohol content. In the view of above needs and great prospects of cultivation of this crop successfully in various region of India, it is necessary to evolve high yielding genotypes for respective locations. Due to the limited improved varieties for high oil yield and herbage yield, its cultivation is not popular among farmers. Therefore, in this regard mutant populations were developed through gamma radiation to create the artificial variability and selection was done to identify the high yielding germplasm of patchouli named as Jor Lab P-1 which would be helpful in doubling the net income of farmers of India (Lal *et al.,* 2018). Then, these superior selected clones were evaluated in four different locations of NE region, where these were compared to the check variety.

As per data from Table 1, the oil yield kg/ha/year was significantly higher in the germplasm Jor Lab P-1 than the check variety Johor. The higher yield is a desired character in patchouli as it is more economically beneficial. Plants of this variety are propagated through cutting and plants are stable for commercial cultivation. The variety Jor Lab P-1 (fig. 1) thus increases earnings of farmers as well as meet the demand of its essential oil in the country.

Table 1. Multilocation data of Patchouli variety (Jor Lab P-1) with check variety (Average of four locations)

Variety	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Fresh herbage yield (kg/ha/year)	Dry herbage yield (kg/ha/year)	Oil (%)	Oil yield (kg/ha/year)	Patchouli alcohol (%)
Jor Lab P-1	112	9.4	7.26	11393.84	3220	3.10	80.5	38.00
Check variety (Johor)	101	7.3	6.89	10798	2446.5	2.15	52.60	32.8

Morpho-agronomic Characteristics

Characters	Range
Plant height (cm)	106-116
Fresh herbage yield (kg/ha/year)	9870-12340
Dry herbage yield (kg/ha/year)	2800-3251
Oil content %	2.85-3.251
Patchouli alcohol %	32-43

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42. EC338785 (EC338785; INGR18042), a Sweet Basil (*Ocimum basilicum*) Germplasm with High Methyl Chavicol Content (> 88.81±2.34 %) in Essential Oil Isolated from Aerial Parts.

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Sweet basil (*Ocimum basilicum* L.) is a pleasant smelling perennial herb of high industrial importance for the essential oil and aroma chemicals. The plant possesses wide range of genetic variability as observed through plant morphology, phenology and oil composition. Traditionally, basil has been extensively utilized in food as a flavoring agent, and in perfumery and medical industries. The basil essential oils are usually extracted from the leaves and flowering tops of basil plants. Through the centuries basil was cultivated for culinary and medicinal purposes in many countries, which created a great diversity of species within the *Ocimum* genus. The genus *Ocimum* comprises more than 150 species and is considered as one of the largest genera of the Lamiaceae family. The *O. basilicum* 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 (Pushpangadan and Bradu, 1995).

The chemical composition of basil oil has been the subject of considerable interest due to extensive diversity observed in the constituents of the basil oils. The plant has the propensity to exhibit chemotypes i.e. morphologically indistinguishable plants of the same *Ocimum* species very often differ clearly in their chemical constituents. 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. Variations in chemical composition of basil oil play an important role in evaluating their utilization and value for industrial applications (Raina *et al*., 2017)

The present exotic germplasm collection of *O. basilicum* EC338785 was imported from USDA, USA in 1992. The germplasm was grown in experimental fields of ICAR-NBPGR 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. Detailed chemical profiling of essential oil isolated from aerial plant parts of EC338785 by GC/MS exhibited methyl chavicol 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 EC338785 (methyl chavicol 88.81 ± 2.34%). Methyl chavicol 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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43. Solan Selection (IC626004; INGR18043), a Malaxis (*Malaxis acuminata*) Germplasm with Yellow Coloured Flowers without any Purple Tinge. Yellowish Green Floral Buds. Greenish Basal Sheath at the Base of Shoot.

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Malaxis acuminata D. Don (syn. *Microstylis wallichii* Lindl.) is a terrestrial, perennial, medicinal orchid, distributed in India in temperate to subtropical Himalayas at an altitude of 1200-2100m (Clarke, 1985). It is an important ingredient of Ashtavarga drug and is used in Ayurveda for the preparation of Chyawanprash, Astavarga churna, Chitrakadi taila, Vachadi Taila, Mahakalyan Taila, Jivaniya ghrita, Mahamayura ghrita, Vajikarma taila, Brahini gutika and Himvana agada (Anonymous, 2006; Balkrishna *et al*., 2012). It is also used to cure tuberculosis and is a potent aphrodisiac (Chauhan, 1990). Due to unscientific harvesting, overexploitation and habitat destruction the existence of *M. acuminata* is under threat and is listed in CITES Appendix-II for ensuring its conservation. Genetic diversity assessment studies conducted at Shilly Farm (altitude 1550 amsl, latitude-N 30º54’30” and longitude E 77º07’30”) under Dr YS Parmar Universityof Horticulture & Forestry, Solan, Himachal Pradesh resulted in isolation of one unique & stablemorphotype (named as Solan Selection) having distinct colour of floral buds, flowers, sheath on base of shoot (rhizome) and pseudobulbs.

Morpho-agronomic Characteristics: The plants of Solan Selection are characterised (Fig.1) by greenish basal sheath (at the base of the shoot in contrast to purplish in wild type), yellowish green floral buds (purplish in wild type), yellow coloured flowers without any purple tinge on their surface (purple tinge in wild type) and pseudobulbs covered by green sheath (purplish in wild type). All theses distinct morphological characters were found consistently stable in successive growing seasons during the years 2013, 2014, 2015, 2016 & 2017.

Associated Characters and Cultivation Practices: *Malaxis acuminata* is successfully regenerated by vegetative propagules i.e. rhizomes and pseudobulbs (Sharma *et al.*, 2014). Each plant produce single rhizome and 2-4 pseudobulbs in a growing season. The basal swollen stem of the plant on senescence develop to single rhizome, which is the economic part and is used in drugs and pseudobulbs give rise to new plants during next growth cycle.

Investigations are continuing at Dr YS Parmar University of Horticulture & Forestry Nauni, Solan to assess the growth & yield performance in respect of total biomass yield with a view to develop a high yielding strain/variety fulfilling the requirement of DUS criteria.

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44. Rama Tulsi/ DOS-1 (IC0627270; INGR18044), a Basil (*Ocimum sanctum*) Germplasm with Number of PGs in leaf. Dry Leaf Recovery (23.10 %). Essential Oil Contents (0.65 %) in Green Herbage and Leaves.

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The holy basil (*Ocimmum sanctum* L. syn. *Ocimum tenuiflorum*) (Family Lamiaceae), is the most sacred herb. It is an excellent herb known as queen of herbs, native of India and is cultivated largely as a house hold species. The most common uses of the holy basil include preparation of herbal tea, healing remedies, cosmetics and as a preservative.

Each and every part of plant are economic parts used in the treatment of various diseases in Indian systems of medicine. India exports large quantity of leaves, plant extract and essential oil in the world market and earns crores of revenue every year. Germplasm constitute the basic quality materials required for the improvement of this crop. Increasing demand of leaves and essential oil in the national and international market calls for developing high yielding varieties with desired marker traits. For the first time, a selection with maximum no. of PGs per leaf and rich in essential oil content (DOS-1) was identified at the Directorate of Medicinal and Aromatic Plants Research, Anand, Gujarat. DOS-1 was also suitable for ratoon crops. DOS-1 was having a stem girth (1.3 cm), plant height (85 cm), plant spread (0.30 m^2), dry leaf recovery (23.10 %), plant spread (52 cm) and essential oil content from green herbage (0.65 %) as compare to Angna (check) which was having stem girth (1.6 cm), plant height (119 cm), plant spread (0.32 m^2) dry leaf recovery (21.0 %) and essential oil (0.35 %) content (Table A). The plant growth parameters and essential oil content could be some important parameters in tulsi which may be used to develop high yielding cultivars. Leaf, petiole, new branches and inflorescence are green in colour at the full flowering stage as compare to check (purplish). The maximum no. of PGs per leaf was observed in DOS-1 (8478) while minimum in Angna (4330) in leaf. The number of PGs were observed just double in DOS-1. The number of PGs and oil content having positive relationship in DOS-1/tulsi. The selection is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics of growth, yield and quality variations. Further, these traits can be used as DUS character for identification of elite germplasm lines and cultivars

45. Sweet basil/ Rudra-2 (IC0627271; INGR18045), a Dwarf Basil (*Ocimum basilicum*) Germplasm with Early Flowering (27.75 days after transplanting).

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Basil (*Ocimum basilicum* L.) is one of the most important aromatic herb belongs to the family Lamiaceae. It originated from India and then reached to warm regions worldwide. In India, basil have been cultivated in Gujarat, Rajasthan, M.P. and U.P. in patches under approximately 2,160 ha area. Basil is cultivated extensively in France, Egypt, Iran, Hungary, Indonesia, Morocco, Greece and Israel, most in Mediterranean countries and in various regions with temperate and hot climates.

Now it is commercially grown for its essential oil, which are rich in three important essential oils *viz*., linalool (20-40 %), methyl chavicol (20-25 %) and eugenol (0-12 %). It also contains tannins and flavonoids. As per geographical origin and major constituents of basil, they are divided into four parts viz., European chemotype (linalool), reunion chemotype (estragole), tropical chemotype (methyl cinnamate) and eugenol chemotype (eugenol). Morphological and chemotypic characterization are the main criterion for selection of suitable morphotype for herbal industry. A wide variation was observed in Rudra-2 and GAB-1 of sweet basil based on their morphological traits. Two main morphotypes cultivated in India and adjoining regions are bunch type panicles and single panicles. The inflorescence was individual type (loose) and purplish green coloured in Rudra-2 as compare to GAB-1 which had bunchy (compact) and light purple coloured inflorescence. The variants with distinct characters' leaf size, plant height, spreads, canopy compactness and branches are available. The minimum growth parameters, especially plant height (53 cm), plant spread (37 cm), stem girth (1.10 cm), internodal space (3.26 cm), number of branches (10), leaf size (8.72 cm^2), leaf petiole length (1.08 cm) and earliest on set of flowering (27.75 days after transplanting) were observed in Rudra-2 as compare to variety GAB-1 which had plant height (105 cm), plant spread (64 cm), stem girth (1.89 cm), minimum internodal space (4.57 cm), number of branches (23), leaf size (12.45 cm^2), leaf petiole length (3.48 cm) and earliest on set of flowering of 39 days after transplanting.Reduced plant height is an important agronomic trait in basil breeding that has potential to be used for proper utilization of resources. Moreover, such traits permit higher plant populations under vertical and horizontal resources utilization. The basil, has an increased plant height as compared to a relatively restricted root system. Therefore, when it was grown in field where strong winds blew during the flowering period, plants suffered from lodging. The reduction in plant height could lead to enhanced lodging resistance. The selection is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics of growth variations. Further, these traits can be used as DUS character for identification of elite germplasm lines and cultivars.

46. Sweet basil/ DOB-1 (IC0627272; INGR18046), a Basil (*Ocimum basilicum*) Germplasm with Upper leaf (Adaxial Surface) Puckering. Light Green Leaf Colour and. Maximum Number of PGs in Mature Leaf.

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Basil (*Ocimum basilicum* L.) known as sweet basil and one of the most important aromatic herb belonging to Lamiaceae (Labiatae) family, comprises perennial herbs and is native to tropical and sub-tropical regions of Asia, Africa and Central-South America. Medicinal plants' genetic resources with enormous diversity are global assets of incalculable value to the present and future generations, and sufficient genetic variability is a prerequisite for efficient selection for crop improvement.

Basil, an economically important herb due to its essential oil, is used in hygiene and cleaning products, perfumes, cosmetics as a local anesthetic and antiseptics. Plant extracts are widely used in traditional medicines for its biologically active constituents that have insecticidal, nematicidal, fungistatic and antibacterial properties. The diverse signatures of basil in appearance, flavors, fragrances, industrial traits, edible and drying oils and natural pigments provide great opportunities for developing new culinary, ornamental and industrial crop with marker traits. Therefore, present registration was undertaken to elucidate the morphological markers with essential oil production in sweet basil. The inflorescence is individual type (loose) and purple in colour in DOB-1 as compare to GAB-1 which has bunchy (compact) and light purple in inflorescence colour. The variants with distinct combination of characters' upper side leaf (adaxial surface) puckering, light green upper leaf colour and maximum number of PGs (15.6/mm^2 leaf area) for high essential oil production in DOB-1 as compare to GAB-1 which had no puckering, green leaf colour and minimum number of PGs (6.4/mm^2 leaf area). The selection is stable, uniform and distinct and hence, may be used as an important allelic source to unravel genetics for morphological marker and quality traits. Further, these traits can be used as DUS character for identification of elite germplasm lines and cultivars.