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Plant Germplasm Registration Notice[@]

The Plant Germplasm Registration Committee (PGRC) of ICAR held its XXXXVIth meeting on December 24, 2021 in virtual mode. 131 proposals were received and examined at ICAR-NBPGR out of which 74 proposals complete in all respects and reviewed by experts were considered for registration. 67 proposals with unique/novel features belonging to 27 species were finally recommended for registration. The information on registered germplasm is published with the purpose to disseminate the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes.

1. RP 5690-20-6-3-2-1 (IC0641981; INGR21176), a rice (*Oryza sativa*) germplasm with resistance to brown planthopper and whitebacked plant hopper. Possessing *bph4, Bph 9*, *Bph 17* and *Bph 32* genes for BPH resistance; and *wbph 9* & *wbph 10* genes for WBPH resistance

G Padmavathi[*], V. Jhansi Lakshmi, M Sheshu Madhav, P Senguttuvel, Ch Suvarna Rani, LV Subba Rao and RM Sundaram
ICAR-Indian Institute of Rice Research, Hyderabad-500030, Telangana, India
[*]*Email: padmaguntupalli6@gmail.com*

Considering the enormous yield losses caused in rice by two dreaded insect pests of rice namely brown planthopper (BPH) and white backed planthopper and (WBPH) for which limited donors are available, a focussed research program is being carried out at ICAR-IIRR, Hyderabad to develop elite lines conferring resistance to both the plant hoppers. An inbred line, RP 5690-20-6-3-2-1 developed from Sona mahsuri/SR 26-B following pedigree method was identified as resistant to planthoppers during seedling stage under controlled conditions against BPH and WBPH population of Hyderabad. It is a medium duration culture (128 days) with tall plant stature (139 cm) possessing long bold grains. It was evaluated in multi-location testing trial *viz.* Planthopper Screening (PHS) trial for two years in 2017 and 2018 against BPH and WBPH populations at 13 hot spots as well as controlled greenhouse conditions in AICRIP entomology program. It exhibited stable and durable reproductive stage resistance against planthoppers at 4 locations continuously for 2 years (Table 1) in 3 locations (IIRR- Hyderabad, Ludhiana and Pantnagar with a mean DS: 3.2 against BPH; at one location (IIRR, Hyderabad) resistance reaction against WBPH (DS: 3.1) and moderate resistance reaction (DS: 4) at another single location (Maruteru) against mixed population of planthoppers. The resistant checks PTB 33 and MO1

Table 1: Glass house and field reaction of *RP 5690-20-6-3-2-1* to BPH, WBPH and mixed population of planthoppers during 2017-2018

S. No.	*Designation*	*Year of testing*	*DS of BPH (Green house reaction)*				*DS of WBPH (Green house reaction)*	*DS of Planthoppers (Field reaction)*
Screening locations			IIRR	LDN	PNT	Mean DS	IIRR	MTU
1	RP 5690-20-6-3-2-1	2017	4.8	2.3	1.7	2.9	2.3	5
		2018	2.8	3.6	4.5	3.6	3.9	3
		Mean	3.8	2.95	3.1	3.2	3.1	4
2	PTB 33 (R check for BPH)	2017	0.5	1.7	2.1	1.4		5
		2018	1.3	1.6	7.6	3.5		1
		Mean	*0.9*	*1.65*	*4.85*	2.4		3
3	MO1 (R check for WBPH)	2017					1.6	9
		2018					4.2	7
		Mean					2.9	8

IIRR: Indian Institute of Rice Research, Hyderabad; LDN: Ludhiana, PNT: Pantnagar, MTU: Maruteru

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[@]*Edited by:* ***Anju Mahendru Singh*** *and* ***Anjali Kak****, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India.*

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recorded mean damage scores ranging from 0.9 to 4.85 and 1.6 to 4.2 respectively (Padmavathi *et al*. 2019; ICAR-IIRR, 2018. Progress Report 2017, Vol 2; ICAR-IIRR, 2019. Progress Report 2018, Vol 2).

Molecular characterization using linked and designed markers reported earlier revealed the presence of a synergistic combination of 4 known BPH Resistance genes (*bph4, Bph 9, Bph 17* and *Bph 32*) and 2 WBPH resistance genes (*wbph 9* & *wbph 10*) imparting stable resistance to the prevailing populations of planthoppers. This line could be exploited as a vital genetic source for imparting durable resistance to BPH and WBPH in recombination breeding programs along with good grain quality and high grain yield.

References

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2. CRR 363-36 (IET19251) (IC640650; INGR21177), a rice (*Oryza sativa*) germplasm with aroma, early maturity (85-90 days) and long slender grain for rainfed uplands

NP Mandal[*], Somnath Roy and Amrita Banerjee

Central Rainfed Upland Rice Research Station, ICAR-NRRI, Hazaribag-825301, Jharkhand, India

[*]*Email: npmandal@hotmail.com*

The rice elite line CRR 363-36 (IET 19251) was developed through pedigree breeding from a cross between Gaurav and Kalinga III at CRURRS (ICAR-NRRI), Hazaribagh. Among the parents Gaurav is a Basmati 370 mutant with excellent grain quality and aroma, and Kalinga III (AC540/Ratna) is an upland variety released for Orissa and Bihar. The CRR 363-36 was developed with an objective to produce a high yielding early maturing variety having excellent grain quality and aroma for rainfed uplands in eastern India because most of the developed upland rice varieties are poor in terms of grain quality and none of them is having aroma. Good grain quality can fetch better premium at the market and partially compensate upland rice farmers for low yield. The line was evaluated as IET 19251 in AICRIP - very early group in 2005 and subsequently tested under Orissa state adaptive trials during 2007-2010. Agro-morphologically, CRR 363-36 is intermediately tall, it flowers in 55-60 days and has excellent long slender grains with good elongation ratio, considerable aroma and acceptable amylose content (Table 1). It is resistant to brown spot and moderately resistant to blast diseases which are the major diseases of uplands, based on National Screening nursey – 2005 data of AICRIP. CRR 363-36 is also resistant to gall midge-1, stem borer and moderately resistant to gall midge-4 & -5 and leaf folder. Due to its very early nature, CRR 363-36 usually escape drought stress under rainfed uplands. This improved elite line can be used as a donor for superior grain quality in upland rice breeding programmes.

Table 1: Salient agro-morphological features of rice elite line CRR 363-36

Characteristics	*CRR 363-36*	*Characteristics*	*CRR 363-36*
Plant type	Intermediate	Kernel breadth(mm)	1.85
Coleoptile colour	Green	Grain L/B ratio	3.45
Early plant vigour	Vigorous	Kernel appearance	LS
Basal leaf sheath colour	Green	1,000 grain weight (g.)	23.55
Leaf blade colour	Green	Threshability	Easy
Leaf pubescence	Pubescent	Husk colour	Straw
Leaf length (cm)	27.74	Hulling recovery (%)	77
Leaf width (cm)	1.24	Milling recovery (%)	65
Leaf angel	Horizontal	Head rice recovery - HRR(%)	52
Days to 50% flowering	55-60	Chalkiness	OC
Panicle exertion	Full	Kernel length after cooking(mm)	9.9
Stigma colour	White	Elongation ratio	1.54

Apiculus colour	Straw	Alkali value	4
No. of effective tillers/plant	14	Amylose content (%)	18.75
No. of panicles/sq.mt	238	Aroma	Present
Plant height (cm)	96		
Plant height (cm)	96		
Panicle length (cm)	23.86		
Panicle type	Compact		
Awning	Absent		
Days to maturity	85-90		
Seed coat(kernel) colour	White		
Kernel length(mm)	6.39		

3. RR 433-2-1 (IET 19252) (IC0560851; INGR21178), a rice (*Oryza sativa*) germplasm tolerant to drought and high yielding for rainfed direct seeded upland conditions

NP Mandal*, **Somnath Roy and Amrita Banerjee**

Central Rainfed Upland Rice Research Station, ICAR-NRRI, Hazaribag-825301, Jharkhand, India

*Email: npmandal@hotmail.com

The rice elite line RR 433-2-1 (IRAT112/Annada) is a derivative of a *tropical japonica* × *indica* cross, of intermediate stature with the better lodging resistance of the *japonica* parent and more responsive to moderate-input management than traditional varieties. This line was developed at CRURRS (ICAR-NRRI), Hazaribag through pedigree breeding. The line (IET19252) was tested under All India Coordinated Rice Improvement Project (AICRIP) trials during 2005-2007, and based on overall performance it was identified as promising for release in the states of Orissa, Gujarat and Maharashtra (irrigated ecology). RR 433-2-1 recorded superior yield potential and stability under drought affected direct seeded conditions in AICRIP trials. Drought tolerance of this elite culture is well documented (Mandal *et al.,* 2010). Under normal conditions, RR433-2-1 recorded average grain yield of 3.0-3.5 t ha^{-1}. Under managed drought experiments across environments, it recorded grain yield of 2.10 t ha^{-1} and 0.60 t ha^{-1} under moderate and severe drought conditions, respectively which is considerably higher that Vandana (1.7 t ha^{-1} and 0.60 t ha-^{1}, respectively) (Verulkar *et al.,* 2010). A study with RR433 showed that it has deeper roots (17.37 cm), higher root volume (20.6) and thicker roots (1.20 mm) than check varieties such as Vandana, Kalinga III and Brown gora (Pushpam *et al.,* 2018). RR 433-2-1 is moderately resistant to Brown spot, Sheath rot and Leaf blast. It is resistant gall midge biotype 4 and moderately resistant to gall midge biotype 1, and moderately resistant to stem borer and leaf folder. Agro-morphologically, RR433-2-1 has intermediate plant height (90-100 cm), very early maturity (95-100 days), non-shattering panicles, long-bold grains (L/B ratio: 2.79), straw hulls and white kernels (Table 1). It possesses good cooking quality (amylose content 23.01% and Gel consistency 25-33 mm) with acceptable physical grain quality (Long bold grains, very occasional chalkiness, kernel length 6.1 mm and kernel breadth 2.18).

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Table 1: Salient agro-morphological features of RR 433-2-1

Characteristics	*RR433-2-1*	*Characteristics*	*RR433-2-1*	*Characteristics*	*RR433-2-1*
Seedling vigour	Good	Maturity group	Early (95-100 days)	Kernel length	6.10 mm
Tillering ability	Medium	Panicle type	Compact	Kernel breadth	2.18 mm
Leaf blade pubescence	Intermediate pubescent	Panicle exertion	Well exserted	Length/ Breadth ratio)	2.79
Leaf blade colour	Pale green	Panicle length	20.5-24.2 cm	Grain type	LB
Leaf angle	Erect	Spikelet fertility	Highly fertile	Kernel colour	White
Ligule colour	White	Threshability	Intermediate	Endosperm type	Non-glutinous
Leaf senescence	Intermediate	Hull colour	Straw	Chalkiness of Endosperm	Present
Ligule shape	2-cleft	Awning	Absent	Head rice recovery	70.8%
Collar colour	Light green	Apiculus colour	Purple	Drought reaction	Tolerant
Culm angle	Erect	Stigma colour	White	Brown spot reaction	MR
Culm strength	Intermediate	Lemma & palea pubescence	Hairy	Leaf blast reaction	MR
Culm number	6 - 10	Grain length	7.50 mm	Leaf folder reaction	MR
Plant height	Intermediate tall (90-100 cm)	Grain width	3.45 mm	Stem borer reaction	MR
Days to 50% flowering	68-72 days	1000-grain weight	24.24 g	Gall midge biotype 1 & 4	MR & R, respectively

4. Kalakeri (IC0640883; INGR21179), a rice (*Oryza sativa*) germplasm tolerant to drought and phosphorus starvation with weed competitiveness

Somnath Roy[1], NP Mandal[1], P Swain[2], Amrita Banerjee[1] and BC Patra[2*]
[1]*Central Rainfed Upland Rice Research Station, ICAR-NRRI, Hazaribag-825301, Jharkhand, India*
[2]*ICAR-National Rice Research Institute, Cuttack- 753006, Odisha, India*
[*]*Email: bcpatracrri@yahoo.com*

Kalakeri is a highly drought tolerant *aus* rice landrace originally from Odisha. The drought tolerant rice variety Vandana (RR 167-982) was developed by using Kalakeri as a tolerant donor (Kalakeri/C22) (Sinha *et al.* 1994). It possesses both vegetative and reproductive stage drought tolerance. In a recent study, several *DTY QTLs* for grain yield under reproductive stage stress such as $qDTY_{1.2}$, $qDTY_{1.3}$, $qDTY_{2.2}$, $qDTY_{2.3}$, $qDTY_{3.2}$ and $qDTY_{6.1}$ were recorded in Kalakeri using QTL-linked SSR markers (Roy *et al.*, 2021). Over the multi-environments trials Kalakeri exhibited leaf rolling and leaf drying scores of 3.0-4.3, indicative of a tolerant genotype. It showed lower spikelet sterility (36.4%) and a higher grain yield than Vandana under reproductive stage drought (ICAR-NRRI Annual Report 2013-14). Kalakeri is a good weed competitive genotype in terms of early emergence of plumule and initial higher leaf area index, tiller number, number of roots/plant and root depth. Under normal conditions, Kalakeri is found to be extra-vigorous (very fast growing, plants at 5-6 leaf stage have 2 or more tillers). It has considerable tolerance to low phosphorus conditions in terms of higher biomass production under low P, and it possess the tolerant (Kasalath type) haplotype in *Phosphorus uptake 1* (*Pup1*) locus, including the *Phosphorus starvation tolerance 1* (*PSTOL1*) gene (Roy et al., 2021). Agro-morphologically, Kalakeri has intermediate plant type (105 cm), maturity 90-95 days, and low tillering ability. It has medium-bold kernel type, and intermediate amylose content (20.7-25.2%) (Table 1)

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Table 1: Agro-morphological characteristics of Kalakeri (IC0640883)

Characteristic	Kalakeri	Characteristic	Kalakeri	Characteristic	Kalakeri
Early plant vigour	Extra vigorous	Leaf width (cm)	1.15	Brown rice length (mm)	6.13
Tillering ability	Low (9 tillers/plant)	Days to 50% flowering (days)	59	Brown rice width (mm)	2.81
Plant height	Intermediate (105 cm)	Panicle length (cm)	25.2	Brown rice length	Medium
Panicle exertion	Well exerted	Panicle axis	Straight	Brown rice shape	Bold
Leaf blade pubescence	Glabrous	Awning	Absent	100-grain weight (g)	2.33
Leaf blade colour	Light green	Apiculus colour	Purple	Grain yield (g)	2.08-3.25 t/ha
Basal leaf sheath colour	Light purple	Stigma colour	White	Aroma	No
Leaf angle	Erect	Lemma and palea colour	Black	Biotic stress susceptibility	Moderately resistant to blast and brown spot (SES score = 4.0)
Flag leaf angle	Erect	Sterile lemma colour	Gold		
Leaf length (cm)	43.0	Seed coat colour	Speckled brown		

5. Hango-2 (IC0640652; INGR21180), a wheat (*Triticum aestivum*) germplasm with novel leaf rust resistance gene *Lr80*. Confers broad spectrum leaf rust resistance.

Subodh Kumar[1], SC Bhardwaj[1*], OP Gangwar[1], VK Vikas[2], Hanif Khan[3], Pramod Prasad[1] and GP Singh[3]
[1]*ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India*
[2]*IARI Regional Station, Wellington-643231, Tamil Nadu, India*
[3]*ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India*
[*]*Email: Subhash.Bhardwaj@icar.gov.in*

Leaf rust, caused by *Puccinia triticina* inflicts more losses on wheat than any other rust Bhardwaj *et al.* 2021). Deployment of rust resistance is an economic, effective and ecologically friendly approach to control this disease. Therefore, identifying new and effective rust resistance sources is always a priority in breeding wheat varieties. Common wheat landraces are valuable sources of genetic diversity for resistance to biotic and abiotic stress resistance (Bansal *et al.* 2013).

Wheat landrace Hango-2 (*LWH2*) collected from the Himalayan area of Hango, District Kinnaur, in Himachal Pradesh in 2006 exhibited a very low infection type (IT;) at the seedling stage to all Indian leaf rust pathotypes (*Puccinia triticina*) pathotypes, except the pathotype 5R9-7 (16-1 old Indian notation) or DBBGB (North American designation) which produced IT 3+ (Table 1).

Genetic analysis based on Agra Local/Hango-2-derived F3 families indicated monogenic control of leaf rust resistance, and the underlying locus was temporarily named *LrH2*. Bulked segregant analysis using 303 simple sequence repeat (SSR) markers located *LrH2* in the short arm of chromosome 2D. An additional set of 10 chromosome 2DS-specific markers showed polymorphism between the parents and these were mapped on the entire Agra Local/Hango-2 F3 population. *LrH2* was flanked by markers cau96 (distally) and barc124 (proximally). The 90 K Infinium SNP array was used to identify SNP markers linked with *LrH2*. Markers KASP_17425 and KASP_17148 showed association with *LrH2*. Comparison of seedling leaf rust response data and marker locations across different maps demonstrated the uniqueness of *LrH2* and it was formally named *Lr80*. The *Lr80* linked markers KASP_17425, KASP_17148 and barc124 were developed for its utilization in marker assisted selection.

Most of the resistance genes identified in the past have minor effect or adult plant resistance. Contrarily *Lr80* is a major gene and can be identified in seedling stage as well as through the linked markers. Identification of *Lr80* from a local wheat is again a testimony that landraces are effective sources of biotic and abiotic resistance. This is the sixth rust resistance gene designated from India in 75 years of rust resistance gene cataloguing in wheat world over. Other *Lr* genes reported from India are *Lr10* (based on the work in Canada), *Lr48*, *Lr49*, *Lr57* and *Lr58*. Since this gene

Table 1: Response of *Lr* genes located on 2DS to different virulent and predominant pathotypes of *Puccinia triticina* in India

Pathotypes		*Lr genes on 2DS chromosome*								*Parental lines*
Indian Designation	*Common name*	*Lr2a (TC)*	*Lr2b (TC)*	*Lr2c (TC)*	*Lr11 (Tc)*	*Lr15 (TC)*	*Lr22a (TC)*	*Lr22b (TC)*	*Lr39 (KS92WRGC15)*	*Hango 2 (Lr80)*
29R45	12-5	;1	;12	3+	3+	0;	3+	3+	0;	;-
5R9-7	16-1	;1	;	3+	;	0;	33+	33+	0;	3+
109R63	77-1	3+	3+	3+	3+	3+	3+	3+	0;	;-
109R31-1	77-2	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R63-1	77-5	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R55-1	77-6	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R127	77-7	3+	3+	3+	3+	3+	3+	3+	0;	;-
253R31	77-8	3+	3+	3+	3+	3+	3+	3+	0;	;-
121R60-1	77-9	;	;	;	3+	3+	3+	3+	0;	;-
377R60-1	77-10	;	;	;	3+	3+	3+	3+	0;	;-
21R55	104-2	;12	;12	3+	3+	0;	3+	3+	0;	;-
21R63	104-3	;12	;12	3+	3+	0;	3+	3+	0;	;-

confers resistance to leaf rust, therefore, it is being used to pyramiding of resistance and breeding wheat varieties.

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Bansal UK, VN Arief, IH DeLacy and H Bariana (2013) Exploring wheat landraces for rust resistance using a single marker scan. *Euphytica* 194: 219–233.

6. HS661 (IC0638606; INGR21181), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm resistant to all pathotypes of yellow (stripe) rust. Possessing rust resistance genes *Yr15* and *Sr25/Lr19*

Dharam Pal[1*], SC Bhardwaj[2], Madhu Patial[1], Subodh Kumar[2], OP Gangwar[2], Pratima Sharma[3] and KV Prabhu[4]

[1]*ICAR-IARI, Regional Station [CHC], Shimla-171004, Himachal Pradesh, India*

[2]*ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India*

[3]*Green Glen Layout, Palm Avenue, Bengaluru-560103, Karnataka, India*

[4]*PPVFRA, NASC Complex, New Delhi-110012, Delhi, India*

**E-mail: dpwalia@rediffmail.com*

Stripe rust or yellow rust caused by fungus *Puccinia striiformis* f. sp. *tritici*, has its impact on the wheat crop grown in 10-12 million hectares (mha) of Northern India (Bhardwaj and Singh 2019). Grain yield loss due to stripe rust ranged from 10-70% (Chen, 2005; Ashmawy and Ragab, 2016). It can cause 100% yield loss if infection occurs at an early stage of growth and the disease continues to develop during the growing season (Afzal *et al*., 2007). Rust resistance breeding program against a multi-racial pathogen is always faced with the problems of complexities of race composition and the evolution of new pathotypes. It is imperative to have choice of parents possessing diverse rust resistance genes for developing and deployment of wheat cultivars with durable resistance for increasing their longevity. In this direction, a rust resistant wheat germplasm HS661, was developed from a cross HS295*2/FLW20(*Lr19*)//HS295*2/FLW13(*Yr15*) through back crossing followed by Bulk- Pedigree method of breeding at Indian Agricultural Research Institute, Regional Station, Shimla. HS661 has been found resistant against all the pathotypes of yellow rust under seedling resistance test at IIWBR, RS, Shimla. Besides, it has shown seedling resistance to all pathotypes of brown rust and stem rust (Table1) (AICRPW&B Progress Report, Crop Protection, 2018). HS661 was found to possess adult plant resistance (APR) to yellow rust at four locations *viz*., Bajaura, Dhaulakuan, Malan and Una. It was also resistant to all the three rusts including yellow rust in Plant Protection Screening Nursery (AICRPW&B Progress Report, Crop Protection, 2018). HS661

Table1: All stage resistance in HS661 against wide array of rust pathotypes

Yellow Rust Pathotypes

Genotype	*46S119*	*110S119*	*78S84*	*110S84*	*238S119*	*110S247*	*T*	*P*	*111S68*	*79S68*	*79S4*	*7S0*	*K*	*6S0*	*20A*	*L*	*N*	*38A*	*Gene*
HS661	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
FLW20	S	S	S	S	S	S	S	S	S	S	S	R	S	S	S	S	S	S	
FLW13	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	
HS295	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	
Agra Local	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	

Brown Rust Pathotypes

Genotype	*11*	*12-2*	*12-5*	*12-7*	*12-8*	*16-1*	*77*	*77-1*	*77-2*	*77-5*	*77-6*	*77-7*	*77-8*	*77-9*	*77A-1*	*77-10*	*104-2*	*104-3*	*104B*	*106*	*108-1*	*162-1*	*162A*	*162-3*	
HS661	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
FLW20	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	
FLW13	R	R	S	S	R	R	R	R	R	S	R	S	R	S	R	S	S	S	R	R	R	R	R	R	
HS295	R	R	S	S	R	R	R	R	S	S	R	S	R	S	R	S	S	S	S	R	R	R	R	R	
Agra Local	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	

Black Rust Pathotypes

Genotype	*11*	*11A*	*14*	*15-1*	*21*	*21-1*	*21A-2*	*24A*	*34-1*	*40*	*40A*	*40-1*	*40-2*	*40-3*	*42B*	*117A*	*117A-1*	*117-1*	*117-2*	*117-3*	*117-4*	*117-5*	*117-6*	*122*	*184*	*295*	
HS661	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	Sr2+R
FLW20	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	
FLW13	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	
HS295	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R	R	R	R	R	R	R	R	R	R	R	R	
Agra Local	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	

was confirmed to possess *Yr15* using molecular marker *gwm11* (Pal *et al*., 2019), also confirmed for presence of *Sr25/Lr19* using STS marker *Gb*.

HS661 possesses good agronomic features *viz*., semi-erect growth habit, waxy flag leaf sheath, tapering ear shape, 88cm of plant height, white ear with white awns, attitude of awns is spreading, the grains are semi-hard and ovate shaped, amber in colour with thousand grain weight of 39g. The rust resistance genes *Yr15* and *Sr25/Lr19* rendering broad spectrum resistance against wide array of pathotypes of all the three rusts along with good agronomic features present in HS661 could be a desirable choice for breeding rust resistant wheat varieties in India.

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7. QBP18-8 (IC0640679; INGR21182), a Wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high hectoliter weight (80.6Kg/hl)

Anju Mahendru Singh[1*], SV Sai Prasad[2], Arvind K Ahlawat[1] and Ram Bihari Shukla[1]

[1]*Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*

[2]*ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India*

**Email: Anju.Singh@icar.gov.in*

Flour recovery is a much sought after trait by the Indian millers as it increases their profit margins. It is also a highly desirable trait for superior chapati quality. Flour recovery is affected by several genetically controlled traits and soil characteristics. Among the genetically controlled traits, hectoliter or test weight is the most important. Test weight determinants are grain shape, diameter, weight and grain density. Genotypes combining all four criteria are less common in Indian wheat varieties. Major wheat varieties have mean test weight between 75-77 Kg/hl. A genotype QBP 18-8 was developed as a pure line from selection of the entry from the HarvestPlus Yield trial and possesses much higher test weight than the prevalent check varieties.

The mean values of test weight in the four agroclimatic zones for wheat *viz*., North Western Plains Zone, the North Eastern Plains Zone, the Central Zone and the Penninsular Zone of India were 81 Kg/hl, 80.6 Kg/hl, 81.3 Kg/hl and 79.7 Kg/hl respectively. Thus, QBP 18-8 recorded significantly higher mean value of 80.6 Kg/hl against the mean value of 75.9 Kg/hl of the popular wheat variety HD3086 and showed a high stability over all the locations. Thus, QBP18-8 is a stable donor for high test weight across varied environments and therefore, can be used in breeding programmes to increase the flour recovery of the new lines.

8. QBI20-14 (IC0640680; INGR21183), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high grain zinc concentration (57mg/kg)

Anju Mahendru Singh*, Shailendra K Jha, Arvind K Ahlawat and Ram Bihari Shukla

[1]*Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*

**Email: Anju.Singh@icar.gov.in*

Development of Bio fortified wheat is an important goal for wheat plant breeders today. In the initial phase, a number of crosses were made with wild species many of which had been reported to have high grain iron and zinc concentration. However, it was soon realized that not only do the wild relatives bring in a lot of linkage drag but in many cases, the high content observed is mainly due to the “concentration effect” in the grain. Therefore, more efforts are now being made to search for high grain iron and zinc in the adapted germplasm and involving wild relatives or progenitors at the most only once in the cross. With such efforts, a number of genotypes responding to soils with even moderate content of available zinc have been developed.

QBI20-14 is one such genotype and it has shown higher levels of grain zinc concentration over five locations as compared to the varietal check GW322 and micronutrient check WB02. The genotype QBI20-14 is also higher in yield as compared to both the checks. Thus, coupled with high grain yield and protein content (13.6%), QBI20-14 is a stable donor of grain zinc for breeding programmes to improve nutritional quality of wheat.

9. QBP18-10 (IC0640681; INGR21184), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high hectoliter (test) weight (80.4 kg/hl) and superior grain appearance

Anju Mahendru Singh[1*], Divya Ambati[2], Arvind K Ahlawat[1] and Ram Bihari Shukla[1]
[1]*Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*
[2]*ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India*
[*]*Email: Anju.Singh@icar.gov.in*

Major wheat varieties have mean test weight between 75-77 Kg/hl. The genotype QBP 18-10 has a much higher test weight. The mean value of test weight in the four locations of NWPZ was 79.6 Kg/hl, in the NEPZ was 79.4 Kg/hl, in the CZ was 80.4 Kg/hl and in the PZ, it was 82.4 Kg/hl. Overall, QBP 18-10 recorded a very high mean value of 80.4 Kg/hl against the mean value of 75.9 of the check variety HD 3086. Thus, along with QBP18-8 (IC640679; INGR21182), QBP18-10 (mentioned at S No. 7 above) is an elite donor for High Test weight.

Moreover, the grain of genotype QBP18-10 is very much like the hard, vitreous and lustrous sharbati grain which gets a better premium in the market. It has recorded very high grain Appearance score (7.1). The grain protein of QBP18-10 is also high (mean value of 12.3%). These traits are invaluable to the milling industry and fetch a better price to the farmer and the miller. Thus, QBP18-10 shows stability for high test weight across varied environments, has a very appealing grain appearance and also has a good protein content above 12% and this genotype can be involved as one of the parents in breeding programmes to increase the flour recovery and market value of the new lines.

10. QBP17-7 (IC0640682; INGR21185), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high grain iron concentration (48.1mg/Kg)

Anju Mahendru Singh[1*], Pradeep K Singh[1], Arvind K Ahlawat[1] and Ram Bihari Shukla[1]
[1]*Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*
[*]*Email: Anju.Singh@icar.gov.in*

Iron is a major component of plant and human enzymes and biomolecules. Wheat grain has higher level of grain zinc and iron concentration as compared to rice and maize kernels. However, the current levels of grain micronutrients in wheat are not sufficient to provide even 50% of the RDA for adults. Since wheat is the staple food in India especially in the Northern and Central parts of the country, iron is an important nutritional trait to be improved by plant breeding efforts called bio-fortification. QBP17-7 is a germplasm developed by intermating of high iron source and high yielding lines. QBP17-7 showed 43.2 mg/Kg (ppm) in NWPZ as against 41.3ppm of the check WB02, 45.2ppm in NEPZ as against 44.6 ppm in WB02 and 55.8ppm in CZ against WB02 with 47.9 ppm. Thus, it has recorded higher mean value zone wise as well overall higher mean (48.1ppm) of grain iron concentration over the bio-fortified variety WB02 having an overall mean of 44.8 ppm in the AIW&BRP. This line has maintained the protein content of 13.1% similar to WB02 (13. 3%). Thus, with its good yielding background, higher iron concentration and high protein content QBP 17-7 is a valuable resource and donor for biofortification.

11. HD3241 (IC0640684; INGR21186), a wheat (*Triticum aestivum* subsp. *aestivum*) germplasm with high sedimentation value (73-75 ml) for greater gluten strength

Anju Mahendru Singh[1], Jang Bahadur Singh[2] and Arvind Kumar Ahlawat[1]
[1]*Div. of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*
[2]*ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India*
[*]*Email: Anju.Singh@icar.gov.in*

India has seen an upsurge in the value based industry in the recent past. The milling and baking industry of India is rapidly expanding and is valued at ~Rs 73 billion. The industrial handling of wheat flour has been a subject of concern in the baking industry of India. The bread and pizza flour requires strong gluten for retaining the carbon dioxide gas released during fermentation of the dough. However, Indian wheat varieties have moderately strong gluten with sedimentation values in the range of 40-50 ml. Therefore, the use of conditioners such as potassium bromate, ascorbic acid *etc.* is rampant in Indian baking industry which is not advisable for consumers' health. Hence, varieties with greater gluten strength for industrial handling and better baking are sought. India could see an upsurge in its export if such varieties are developed using the high trait donors. Sedimentation test is an indicator of gluten content and gluten strength.

HD 3241 was identified during the screening of germplasm received from CIMMYT as an entry in the trials for quality traits. It is an elite germplasm with high yield, resistance to all the three rusts and has height of 110-113cm & 160 tillers/meter. HD3241 was analysed for quality traits also and was promoted to Quality Component and Wheat Biofortification Nursery (QCWBN) planted at 12 locations during 2018-19 under the AIW&BRIP. HD3241 was found to be excellent in its SDS-Sedimentation Value (SV) in all the four zones. It showed SV of 70ml and 77ml in NWPZ and NEPZ respectively and 76ml across CZ and PZ. Thus, the mean value of HD3241 over all the four zones was found to be 75 ml which is the highest reported for any of the genotypes tested so far in the AIW&BIP. HD3241 also has a Protein content of 12.6% and Hectoliter (Test) weight of 78.4 kg/hl and also has hard and lustrous grains. Therefore, HD3241 is a highly stable donor of very high sedimentation value for use in wheat breeding programmes for bread making quality.

12. IC290156 (IC290156; INGR21187), a wheat (*Triticum aestivum*) germplasm with resistant to stripe rust pathotypes 46S119 and 47S103

Sundeep Kumar[1*], Anjan Kumar Pradhan[1], Amit Kumar Singh[1], Neeraj Budhlakoti[1], Dwijesh Chandra Mishra[1], Divya Chauhan[1], Suneel Kumar Meena[1], Subodh Kumar[2], SC Bhardwaj[2], Anil Rai[3] and Kuldeep Singh[3]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India*

[2]*ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India*

[3]*ICAR-Indian Agricultural Statistics Research Institute, Pusa Campus-110012, New Delhi, India*

[*]*Email: sundeepksharma77@rediffmail.com*

Stripe rust is the most damaging and widely prevalent disease which caused by *Puccinia striiformis* f. sp. *tritici* (Pst) in wheat. It causes significant yield losses in almost every part of the world where cool and humid conditions persist during crop season. Yield losses due to this disease vary from 10 to 40% which depends upon various factors like severity level, susceptibility of cultivars, stage of infection, rate of disease development, and duration of disease. In India, stripe (yellow) rust is the major disease in North West Plain Zones (NWPZ) especially sub-mountainous parts of Punjab, Haryana, and Western Uttar Pradesh, the major wheat growing regions of India. Occurrence of stripe rust has also been observed frequently in Jammu & Kashmir, Punjab, Himachal Pradesh, *tarai* regions of Uttarakhand and western Uttar Pradesh. However, a major outbreak of stripe rust was observed in the North Western Plain Zone (NWPZ) and the Northern Hills Zone (NHZ) of India in 2006 and 2012–13 which caused heavy yield losses. Keeping in consideration an experiment was conducted on a set of 391 wheat germplasm lines comprised of Indian landraces, Indigenous germplasm collection and some exotic lines and breeding stocks. These germplasm lines were evaluated separately against four pathotypes 46S119, 238S119, 47S103 and 110S119 for two consecutive years 2018 and 2019 winter season (8 environments). In addition, a genome wide association study (GWAS) was also preferred to identify QTLs/genes associated with stripe rust resistance.

The germplasm line IC290156 which showed the presence of resistance-associated favourable alleles and therefore showed high disease severity index for stripe rust. This germplasm line was found resistant against two pathotypes i.e., 46S119 and 47S103. It is also associated with a candidate gene TraesCS6D02G384800, that functions as leucine-rich repeat receptor-like protein kinases (LRR) which play key role in pathogen recognition and disease resistance. The study also revealed 20 novel QTLs, which 11 QTLs for 46S119 and 47S103(T) pathotypes distributed on 2DL, 3AL, 3B, 3DS, 4DL, 5BS and 6DL which are linked with IC290156 line. This line is a potential genetic resource for stripe rust resistance, which can be further used in wheat improvement programme.

13. IC321906 (IC321906; INGR21188), a wheat (*Triticum aestivum*) germplasm with terminal heat tolerance

Sundeep Kumar[1*], Jyoti Kumari[1], Nabin Bhusal[2], Anjan Kumar Pradhan[1], Neeraj Budhlakoti[3], Dwijesh Chandra Mishra[3], BK Meena[4], Divya Chauhan[1], Suneel Kumar[1], Amit Kumar Singh[1], Gyanendra Pratap Singh[4], Kuldeep Singh[1] and Sindhu Sareen[4]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India*

[2]*Agriculture and Forestry University, Bharatpur 44200, Nepal*

[3]*ICAR-Indian Agricultural Statistics Research Institute, Pusa Campus-110012, New Delhi, India*

[4]*ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India*

[*]*Email: sundeepksharma77@rediffmail.com*

A comprehensive study was conducted to identify heat tolerant wheat lines from an association mapping panel of 205 wheat accessions, evaluated under late sown conditions in India at three different locations (Delhi, Hisar and Karnal) for 3 consecutive years (2015-2017). Planting was done in three replications on each location. In the field screening, data was recorded for 16 agronomic traits such as days to heading (DH), days to anthesis (DA), days to physiological maturity (DM), chlorophyll fluorescence (CFL), cell membrane stability (CMS), grain filling duration (GFD), grain weight/spike (GW, g), grain numbers/spike (GN), grain numbers/m (GNM), productive tillers/m (PTL), plant height (PHT, cm), 1,000 grain weight (TGW, g), biomass (BM, gm–2), grain yield (GY, gm–2), grain filling rate (GFR), and harvest index (HI, %) to find out the variation among studied wheat accessions. Stability analysis and AMMI biplot was also performed to analyze the stable performance of genotypes across the environment and years. Genotyping using a high density 35 K array, revealed a large number of SNPs that could be used for the GWAS analysis. In total, 69 QTLs were identified for the ten agronomic traits.

The favourable alleles for each QTL region were identified by comparing the extreme phenotypic values in association mapping panel. The analysis revealed heat tolerant germplasm lines based on presence of favourable alleles for few accessions *viz*. HD2888, IC611071, IC611273, IC75240, IC321906, IC416188 and J31-170. Among these germplasm lines, co-localized QTLs were found for IC321906 accession showing favourable alleles for 3 different traits *viz*. GY (1), GFR (7) and BM (2). This accession is a variant of C306 (a popular drought tolerant wheat cultivar released in 1960's) as its parent from Jharkhand is being proposed to be registered as genetic stock for heat tolerance. This is a potential genetic resources for heat tolerance, which can be further used in wheat improvement programmed.

14. BNSR6 (IC0641982; INGR21189), a wheat (*Triticum aestivum*) germplasm having high Fe (43.8 ppm), Zn (48.6 ppm) and protein (14.3 %)

Sewa Ram[1*], OP Gupta[1], Vanita Pandey[1], Sunil Kumar[1], BS Tyagi[1], Gopalareddy K[1], VS Sohu[2] and GP Singh[1]

[1]*ICAR-Indian Institute of Wheat and Barley Research, Karnal 132001, Haryana*

[2]*Punjab Agricultural University, Ludhiana -141004, Punjab*

[*]*Email: sewa.ram@icar.gov.in*

Worldwide over 2 billion people suffer from iron (Fe), zinc (Zn) and/or other (multiple) micronutrient deficiencies. In India, 48% of children under the age of 5-10 years have zinc/iron or some other micronutrient deficiency. Zinc is one of the important micronutrient for normal growth and development. BNSR 6 was developed at ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR) by crossing DPW 621-50 // GLUPRO*3 / PBW 568. The hand threshed grains of 10 centres in QCWBN comprising all the major wheat growing zones of the country has been analysed for grain iron and zinc concentration and 11 centres for grain protein concentration. BNSR 6 was found to be superior for grain zinc concentration (48.6 ppm), grain iron concentration (43.8 ppm), and grain protein concentration (14.3 %) over the locations to all the check var`ieties (Table 1 and 2). Thus, BNSR 6 would be a potential source to be utilized in future breeding programs to develop high yielding bread wheat varieties with enhanced grain zinc, iron, and protein concentration.

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Table1: Grain iron and zinc concentration of BNSR 6 and check varieties at 10 locations during 2020-21

Zone	Location	*Genotype*							
		BNSR 6		*WB02*		*HD3226*		*GW322*	
		Zn	*Fe*	*Zn*	*Fe*	*Zn*	*Zn*	*Fe*	*Zn*
NWPZ	Karnal	39.8	38.7	35.1	36.9	31.0	32.5	35.0	33.6
	Hisar	47.1	48.6	44.4	42.8	35.8	42.1	40.5	40.1
	Delhi	61.9	42.3	59.1	39.9	48.7	53.3	40.0	52.4
	Ludhiana	41.4	48.5	37.4	41.6	33.7	34.4	37.5	35.5
NEPZ	Kanpur	39.4	33.1	38.0	34.0	32.3	40.6	35.2	38.4
	Varanasi	35.0	38.9	34.6	38.0	29.2	33.2	37.9	34.2
CZ	Indore	53.7	44.5	51.1	40.2	42.8	50.7	42.7	47.4
	Vijapur	55.0	43.2	56.1	46.5	44.1	49.6	45.5	49.5
PZ	Pune	58.4	44.8	50.0	44.2	42.4	46.7	40.6	47.8
	Dharwad	54.0	51.8	37.6	43.1	29.9	31.2	39.8	34.9
Mean (National)		48.6	43.4	44.3	40.7	37.0	41.3	39.5	41.4

Table 2: Grain protein concentration of BNSR 6 and check varieties at 11 locations during 2020-21

Zone	*Location*	*Genotype*			
		BNSR 6	*WB02*	*HD3226*	*GW322*
NWPZ	Karnal	14.7	13.8	12.8	11.1
	Hisar	12.8	12.8	11.2	10.5
	Delhi	16.1	15.7	14.5	12.5
	Ludhiana	14.4	13.2	12.8	11.2
NEPZ	Kanpur	11.5	11.6	11.1	9.2
	Varanasi	12.9	12	11.9	10.1
CZ	Indore	14	14.5	13.7	10.8
	Vijapur	14	14.6	13.5	11
PZ	Pune	15.3	15.1	14	11.1
	Dharwad	17.3	16	13.5	10.9
	Niphad	14.7	13.8	13.1	10.9
Mean		14.3	13.9	12.9	10.9

15. HI 8807 (IC0641983; INGR21190), a wheat (*Triticum durum*) germplasm with resistance to stem, leaf, stripe rusts and Karnal bunt.

Divya Ambati, Rahul M Phuke, SV Sai Prasad, Jang Bahadur Singh, Prakasha TL[*] and Dilip Kumar Verma
ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India
[*]*Email: prakash7385@gmail.com*

Durum wheat (*Triticum turgidum* subsp. *durum* (Desf.) Husnot) is the second most important cultivated wheat species. Globally, it is cultivated in 17 million ha, with a production of 38.1 million tonnes. Rainfall, biotic (pests and diseases) and abiotic (drought, sunlight, cold, and salinity) stresses found to affect durum wheat productivity (Xynias *et al*., 2019). Central and peninsular zones comprising of Madhya Pradesh, Gujarat, Maharashtra and Karnataka states are the major durum wheat growing regions in India. Among diseases, stem and leaf rusts are major diseases in these zones. Managing diseases through host plant resistance is the most economical and viable strategy to manage diseases. Diverse genetic base is required to minimize crop losses caused by these ever-evolving pathogens. Identifying and utilizing multiple disease resistant along with high yielding genotypes is important in durum wheat improvement.

HI 8807 (HI 8695/ HI 8663// HI 8663), a semi erect durum wheat genotype with strong waxiness on leaf sheath and spike, white, dense tapering spike and without glume pubescence. It was identified to be resistant to stem, leaf and stripe rusts in multi-location testing *viz*., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2017 to 2021 (Table 1). It showed resistance to Karnal bunt disease (Table 2) over two years of testing at different locations. HI 8807 showed superiority in mean weighted grain yield superiority of 0.4 to 4.3% in NIVT and AVT-I in comparison to bread wheat check varieties. As the availability of multiple disease resistant high yielding genotypes is rare, HI 8807 can be used as potential resistance donor to breed varieties against these multiple pathogens and also a source of high grain yield.

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Table 1: Disease data of HI 8807 in comparison with check varieties over years

Year of testing	*Trial*		*Stem rust*		*Leaf rust*				*Stripe rust*	
			South		*South*		*North*		*North*	
			HS	*ACI*	*HS*	*ACI*	*HS*	*ACI*	*HS*	*ACI*
2017-18	NIVT 3B	HI 8807	10MS	2.5	10MS	1.5	TR	0.0	10S	3.4
		HD 2864 (c)	5MR	0.9	5MS	1.3	30S	4.9	80S	59.0
		HD 2932 (c)	30MR	6.3	80S	15.1	70S	21.0	90S	58.0
2018-19	AVT I	HI 8807	20MS	3.3	5MS	0.6	20S	2.8	20MS	3.4
		HD 2864 (c)	10S	2.8	40S	6.5	20S	6.0	100S	61.8
		HD 2932 (c)	20MS	8.4	40S	19.4	90S	34.6	80S	55.0
2019-20	EPPSN	HI 8807	10MS	2.2	TMS	0.3	20S	7.6	20MS	4.9
2020-21	MDSN	HI 8807	10S	2.7	20MS	2.7	0	0	5S	1.7

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

Source: AICW&BIP – Crop Protection Report (2017-21)

Table 2: Disease score of Karnal bunt

Year of testing	*Trial*		*Karnal bunt (%)*							
			Jammu	*Hisar*	*Delhi*	*Ludhiana*	*Pantnagar*	*Dhaulakuan*	*HS*	*Avg*
2018-19	AVT I	HI 8807	2.7	1.6	8.8	1.0	-	-	8.8	3.5
		HD 2864 (C)	12.2	5.6	3.3	8.0	-	-	12.2	7.3
2019-20	EPPSN	HI 8807	2.4	6.7	0.0	0.0	2.5	1.3	2.2	6.7
2020-21	MDSN	HI 8807	-	-	-	-	-	-	7.4	1.9
		HD 2967	-	-	-	-	-	-	12.5	6.0

16. HI 8812 (IC0641984; INGR21191), a wheat (*Triticum durum*) germplasm with resistance to stem, leaf, stripe rusts and flag Smut. High yielding.

Rahul M Phuke, Divya Ambati, SV Sai Prasad, Jang Bahadur Singh, Prakasha TL* and Dilip Kumar Verma
ICAR-IARI Regional Station, Indore-452001, Madhya Pradesh, India
**Email: prakash7385@gmail.com*

Global wheat production is affected by many biotrophic fungi like *Puccinia* (causing rust diseases) and *Urocystis Agropyri* (causing flag smut). The flag smut inoculum can survive in soil for 7-10 years. Therefore, breeding varieties which are resistant to these pathogens is extremely important in managing these diseases. Durum wheat is cultivated in central and peninsular parts of India. Developing resistant varieties with broader genetic base is the need of the hour owing to rapid evolution of these pathogens.

HI 8812 (HI 8680/ HI 8663), is a erect durum wheat genotype with strong waxiness on was identified to be resistant to stem, leaf and stripe rusts and flag smut in multi-location testing *viz*., Plant Pathological Screening Nursery (PPSN), Elite PPSN and Multiple Disease Screening Nursery (MDSN) from 2017 to 2021 (Table 1). It showed resistance to flag smut disease (Table 2) over two years of testing at different locations. HI 8812 showed superiority in mean weighted grain yield superiority of 2.1 to 3.2% in NIVT and AVT-I in comparison to check varieties. As the availability of multiple disease resistant high yielding genotypes is rare, HI 8812 can be used as potential resistance donor to breed varieties against these multiple pathogens and also a source of high grain yield.

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Table 1: Disease data of HI 8812 in comparison with check varieties over years

Year of testing	*Trial*		*Stem rust*		*Leaf rust*				*Stripe rust*	
			South		*South*		*North*		*North*	
			HS	*ACI*	*HS*	*ACI*	*HS*	*ACI*	*HS*	*ACI*
2017-18	NIVT 4	HI 8812	TMS	0.2	20MS	3.0	5MR	0.3	10MS	3.8
		HI 8713 (c)	30S	14.3	30S	3.9	20S	2.9	10S	3.3
		HI 8737 (c)	30S	13.7	20S	2.7	10MS	1.7	20MS	3.3
2018-19	AVT I	HI 8812	5MS	2.0	20MS	2.6	20S	2.6	10S	3.4
		HI 8713 (c)	10MS	1.6	5MR	0.3	10S	3.4	20S	3.9
		HI 8737 (c)	40S	11.0	20MS	3.0	20S	3.3	15S	3.0
2019-20	EPPSN	HI 8812	10MS	4.4	TMR	0.1	15S	8.0	40S	6.2
2020-21	MDSN	HI 8812	10S	2.7	15MR	2.1	5S	1.0	5S	1.7

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

Source: AICW&BIP – Crop Protection Report (2017-21).

Table 2: Disease score of Flag smut

Year of testing	*Trial*		*Flag smut (%)*					
			Ludhiana	*Hisar*	*Durgapura*	*Karnal*	*Highest Score*	*Average*
2018-19	AVT I	HI 8812	0.0	0.0	0.0	4.9	4.9	1.2
		HI 8737(C)	0.0	8.5	0.0	1.3	8.5	2.1
		HI 8713 (C)	0.0	9.6	0.0	2.3	9.6	3.0
2020-21	MDSN	HI 8812	-	-	-	-	0	0

17. RWP-2018-32 (IC0641985; INGR21192), a wheat (*Triticum aestivum*) germplasm tolerant to heat stress with lower grain yield reduction. Higher grain number and higher grain weight under heat stress

Mamrutha HM*, Hanif Khan, Om Parkash Tuteja, Rinki, Gopalareddy K, Sonu Singh Yadav, Satish Kumar , CN Mishra, SK Singh, Gyanendra Singh and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

**Email: mamrutha.M@icar.gov.in*

The wheat genotypes RWP-2018-32 (HD3131/DBW90) was developed at ICAR-IIWBR, Karnal. This entry was evaluated in national multi-location heat tolerance trial (MLHT1) during the year 2018-19 and 2019-20 crop seasons and was evaluated at Durgapura, Hisar, Karnal, Ludhiana, Kanpur, Pusa, Ranchi, and Sabour centres which are hot spot locations for heat stress. RWP-2018-32 (0.90) has showed Heat Susceptibility Index (HSI) values lower than checks, DBW150 (0.94), Raj3765 (0.93) and HD2932 (1.22). RWP-2018-32 recorded lower yield reduction (27%) compared to checks (Table 1) except WH730. Lower yield reduction (YR) under heat stress is the important character of a heat tolerant genotype. This genotype was found to be promising for other traits like biomass plot^{-1} (BM), grain number spike^{-1} (GNS), grain weight spike^{-1} (GWS) and grain yield^{-1} plot (GY) under late sown condition (Table 2). Thus, RWP-2018-32 can serve as a potential source to be utilized in future breeding programs to develop heat tolerant wheat varieties.

Table 1: The HSI and yield reduction (%) of wheat genotypes over years (2018-19 & 2019-20)

	HSI			*Yield Reduction (%)*		
Genotype	*2018-19*	*2019-20*	*Mean*	*2018-19*	*2019-20*	*Mean*
RWP-2018-32	0.87	0.94	0.90	31.5	23.3	27.4
DBW150(C)	1.06	0.82	0.94	38.4	20.3	29.4
HD2932(C)	1.22	1.19	1.22	44.1	29.6	36.9
Raj3765(C)	1.06	0.79	0.93	38.4	19.7	29.1
WH730(C)	0.89	0.91	0.88	30.8	22.6	26.7

Table 2: Pooled data of agro-morphological traits of wheat genotype under MLHT1 2018-19 & 2019-20 under late sown condition

Genotype	*DH*	*DM*	*PT/3mt*	*BM(g)*	*PH(cm)*	*GNS*	*GWS(g)*	*GY(g)*
RWP-2018-32	81	109	293.59	4597.13	89.44	56.64	2.18	1325
DBW150 (C)	78	106	275.88	4750.63	95.53	50.88	1.96	1248
HD2932 (C)	80	108	285.06	4289.38	89.97	48.34	1.80	1270
RAJ3765 (C)	76	106	293.53	4318.75	89.15	49.26	1.96	1270
WH730 (C)	79	104	296.12	4512.24	98.7	51.6	2.01	1302

18. DBW302 (IC0641986; INGR21193), a wheat (*Triticum aestivum*) germplasm with resistance to black and brown rusts. Resistant to Karnal bunt and flag smut.

Hanif Khan[1*], Ravish Chatrath[1], Om Parkash[1], CN Mishra[1], Gopalareddy K[1], OP Gangwar[2], Raj Kumar[1], Satish Kumar[1], Mamrutha HM[1], Poonam Jasrotia[1], SC Bhardwaj[2], Sudheer Kumar[1], Sunil Kumar[1], Gyanendra Singh[1] and GP Singh[1]
[1]*ICAR-Indian Institute of Wheat and Barley Research Karnal-132001, Haryana, India*
[2]*ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India.*
[*]*Email: Hanif.Khan@icar.gov.in*

Combining resistance genes in wheat breeding to facilitate the development of more durable resistances is a well-known procedure in wheat breeding (Bhardwaj, 2013; Khan et al. 2021). Wheat breeder's strategy has been to utilize germplasm sources that are as diverse as possible for rust resistance. Availability of resistance against multiple diseases of wheat will speed up the breeding process and ensure such targeted resistance combinations are present in the breeding lines.

DBW302 has been developed from cross between DBW112/HD3108 through pedigree method of breeding. Its multi-location testing for yield traits was done at six locations in the Special High Yield Potential Trial (SPL-HYPT 2018-19) under all India Coordinated Wheat Improvement trials. The proposed genotype was found resistant against black/stem and brown/leaf rusts and moderately resistant against yellow/stripe rust of wheat under multi-location Plant Pathological Nursery. Based on its resistance to three rusts the entry was selected for evaluation in Multiple Disease Screening Nursery (MDSN).

During 2020-21, MDSN was conducted at the centres: for stem rust: Mahabaleshwar, Indore, Dharwar, Niphad and Wellington; for stripe rust: Ludhiana, Pantnagar, Hisar, Dhaulakaun, Malan, Almora and Karnal; for leaf rust (N): Delhi, Ludhiana, Hisar and Karnal; for leaf rust (S): Mahabaleshwar, Indore, Dharwar, Niphad and Wellington; for Karnal bunt: Delhi, Dhaulakaun, Pantnagar, and Ludhiana; for flag smut: Hisar, Ludhiana and Durgapura; for powdery mildew: Dhaulakaun, Malan, Jammu, Pantnagar, and Malan; for foliar aphid: Nphad, Ludhiana, Karnal and Shillongani.

Table 1: Average disease scores under multi-location testing in MDSN (2020-21)

Genotype	*Average coefficient of infection (ACI) of rust*				*Karnal %*	*Flag Smut %*
	Stem	*Leaf (South)*	*Leaf North)*	*Stripe*		
DBW302	2.7	5.4	3.0	6.2	2.7	2

Based on multilocation testing DBW302 was found to be resistant to wheat rusts as indicated by low ACI; stem rust 2.7, leaf rust (South) 5.4 and leaf rust (North) 3.0, Karnal bunt (2.7%) and flag smut (2%) (Table1) following disease score 0-100 scale (Loegering, 1959). It was found to be moderately resistant to and stripe rust (ACI 6.2) powdery mildew (4) and foliar aphids (grade 3). Plants of DBW302 medium tall statured with average height of 107 cm and has maturity duration of 155 days in NWPZ under timely sown conditions. Grains are hard textured with amber colour and has 1000 gain weight of 42g. Overall DBW302 has multiple disease resistance in good agronomic background.

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19. IIWBR DN 502 (IC0640669; INGR21194), a wheat (*Triticum aestivum*) germplasm having Glu-D1 double null with lowest sedimentation volume in the background of PBW 502 and suitable for biscuit making.

Sewa Ram[1*], Sneh Narwal[2], BS Tyagi[1] and GP Singh[1]
[1]*ICAR-Indian Institute of Wheat and Barley Research Karnal-132001, Haryana, India*
[2]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi, India.*
[*]*Email: sewa.ram@icar.gov.in*

There are limited numbers of varieties having characteristics suitable for biscuit making in India. This is primarily because of more emphasis has been given for improving hard wheat with medium strong gluten suitable for chapati. However, soft wheat with week and extensible gluten is required for biscuit making. Breeding for soft wheat products can be expedited by using molecular markers for soft grain texture and week gluten. In this investigation *Glu-D1* double null trait of NAP HAL has been transferred into high yielding backgrounds of PBW502 using molecular marker assisted selection and microlevel tests.

The crossing was initiated during 2005-06 using PBW502 as recurrent parents and Nap Hal as donor and subsequently advanced into higher generations using molecular markers and microlevel tests for sedimentation volume. Advanced lines of the crosses between PBW502 and Nap Hal were evaluated for grain hardness, sedimentation volume and biscuit making quality during 2015-2016; 2016-17 and 2017-18 and 2018-19 and low sedimentation lines stable across years with high biscuit spread factor (>11.0) and high yield potential were identified.

The sedimentation value of advanced lines of the cross between PBW 502 and Nap Hal exhibited sedimentation value in low range (1.8 to 3.9). Mixograph analysis also showed significant reduction in Mixograph Peak Time (MPT) in advanced generations as compared to varieties indicating potential for better biscuit making quality. There was significant reduction in time to peak parameter (from 2.50 minute in PBW 502 to 0.90 minute in advanced line) indicating very weak nature of the gluten caused by *Glu-D1* double null and thus suitable for biscuit making.

Table 1: Sedimentation volume of PBW 502 and *Glu-D1* double null line (IIWBR DN 502) measured across the years (2016-2019). Now the advanced line is at $BC_2 F_9$ stage (2020-21).

Cultivars and Cross combinations	*Sedimentation volume in cc (1 g test)*				
	2016	2017	2018	2019	Mean
PBW 502	7.5	7.2	7.4	7.3	7.4
NAP HAL	3.6	3.6	3.4	3.5	3.5
IIWBR DN 502 (PBW502/*2/NAP HAL)	2.7	2.6	2.3	2.5	2.5

20. DBW308 (IC0640675; INGR21195), a wheat (*Triticum aestivum*) germplasm highly resistant to blast, brown rust as well as black and yellow rust diseases of wheat

Hanif khan[1*], Om Parkash[2], CN Mishra[1], Gopalareddy K[1], OP Gangwar[2], Raj Kumar[1], Satish Kumar[1], Mamrutha HM[1], Poonam Jasrotia[1], SC Bhardwaj[2], Sudheer Kumar[1], Sonu Singh Yadav[1], Gyanendra Singh[1], Ravish Chatrath[1] and GP Singh[1]
[1]*ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India*
[2]*ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India*
[*]*Email: Hanif.Khan@icar.gov.in*

Wheat blast (WB) disease reported first time from Brazil in 1985 has recently emerged as in Bangladesh in the year 2016, thereby putting a threat to wheat in the entire South Asia. A very high propensity of WB becoming pandemic to a particular geographical localization takes the threat to the next level. Therefore, it is imperative to developed resistant varieties/genetic stock efforts in collaboration with national and international partners. Also, wheat rusts are widely distributed across all the major wheat-growing regions in the world. Regular shifts in virulences pose a major challenge to achieving durable rust resistance. Wheat breeder's strategy has been to utilize germplasm sources that are as diverse as possible for rust resistance.

DBW308 has been developed from cross between HD3108/HD2967 through pedigree method of breeding. Its multi-location testing for yield traits was done at 20 locations in the National Initial Varietal Trial 1A (NIVT-1A) under all India Coordinated Wheat Improvement trials (2019-20). The proposed genotype was found highly resistant (score 0, 0) against wheat blast during at International WB screening facility of CIMMYT, Jassore, Bangladesh screened in two different dates of sowing, at three locations i.e. US, Okinawa and Quirusillas (Bolivia) during 2019-20 and at two locations *i.e.* Jassore, and Quirassallis at two different dates of sowing during 2020-21 (Table 1).

Table 1: Data testing under PPSN (22 locations) and International WB screening facility of CIMMYT (three locations two years)

Genotype	*Average coefficient of infection (ACI) of rust*				*Av. WB score 2019-20*	*Av. WB score 2020-21*
	Stem	*Leaf (South)*	*Leaf North)*	*Stripe*		
DBW308	2.6	2.1	2.6	10.2	0	0
Susc. Check	77.5	77.5	70.0	72.5	100	100

Besides, screening for various wheat diseases Plant Pathological Screening Nursery (PPSN 2019-20) at 23 locations viz. Bajaura, Malan, Dhaulakuan, Gurdaspur, Ludhiana, Jammu, Hisar, Karnal, Durgapura, Delhi, Pantnagar, Faizabad, Kanpur, Indore, Powarkheda, Vijapur, Junagadh, Pune, Niphad, Mahabalseshwar, Dharwad, Wellington. Based on multilocation testing DBW308 was found to be resistant to all the three rusts of wheat as indicated by low ACI (stem rust 2.6, leaf rust 2.1 south, 2.6 north and stripe rust 10.2) (Table 1). It is thus highly resistant to brown (leaf) and black (stem) rusts and moderately resistant to yellow(stripe) rust based on 23 locations data. It would provide genetic variability for developing wheat blast and rust resistant wheat varieties for all the zones.

21. HW5073 (IC0640676; INGR21196), a wheat (*Triticum aestivum*) germplasm with adult plant minor stem rust resistance gene *Sr2* with pleiotropic effect on leaf rust (*Lr27*) and stripe rust (*Yr30*) resistance

Vikas VK[1], Aravindh R[2], Sivasamy M[1], Ganesamurthy K[2], Jayaprakash P[1], Gopalakrishnan C[2], Sundeep Kumar[3], Geetha M[1], Nisha R[1], Shajitha P[1], John P[1], Sindhu PA[1] and GP Singh[4]
[1]*ICAR-IARI Regional Station, Wellington-643231, Tamil Nadu, India*
[2]*Tamilnadu Agricultural University, Coimbatore -641003, Tamil Nadu, India*
[3]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India*
[4]*ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India*
**Email: vikaswtn21@gmail.com*

Wheat is one of the most widely consumed cereal crops worldwide that provides 20% of dietary calories and protein. In India, wheat is the most important cereal crop after rice with a production of 107.18 MT during 2019-20. But with the rapidly increasing population, India will need more than 140 million tons of wheat by 2050. Among many factors, intensified agricultural practices and climate change have increased the incidence of pathogens in wheat in the recent years. Stem and leaf rust diseases continually pose threat to wheat production. In recent years, climate change and intensive crop cultivation practices are making powdery mildew as a potential threat to wheat production. Deploying resistant cultivars are the most economic, reliable and sustainable way to manage the stem rust, leaf rust and powdery mildew of wheat. Most of the rust resistance genes are all stage resistance (ASR)/major gene and therefore succumb to new variants of the respective pathogen soon after their deployment, whereas adult plant resistance (APR)/minor genes have small to intermediate effects when present alone. High and durable rust resistance can be achieved by combining the ASR and APR genes together.

Using conventional selection system, it is difficult to select two or more genes in a single genotype. In such a situation, phenotype neutral selection based on marker-trait association along with adult plant reaction become inevitable. Stem rust, leaf rust and powdery mildew resistance genes, *Sr2/Lr27/Yr30*, *Sr24/Lr24* and *Sr36/Pm6* were pyramided in the background of HD2833 cultivar through marker assisted backcross approach. Presence of the resistance genes were carried out using molecular markers, *gwm533* (*Sr2*+) (Spielmeyer *et al.*, 2003), *Sr24#12* (*Sr24/Lr24*) (Mago *et al*., 2005) and *stm773-2* (*Sr36/Pm6*) (Tsilo *et al*., 2008), in the pyramided lines. Stable and high yielding line (HW5073) was selected at BC4F7 generation and further evaluated for four seasons in two years. Adult plant reaction of pyramided lines showed resistance to the stem rust, leaf rust and powdery mildew pathotypes prevailing in India. Using gene pyramids of minor (*Sr2/Lr27/Yr30*) and major resistance genes (*Sr24/Lr24* and *Sr36/Pm6*) that confer resistance to the predominant pathotypes of stem rust, leaf rust and powdery mildew could impart durability to the cultivars than single gene deployment. Genetic stock can diversify the rust resistance genes among the wheat germplasm and provide a vital source for imparting durable rust resistance in wheat.

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22. DCMS 22A & DCMS 22B (IC0640654 & IC0640655; INGR21197), a new cytoplasmic genetic male sterile wheat (*Triticum aestivum*) in DBW 16 background with CMS source MTSA 2A

SK Singh*, Pradeep Sharma, Satish Kumar, Suresh Kumar, RP Gangwar, Snehanshu Singh and GP Singh
ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India
Email: sksingh.dwr@gmail.com

Exploitation of heterosis and development of hybrids is an innovative approach in cereals for breaking yield barriers and realizing higher yields.

The proposed genetic stock DCMS 22A was developed using MTSA 2A based CMS 2A (MTSA 2A/8*RAYON) as female parent in first cross with Indian advanced variety DBW 16 as male parent. After initial cross, 8 generations of backcrosses were made with the variety DBW 16 used as recurrent parent. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 22A (Table 1).

The heading period in DCMS 22A ranged from 95-109 days with mean of 100 days whereas average plant height was 95 cm with range of 92-100 cm. Compared to this, the maintainer line DCMS 22B showed similar average days to heading of 100 days with plant height of 98 cm. These features are helpful in synchronised flowering and better pollen movement for maximum seed set.

It may be concluded that the proposed genetic stock DCMS 22A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS22A and its maintainer for quantitative traits

Year	*DCMS22A (CMS- A line)*			*DCMS 22B (DBW 16: B line)*	
	Male sterility(%)	*Days to heading*	*Plant height(cm)*	*Days to heading*	*Plant height(cm)*
2015-16	100	98	94	98	98
2016-17	100	95	92	95	98
2017-18	100	97	92	97	98
2018-19	100	109	100	110	97
Mean	100	100	95	100	98

23. DCMS 23A & DCMS 23B (IC0640656 & IC0640657; INGR21198), a New cytoplasmic genetic male sterile line of wheat (*Triticum aestivum* subsp. *aestivum*) in DBW 16 background with CMS source Chuan 13A

SK Singh*, Satish Kumar, Pradeep Sharma, Suresh Kumar, RP Gangwar, Snehanshu Singh and GP Singh
ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India
Email: sksingh.dwr@gmail.com

The proposed genetic stock DCMS 23A was developed using CHUAN 13A based CMS 8A (CHUAN13A/5/7*ATTILA/3/HUI/CARC//CHEN/CHTO/4/ATTILA) as female parent in first cross with Indian advanced variety DBW 16 as male parent. After initial cross, 8 generations of backcrosses were made with DBW 16 as recurrent parent in order to recover its agronomic background. In this process, more than 100 spikes were pollinated. In every generation, five spikes of recipient population were bagged just after emergence from the flag leaf in order to ensure complete male sterility as indicated by no seed set.

After eight backcross generations, the resultant male sterile line was planted in the field along with recurrent parent as maintainer line. The newly developed CMS lines were pollinated with maintainer lines for getting seeds for next generation. For the purpose, the CMS line was planted along with maintainer line in 2B: 4A: 2B row ratio and all the recommended agronomic practices were adopted to raise a good crop during four consecutive crop seasons of 2015-16, 2016-17, 2017-18 and 2018-19. Five randomly selected spikes of these CMS lines were bagged at just after emergence from flag leaf and the seed set was observed in these un-pollinated spikes for calculating seed set percentage. The data were also recorded on days to heading and plant height for evaluating their suitability to hybrid wheat programme. The seed set was observed among these lines and the results indicated no seed set in the bagged un-pollinated spikes of the CMS lines. This indicated complete male sterility in the new CMS line DCMS 23A (Table 1).

The heading period in DCMS 23A ranged from 95-108 days with mean of 100 days whereas average plant height was 97 cm with range of 96-98 cm. Compared to this, the maintainer line DCMS 23B showed similar average days to heading of 100 days with plant height of 98 cm which is in tune to CMS line. This similar feature is helpful in synchronised flowering and pollen movement for maximum seed set.

It may be concluded that the proposed genetic stock DCMS 23A may be used intensively for development of hybrid wheat for Indian conditions so that new breakthrough may be achieved in wheat productivity.

Table 1: Performance of DCMS23A and its maintainer for quantitative traits

Year	*DCMS23A (CMS- A line)*			*DCMS 23B (DBW 16: B line)*	
	Male sterility(%)	*Days to heading*	*Plant height(cm)*	*Days to heading*	*Plant height(cm)*
2015-16	100	98	96	98	92
2016-17	100	95	96	95	104
2017-18	100	97	98	97	99
2018-19	100	108	98	109	97
Mean	100	100	97	100	98

24. WAPD 1508 (IC0640666; INGR21199), a wheat (*Triticum aestivum*) germplasm with triple gene dwarf genotype possessing bold seeds and longer spikes

SK Singh, Satish Kumar, Pradeep Sharma, OP Gupta, Suresh Kumar and GP Singh
ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India
*Email: sksingh.dwr@gmail.com

The wheat growing areas in the country are experiencing a kind of stagnation in yield levels. The agronomic manipulations for fertiliser dose and schedule are being done for developing high yielding genotypes for irrigated timely sown conditions. Such manipulations sometimes lead to increased biomass that result in lodging during crop stages. Research efforts at IIWBR resulted in selection of dwarf transgressive segregants that resulted in development of 38 short statured genotypes.

The proposed germplasm line WAPD 1508 was developed from the cross 35IBWSN 159/34IBWSN 24//23ESWYT 43 following modified pedigree method. The first cross was made between 35IBWSN 159 [Croc_1/*Ae. Squarrosa* (205)// Kauz/3/Attila] and 34IBWSN 24 [Altar 84/*Ae. squarrosa* (219)//Seri] and the resultant F1 was again crossed with pollen parent 23ESWYT 43 [Munia/CHTO/3/PFAU/ BOW// VEE#9/4/Chen/ *Ae. squarrosa* (Taus) //BCN]. The dwarf plants from the segregating populations of this three-way cross were selected and fixed. The proposed entry WAPD 1508 is characterised for presence of dwarfing genes through molecular markers for genes *Rht B1b (237bp), Rht D1b (254 bp) and Rht 8 (192 bp)* alongwith check varieties DBW 93, DM 6 and DM 7. WAPD 1508, DM 6 and DM7 were confirmed as triple gene dwarf genotypes whereas DBW 93 has two dwarfing genes. Initially WAPD 1508 was evaluated for agro-morphological traits alongwith check DBW 93 during 2016-17 in PYT at Karnal. Thereafter, two triple gene dwarf checks DM6 and DM7 were included for comparison of agro-morphological traits. After its better performance for various agro-morphological traits, WAPD 1508 was evaluated in multi-locational National Genetic Stock Nursery (NGSN) at 32 locations during 2019-20 and 31 locations during 2020-21.

The entry WAPD 1508 showed promising performance during three years of evaluation at Karnal location under timely sown irrigated conditions (Table.1). On mean basis of three years' data (2016-17 to 2018-19), it showed mean yield of 64.4q/ha which was 24.3% higher than the best check variety DBW 93 (51.8q/ha). The short statured nature with plant height 70 cm was comparable to other dwarf checks DM 6 and DM 7 that indicated its suitability for non-lodging. It was earliest in heading (93 days) and possessed bolder grains (42.0g TGW) longer spike (13.0cm), high harvest index (39.2%). It but has more grain filling period of 47 days that supported proper grain development. During 2019-20 and 2020-21, it was evaluated in NGSN at 32and 31 locations, respectively across the country representing all 5 wheat growing zones. In NGSN, WAPD 1508 showed higher yield than the other triple gene dwarf checks DM 6 & DM 7 and was at par to the DBW 93. It also showed longer spikes and bolder seeds than the checks and comparable performance for heading, maturity and plant height.

Based on above results, it may be concluded that the germplasm line WAPD 1508, a triple gene dwarf statured genotype is suitable for high potential areas where more yield can be harvested by manipulating agronomic package of practices. Increased fertiliser dose may be supported by its dwarf stature leading to non-lodging conditions. It may also be suitable for mechanised farming system. In view of its traits, it can be further utilised as potential donor in developing dwarf high yielding genotypes suitable to mechanised farming.

Table 1: Performance of WAPD 1508 for yield and component traits during 2016-17 to 2018-19

Genotypes	*DH (days)*	*DM (days)*	*PH (cm)*	*TPM*	*SPL (cm)*	*GPS*	*TGW (g)*	*GY (q/ha)*	*HI (%)*	*Dwarfing genes*		
										Rht B1b	*Rht D1b*	*Rht 8*
WAPD 1508	93	140	70	157	13.0	59	42.0	64.4	39.2	+	+	+
DM 6 ©	96	138	65	163	11.5	77	23.5	30.0	26.7	+	+	+
DM 7 ©	95	138	64	165	12.0	78	23.0	35.0	27.0	+	+	+
DBW 93©	94	136	90	129	9.0	56	40.7	51.8	36.1	-	+	+

DH-Day to heading, DM-Days to maturity, PH-Plant ht., TPM- Tillers per meter length, SPL-Spike length, GPS- Grains per spike, TGW- 1000 grains wt., GY-Gr yield, , HI- harvest index

25. DWAP 18-07 (IC0640667; INGR21200), a wheat (*Triticum aestivum*) germplasm with highly tolerant to water stress conditions of warmer areas and Low yield reduction under stress

SK Singh, Pradeep Sharma, OP Gupta, Suresh Kumar, Rinki and GP Singh
ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India
*Email: sksingh.dwr@gmail.com

The wheat growing areas in the country are experiencing warmer climatic conditions in present climatic scenario. The high temperature conditions coupled with water scarcity conditions becomes more crucial for harvesting good wheat yields. In such areas, AICRP on wheat & barley has advocated restricted irrigation condition in which one pre-sowing irrigation and another irrigation at 45 DAS is given. The wheat improvement for warmer areas programme of the ICAR-IIWBR has developed number of elite lines for such conditions using shuttle breeding approach for target oriented wheat improvement.

The germplasm line DWAP 18-07 was developed from the cross HW 1080/DBW 17 following modified pedigree method. The segregating generations were evaluated at Karnal and 8 shuttle breeding centres in CZ and PZ for target oriented selection. It was evaluated at 10 locations in all four zones i.e., Karnal in NWPZ, Ayodhya in NEPZ, Jabalpur, Junagadh, Vijapur and Bilaspur in CZ and Akola, Niphad and Dharwad in PZ under timely sown irrigated condition and timely sown restricted irrigation condition in replicated trials. The check varieties are the latest commercial cultivars of all the zones for various production conditions. The yield data was analysed location wise to estimate the stress susceptibility index (Fischer & Maurer, 1978) and percent reduction of yield under stress conditions (Choukan *et al.*, 2006). The pooled analysis of SSI and Red (%) indicated wide range of variability among the genotypes in the experiment. In general, the genotypes having SSI <1.0 is considered as stress tolerant genotypes.

The proposed genotype DWAP 18-07 showed least SSI of 0.14 (Table 1) alongwith least reduction in yield under stress conditions (3.54) which reflects its high tolerance nature to water scarcity conditions.

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Table 1: Stress susceptibility index of selected entries of wheat in multilocations

S. No.	Entry	Stress susceptibility index (SSI)											Reduction in yield under stress (%)
		Akola	Ayodhya	Jabalpur	Niphad	Dharwad	Junagadh	Powarkheda	Vijapur	Bilaspur	Karnal	Pooled	
1	DWAP 18-07	0.50	0.91	0.12	0.71	0.60	1.21	2.59	0.85	-0.70	-4.89	0.14	3.54
2	DBW 110 ©	-0.13	0.66	4.43	1.16	0.80	1.16	4.97	1.13	1.04	-3.62	0.66	17.04
3	DBW 93 ©	1.25	0.59	-24.67	0.79	0.90	0.83	2.68	1.52	1.23	0.53	0.70	18.05
4	HD 2967 ©	-3.13	1.42	-6.52	1.06	1.30	0.89	-1.30	-0.13	1.10	1.06	1.04	26.59
5	HD 2932 ©	1.84	0.59	8.84	0.91	0.98	0.86	0.74	1.00	0.73	1.31	1.12	28.79
6	GW 322 ©	0.84	2.15	3.58	1.01	1.07	1.11	3.46	1.77	1.11	2.65	1.25	31.99
7	MACS 6222 ©	1.57	0.68	1.72	1.09	1.05	1.15	-0.93	0.79	0.89	-0.44	1.28	32.78
8	DBW 222 ©	0.05	2.23	3.61	1.18	1.01	1.43	1.27	1.18	0.77	2.02	1.29	33.05

26. TAW 33 (IC0631397; INGR21201), a wheat (*Triticum aestivum*) germplasm with high grain hardiness index

BK Das[1], Abhijit Shitre[1], Gautam Vishvakarma[1], Sudhakar Mali[1], SG Bhagwat[1], Potdukhe N R[2], Swati Bharad[3], BD Gite[4], Gadekar DA[5], Suresh Dodke[6] and UG Kachole[6]

[1]*Nuclear Agriculture & Bio-Technology Division, BARC-400094, Maharashtra, India*
[2]*Cotton research unit, Dr. PDKV, Akola 444104, Maharashtra, India*
[3]*Wheat research unit, Dr. PDKV, Akola 444104, Maharashtra, India*
[4]*ARS, Washim-444505, Maharashtra, India*
[5]*College of Agriculture, Muktainagar-426306, Maharashtra, India*
[6]*ARS, Niphad, Dist Nasik-422303, Maharashtra, India*
[*]*Email: bkdas@barc.gov.in*

Wheat is second largest staple food for the world after rice and consumed in different types of end products like breads, biscuits, cakes, noodles, pasta, chapati *etc.* One of the fundamental means of classifying wheat as hard or soft wheat is through its endosperm texture. It impacts significantly on the milling process affecting flour particle size and milling yield (1). The quality of the end product ultimately depends on the viscoelastic properties of gluten proteins and physical properties of the wheat flour being used for the preparation of dough. These physiochemical parameters include grain hardness index, colour of the flour, quantity and quality of gluten proteins, starch content, size and packing of starch and protein granules in wheat kernel. Among these, grain hardiness index is most important physical quality parameter which determines starch damage and particle size during milling of wheat grains. Soft grain with low protein content are required for cake and biscuits making where as hard grain and high protein content are suitable for bakery products (2). High grain hardness index is correlated with more damaged starch causing more water absorption and keeping the end-product soft for longer duration.

Taw 33 is a stable *T. aestivum* genotype developed through conventional breeding and recurrent selection. The parents used in the crossing were HD2385/ FLW2. TAW33 was tested for grain hardiness and other morphological traits over a period of two years from 2016-17 to 017-18 in ICAR trials. This genotypes has consistently exhibited the highest grain hardiness index among the 52 *T. aestivum* genotypes tested in AICRP during the years 2017-18. TAW 33 recorded grain hardiness index as high as 102 against that of the check varieties which ranged from 32.8 to The genotype TAW33 also possessed the 5+10 subunits of glutenin which impart strength to dough resulting in strong dough that is suitable for bread making. Thus, TAW 33 having highest grain hardiness index with 12% protein content and 5+10 glutenin subunits will be a very valuable genotype as a potential donor in wheat quality improvement programme. TAW33 also has very good agronomical traits like long panicle, bold lustrous grain and very sturdy stem which resist the crop lodging at the time of maturity.

The other Agronomical and quality traits of TAW33 and check varieties are given in Table 1.

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Table 1: Agronomical and quality traits of TAW33 and check varieties

	UP2672	*C306*	*NIAW1415*	*HS490*	*DDW42*	*TAW33*
Protein content	13	11.6	11.5	11.2	11.9	12
Sedimentation value	62.2	46.8	48.8	43.4	44.7	52.3
Tiller No	92	89	84	89	86	103
TGW	41	38	39	39	40	40
Yield (gm/m2)	415	340	399	337	376	393
Grain appearance score	5.8	6.6	5.2	4.7	5.5	6.1
Hectoliter weight	77.1	80.4	76.1	73.8	78.4	77.8

27. BHS 478 (BBM 800) (IC0640686; INGR21202), a barley (*Hordeum vulgare*) germplasm with seedling resistance against all races of leaf and stripe rust and Adult plant resistance to yellow rust and leaf rust

Madhu Patial, Dharam Pal, SC Bhardwaj, KK Pramanick and OP Gangwar
[1]*IICAR-IARI Regional Station, Shimla 171004, Himachal Pradesh, India*
[2]*ICAR-IIWBR, Regional Station, Shimla-171002, Himachal Pradesh, India*
[*]*Email: mcaquarian@gmail.com*

BHS 478 (BBM 800) is a barley (*Hordeum vulgare L.*) line resistant against stripe, leaf and stem rust. It has shown highest degree of resistance against all the prevailing pathotypes of stripe and leaf rust at seedling stage and is resistant to both the rust at adult plant stage. BHS 478 (BBM 800) also showed resistance or moderately resistance response against all the pathotype of stem rust (except for pathotype *11* showing moderately susceptible response) at seedling stage and also resistant response (5S) at adult plant stage (Table 1). This line is developed following pedigree method of breeding involving crosses between barley breeding material BHS 385 and registered barley genetic stock BHS 369 at ICAR- IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Center, Shimla (H.P.).

BHS 478 (BBM 800) has semi spreading growth habit with medium maturity (169 days) under Northern Hill condition. The average yield is 3.23 t/ha under rainfed condition of Northern Hill Zone of All India Co-ordinated trials 2019-20. The distinguish features of BHS 478 (BBM 800) are six-rowed; hulled; semi-spreading growth habit; semi-erect flag leaf attitude; green leaves; white colour of ear at maturity and thousand grain weight of 45 grams.

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Table 1: Reaction to major diseases

Diseases	*Condition*	*Year*	*Response of Proposed Genetic stock BHS 478 (BBM 800)*	*Page No.*
Stripe Rust (Resistant to yellow rust)	IBDSN (APR)	2018-19	ACI= 0.0 HS= 0	3.7 of Reference (i)
	NBDSN (APR)	2019-20	ACI=8.6	3.14 of Reference (ii)
	NBDSN (Seedling)	2019-20	R (Resistant to all races)	3.28 of Reference (ii)
Leaf Rust (Resistant to brown rust)	NBDSN (APR)	2019-20	HS= 5S	3.14 of Reference (ii)
	NBDSN (Seedling)	2019-20	R (Resistant to all races)	3.28 of Reference (ii)
Stem Rust (Resistant to black rust)	NBDSN (APR)	2019-20	HS=5S	3.14 of Reference (ii)
	NBDSN (Seedling)	2019-20	R (Resistant) to moderately resistant (MR) response to all races (Except for race 11 showing moderately susceptible response)	3.28 of Reference (ii)

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

28. DWRBG4 (IC0641987; INGR21203), a barley (*Hordeum vulgare* subsp. *vulgare*) germplasm with combination of high beta-glucan (7.5% dwb) and high protein (13.2%)

Rekha Malik[*], **Dinesh Kumar, RPS Verma, Ajit Singh Kharub, Lokendra Kumar, Jogendra Singh, Chuni Lal, Poonam Jasrotia, Surendra Singh, Rajendra Kumar and GP Singh**

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

[*]*Email: rekha.malik@icar.gov.in*

DWRBG-4 (Tested as RMB11) is a two-row hulled barley genotype derived from a cross DWR30/Shebac and further advanced through pedigree selection of plant breeding approach. RMB11 was evaluated in Barley Quality Screening Nursery in AICRIP trials during 2020-21 along with checks at five locations and as expected, gave high score of protein and beta glucan percentage which is a rare found combination in two row hulled barley. DWRBG-4 has shown higher level of beta glucan content (7.5% dwb) which is higher than the malt varieties (4.2 to 6.2 % dwb) and DWR 30 (6.9% dwb), the previously registered germplasm for this trait (Table 1). Also, this genotype has higher level of protein content (13.2% dwb) which is higher than registered varieties (11.5 to 12.3 % dwb) and comparable to previously registered genetic stock BK1127 (13.8% dwb) (Table 2). This unique combination of high protein and high beta glucan is very much desirable for health food industry and is not yet reported or registered till date in Indian barley germplasm. DWRBG-4 is the outcome of institute barley breeding programme and can serve as potential candidate genotype across AICWBIP for introgression of quality traits in barley. Average values for agro-morphological traits were observed as 50% flowering in 92 days and matured in 138 days. Plant height was measured 114 cm and foliage colour was light green. The genotype other traits calculated are 1000 grain weight (55.1g), test weight (61.8) and starch content (59.4).

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Table 1: Beta glucan content (% dwb) from different locations in AICWBIP BQSN 2020-21

Code	*Genotype*	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	*Average*
R-11	DWRBG-4 (RMB -11)	7.7	5.5	6.9	8.8	7.6	8.3	7.5
M-17	DWRUB52 (c)	5.4	4.2	4.4	5.2	5.1	5.3	4.9
M-18	DWRB101 (c)	5.4	4.4	5.9	5.0	5.1	5.0	5.1
M-23	DWRB182 (c)	4.2	4.2	4.4	4.7	4.0	4.0	4.2
M-27	BK 306	3.8	4.3	4.4	4.7	4.5	4.5	4.4
M-33	DWRB 197	6.3	6.4	6.6	6.4	6.5	5.9	6.4

Table 2: Protein content (% dwb) from different locations in AICWBIP BQSN 2020-21

Code	*Genotype*	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	*Average*
R-11	DWRBG-4 (RMB -11)	12.0	15.5	13.0	12.7	12.6	13.1	13.2
M-17	DWRUB52 (c)	12.0	11.6	14.5	12.0	9.7	12.5	12.1
M-18	DWRB101 (c)	12.1	11.7	12.8	11.7	9.6	11.1	11.5
M-23	DWRB182 (c)	12.2	11.6	14.2	13.2	12.1	10.4	12.3
M-2	BK1127	13.0	15.1	15.4	15.1	10.4	13.6	13.8
M-27	BK 306	12.5	13.7	13.8	11.5	11.5	11.4	12.4

#Predicted values through NIR

29. DWRBG1 (IC0641988; INGR21204), a barley (*Hordeum vulgare*) germplasm with combination of low grain beta-glucan (3.8%) and higher grain protein content (13%)

Dinesh Kumar[*], **RPS Verma, Sneh Narwal, Rekha Malik, Ram Pal Saini and GP Singh**

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

[*]*Email: Dinesh.Kumar3@icar.gov.in*

DWRBG 1 (tested as ICARDA 5) is a two-row hulled barley genotype, selected from PYT- 2014-15 entry number-41 of ICARDA. It has been identified for lower grain beta glucans content coupled with desirable protein content. Grain beta glucan (β1-3, 1-4 glucan) content is a very important component in determining the malting quality of any malt barley genotype. In case of malt barley, the beta glucan content should be as low as possible and not higher than 4%. Higher content of beta glucans poses a problem in proper modification of endosperm as after the dissolution of cell wall (where major component is beta glucan), the starch hydrolysing agents can only gain entry to the starch molecules. Genotype is the major determinant of grain beta glucan content and is also influenced by environment. Barley is grown in short days in India with a limited grain filling window and getting low grain beta glucans content is a challenge. The identified genotype DWRBG1 has low grain beta glucans content of 3.67% (Table 1). Further, protein content is a very important quality trait influencing malting and brewing quality of barley grain. Very high protein content (> 14%) in the grain impacts adversely the malt extract yield. Very low content of protein (<9.0%) is also not desirable since in brewing process yeasts need optimum quantity of amino acids for growth. In case of malt-based food products, good quantity and quality of protein is required. Nowadays brewing industry also requires higher protein content (12-13%), especially to get higher diastatic power and free amino nitrogen especially in cases wherever adjuncts are being used or higher protein derived components are required in the end product. The genotype DWRBG1 has average protein content of 12.81% (Table 2) and is very unique in the sense that it has low grain beta glucans content also. Thus, DWRBG1 is a potential genotype which can be used as donor parent for improving the quality in malt barley.

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Table 1: Grain beta glucan (%dwb) in ICARDA-5 at different locations during 2019-21

Genotype	*2019-20*	*2020-21*						*Mean*
	Karnal	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	
ICARDA 5	2.9	3.6	3.9	4.3	4.1	3.3	3.8	3.7
DWRUB 52 (c)	4.9	5.4	4.2	4.4	5.2	5.1	5.3	4.9
DWRB 101 (c	4.7	5.4	4.4	5.9	5.0	5.1	5.0	5.1
DWRB-182 (c)	3.3	4.2	4.2	4.4	4.7	4.0	4.0	4.1
DWR 37 (c)*	-	4.8	4.4	4.8	5.0	5.4	4.8	4.9
DWR 39 (c)*	-	4.6	2.9	NA	NA	4.4	4.2	4.0

*Registered stocks for the trait

Table 2: Grain protein content in ICARDA-5 at different locations during 2019-21

Genotype	*2019-20*			*2020-21*						*Mean*
	Karnal	*Hisar*	*Pantnagar*	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	
ICARDA 5	11.1	13.5	10.6	13.9	12.9	13.9	14.0	12.0	11.4	12.6
DWRUB 52 (c)	10.6	13.4	9.8	12.0	11.6	14.5	12.0	9.7	12.5	11.8
DWRB 101 (c)	11.1	13.0	10.2	12.1	11.7	12.8	11.7	9.6	11.1	11.5
DWRB-182 (c)	11.7	12.8	11.5	12.2	11.6	14.2	13.2	12.1	10.4	12.2
DWR 37 (c)*	-	-	-	14.6	16.3	12.9	12.8	15.5	13.2	14.2
DWR 39 (c)*	-	-	-	15.8	16.6	NA	NA	NA	NA	16.2

*Registered stocks for the trait

30. DWRBG 3 (IC0641990; INGR21205), a barley (*Hordeum vulgare*) germplasm with combination of low grain beta-glucan content (3.88%) and desirable thousand grain weight (45g)

Dinesh Kumar[*]**, RPS Verma, Sneh Narwal, Rekha Malik, Ram Pal Saini and GP Singh**
ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India
[*]*Email: Dinesh.Kumar3@icar.gov.in*

DWRBG-3 (tested as ICARDA-9) is a two-row hulled barley genotype, selected from PYT-2014- 15 entry number-93 of ICARDA. It has been identified for lower grain beta glucans content coupled with desirable thousand grain weight (44-46 g). Grain beta glucan (β 1-3, 1-4 glucan) content is a very important component in determining the malting quality of any malt barley genotype. In case of malt barley, the beta glucan content should be as low as possible and *not higher than 4%*. Higher content of beta glucans poses a problem in proper modification of endosperm as after the dissolution of cell wall (where major component is beta glucan), the starch hydrolysing agents can only gain entry to the starch molecules. Genotype is the major determinant of grain beta glucan content and is also influenced by environment. Barley is grown in short days in India with a limited grain filling window and getting low grain beta glucans content is a challenge. The identified genotype DWRBG-3 has low grain beta glucans content of 3.87% Table 1). Further, thousand grain weight (TGW) is an important contributor of grain yield and quality. For malt purpose barley, thousand grain weight of 44-46 g is desirable for two row barley variety. The genotype DWRBG-3 has TGW of 45 grams (Table 2), which is well in required/ desirable range. Usually, two rowed barleys have higher thousand grain weight as compared to six rowed barleys. Lower thousand grain weight may result in lower yields and lower values of malt extract. Very high thousand grain weight (> 48 g) lead to under modification of grains during malting (conversion of endosperm starch in to sugars), as during steeping stage water may not reach to core of grain and poor ignition of aleurone layer for secretion of amylases, leading to undigested starch in some parts of endosperm. Genotype or variety is the major determinant of thousand grain weight, but is also affected by environment, cultural practices and biotic/abiotic stresses. Thus, DWRBG-3 is a potential genotype which can be used as donor parent for improving the quality in malt barley.

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Table 1: Grain beta glucan (%db) in DWRBG-3 (ICARDA-9) at different locations during 2019 - 2021

Genotype	*2019-20*	*2020-21*						*Mean*
	Karnal	*Hisar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	
ICARDA-9	3.8	3.7	3.0	4.2	4.3	3.7	4.4	3.87
DWRUB 52 (c)	4.9	5.4	4.2	4.4	5.2	5.1	5.3	4.93
DWRB 101 (c)	4.7	5.4	4.4	5.9	5.0	5.1	5.0	5.07
DWRB-182 (c)	3.3	4.2	4.2	4.4	4.7	4.0	4.0	4.11
DWR 37*	NT	4.8	4.4	4.8	5.0	5.4	4.8	4.87
DWR 39*	NT	4.6	2.9	NA	NA	4.4	4.2	4.03

*Registered stocks for the trait

Table 2: Thousand grain weight in DWRBG-3 (ICARDA-9) at different locations during 2019 - 21

Genotype	*2019-20*			*2020-21*					*Mean*
	Hisar	*Karnal*	*Pantnagar*	*Karnal*	*Ludhiana*	*Durgapura*	*Pantnagar*	*Kanpur*	
ICARDA-9	50.7	43.5	45.9	45.9	46.4	41	42.7	50.2	45.8
DWRUB 52 (c)	56.1	40.5	47.1	47.1	49.3	48.4	33.8	51.4	46.7

DWRB 101 (c)	52.9	47.9	50.1	50.1	49	55.5	49.6	51.3	50.8
DWRB-182 (c)	43	41.2	43.0	39.9	43.9	44.2	41.1	49.9	43.3
DWR 37*	NT	NT	41.2	NT	47.7	50.7	52.9	52.8	49.1
DWR 39*	NT	NT	39.9	NT	24.6	44.7	NA	NA	36.4

*Registered stocks for the trait

31. DWRBG5 (IC0641991; INGR21206), a huskless barley (*Hordeum vulgare*) germplasm with high thousand grain (43.5g) weight, bold grain percentage (63.2%) and protein content (14.7%)

Jogendra Singh*, RPS Verma, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Rekha Malik, Charan Singh, Ajit Singh Kharub and GP Singh

ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India

Email: jogendra.singh2@icar.gov.in

DWRBG-6 (DWRB217) is a six-row hulless barley genotype, selected from exotic (INBYT-(2013)- HI-2, ICARDA) breeding material (PETUNIA2/M112). DWRBG-6 was *screened for stripe rust at 7 locations in National Barley Disease Screening Nursery (NBDSN) during 2019-20*. DWRBG-6 exhibited resistance to stripe rust with ACI= 4.0 and HS=10S, while the huskless checks Karan16, NDB943, PL891 and infector were highly susceptible (Table 1).

This genotype was also screened in Seedling Resistance Tests (SRT) against 7 pathotypes for infection response during 2019-20. DWRBG-6 exhibited resistance against five currently prevailing pathotype (M, G, Q, 6S0 and 7S0) including the two new pathotypes (Table 2). This also supports the field screening results with the currently prevailing pathotypes. The check varieties showed susceptible reaction against all 7 pathotypes except PL 891 having resistant response to pathotype 24.

The starch content was registered 63.7%, which is 1.3% higher than better checks (Table 3).The genotype also had 72.3 kg/hl test weight and protein content 13.6%.

Agro-morphological and quality traits: DWRBG-6 flowers in 92 days and matures in 135 days. Its average plant height is 106 cm and has 117 tillers/meter. The average spike length is 6.9 cm with 73 grains and thousand grain weight of 38.2g.

References

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Table1: Stripe rust reaction of DWRBG-6 (DWRB-217) at adult plant stage during 2019-20

Genotype	*Durgapura*	*Ludhiana*	*Bajaura*	*Jammu*	*Karnal*	*Hisar*	*Almora*	*ACI*	*HS*
DWRBG-6	5MR	10S	0	10MS	5MS	0	NG	4.0	10S
Karan16 ©	60S	40S	20S	40S	5MS	0	10S	24.9	60S
NDB943©	100S	80S	80S	60S	0	0	NG	53.3	100S
PL891©	10MR	0	30S	0	60S	60S	0	22.0	60S
Infector	100S	60S	100S	80S	100S	84.00	100S	88.6	100S

Table 2: Stripe rust reaction of DWRBG-6 (DWRB-217) at seedling resistance during 2019-20

Genotype	Pathotypes						
	57	24	M	G	Q	6S0	7S0
DWRBG-6	S	MS	R	R	R	R	R
Karan16 ©	S	S	S	MS	S	S	S
NDB943©	S	S	S	NG	S	S	S
PL891©	NG	R	NG	NG	S	NG	S

Table 3: Starch content of DWRBG-6 (DWRB-217) at different locations during 2019-20

Genotype	*Starch content (% db)*						
	Durgapura	*Pantnagar*	*Kanpur*	*Hisar*	*Karnal*	*Ludhiana*	*Mean*
DWRBG-6	65.6	64.5	65.0	61.5	64.3	61.0	63.7
Karan16 ©	65.8	60.2	63.8	60.1	63.4	61.3	62.4
NDB943©	65.1	NA	62.8	59.8	63.6	60.9	62.4
PL891©	63.0	59.8	61.7	60.0	61.4	62.0	61.3

32. DWRBG6 (IC0641992; INGR21207), a huskless barley (*Hordeum vulgare*) germplasm with adult plant resistance to stripe rust, seedling resistance to new pathotypes 6S0 and 7S0 and high starch content (63.7%).

Jogendra Singh[1*], RPS Verma[1], Sudheer Kumar[1], OP Gangwar[2], Dinesh Kumar[1], Chuni Lal[1], Lokendra Kumar[1], Rekha Malik[1], Charan Singh[1], AS Kharub[1] and GP Singh[1]
[1]*ICAR-Indian Institute of Wheat and Barley Research Karnal-132001, Haryana, India*
[2]*ICAR-IIWBR Regional Station, Shimla-171002, Himachal Pradesh, India*
[*]*Email: jogendra.singh2@icar.gov.in*

DWRBG-6 (DWRB217) is a six-row hulless barley genotype, selected from exotic (INBYT-(2013)- HI-2, ICARDA) breeding material (PETUNIA2/M112). DWRBG-6 was *screened for stripe rust at 7 locations in National Barley Disease Screening Nursery (NBDSN) during 2019-20*. DWRBG-6 exhibited resistance to stripe rust with ACI= 4.0 and HS=10S, while the huskless checks Karan16, NDB943, PL891 and infector were highly susceptible (Table 1).

This genotype was also screened in Seedling Resistance Tests (SRT) against 7 pathotypes for infection response during 2019-20. DWRBG-6 exhibited resistance against five currently prevailing pathotype (M, G, Q, 6S0 and 7S0) including the two new pathotypes (Table 2). This also supports the field screening results with the currently prevailing pathotypes. The check varieties showed susceptible reaction against all 7 pathotypes except PL 891 having resistant response to pathotype 24. The starch content was registered 63.7%, which is 1.3% higher than better checks (Table 3). The genotype also had 72.3 kg/hl test weight and protein content 13.6%.DWRBG-6 flowers in 92 days and matures in 135 days. Its average plant height is 106 cm and has 117 tillers/meter. The average spike length is 6.9 cm with 73 grains and thousand grain weight of 38.2g.

References

Anonymous (2020) Progress report of AICRP on Wheat and Barley. 2019-20. Barley Improvement. (Eds. RPS Verma, AS Kharub, Dinesh Kumar, Chuni Lal, Lokendra Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Charan Singh, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and Gyanendra Pratap Singh). ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. pp 3.14-3.16.

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Table1: Stripe rust reaction of DWRBG-6 (DWRB-217) at adult plant stage during 2019-20

Genotype	*Durgapura*	*Ludhiana*	*Bajaura*	*Jammu*	*Karnal*	*Hisar*	*Almora*	*ACI*	*HS*
DWRBG-6	5MR	10S	0	10MS	5MS	0	NG	4.0	10S
Karan16 ©	60S	40S	20S	40S	5MS	0	10S	24.9	60S
NDB943©	100S	80S	80S	60S	0	0	NG	53.3	100S
PL891©	10MR	0	30S	0	60S	60S	0	22.0	60S
Infector	100S	60S	100S	80S	100S	84.00	100S	88.6	100S

Table 2: Stripe rust reaction of DWRBG-6 (DWRB-217) at seedling resistance during 2019-20

Genotype	*Pathotypes*						
	57	*24*	*M*	*G*	*Q*	*6S0*	*7S0*
DWRBG-6	S	MS	R	R	R	R	R
Karan16 ©	S	S	S	MS	S	S	S

NDB943©	S	S	S	NG	S	S	S
PL891©	NG	R	NG	NG	S	NG	S

Table 3: Starch content of DWRBG-6 (DWRB-217) at different locations during 2019-20

Genotype	*Starch content (% db)*						
	Durgapura	*Pantnagar*	*Kanpur*	*Hisar*	*Karnal*	*Ludhiana*	*Mean*
DWRBG-6	65.6	64.5	65.0	61.5	64.3	61.0	63.7
Karan16 ©	65.8	60.2	63.8	60.1	63.4	61.3	62.4
NDB943©	65.1	NA	62.8	59.8	63.6	60.9	62.4
PL891©	63.0	59.8	61.7	60.0	61.4	62.0	61.3

33. IML 21 (IC0640688; INGR21208), a maize (*Zea mays*) germplasm resistant to *Turcicum* Leaf Blight (TLB)

Shyam Bir Singh[1*], SI Harlapur[2], N Mallikarjuna[3], R Devlash[4], H Rajashekara[5], KS Hooda[6], Chikkappa GK[7], Bhupender Kumar[6], Ramesh Kumar[6], Santosh Kumar[1], Parveen Bagaria[6], RK Kasana[1], Sushil Kumar[1], SS Gangoliya[7], N Sunil[8], Yatish KR[8], BS Jat[6], Krishan Kumar[6] and Sujay Rakshit[6]

[1]*Regional Maize Research and Seed Production Centre, ICAR-IIMR, Begusarai-851101, Bihar, India*
[2]*University of Agricultural Sciences, Dharwad-580005, Karnataka, India*
[3]*Zonal Agricultural Research Station, V.C. Farm, Mandya-571405, Karnataka, India*
[4]*CSKHPKV, HAREC, Bajaura, Distt. Kullu-175125, Himachal Pradesh, India*
[5]*ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand, India*
[6]*ICAR-Indian Institute of Maize Research PAU, Campus, Ludhiana-141004, Punjab, India*
[7]*ICAR-IIMR Unit, Pusa Campus-110012, New Delhi, India*
[8]*WNC (ICAR-IIMR), Hyderabad-500030, Telangana, India*
[*]*Email: singhsb1971@rediffmail.com*

Maize (*Zea mays* L.) is one of the most versatile emerging crops with its highest genetic yield potential among the cereals. The major reason for low productivity of maize in India is losses caused by various biotic and abiotic stresses. Among the various biotic stresses, foliar diseases namely, turcicum leaf blight (TLB) also called northern corn leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs. (syn. *Heliminthosporium turcicum* Pass.) is of worldwide importance and one of the most important diseases in India. This foliar disease occurs in high humidity and moderate temperature areas. It also results upto 70% loss in the yield. The fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al*. 2013; De-Rossi *et al*., 2015). Host plant resistance is considered as most practical and economically viable method of plant disease management (Wathaneeyawech *et al,* 2015: Hooda *et al*, 2018). The inbred IML 11 is developed at Regional Maize Research and Seed Production Centre (ICAR-IIMR), Begusarai following pedigree method using commercial maize hybris as source material. Under hot spot locations (Dharwad, Mandya, Almora and Bajaura) for TLB, the line IML 21 (IMLSB 343-2) displayed a mean disease score of 2.6 at par with the resistant check i.e. 2.6 while the susceptible check 7.9.

A set of 237 newly developed maize inbred lines along with resistant (LM 13, CL 4, NAH 1137) and local susceptible (CM 202, CM 600) inbred line as check were evaluated against TLB under artificial epiphytotic conditions. The trial was conducted during kharif season of 2017 and 2018 at TLB hot-spot locations, *viz*., Dharwad, Mandya, Almora and Bajaura. In 2017, the trial was conducted in randomized complete block design whereas in 2018 it was conducted in alpha design. Spore suspension of *E. turcicum* isolates was prepared in lab and sprayed by using atomizer at three to four leaf stage of each and every maize plants twice in an interval of two days to ensure proper inoculation. The disease reaction was recorded by using 1 to 9 scales as suggested by Hooda *et al.* (2018). Disease scoring was commenced from six-eight leaves stage (approximately 45 days after planting) and continued on weekly basis for 6 weeks. The genotypes showing disease score between 0.0–3.0 were considered as resistant (R), 3.1-5.0 as moderately resistant (MR), 5.1- 7.0 as moderately susceptible (MS), >7.0 as susceptible (S). The disease reaction was recorded on five plants in the middle of the row and it was averaged to calculate TLB overall mean disease score of each line. The overall mean TLB score calculated across locations over two years was considered to classify inbred lines into resistant, moderately resistant, moderately susceptible and susceptible inbred lines. Out of 237 inbred lines, 41 inbred lines were resistant with TLB score <3.0, 181 lines were moderately resistance with TLB score 3.1-5.0 and 15 inbred lines were moderately susceptible with TLB score 5.1 to 7.0 (Singh *et al*. 2018). The Inbred lines were also evaluated for maturity and yield traits during rabi-2017-18 and 2018-19 and RMR&SPC, Begusarai. Out of the 41 resistant inbred lines, four best TLB resistant lines along with high yield per se performance as mentioned in Table 1 were identified for registration.

IML 21 is a late maturing high yielding line resistant to Turcicum Leaf Blight (disease mean score 2.6 on the scale of 1-9), medium height, medium ear placement, straight attitude of lateral tassel branches, sparse spikelets of tassel, yellow round shaped and semi-dent/semi-flint kernels. It is derived from normal maize segregating progeny by continuous selfing following pedigree breeding method. IML 21 is high yielding maize inbred line with yield potential of 33.1 q/ha. This inbred is also suitable for cultivation during *rabi* season. It also has good seed setting to be used as seed parent under commercial seed production. The inbred has straight kernel rows and semi-dent or semi flint kernels.

Disease scorer for TLB (*Kharif*-2017 & 2018), maturity and yield (*rabi*-2017-18 & 2018-19) of identified newly developed maize inbred lines

References

De-Rossi RL, ML Reis and R Brustalin (2015) Fungal baseline for mycelia sensitivity of *Exserohilum turcicum*, causal agent of northern corn leaf blight. *Summa Phytopathol.* 41(1): 25-30.

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Wathaneeyawech S, P Sirithunya, and P Smitamana (2015) Collections, isolations, morphological study of *Exserohilum turcicum* and screening resistant varieties of corn to Northern Corn Leaf Blight disease. *Int.J. Agri. Techn.* 11(4): 937-952.

Table 1: Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (rabi-2017-18 & 2018-19) of identified newly developed maize inbred lines

S.No.	*Name of inbred*	*Another name*	*TLB score*	*Reaction*	*Days to 50% anthesis (rabi)*	*Days to 75 % dry husk maturity (rabi)*	*Grain yield (q/ha)*	*Maturity group*
1	IML 21	IMLSB-343-2	2.6	R	125	163	33.1	Late
2	IML 11	IMLSB-334B-1	2.6	R	122	158	28.2	Late
3	IML 13	IMLSB-1041-4-1	2.4	R	112	155	36.4	Medium
4	IML 12	IMLSB-446-2	2.5	R	107	147	31.9	Medium
		Resistant Check (CL 4/ NAH 1137	2.4	R	--	--	--	--
		Susceptible check (CM 200)	7.9	S	--	--	--	--

34. IML 12 (IC0640689; INGR21209), a maize (*Zea mays*) germplasm with resistance to *Turcicum* Leaf Blight (TLB)

Shyam Bir Singh[1*], KS Hooda[2], Chikkappa GK[3], Bhupender Kumar[2], Ramesh Kumar[2], Santosh Kumar[1], Parveen Bagaria[2], SI Harlapur[4], N Mallikarjuna[5], R Devlash[6,] H Rajashekara[7], RK Kasana[1], Sushil Kumar[1], SS Gangoliya[3], N Sunil[8], Yatish KR[8], BS Jat[2], Krishan Kumar[2] and Sujay Rakshit[2]

[1]*Regional Maize Research and Seed Production Centre, ICAR-IIMR, Begusarai-851101, Bihar, India*

[2]*ICAR-Indian Institute of Maize Research PAU, Campus, Ludhiana-141004, Punjab, India*

[3]*ICAR-IIMR Unit, Pusa Campus-110012, New Delhi, India*

[4]*University of Agricultural Sciences, Dharwad-580005, Karnataka, India*

[5]*Zonal Agricultural Research Station, V.C. Farm, Mandya-571405, Karnataka, India*

[6]*CSKHPKV, HAREC, Bajaura, Distt. Kullu-175125, Himachal Pradesh, India*

[7]*ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand, India*

[8]*WNC (ICAR-IIMR), Hyderabad-500030, Telangana, India*

[*]*Email: singhsb1971@rediffmail.com*

Maize (*Zea mays* L.) is one of the most versatile emerging crops with its highest genetic yield potential among the cereals. The major reason for low productivity of maize in India is losses caused by various biotic and abiotic stresses. Among the various biotic stresses, foliar diseases namely, turcicum leaf blight (TLB) also called northern corn leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs. (syn. *Heliminthosporium turcicum* Pass.) is of worldwide importance and one of the most important diseases in India. This foliar disease occurs in high humidity and moderate temperature areas. It also results upto 70% loss in the yield. The fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al*. 2013; De-Rossi *et al*., 2015). Host plant resistance is considered as most practical and economically viable method of plant disease management (Wathaneeyawech et al, 2015: Hooda et al, 2018). The inbred IML 11 is developed at Regional Maize Research and Seed Production Centre (ICAR-IIMR), Begusarai following pedigree method using commercial maize hybris as source material. Under hot spot locations (Dharwad, Mandya, Almora and Bajaura) for TLB, the line IML 12 (IMLSB 446-2) displayed a mean disease score of 2.5 at par with the resistant check i.e. 2.4 while the susceptible check 7.9.

A set of 237 newly developed maize inbred lines along with resistant (LM 13, CL 4, NAH 1137) and local susceptible (CM 202, CM 600) inbred line as check were evaluated against TLB under artificial epiphytotic conditions. The trial was conducted during kharif season of 2017 and 2018 at TLB hot-spot locations, *viz*., Dharwad, Mandya, Almora and Bajaura. In 2017, the trial was conducted in randomized complete block design whereas in 2018 it was conducted in alpha design. Spore suspension of *E. turcicum* isolates was prepared in lab and sprayed by using atomizer at three to four leaf stage of each and every maize plants twice in an interval of two days to ensure proper inoculation. The disease reaction was recorded by using 1 to 9 scales as suggested by Hooda *et al*. (2018). Disease scoring was commenced from six-eight leaves stage (approximately 45 days after planting) and continued on weekly basis for 6 weeks. The genotypes showing disease score between 0.0–3.0 were considered as resistant (R), 3.1-5.0 as moderately resistant (MR), 5.1- 7.0 as moderately susceptible (MS), >7.0 as susceptible (S). The disease reaction was recorded on five plants in the middle of the row and it was averaged to calculate TLB overall mean disease score of each line. The overall mean TLB score calculated across locations over two years was considered to classify inbred lines into resistant, moderately resistant, moderately susceptible and susceptible inbred lines. Out of 237 inbred lines, 41 inbred lines were resistant with TLB score <3.0, 181 lines were moderately resistance with TLB score 3.1-5.0 and 15 inbred lines were moderately susceptible with TLB score 5.1 to 7.0 (Singh et al. 2018). The Inbred lines were also evaluated for maturity and yield traits during rabi-2017-18 and 2018-19 and RMR&SPC, Begusarai. Out of the 41 resistant inbred lines, four best TLB resistant lines along with high yield per se performance as mentioned in Table 1 were identified for registration. IML 12 is a medium maturing high yielding line resistant to Turcicum Leaf Blight (disease mean score 2.5 on the scale of 1-9), medium height, medium ear placement, straight attitude of lateral tassel branches, sparse spikelets of tassel, yellow round shaped and flint kernels. It is derived from normal maize test cross progeny by continuous selfing following pedigree breeding method.

IML 12 is high yielding maize inbred line with yield potential of 31.9 q/ha. This inbred is also suitable for cultivation during rabi season. It also has good seed setting to be used as seed parent under commercial seed production. The inbred has straight kernel rows and semi-dent or semi flint kernels.

References

De-Rossi RL, ML Reis and R Brustalin (2015) Fungal baseline for mycelia sensitivity of *Exserohilum turcicum*, causal agent of northern corn leaf blight. *Summa Phytopath*. 41(1): 25-30.

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Table1: Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (rabi-2017-18 & 2018-19) of identified newly developed maize inbred lines

S.No	*Name of inbred*	*Another name*	*TLB score*	*Reaction*	*Days to 50% anthesis (rabi)*	*Days to 75 % dry husk maturity (rabi)*	*Grain yield (q/ha)*	*Maturity group*
1	IML 12	IMLSB-446-2	2.5	R	107	147	31.9	Medium
2	IML 21	IMLSB-343-2	2.6	R	125	163	33.1	Late
3	IML 11	IMLSB-334B-1	2.6	R	122	158	28.2	Late
4	IML 13	IMLSB-1041-4-1	2.4	R	112	155	36.4	Medium
		Resistant Check (CL 4/ NAH 1137	2.4	R	--	--	--	--
		Susceptible check (CM 200)	7.9	S	--	--	--	--

35. IML 13 (IC0640690; INGR21210), a maize (*Zea mays*) germplasm resistant to *Turcicum* Leaf Blight (TLB)

Shyam Bir Singh[1*], KS Hooda[2], Chikkappa GK[3], Bhupender Kumar[2], Santosh Kumar[1], Ramesh Kumar[2], N Sunil[4], Yatish KR[4], Krishan Kumar[2], BS Jat[2], SI Harlapur[5], N Mallikarjuna[6], H Rajashekara[7], R Devlash[8], Parveen Bagaria[2], RK Kasana[1], Sushil Kumar[1], SS Gangoliya[3] and Sujay Rakshit[2]

[1]*Regional Maize Research and Seed Production Centre, ICAR-IIMR, Begusarai-851101, Bihar, India*

[2]*ICAR-Indian Institute of Maize Research PAU, Campus, Ludhiana-141004, Punjab, India*

[3]*ICAR-IIMR Unit, Pusa Campus-110012, New Delhi, India*

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Maize (*Zea mays* L.) is one of the most versatile emerging crops with its highest genetic yield potential among the cereals. The major reason for low productivity of maize in India is losses caused by various biotic and abiotic stresses. Among the various biotic stresses, foliar diseases namely, turcicum leaf blight (TLB) also called northern corn leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs. (syn. *Heliminthosporium turcicum* Pass.) is of worldwide importance and one of the most important diseases in India. This foliar disease occurs in high humidity and moderate temperature areas. It also results upto 70% loss in the yield. The fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al.* 2013; De-Rossi *et al.*, 2015). Host plant resistance is considered as most practical and economically viable method of plant disease management (Wathaneeyawech et al, 2015: Hooda et al, 2018). The inbred IML 11 is developed at Regional Maize Research and Seed Production Centre (ICAR-IIMR), Begusarai following pedigree method using Non QPM pool as source material. Under hot spot locations (Dharwad, Mandya, Almora and Bajaura) for TLB, the line IML 13 (IMLSB 1041-4-1-1) displayed a mean disease score of 2.4 at par with the resistant check i.e. 2.4 while the susceptible check 7.9.

A set of 237 newly developed maize inbred lines along with resistant (LM 13, CL 4, NAH 1137) and local susceptible (CM 202, CM 600) inbred line as check were evaluated against TLB under artificial epiphytotic conditions. The trial was conducted during kharif season of 2017 and 2018 at TLB hot-spot locations, *viz*., Dharwad, Mandya, Almora and Bajaura. In 2017, the trial was conducted in randomized complete block design whereas in 2018 it was conducted in alpha design. Spore suspension of *E. turcicum* isolates was prepared in lab and sprayed by using atomizer at three to four leaf stage of each and every maize plants twice in an interval of two days to ensure proper inoculation. The disease reaction was recorded by using 1 to 9 scales as suggested by Hooda *et al.* (2018). Disease scoring was commenced from six-eight leaves stage (approximately 45 days after planting) and continued on weekly basis for 6 weeks. The genotypes showing disease score between 0.0–3.0 were considered as resistant (R), 3.1-5.0 as moderately resistant (MR), 5.1- 7.0 as moderately susceptible (MS), >7.0 as susceptible (S). The disease reaction was recorded on five plants in the middle of the row and it was averaged to calculate TLB overall mean disease score of each line. The overall mean TLB score calculated across locations over two years was considered to classify inbred lines into resistant, moderately resistant, moderately susceptible and susceptible inbred lines. Out of 237 inbred lines, 41 inbred lines were resistant with TLB score <3.0, 181 lines were moderately resistance with TLB score 3.1-5.0 and 15 inbred lines were moderately susceptible with TLB score 5.1 to 7.0 (Singh et al. 2018). The Inbred lines were also evaluated for maturity and yield traits during rabi-2017-18 and 2018-19 and RMR&SPC, Begusarai. Out of the 41 resistant inbred lines, four best TLB resistant lines along with high yield per se performance as mentioned in Table 1 were identified for registration.IML 13 is a medium maturing high yielding line resistant to Turcicum Leaf Blight (disease mean score 2.4 on the scale of 1-9), medium height, low ear placement, curved attitude of lateral tassel branches, dense spikelets of tassel, yellow round shaped and flint kernels. It has low ASI (3days). It is derived from non-QPM pool, (a normal maize population) following pedigree breeding method.

IML 13 is high yielding maize inbred line with yield potential of 36.4 q/ha. This inbred is also suitable for cultivation during rabi season. It also has good seed setting to be used as seed parent under commercial seed production. The inbred has straight kernel rows and flint kernels. It is also moderately tolerant to waterlogging.

Table 1: Disease scorer for TLB (Kharif-2017 & 2018), maturity and yield (*rabi*-2017-18 & 2018-19) of identified newly developed maize inbred lines

S. No.	*Name of inbred*	*Another name*	*TLB score*	*Reaction*	*Days to 50% anthesis (rabi)*	*Days to 75 % dry husk maturity (rabi)*	*Grain yield (q/ha)*	*Maturity group*
1	IML 13	IMLSB-1041-4-1	2.4	R	112	155	36.4	Medium
2	IML 12	IMLSB-446-2	2.5	R	107	147	31.9	Medium
3	IML 21	IMLSB-343-2	2.6	R	125	163	33.1	Late
4	IML 11	IMLSB-334B-1	2.6	R	122	158	28.2	Late
		Resistant Check (CL 4/ NAH 1137	2.4	R	--	--	--	--
		Susceptible check (CM 200)	7.9	S	--	--	--	--

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36. WN 585 (IC0624599; INGR21211), a finger millet (*Eleusine coracana*) germplasm with early flowering & early maturity (100-110 days), red grain & high yield

Harshal Eknath Patil[1], Gopal D Vadodariya[1], Brijeshkumar K Patel[1] and M Elangovan[2]

[1]*Hill Millet Research Station, Navsari Agricultural University, Waghai-394730, Gujarat, India*

[2]*ICAR-Indian Institute of Millets Research, Hyderabad, Telangana 500030, India*

**Email: harshalpatil@nau.in*

The proposed culture, WN-585 is early flowering, early maturing and high yielding red grain genotype have been developed through selection from local germplasm collected from the Dangs district by Hill Millet Research Station, NAU, Waghai, Dangs, Gujarat. The WN-585 was tested under various categories of station trials at Waghai, Varanasi and Dahod centers as well as tested in 20 AICRP small millets locations across seven states at national level from 2017-18, 2018-19 to 2019-20.

The early maturing (100-110 days) culture WN-585 (3065 kg/ha) performed well with 21.3 % and 13.7 % grain yield superiority over national check 'VL-149' and 'VL-352', respectively in Gujarat. At national level, it showed 19.6 % grain yield improvement over national check 'VL-352'. The genotype 'WN-585' yields on an average 2607 kg/ha of grain yield which was 15.3, 19.6, 5.4 and 4.2 per cent higher than national checks GPU-47, VL-352, PR-202 and VL-376, respectively in 20 locations across the All India Coordinated trials conducted during 2017-18, 2018-19, 2019-20 at Gujarat, Maharashtra, Odisha, Tamilnadu and Telangana under rainfed conditions. (Annexure - I & II). Also, WN-585 yielded 6369 kg/ha of fodder yield with 14.5 per cent increased yield over national check VL-352 in All India Coordinated trials conducted during 2017-18, 2018-19, 2019-20 at Gujarat, Maharashtra, Odisha, Tamilnadu and Telangana under rainfed conditions. (Annexure - III).

With respect to pest and diseases, it was found superior to checks and moderately resistant for the same. Considering the increasing demand of red grain culture 'WN-585' with early maturing, high yield potential culture, desirable grain quality and moderately resistant to foot rot and blast disease. It is proposed to best culture for early maturing finger millet growing dry lands, hill and tribal areas of India. Hence it can be used directly in recombination breeding for induction of earliness with red grain colour and high grain yield.

37. CCB 12 (IC0641999; INGR21212), a cotton (*Gossypium barbadense*) germplasm with cleistogamous flower and three locule bolls

KPM Dhamayanthi*, A Manivannan and K Rathinavel
ICAR-CICR Regional Station, Coimbatore-641003, Tamil Nadu, India
Email: dhamayanthikpm@gmail.com

Cleistogamy, a breeding system in which plants produce unopened flowers, and this feature facilitates self-pollination, this phenomenon has received increasing attention in recent years. It is present in 693 angiosperm species, distributed over 228 genera and 50 families. Recent investigations have indicated that evolution of cleistogamy in these taxa may be influenced by the occurrence of heterogeneous environments, inbreeding depression and geitonogamy. Cleistogamy mechanism helps in ensuring the self-pollination by which genetic purity is reserved.

Gossypium barbadense grows indeterminately and flowers; flower buds are denoted as squares. The flower bud is surrounded by three bracts and forms a pyramid-like shape. The first square is typically appearing on node 5 or 6 in about 37 to 39 days after sowing. Anthesis takes place approximately 24 days after the formation of first square. The bloom process takes several days, and bloom age can be estimated by the bloom characteristics. On the day a flower opening, it appears yellow in color. Pollination in a flower usually occurs within a few hours of flower opening.

A three way cross (SN (SN x ICB 75) 7-1-6-2) was made during 2012-2013 crop season. Among the F3 population a single plant bearing flowers (cleistogamous) in different nature from that of the parents was isolated. The identified plant is semi spreading type with an average height of 133 cm, with sympodia ranging from 6 to 7 per plant. The cultivar exhibited solitary bolls, ovate in shape with pointed tip. At present, this cultivar is in F8 generation. It was evaluated for three years to study the flowering patter during the phenology, seed cotton production an d fiber quality, at ICAR-CICR Regional Station, Coimbatore and subsequently, confirmative trials were conducted at ICAR-CICR, Nagpur, MPKV, Rahuri and ICAR- CICR Regional Station, Sirsa, under diverse agro climatic zones. The morphological observations recorded in all the locations have confirmed that the cultivar is true to type with cleistogamous flowers. Average seed cotton yield of 7.5 q/ha was recorded. This cultivar is rated under ELS category as per the fibre quality parameters with the staple length of 35 mm, strength of 34 g/tex and micronaire of 2.5 µ/inch.

Occurrence of cleistogamous flowers in *G. barbadense* is very rare phenomenon. The identified cultivar was from an intra barbadense cross (Suvin x (Suvin x ICB-75) and found stable for cleistogamous flower production. The trait is controlled by two recessive genes (cg1 and cg2) and can be transferred in populations through breeding methods, like haploidisation or backcrosses. Digenic inheritance of 15:1 is reported for this trait. The petals are locked each other as to prevent the opening of the flower, thereby excluding the possibility of cross-pollination. This character in breeding lines would be of great importance for maintaining genetic purity in often-cross pollinated crops like cotton.

38. CNH 204710 (IC0641997; INGR21213), a cotton (*Gossypium hirsutum*) germplasm with ginning outturn percentage of 43.9%

SM Palve* and Nita Kate
ICAR-Central Institute for Cotton Research, Nagpur-440010, Maharashtra, India
Email: smpalve@gmail.com

Ginning outturn (GOT) is an important component of fibre yield in cotton as it is directly associated with lint. The amount of lint borne on a single seed is a matter of considerable economic importance. It is commonly represented as the ginning percent. GOT is the ratio of weight of lint to the weight of seed-cotton (lint and seed) expressed as percentage. It is much used measurement in cotton production, marketing and ginning. Ginning out-turn is a useful indicator of the performance of a genotype. Since, cotton lint is considered to be the most economic and valued from textile industries and fabrics manufacturing point of view. The measurement of lint as an index or in terms of percentage helps to identify varieties/ genotypes producing more lint. Genotypes with high ginning out-turn values are thus preferable, because they yield more lint.

CNH 204710 was developed from an interspecific cross involving *G. barbadense* (Gb) and *G. hirsutum* (Gh) species. A backcross inbred population was developed involving *G. hirsutum* cv. Suraj as a recurrent parent and *G. barbadense* cv. Suvin as a donor. Crosses were made between Suraj as female parent and Suvin as the male parent during 2013- 14 at ICAR-Central Institute for Cotton Research, Nagpur. The F_1 (Suraj × Suvin) was then backcrossed to Suraj to produce BC_1F_1 population during 2014. In 2015, BC_1F_1 population was grown and extensively self-pollinated. In subsequent generations up to BC$_1$F$_6$, continued self-pollination of selected single plant progenies was done. The field experiment was conducted during 2018-19, 2019-20, and 2020-21 at ICAR-Central Institute for Cotton Research, Nagpur with 19 BC1 families of 4-14 plants per family and tested for yield components and fibre properties.

CNH 204710 is morphologically typical of upland cotton with hairy leaves and stem. It has normal leaf shape, higher internode length, long duration of 170-190 days maturity and growth habit similar to the varieties Suraj and NH 615. The introgression line CNH 204710 was selected on the basis of the results of 3-year field trials for superior ginning outturn percentage of 43.9 % than those of the released check varieties Suraj and NH 615. NH 615 is regularly being used as zonal check for Central zone had ginning outturn of 36.9 % and quality check Suraj had 36.2 %. The donor parent Suvin had ginning outturn of 31.6 %. The identified introgression line CNH 204710 had upper half mean length of 29.1 mm, fibre strength of 26.5 g/tex and boll weight of 4.8 g. Fibre length of CNH 204710 was comparable to NH 615 (28.6 mm). Overall, CNH 204710 a high GOT (43.9 %) introgression line is an excellent source for cotton breeding programs.

39. DPB-1 (IC0632628; INGR21214), a broccoli (Brassica *oleracea* var. *italica*) germplasm with purple heading

Pritam Kalia, Shrawan Singh[*] and BS Tomar
Division of Vegetable Science, ICAR-IARI, Pusa Campus-110012, New Delhi, India
[*]Email: singhshrawan@rediffmail.com

Nutritionally, broccoli is a very important vegetable crop because it is rich source of health benefiting anticancer glucosinolates and dietary minerals and vitamins. Broccoli is rich source of health beneficial glucosinolates such as glucoraphanin and glucoiberin. It has diverse variants for attractive colours such as green, purple and light yellow. The green is most common but purple colour is most attractive with added value of anthocyanin. Although, a purple heading variety 'Palam Vichitra' is developed for Indian condition but it takes long period (110-120 days after transplanting) and have dull shade of purple colour. While, the major demand arises near metro cities particularly in north Indian condition, hence it was essential to develop genotype having short harvest period 85-95 days) and attractive purple heads to fulfil the rising demand.

A new purple heading genotype with purple head was derived by recurrent selection from a segregating exotic material. The new genotype 'Delhi Purple Broccoli-1' was developed by recurrent selection. For this, the plant with purple colour head was selected and selfed by bud-pollination. From its progeny the selection and selfing process was continued for two more generation and each time, plants were selected with desirable traits such as medium head size, fine to medium size buds, partial to compact, medium to intense purple heads, early maturity, seed production capacity etc. The fixed genotype was designated as 'Delhi Purple Broccoli-1'. It is distinct from the only purple heading broccoli 'Palam Vichitra' in India. Palam Vichitra takes 120 days after transplanting for maturity and produce seeds only in hills. While, the Delhi Purple Broccoli takes around 85-95 days after transplanting and produce seeds profusely in plains of north India during winter season. The distinguishing features between heads of both can be seen from. Its average head width is 17.6 cm, head length 15.6 cm and weight ranges from 600-750 g. It is rich in anthocyanin (30.31±0.68 mg/100g fw), higher than Palam Vichitra (17.8 mg/100 g fw). It is suitable for staggered sowing/planting from September to October, hence, has a longer harvest window, a desirable trait for market.

Delhi Purple Broccoli-1 is a medium stature variety and suitable to accommodate a greater number of plants per unit area. Unlike Palam Samridhi, it doesn't produce side spears which attract farmers for single harvest. Similar to other broccoli, it needs to be harvested with stalk when heads are compact, buds are well grown but still unopened and looks attractive. Yield potential of Delhi Purple Broccoli-1 is 21.8 t/ha, higher than Palam Samridhi (14.1 t/ha) and Pusa KTS-1 (15.60 t/ha). Important plant and yield traits are given in Table 1 and year-wise yield comparison in Table 2.

Table 1: Horticultural traits of Delhi Purple Broccoli-1 alongwith checks in Delhi condition

Character	*Days to harvest (after transpla nting)*	*Spacing (cm)*	*Plant height (cm)*	*Plant spread (cm)*	*Gross plant weight (g)*	*Seed yield (g/plant)*	*Marketable head weight (g)*	*Net head weight (g)*	*Marketable yield (t/ha)*
Delhi Purple Broccoli-1	85-95	45 × 45	52.5	48.3	1350		570	450	21.5
Palam Vichitra	120	60 × 45	63.2	60.0	1870		730	720	23.9

Table 2: Year-wise marketable yield of Delhi Purple Broccoli-1 genotype at IARI, New Delhi

Entry	*Marketable head yield (tonnes/ha)*					*Avg. marketable yield (tonnes/ha)*	*Maturity**
	2015-16	*2016-17*	*2017-18*	*2018-19*	*2019-20*		
Delhi Purple Broccoli-1	27.0	20.8	21.5	19.5	20.3	21.8	December – January
Palam Vichitrai	-	22.8	23.9	25.0	26.5	26.4	February - March

*Due to temperature requirement for head initiation and development.

40. 635414 (IC0635414; INGR21215), a bottle gourd (*Lagenaria siceraria*) germplasm resistant to powdery mildew

Dhananjaya MV[*], Sandeep Kumar GM, Varalakshmi B and Mahesh B
ICAR-Indian Institute of Horticultural Research, Bengaluru-560089, Karnataka, India
[*]Email: Dhananjaya.MV@icar.gov.in

Introduction

Bottle gourd [*Lagenaria siceraria* (Mol) Standle; 2n = 22] commonly known as 'white flowered gourd' or 'calabash gourd' belongs to the family Cucurbitaceae. Its fruits are known for good nutritive value. It is rich source of vitamins, minerals and also possess diuretic, antioxidant, cardio protective properties (Barot *et al*. 2015). Acceptability for fruit shape varies with the region and segment. The Southern parts of the country prefer cylindrical shape, whereas North and north eastern regions prefer round to oblong shaped fruits. For achieving quick cultivar development in the desired shape, presence and utilization of resistance source in the desired fruit shape is well appreciated by the breeders in the development of varieties/hybrids with resistance. Keeping in view, ICAR-IIHR, Bengaluru has come out with genetic stocks having resistance to major biotic stress *i.e* powdery mildew which is confronting the farmers. A promising genetic stock BG-8-1with elongated straight shape fruits with green stripes was developed through individual plant selection from an open pollinated population collected and maintained in the germplasm. It was found to be resistant for powdery mildew disease reaction. Plants are monoecious, annual vine with soft pubescence and produces white solitary flowers during evening hours. It takes an average of 54.18days for first female flower appearance at 17.33 node. Fruits are elongated straight shape with green stripes with a length of 35.05 cm and circumference 25.66 cm. It also produces 4.88 number of fruits per plant with a marketable yield of 32.20 t/ha (Table 1).

Table 1: Morphological, quality traits and disease reaction of BG-8-1

Sl. No	*Character*	*BG-8-1*
Morphological Traits		
1.	Days to first female flower appearance	54.18
2.	Node on which first female flower appeared	17.33
3.	Number of female flower	10.15
4.	Number of fruits per plant	4.88
5.	Yield /ha	32.20
Fruit quality traits		
6.	Fruit length(cm)	35.05
7.	Fruit circumferance (cm)	24.25
8.	Fruit weight(kg)	1.10
9.	Fruit shape	Elongated straight with green stripes
Disease reaction		
10.	Powdery Mildew	13.58 (PDI) 300.00 (AUDPC)

Fruits are medium, elongated straight with stripes on the surface of the fruits and shows resistant reaction for powdery mildew disease. It is a typical warm season vegetable, it cannot with stand frost and usually prefers hot and moist climate for cultivation. Seeds are sown from January to February for summer crop, June to July for rainy season crop and October - November for Rabi season. Land should be prepared well before planting by repeated ploughing and harrowing, 20-25 tonnes of farm yard manure/ha should be broadcasted after the first ploughing. Apply the recommended fertilizer mixture of 75 kg N, 100 kg P2O5 and 35-70 K2O/ha in two to three splits. Seeds are sown on raised beds of 15- 30cm height, 1-1.5 m width during rainy season by maintaining a spacing of 1.6 m between the rows and 1 m between the plants. Two to three seeds were sown per hill and covered with soil and light irrigation was given. Thinning of seedling should be done 25-30 days after sowing, retaining one healthy seedling per hill. Plants should be properly trained on the supporting structure to facilitate intercultural operations, thereby it reduces the incidence of pest and disease.

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41. VRT4-55-20 (HCP/YSR-6/) (IC0637253; INGR21216), a tomato (*Solanum lycopersicum*) germplasm with broad spectrum resistance to tomato leaf curl virus (ToL CV) with *Ty-2* and *Ty-3* genes

Prasanna HC[1], Yerasu Suresh Reddy[1*] and Major Singh[2]

[1]*ICAR-Indian Institute of Vegetable Research, Varanasi–221305, Uttar Pradesh, India*

[2]*ICAR-Directorate of Onion and Garlic Research, Pune-410505, Maharashtra, India*

[*]*Email*: *yerasusureshreddy@gmail.com*

Wild relatives of crops are good source of allelic variation that can boost the genetic improvement of agriculturally important crops. Resistance breeding against Tomato (yellow) leaf curl disease (TYLCD/ToLCD) got benefited from wild relatives of tomato (*Solanum lycopersicum* L.). Resistance to tomato-infecting begomoviruses has been successfully introgressed from different wild species of tomato like *Solanum pimpinellifolium, Solanum peruvianum, Solanum chilense* and *Solanum habrochaites* (*Ji et al*., 2007b). From these sources, a few resistance genes have been introgressed into cultivated tomatoes. Among them *Ty2* and *Ty3* genes are well characterized and fine mapped using molecular markers.

Tomato line VRT4-55-20 with *Ty2* and *Ty3* genes pyramided was developed at ICAR-Indian Institute of Vegetable research, Varanasi. It has good resistance against ToLCV. VRT4-55-20 was developed through marker assisted selection from F_2 populations of a cross between FLA478-6-1-11 × CLN2498C and FLA478-6-1-11 × CLN1621E. The lines CLN2498C and CLN1621E carry *Ty-2* gene. The line FLA478-6-1-11 carries *Ty-3* gene (Prasanna *et al*., 2015). VRT4-55-20 showed a higher level of resistance in agro inoculation test with two bipartite Tomato leaf curl New Delhi virus (ToLCNDV) and Tomato leaf curl Palampur virus (ToLCPalV), and a monopartite Tomato leaf curl Bangalore virus (ToLCBV). VRT4-55-20 showed high level of resistance under natural epiphytotic conditions also. Cultivars Kashi Vishesh and Punjab Chhuhara were used as susceptible checks and they showed disease symptoms in all the experiments (Prasanna *et al*., 2015).

The pyramided line VRT4-55-20 recorded an average fruit yield of 1.28 kg per plant. The fruits of the line plum shaped with a per carp thickness of 0.5 cm with an average locule number of 2 per fruit. TSS of 3.6 Brix was recorded. Fruit have distinctive thick green shoulder.

VRT4-55-20 can be used in different future tomato ToLCV resistance breeding programmes like the line can be tried as a parent in hybrid development programmes and the line can be used as source of *Ty-2* and *Ty-3* genes in gene pyramiding programmes with other economically important genes. Importantly, the line can be used in developing resistant cultivars for green fruit shoulder tomato market segment.

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42. BR-207 (IC0642000; INGR21217), a cauliflower (*Brassica oleracea* var. *botrytis*) germplasm single dominant resistant gene to black rot disease caused by *Xanthomonas campestris* pv. *campestris* race 1

Pritam Kalia[1], Partha Saha, SR Sharma, Shrawan Singh and Dinesh Singh

[1]*Division of Vegetable Science, ICAR-IARI, Pusa Campus-110012, New Delhi, India*

[2]*ICAR-IARI Regional Station, Katrain, Himachal Pradesh-175129, India*

[3]*ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi-110012, India*

[*]*Email: partha.saha@icar.gov.in*

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is one of the most important winter vegetable grown widely in India. Among the various diseases, black rot caused by *Xanthomonas campestris* pv. *campestris* (*Xcc*) (Pammel) Dowson is the most devastating disease of cauliflower worldwide including India (Singh and Dhar, 2011; Saha et al., 2014; Saha et al., 2015; Saha et al., 2021). The line 'BR-207' is resistant to black rot disease caused by *Xcc* race 1. It was developed from progeny selection of a cross of S. No. 15 (susceptible genotype) and MGS-2-3 (resistant) by Division of Vegetable Science, ICAR-IARI, New Delhi, India. The line carries a single dominant resistant gene (Saha *et al*., 2015).

The resistant line BR 207 belongs to mid-late maturity group with semi erect growth habit and medium in height (45–50 cm). The leaves are light green, medium in size with medium puckering habit. The curds are medium, compact and creamy white with an average weight of 350 g. The reaction of the plant at adult stage showed resistant reaction with mean disease score of 1.2 and 100 % plants were resistant (Table 1) (Saha *et al*., 2012).

The curd matures in the month of mid-January requiring 16-20°C temperature for curd initiation and development. The crop gets ready to harvest in 75 days after transplanting in its normal growing season. The flowers of 'BR-207'are yellow and stalk length is medium and flowering occurs during March. The line can be a useful source for transferring the resistant gene in commercially susceptible variety (s) or to develop hybrid (s). For each inoculated leaf, disease scores were taken at 21 days post inoculation. The severity of symptoms was assessed on a six-point scale of 0–9based on the relative lesion size as 0 = no symptoms,1 = small necrosis or chlorosis surrounding the infection point, 3 = typical small V-shaped lesion with black veins, 5 = typical lesion half way to the middle vein, 7 = typical lesion progressing to the middle vein, and 9 = lesion reaching the middle vein (Vicente et al. 2002).

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Table 1: Response of BR-207 and commercial cauliflower varieties to black rot disease in four different season/environment after artificial inoculation with black rot pathogen (Xcc race 1)

Genotype/lines	*Mean disease score 21 days' post inoculation Environment 1/ season 1 (a)*	*PDI at 60 days after inoculation Environment 2/ season 2 (b)*	*PDI at 60 days after inoculation Environment 3/ season 3 (c)*	*PDI at 60 days after inoculation Environment 4/ season 4 (d)*	*Disease reaction**
BR-207	1.2	0.2	0.80	1.0	Resistant
Pusa Himjyoti	9.0	8.2	9	8.6	Highly susceptible
Pusa Sharad	9.0	7.4	8.6	8.2	Highly susceptible

43. PC-1 (IC0642001; INGR21218), a cauliflower (*Brassica oleracea* var. *botrytis*) germplasm rich in anthocyanin (40.6±2.74 mg/100g FW)

Shrawan Singh* and Pritam Kalia

Division of Vegetable Science, ICAR-IARI, Pusa Campus-110012, New Delhi, India

**Email: singhshrawan@rediffmail.com*

Speciality foods are major attraction of premier high-end market. In cauliflower, colourful curds orange, purple and green are gaining popularity in global and Indian markets. Anthocyanins have strong free radical scavenging activity and, thereby, good for health. These compounds help in neutralizing reactive oxygen species (ROS) and reactive nitrogen species (RNS), thereby reducing the oxidative stress (Ozcan and Ogun, 2015).

The 'PC-1' is a new purple curding genotype of Indian cauliflower which is developed by recurrent selection from a segregating material of 'Sicilian Purple' type. The 'Sicilian purple' is botanically an intermediate of broccoli and cauliflower and appears closer to broccoli. It forms curd-like heads at a temperature range of 16 to 25°C and does not require vernalisation but needs cold temperature for bolting and flowering. Hence, it produces attractive full-size cauliflower-like curds during December–March months, set seeds profusely, and is easily crossable with Indian cauliflower. Unlike 'Graffiti', it accumulates anthocyanin only in 'pre-floral rudimentary buds' demonstrating the difference in genetic regulation of anthocyanin content between the two varieties.

Anthocyanin content in 'PC-1' was observed to increase up to 21st day of curd formation when it was recorded to be 41.2 mg/100 g fw. However, it declines afterward to 34.2 mg/100 g fw on 24th day of curd initiation. Hence, the ideal stage of harvesting is 21 – 24 days after curd initiation. This may slightly vary from planting time, growing region and nutrition status. This has no deformity in curd portion in homozygous or heterozygous state, hence, can be used for heterosis breeding by developing CMS lines or self-incompatible lines in purple background.

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44. DCA-295 (IC0642004; INGR21219), a chilli (*Capsicum annuum*) germplasm resistant to chilli veinal mottle virus disease and a good general combiner for yield and quality traits

Prabhudeva Ajjappalavara[1*], Megharaj KC[2], TB Allolli[2], HB Patil[2], Revanappa[3], Abdul Kareem M[4], MH Tataga[4] and Ratnakar Shet[4]

[1]*UHS, Horticultural Research & Extension Center, Haveri-581110, Karnataka, India*

[2]*College of Horticulture, Bagalkot-587104, Karnataka, India*

[3]*Horticulture Extension Education Unit, Yadgir-585201, Karnataka*

[4]*College of Horticulture, Sirsi, Uttara Kannada - 581 401, Karnataka, India*

[*]*Email: prabhudev.ajjappalavar@uhsbagalkot.edu.in*

As chilli is an economically important crop due to its significant value in regional as well as export market, the chilli production is taken up throughout the year mainly by the small farmers both in high and lowlands under rain-fed as well as irrigated conditions. In India, chilli veinal mottle virus (ChiVMV) is an economically important viruses causing yield loss to an extent of 50 per cent when the crop becomes infected at early stage. The predominance of ChiVMV during *Kharif* season is dominant because of favoured micro climatic condition. Hence, Identification of superior resistant lines for ChiVMV is very essential for the improvement of yield as well as the national productivity and also the national economy.

Forty-nine chilli genotypes were evaluated for virus complex in the open field under unsprayed condition during *Kharif* 2015 and the results obtained that virus infection was ranged from 16.36% to 89.72%. The lowest per cent incidence was found in DCA-295 (16.36%), DCA- 107 (17.36%) and DCA-154 (17.86%). The selected accessions evaluated against chilli veinal mottle virus through mechanical inoculation under shade net condition during *Kharif* season indicated that three genotypes (DCA-295, DCA-154 and DCA-107) were found to be immune showing no symptoms at both 30 and 45 days after mechanical inoculation for four consecutive *kharif* (2016, 2017, 2018 and 20219) season.

In order to understand the genetics of the resistance against Chilli veinal mottle virus, the F2, BC1 and BC2 generations were developed by using immune germplasm to develop the population (Byadgi Dabbi x DCA-295, Byadgi Kaddi x DCA-295) and these populations were screened for the resistance through artificial inoculation to study the genetic inheritance pattern in the DCA-295 germplasm. The inheritance studies in the Byadgi Dabbi x DCA-295, Byadgi Kaddi x DCA-295 derived advanced populations showed that it is governed by single recessive gene. The tester DCA-295 was identified as a good general combiner for plant height, canopy spread (N-S), canopy spread (E-W), green chilli average fruit weight, ascorbic acid and total chlorophyll.

45. VRRAD-12 (A line) & VRRAD-204 (B line) (IC0642005 & IC0642006; INGR21220), Cytoplasmic Male Sterile and maintainer lines of radish (*Raphanus sativus*) with lyrate leaf shape and blunt root: Good combiner for yield (12.5-33.6%), root length (6.5-32.4%) and root weight (17.2-30.0%)

BK Singh[*] and PM Singh

ICAR-Indian Institute of Vegetable Research, Varanasi-221305, Uttar Pradesh, India

[*]*Email: bksinghkushinagar@yahoo.co.in*

Radish (*Raphanus sativus* L.) is a most important salad crop belongs to Brassicaceae family which is grown round the year for fleshy roots and soft leaves. Heterosis (hybrid vigour) is of commercial importance for commercialization of F_1 hybrids in various vegetable crops, and is being facilitated by use of cytoplasmic male sterility (CMS) and self-incompatibility (SI) in radish. Nonetheless, the SI system in most of the radish genotypes is very weak; hence, there is always chance to get undesirable sibs in hybrid seeds. Therefore, in radish, CMS system is mostly preferred genetic emasculation technique for triggering the F_1 hybrid development, and cost-effective and easy hybrid seed production commercially.

First hybrid radish was developed by Frost (1923); moreover, CMS was first identified in a cultivar of Japanese radish by Ogura (1968) popularly known as Ogura-CMS; and thereafter, it has been transferred into different *Brassica* vegetables. Although radish is the most important salad crop in India because of availability and uses of roots round-the-year, yet only ICAR-IIVR, Varanasi, UP among Public Sector Institutes in India priorities its research on development of CMS lines and CMS-based hybrids. Realizing the importance and advantage of CMS lines especially in easy maintenance of female parent, harnessing heterotic vigour for economic traits (root length, root weight, marketable yield, earliness, uniformity produce, heat tolerance), and cheaper & quality seed production of F_1 hybrids; ICAR-IIVR, Varanasi, UP has developed CMS lines by backcross method and identified better hybrids (Singh et al. 2018, Singh and Singh 2020, Singh et al. 2021). The Ogura-CMS line 'VRRAD-12 or A Line', was developed by crossing CMS plants from open population with an elite line 'VRRAD-204 or B Line or Maintainer Line' which is having better combining ability, higher heterosis for economic traits (12.5-33.6% for marketable root) and suitable for winter season cultivation (Singh and Singh 2020). Significant heterotic hybrids for yield, longer roots, earliness, vigour consistency and uniformity have also been reported previously by many researchers (Kutty and Sirohi 2003, Singh *et al*. 2018, Kochetov and Sinyavina 2019).

CMS line VRRAD-12 is having lyrate type of leaf morphology (leaf division incision), develops white root with blunt-end (non-tapering) during winter season, bears white flower and ready to seed harvest in about 4.5 months after transplanting of stecklings. The quantitative traits of VRRAD-12 for consecutively three years (2017-18, 2018-19 and 2019-20) were observed as 45.7, 42.2 & 38.5 days to first root harvest; 273.5, 261.3 & 246.5 g gross plant weight; 190.3, 172.4 & 152.6 g root weight; 24.8, 23.1 & 22.4 cm root length; 37.5, 39.1 & 44.8 cm shoot length; 3.6, 3.7 & 3.4 cm root diameter; 11.3, 11.0 & 10.5 number of leaf; 60.2, 59.5 and 56.4 t/ha marketable yield; 41.6, 37.8 & 43.1 days to 50% flowering; 410.3, 391.6 & 426.8 pods/plant; 3.7, 3.8 & 3.8 seed/pod; and 12.9, 13.5 & 13.9 g of 1000 seed weight. Moreover, the economic parameters of its maintainer VRRAD-204 during 2017-20 were observed as 42.8, 42.3 & 36.5 days to first root harvest; 258.9, 251.6 & 238.3 g gross plant weight; 184.5, 170.4 & 151.8 g root weight; 24.1, 23.2 & 22.6 cm root length; 35.9, 37.1 & 42.7 cm shoot length; 3.6, 3.5 & 3.3 cm root diameter; 11.5, 11.1 & 10.6 number of leaf; 58.8, 56.4 and 53.7 t/ha marketable yield; 41.0, 38.1 & 42.5 days to 50% flowering; 400.5, 385.4 & 419.8 pods/plant; 3.8, 3.6 & 3.6 seed/pod; and 13.2, 12.4 & 13.3 g of 1000 seed weight. In conclusion, newly developed CMS line VRRAD-12 would be very effective in harnessing heterotic potential, developing CMS-based F_1 hybrids suitable for winter season, and cost-effective commercial hybrid seed production in radish.

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46. DPPMR-09-1 (IC0642003; INGR21221), a pea (*Pisum sativum* subsp. *hortense*) germplasm resistant to powdery mildew disease

Akhilesh Sharma[*] and DK Banyal

Dept. of Vegetable Science & Floriculture, CSKHPKV, Palampur-176062, Himachal Pradesh, India

[*]*Email: assharmaakhil1@gmail.com*

Garden pea (*Pisum sativum* L; 2n=2x=14), belonging to family Leguminosae is an important cool season vegetable crop grown throughout the world for its tender green pods, seeds and foliage. Garden pea is quite palatable and excellent food for human consumption, which is eaten as fresh, canned, frozen and in dehydrated forms. Green peas are rich in health promoting phytonutrients, minerals, vitamins and antioxidants. Powdery mildew in garden pea caused by *Erysiphe pisi* DC. is a serious disease that can cause 25-50 per cent yield losses (Fondevilla and Rubiales 2012). Genetic resistance is quite effective as it is more cost-effective and environment friendly than fungicide applications. In this perspective, hybridization programme was initiated involving diverse parents to isolate powdery mildew resistant progenies with superior attributes during 2004. Line DPPMR-09-1 was isolated in BC1F5 generation from the cross '(VRPMR-10 × Sugar Giant) × VRPMR-10' during 2010 (Sharma *et al*. 2013). The line was further screened for powdery mildew reaction over the years in different locations and showed resistant reaction both under field (Table 1) and *in vitro* (Table 2) conditions. The line is a good resistant source for powdery mildew disease and can be utilized for developing powdery mildew resistant varieties.

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Table 1: Reaction of garden pea genotypes to Powdery mildew disease under field conditions

Genotypes	*2014*	*2017*	*2018-19*	*2019-20*	*2020-21*	*Overall*	
	Kukumseri		*Palampur*			*Infection type*	*Reaction type*
DPPM-65	3	3	3	3	3	3	MS
DPPM-74	3	3	3	3	3	3	MS
DPPMFWR-27	4	4	3	3	3	4	S
DPPMFWR-30	2	2	2	1	2	2	MR
DPPMR-09-1	1	1	1	1	1	1	R
Lincoln	4	4	4	4	4	4	S
Palam Priya	3	4	3	3	3	4	S
Azad P-1	4	4	4	4	4	4	S
Pb-89	3	2	2	2	2	3	MS

Where, R-Resistant; MR-Moderately resistant; MS-Moderately Susceptible; S-Susceptible

Table 2: Reaction of garden pea genotypes to Powdery mildew disease under in-vitro conditions

Genotypes	*Naturally ventilated polyhouse*				*Detached leaf assay*		*Overall*	
	Infection type			*Disease reaction*	*Infection type*	*Disease reaction*	*Infection type*	*Disease reaction*
	2018-19	*2019-20*	*2020-21*					
DPPMFWR-30	2	2	2	MR	2	MR	2	MR
DPPMR-09-1	1	1	1	R	1	R	1	R
Lincoln	4	4	4	S	4	S	4	S
Palam Priya	4	4	3	S	4	S	4	S
Azad P-1	4	4	4	S	4	S	4	S
Pb-89	2	2	2	MR	2	MR	2	MR

Where, R-Resistant; MR-Moderately resistant; MS-Moderately Susceptible; S-Susceptible

47. EC762384 (EC762384; INGR21222), a cowpea (*Vigna unguiculata*) germplasm with dense pubescence

Kuldeep Tripathi[1*], AK Parihar[2], Niranjana Murthy[3], Revanasidda[2], DP Wankhede[1], Neeta Singh[1], SK Deshpande[4], Gayachara[1] and Ashok Kumar[1]

[1] *ICAR-National Bureau of Plant Genetic Resources, Pusa Campus—110012, New Delhi, India*

[2] *ICAR-ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India*

[3] *University of Agricultural Sciences, Bengaluru-560065, Karnataka, India*

[4] *University of Agricultural Sciences, Dharwad-580005, Karnataka, India*

[*] *Email: kuldeep.tripathi@icar.gov.in*

Cowpea is a climate resilient multipurpose leguminous crop cultivated in tropics. Identification of trait specific germplasm is prerequisite to meet the present and future needs of cowpea breeding programme. After characterizing more than 5,000 accessions at the ICAR-NBPGR, New Delhi, a rare and unique cowpea accession, namely EC762384, was identified with very high pubescence. This unique accession had very prominent trichomes on the entire plant that was visible to the naked eye. Pubescence is measured by counting number of trichomes on leaf. Younger leaves exhibited higher pubescence (185.3±35.39 and 137.5±38.18, respectively) compared to mid-age (163.7±36.94 and 132.4±38.91, respectively) and older leaves (112.4±25.79 and 97.5±27.75, respectively). It is a unique and stable character consistently observed over the years (*kharif*, 2019-2020 and 2020-2021) and locations (NBPGR, Issapur farm, IIPR, Kanpur, UAS Dharwad and UAS Bengaluru). The identified accession can be used in the hybridization programme for various genetical studies and development of cowpea varieties with high pubescence. In addition, further studies on this genetic resource may provide insights in insect tolerance and defence mechanism through phenotyping under controlled conditions.

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48. IC241473 (IC241473; INGR21223), a lentil (*Lens culinaris*) germplasm with multiflowering and multipodding with fasciated stem.

Kuldeep Tripathi*[1], Gyan P Mishra[2], Gayacharan[1], HK Dikshit[2], Padmavati G Gore[1], Dileep Tripathi, Reena Mehra[3], Neeta Singh[1], Ashok Kumar[1], Ashutosh Sarker[3] and Kuldeep Singh[4]

[1]*ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India*

[2]*ICAR-Indian Agricultural Research Institute, New Delhi-110012, India*

[3]*International Center for Agricultural Research in the Dry Areas, Amalaha-466 113, Madhya Pradesh India*

[4]*International Crops Research Institute for the Semi-Arid Tropics, Patancheru-502324, Telangana, India*

**Email: kuldeep.tripathi@icar.gov.in*

The inflorescence in lentil is racemose, with usually one to three flowers per peduncle. Multi- flowering (MF) accessions can be identified with an expression of three or more flowers at one or multiple flowering nodes. Multi-flowering clusters have been documented for a few flowering nodes in *Pisum sativum* (up to five FPP), chickpea (upto nine FPP), lentil (up to seven FPP) (Mishra *et al*., 2020). The phenotypic characterization of entire lentil accessions (2,324) of Indian genebank, ICAR-NBPGR, New Delhi lead to the identification of a unique multi-flowering germplasm accession, IC241473, in cultivated lentil (*Lens culinaris* Medik.), forming up to 16 flowers per peduncle at multiple flowering node. Besides, this accession was also having a fasciation of the main stem. The multi-flowering expression was observed under field conditions at ICAR-NBPGR, New Delhi, India, consecutively during the winter seasons of year 2017-18, 2018-19, 2019-20 and was validated at NBPGR, New Delhi, NBPGR, RS, Ranchi and ICARDA, Amlaha (Madhya Pradesh) during 2020–2021. Unlike earlier reported fasciated accessions in legumes, this fasciated accession showed stable multi- flowering expression over the years and locations and was also found fertile with fully developed reproductive organs. This unique and novel germplasm accession can be utilized for genetic studies to identify the locus regulating the multi-flowering trait in lentil and its association with environmental factors.

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49. EC398949 (EC398949; INGR21224), a mung bean (*Vigna radiata*) germplasm with ability to maintain a cool canopy even under moisture stress

SK Raina[1]*, Jagadish Rane[2], Nikhil Raskar[2], AK Singh[2], V Govindasamy[3], Mahesh Kumar[2], SC Ekatpure[4], PS Minhas[2] and SM Sultan[1]

[1]*ICAR-NBPGR Regional Station, Srinagar-190019, Jammu & Kashmir, India*

[2]*ICAR-National Institute of Abiotic Stress Management, Pune-413115, Maharashtra, India*

[3]*ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*

[4]*Kerala Agricultural University, Thrissur-680656, Kerala, India*

**Email: Susheel.Raina@icar.gov.in*

Mungbean [*Vigna radiata* (L.) Wilczek] is an important warm season contributing to nutritional security of vegetarian population of South-east Asia. It is a rich source of carbohydrates, protein (27%), folate and iron (Noble *et al*., 2017). Drought stress during vegetative stage reduces plant size, root growth, leaf area, pod number and harvest index which ultimately lead to reduced grain yields (Raina *et al*., 2016). Canopy temperature is an important physiological trait associated with drought tolerance. Under limited soil moisture conditions, cooler canopy genotypes maintain relatively higher transpiration rates compared to genotypes with higher canopy temperature. Cooler canopy was positively associated with grain yield in rice, sugarcane, chickpeas, pearl millet and soybean under water deficit conditions (Bazzer and Purcell, 2020). Deviation of temperature of plant canopy from air temperature known as Canopy temperature depression (CTD) is an indicator of overall plant water status. Based on evaluation in field conditions in year 2014 and 2015, a landrace accession VC-6173-C (EC-0398949) imported from Thailand was found to have significantly (*p*<0.01) cooler canopy compared to the local check Vaibhav under drought conditions. The canopy temperature depression (CTD) of this accession under drought stress conditions varied from 5.18 - 8.0°C. Since CTD is an effective surrogate trait for screening drought tolerant genotypes, the identified accession has potential utility in breeding drought-tolerant mungbeans. VC-6173-C can also serve as a valuable genetic stock to decipher role of canopy temperature in contributing to drought tolerance in this fast growing legume crop.

The data on associated agro-morphological traits is given in Table 1.

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Table 1: Associated agro-morphological traits in VC-6173-C

Agro-morphological trait	*VC-6173-C*
Days to 50% flowering (days)	38
Plant height (cm)	27.25
Pods/plant	18.2
Pod length (cm)	5.72
Seeds/pod	5.47
Yield under drought(gm/plant)	1.8-4.55

50. EC414478 (INGR21225), a unique seed morphotype of pea (*Pisum sativum*) germplasm with extended funiculus.

Kuldeep Tripathi[1*], Padmavati G Gore[1], Ruchi Bansal[1], Gayacharan[1], Vinod Kumar[1], Neeta Singh[1], Chithra Devi Pandey[1], BB Sharma[2], SB Choudhary[3], AK Parihar[4] and, Ashok Kumar[1]

[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India*

[2]*ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*

[3]*ICAR-National Bureau of Plant Genetic Resources, Ranchi, Jharkhand- 834003, India*

[4]*ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India*

[*]*Email: kuldeep.tripathi@icar.gov.in*

A unique seed morphotype of pea (*Pisum sativum* L.) with extended funiculus was identified during mega germplasm characterization programme at ICAR-NBPGR, New Delhi undertaken during *Rabi* 2019–2020. Based on comparative study with selected accessions (seven) for seed morphology, imbibition and physiological behaviour, this accession was identified with very distinct and intact funiculus at maturity and higher rate of water uptake. It was a novel report of seed morphotype in pea with extended funiculus. All the accessions selected for imbibition behaviour study were of the same moisture content. Imbibition curves clearly indicated that water absorption and weight gain of the seeds were highest in atypical accession as compared to normal cultivars used in the study. All the accessions selected for this study were of the same moisture content (~10.5%). Imbibition curves indicated that the seeds' water absorption and weight gain were highest in EC0414478 accession compared to checks and the accessions used in the study. The highest water uptake was observed in seeds with completely intact funiculus compared with completely varnished hilum and completely removed funiculus. When the reading was taken on the 4th day, germination speed was also fast in the EC0414478 compared to all other accession used in the study. Funicle was remain intact with seed in 1-month old seedlings that indicate uniqueness of atypical accession in holding funicle as fixed character. In the present study, we observed the physiological response and growth of different pea accessions by measuring chlorophyll, RWC and biomass at the early vegetative stage. Our results indicated that EC0414478 showed the highest biomass along with the chlorophyll and RWC in response to drought. Drought tolerance in EC0414478 is attributed to maintaining high moisture content and chlorophyll to sustain active metabolism and growth under limited water conditions. A detailed investigation is required to assess the drought tolerance potential of identified accessions under field conditions. For trait stability, this unique accession was evaluated under multi-location trial at four locations *viz.* ICAR-NBPGR, Issapur Farm, NBPGR, RS, Ranchi, ICAR-IARI, New Delhi and ICAR-IIPR, Kanpur in *rabi* 2020-21 and this unique trait was expressed across the locations.

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51. IC251442 (INGR21226), a rice bean (*Vigna umbellata*) germplasm insensitive to photo-period and thermo-period

Aditya Pratap[1*], PS Basu, Sanjeev Gupta[1], Latha Madhavan[2] and NP Singh[1]

[1]*Indian Institute of Pulses Research, Kanpur, Uttar Pradesh-208024, India*

[2]*ICAR-NBPGR Regional Station, Thrissur-680656, Kerala, India*

[*]E-mail: adityapratapgarg@gmail.com

Mungbean and blackgram are the most popular pulse crops of the *Vigna* group and India is their largest producer, consumer and importer in the world (Pratap *et al*. 2012). Both these crops can be grown across a wide range of adverse soil and climatic conditions, and seasons (spring, summer, winter and rainy seasons) in different parts of the country as a sole, relay or intercrop (Pratap *et al*. 2013). Therefore, these crops also offer an opportunity for their horizontal as well as vertical expansion in large areas. However, the biggest hindrance in horizontal expansion of blackgram and mungbean in India is their photo- and thermo-sensitive behaviour which necessitates breeding of an array of genotypes for different agro-climatic zones of the country. Photo–thermo period sensitivity makes these crops vulnerable to photoperiod and temperature fluctuations, thereby affecting their yield potential drastically, especially when the same variety of these crops is grown across different seasons. Therefore, there is a need to develop cultivars which are largely insensitive to photo- and thermo-period and can be grown over large areas across seasons and agro-climatic zones. However, breeding for photo- and thermo-insensitivity requires robust donors for this trait without a possibility of linkage drag. Keeping this in view, this study aimed at identification of photo- and thermo-insensitive donors in the *Vigna* species so that these could be utilized in mungbean and blackgram improvement programmes through introgression breeding.

A set of 56 accessions of *Vigna* belonging to 13 species (eight accessions of *V. trilobata*, seven of *V. umbellata*, five each of *V. mungo* and *V. hainiana*, four each of *V. sylvestris* and *V. vexillata*, three each of *V. radiata*, *V. sublobata, V. dalzelliana* and *V. pilosa*, and one each of *V. glabrescens, V. trinernia* and *V. unguiculata*) and eight cultigens (four each of mungbean and blackgram) was grown under natural field conditions in the tropical climatic conditions of Kanpur (26°28′ N, 80°24′E) in two consecutive years (2011-13). All the individual plots of 56 accessions were observed every alternate day and the dates of important phenological events and characterization parameters as per NDUS guidelines (IIPR, 2010) were recorded. Viability of the fresh pollen samples in those accessions which survived through the rainy, summer and winter seasons was determined on the basis of observations on stainability of fresh pollen grains. On the basis of phenological events, physiological parameters as well as pollen viability studies, two accessions, viz., *V. umbellata* (IC251442) and *V. glabrescens* (IC251372) were identified to be largely photo- and thermo-period tolerant. Both these accessions behaved normally and were able to flower and set pods at extreme temperatures as high as 43.9°C and as low as 2.7°C. Pollen viability studies were also conducted which recorded viable pollen (>75% at 2.7°C and >85% at 41.9°C) and normal pollen tube growth at both the extremes of temperature. The identified *V. glabrescens* accession has long, constricted pods and dark green, mottled seeds while *V. umbellata* has smooth, curved pods and shining, oval, large seeds. Both these accessions have several other desirable characters besides photo- and thermo-period tolerance, such as long and bold pods, profuse branching and resistance to all major diseases of *Vigna* species, and therefore these could be potential donors for the above traits in *Vigna* through introgression breeding. Earlier *V. radiata* X *V. umbellata* and *V. mungo* X *V. umbellata* crosses have been successfully generated to transfer resistance to MYMV and other desirable traits into mungbean (Singh et al. 2003; Chaisen et al. 2013) and urdbean (Pal et al., 2005). Both these accessions are currently being utilized in developing photo–thermo tolerant genotypes in cultivated *Vigna* species.

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52. IPF 2014-13 (IC0640782; INGR21227), a pea (*Pisum sativum*) germplasm resistant to rust and powdery mildew

AK Parihar[1*], GP Dixit[1], Arpita Das[2], Deepa Saxena[3], Deepak Singh[4], KD Singha[5], KPS Kushwaha[6], Ramesh Chand[7], RS Bal[8], S Chandra[9], Sanjeev Gupta[1], RK Mishra[1] and Anil K Singh[1]

[1]*ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India*

[2]*Bidhan Chandra Krishi Viswavidyalaya, Nadia-741252, West Bengal, India*

[3]*Chandra Shekhar Azad University of Agriculture &Technology, Kanpur-208002, Uttar Pradesh, India*

[4]*ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*

[5]*Assam Agricultural University, Shillongani-782002, Assam, India*

[6]*G.B. Pant University of Agriculture & Technology, Pantnagar-263145, Uttarakhand, India*

[7]*Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India*

[8]*Punjab Agricultural University, Gurdaspur-143521, Ludhiana, Punjab, India*

[9]*Narendra Deva University of Agriculture & Technology, Faizabad -224229, Uttar Pradesh, India*

[*]*Email: ashoka.parihar@gmail.com*

Field pea is considered as an important winter season pulse crop of India and is being cultivated mainly in states of Uttar Pradesh, Madhya Pradesh, Bihar, Assam and Odisha (Anonymous 2021). Being a worthy source of quality protein, starch, minerals and vitamins, it is an important component in many food industries (Parihar *et al*. 2016). Considering the importance of this legume, significant contributions have been made in the recent past toward genetic improvement and cultivar development in our country. Unfortunately, biotic stresses particularly rust and powdery mildew have been the major constriction in field pea cultivation and both diseases can cause noteworthy yield loss under congenial condition (Parihar *et al*. 2020a). The *Uromyces viciae-fabae* (Pers de Bary) is the causal organism for pea rust in tropical and subtropical regions *viz*. India and China (Singh *et al*., 2015; Das *et al*. 2019). This pathogen mainly appears on aerial parts during the reproductive stage of the crop which led towards reduction of photosynthetic area and subsequent yield losses ranges from 57– 100% (Upadhyay and Singh, 1994). The disease occurrence at early stages could result in total failure of the crop. Hence, management of rust is a crucial attempt for sustainable field pea production. However, chemical control is not holistic move towards controlling pea rust owing to intricacy in pathogen manners. This airborne pathogen has wider host range and lack of durability in resistance with quantitative nature of inheritance these factors complicating disease management (Barilli *et al*., 2009a). Therefore, exploitation of host pathogen resistance is the most modest approach of rust control (Rubiales *et al*., 2013). However, so far in field pea, only incomplete resistance is reported against *U. viciae-fabae* (Xue and Warkentin, 2002; Chand *et al*., 2006) and *U. Pisi* (Barilli *et al*., 2009c). Thus, recognition of stable and durable resistance genotypes of field pea against rust, followed by utilization of these genotypes as donors in a resistance breeding program would be a best strategy for disease management in a trustworthy way. During recent past sincere efforts have been made and numbers of genotypes have been developed with good level of resistance to rust. As mentioned above resistance against this pathogen is partial and influenced by environmental factors. Therefore, the magnitude of environmental and genotype-by-environment interaction was assessed to understand the dynamism of resistance and identification of durable resistant genotypes through multi-location and multi- year evaluation for rust. A panel of 23 promising field pea genotypes was assessed under inoculated conditions for rust disease for two consecutive years at six locations in India. Genotype namely IPF-2014-16 and IPF- 2014-13 identified as "ideal" genotypes, which can be recommended for release and exploited in a resistance breeding program for the region confronting field pea rust.

The genotype IPF 2014-13 is tall type (177-211 cm) and leafy type. It has white colour flowers, white & round seed and yellow cotyledon. It flowered and matured in 65-70 days and 120-122 days respectively with 20.0-22.0 gm 100- seed weight. The average yield of the genotype is more than 2.0t/ha. This genotype also has powdery mildew resistance and good yield potential (20-22 qt/ha). It can be grown on different type of soil; however, a well drained soil is essential to achieve good yield potential of this genotype. The field should be well prepared by two to three ploughings. The seed treatment should be done with fungicide like Thirum/ Captan/Carbendazim @ 3.0 g/kg seed + rhizobium culture @ 1 packet/10 kg + Trichoderma @ 4.0 g/kg at 4-5 days before sowing. The optimum sowing time is October 15-Novemebr 15 with 75-80 kg/ha seed rate. If available, about 20 tonnes of organic manures should be incorporated in the soil at the time of land preparation. This should be supplemented with 20-30kg/ha nitrogen as starter dose in basal dressing forms at the time of sowing. The phosphorus and potassium should be applied as a basal dose based on soil test. If soil is deficient in these nutrients, apply 40kg/ha P2O5 with 20-30 kg K2O and 20kg Sulphur per hectare. For Zinc deficiency 0.5 per cent Zinc sulphate +0.25 per cent lime should be applied after the appearance of deficiency symptoms. First irrigation should be given at 45 days and second, if needed, at pod filling stage. This genotype has good worth as a donor in future fieldpea breeding programme towards development of fieldpea varieties with good level of resistance against rust and in other basic studies.

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53. DRMR 2018-37 (IC0640707; INGR21228), an Indian mustard (*Brassica juncea*) germplasm with white rust resistance

HS Meena[*], PD Meena, VV Singh, KH Singh, Arun Kumar, BL Meena, HK Sharma, AK Thakur, MD Meena and PK Rai

ICAR-Directorate of Rapeseed Mustard Research, Bharatpur-321021, Rajasthan, India

[*]*Email: singh_hari2006@yahoo.co.in*

Indian mustard (*B. juncea* L.) is an important oilseed crop of the Indian subcontinent and contributes more than 80% of the total rapeseed-mustard production of the country. It has significant role in edible oil economy of India and perform amazing role in human and animal diet. It is cultivated under a wide range of cropping systems and principally grown as a winter (*Rabi* season) crop generally on conserved moisture or through pre-sowing irrigation. Rapeseed-mustard crops affected by several diseases at different growth stages cause high yield losses. Hence, a wide gap exists amongst the potential and realized yield at the farmers' field. White rust is a major disease of *Brassica*, prevalent worldwide and causes high yield reductions of Indian mustard under severe conditions. The conventional management of using chemical pesticides is very difficult in mustard crop and a problem of reduced efficacy of pesticide arises due to development of resistance by pathogen. Thus, development of disease resistant varieties is the best approach to minimize the yield losses. Therefore, it is highly needed to have good sources of white rust resistance that can be exploited for development high-yielding resistant varieties.

The genotype DRMR 2018-37 was derived from a cross between DRMR 2019 x NRCDR 2 at ICAR-DRMR, Bharatpur. This genotype was isolated as a pure line through pedigree selection and found promising for white rust resistance. It was screened under AICRP-RM plant pathological trials during 2018-19 to 2020-21 at 6-12 locations under natural and artificial conditions. Further, it was also screened at Bharatpur during main *Rabi* season (2018-19 & 2019-20) and during off-season *Kharif* (2018 & 2019) at IARI Regional station, Wellington (Hot spot for white rust), Tamilnadu. White rust resistance of the proposed genotype was also confirmed through molecular markers (At541560 and At2g36360). Pooled summary over the years and locations indicates that proposed genotype DRMR 2018-37 has least WR disease severity (%), zero stag head (%) and revealed immune reaction at hot spot as compared to resistant and susceptible checks (Table 1). The proposed genetic stock DRMR 2018-37 was found to possess AcB1-A5.1 WR resistant locus. Therefore, genotype DRMR 2018-37 revealed high resistance against white rust at both molecular and phenotypic level and it can be utilized in breeding programmes for development of high-yielding white rust resistant varieties. Genotype DRMR 2018-37 will be a very good addition to existing gene pool in germplasm repository for white rust resistance. Hence, this promising line needs protection through germplasm registration.

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Table 1: Pooled summary of reaction over the years on DRMR 2018-37 and checks to white rust under natural & artificial conditions in AICRP-RM pathological trials during 2018-19 to 2020-21 and at Wellington during *Kharif* 2018 & 2019

Entries	*WR Severity (%)*		*Stag head (%)*		*WR (Scale: 0-9)*
	Natural conditions (12)	*Artificial conditions (6)*	*Natural conditions (7)*	*Artificial conditions (3)*	*Wellington (Hot spot for WR)*
DRMR 2018-37	5.1	8.1	0.0	0.0	0
BIOYSR (RC)	19.2	11.8	7.1	19.9	3
Rohini (SC)	29.8	35.1	18.3	20.8	9

*Values in parenthesis representing the number of locations

54. PBS 29079B (IC0642010; INGR21229), groundnut (*Arachis hypogaea* subsp. *hypogeae*) germplasm with high hundred kernel weight (85.36 g)

Kona Praveen[1*], Gangadhara K[2], Ajay BC[1], Narendra Kumar[1], SK Bera[1], AL Rathnakumar[3], Radhakrishnan T[1], Kirti Rani[1], Dagla MC[4], Hariprasanna K[5], Manivel P[6], Mathur RK[7], Chuni Lal[8] and HK Gor[1]
[1]*ICAR-Directorate of Groundnut Research, Junagadh-362001, Gujarat, India*
[2]*ICAR- CTCRI Research Station, Kandukur-534456, Andhra Pradesh, India*
[3]*ICAR-Indian Institute of Oilseeds Research, Hyderabad-500030, Telangana, India*
[4]*ICAR-Indian Institute of Maize Research, Ludhiana -141004, Punjab, India*
[5]*Centre for Rabi Sorghum, ICAR-IIMR, Solapur-413006, Maharashtra, India*
[6]*CTRI, Research Station, Vedasandur-624710, Tamil Nadu, India*
[7] *ICAR-Indian Institute of Oil Palm Research, Pedavegi-53450, Andhra Pradesh, India*
[8]*ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India*
[*]*Email: kona.praveen@icar.gov.in*

Kernel with good quality attributes determines the export potential of groundnut. Large/bold seed with high hundred kernel weight (>55 g) coupled with some quality attributes is one of the major prerequisite for exploiting any groundnut variety for confection purpose (Nigam *et al.*, 1989; Dwivedi and Nigam, 1995). At ICAR-Directorate of Groundnut Research, Junagadh a novel advanced breeding line of groundnut, PBS 29079B was developed from the cross Somnath x J 11 using pedigree method.

It is a Virginia runner with decumbent growth habit and semi spreading type. It bears alternate flowering with compound inflorescence. Leaves are dark green with ovate shape and less hairy. Pods are medium reticulated with shallow constriction and slightly beaked and tan seed colour. It recorded significant difference for seed characters like hundred kernel weight (HKW), kernel length (KL), kernel width (KW) when compared with checks, RG 599-3, Mallika and Girnar 2 over 2018 to 2020 year seasons (Table 1). At

Bikaner it recorded large mean seed size (HKW -121.9 gm; KL- 2.21 cm and KW- 1.03 cm) with moderate oil (48%) and high protein 30.39%) in two seasons. The overall mean for seed size in four seasons is 85.36 g of HKW, 1.84 cm of KL and 0.88 cm of KW.

In addition to seed size this line contains good amount of protein (30%) and moderate oil (45-48%). It is highly suitable for confection purpose and gives good yield under sandy soils especially in Rajasthan. General package of practices for large seed groundnut crop production are applicable to this advanced breeding line production.

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Table 1: Comparison of PBS 29079B genotype with best check over seasons for different traits

	HKW	*KL*	*KW*			*HKW*	*KL*	*KW*	*% of superiority over check*
Kharif, 2018									
PBS29079B	79.64	1.98	0.99	Best Check	Mallika	54.36	1.35	0.8	31.74
Summer, 2019									
PBS29079B	71.27	1.81	0.93	Best Check	GJGHPS1	51.33	1.61	0.8	27.97
Kharif, 2019									
PBS29079B									
Junagadh	73.2	1.71	0.74	Best Check	Mallika	49.04	1.69	0.69	33.00
Bikaner	121.97	2.26	1.03		RG559-3	87.44	1.92	0.94	28.31
Summer, 2020									
PBS29079B	72.69	1.92	1.12	Best Check	GJGHPS1	54.35	1.6	0.94	25.23
Kharif,2020									
PBS29079B									
Junagadh	75.33	1.7	0.8	Best Check	Mallika	52.33	1.6	0.73	30.53
Bikaner	121.97	2.17	1.06		RG559-3	88.33	1.98	0.89	27.58

55. M-571 (IC0642011; INGR21230), a dwarf pistillate line of castor (*Ricinus communis)* condensed internodes, convergent branching, cup shaped leaves and loose spike showing resistant to *fusarium* wilt and leafhopper

C Lavanya*, Santhalakshmi PM and Duraimurugan P
ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-500030, Telangana, India
**Email: c.lavanya@icar.gov.in*

M-571 is an S type pistillate line developed through mutation breeding using gamma ray irradiation of VP-1 seed followed by pedigree method of selection for wilt resistant pistillate line in wilt sick plot. Morphological characters were recorded as red stem color, triple bloom, condensed internodes, 10-15 nodes to primary, cup shaped leaves, convergent branching, conical, long (45-50 cm) spike with loose capsules, pistillate with ISF, spiny capsules (Lavanya and Gopinath, 2008). It is distinct to other registered pistillate lines like IPC-15 (INGR 19017) with papaya leaf type and DPC-16 (INGR 140003) with purple stem and zero bloom.

M-571 is also a good combiner for number of effective spikes per plant (Lavanya and Chandramohan, 2003, Lavanya *et al*, 2006) and used for development of several high yielding experimental castor hybrids.Castor wilt (*Fusarium oxysporum* f. sp. *ricini* Nanda and Prasad) is the most important disease of castor resulting in 30-100% loss of plant population in wilt endemic areas where mono-cropping is followed without crop rotation. Screening of M-571 consecutively for three years (2013-14, 2014-15 and 2018-19) at IIOR-Hyderabad in wilt sick plot using standard screening procedures used in AICRP on castor indicated <10% to<20% wilt incidence (Santhalakshmi *et al*., 2016).

M-571 also showed resistant reaction to leafhopper (hopper burn grade of 0 to 1 on 0–4 scale, while susceptible check DPC-9 recorded maximum hopper burn grade of 4consecutively for two years (2013-14 and 2014-15) at ICAR-IIOR, Hyderabad. Screening at three hot spot locations-IIOR, Hyderabad, Palem (Telangana) and Yethapur (Tamil Nadu) during 2015-16 revealed resistant reaction of M-571 with hopper burn grade of 1 on 0–4 scale and low infestation of leafhopper (7.4 to 35.3 leafhoppers/ 3 leaves/plant) in all three locations. Susceptible checks (DCS-107, DCH-177 and DPC-9) recorded susceptible reaction of 3-4 hopper burn grade and high infestation of leafhopper (40.2 to84.9 leafhoppers/3 leaves/plant) (Source: DOR/IIOR Annual Report, 2013-14 to 2015- 16).

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56. IC0610001-60/Pune 2 (INGR21231), an oil palm (*Elaeis guineensis*) germplasm with Short stature (28.9 cm), high FFB (243.91 kg) and more number of bunches

Bhagya HP[1*], RK Mathur[1], G Ravichandran[1], P Murugesan[2], K Sunil Kumar[2], D Ramajayam[3], Anitha P[1], B Kalyana Babu[1], G Somasundaram[4] and SN Rahana[4]

[1]*ICAR-Indian Institute of Oil Palm Research, Pedavegi-534450, Andhra Pradesh, India*

[2]*ICAR-CTCRI, Thiruvananthapuram-695017, Kerala, India*

[3]*ICAR-NRC, Banana, Thiruchirapalli-620 102, Tamil Nadu, India*

[4]*ICAR-IIOPR, Regional Station, Palode-695562, Kerala, India*

[*]*Email: Bhagya.HP@icar.gov.in*

Oil palm is very important crop for fulfils the edible oil requirement of our country. As compared to other annual oil yielding crop this is giving more oil yield (5-6 t/ha). Oil palm breeding programme mainly depending male (sterile *Pisifera*) and female parent (fertile *Dura*) for hybrid seed production. Commercial material for farmer cultivation is *Tenera*, this can be obtained by crossing of fertile *Dura* and sterile *Pisifera*.

Harvesting is a major problem in oil palm plantation due to more height of the palm, upto 15 years we can easily harvest by using chisel and aluminium pole. After 20-year plantation by using poles we can harvest but risk factors are more due to unbalancing of pole and chances of falling bunches on person and identification of right stage of ripening *etc.* If we develop low height increment hybrids, life of plantation can be extended for few years instead of uprooting plantation. For developing low increment *Tenera* hybrid, we need low height increment *Dura* genotype and dwarf *pisifera*. But dwarf *pisifera* is very rare, so we have to select elite dura with low height increment will lead to development of dwarf hybrids. By this we can improve the yield and hasten the life of plantation and harvesting can be made easy. More number of bunches and high yield genotypes are ideal for developing dwarf hybrids for commercial production. This identified genotype is belonging to base collected germplasm from ICAR-IIOPR and it is 28.9 cm annual height increment with high FFB yield of 243.91 kg and total dry matter of 364.56 kg and more number of bunches (14) (Table 1). So this dura will serve as base genetic material for development of mother dura blocks for commercial production of *Tenera* hybrid in oil palm breeding programme.

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Table 1: Trait description accession: IC061001-60 (Pune-2)

Traits	*2015-16*	*2016-17*	*2018-19*	*Average*
Annual height increment (cm)	28.28	28.06	30.37	28.90
Number of bunches	14	14	11	13
FFB yield (Kg/palm/year)	267	267.48	197.26	243.91
Average bunch weight (kg)	19.07	19.11	17.93	18.76
Total Dry matter (kg)	372.88	357.37	363.43	364.56

57. IC0610001-59/Pune 1 (INGR21232), an oil palm (*Elaeis guineensis*) germplasm with low annual height increment (25.25cm) and high FFB (211.33 kg)

Bhagya HP[1*], RK Mathur[1], G Ravichandran[1], P Murugesan[2], K Sunil Kumar[2], D Ramajayam[3], Anitha P[1], B Kalyana Babu[1], G Somasundaram[4] and SN Rahana[4]

[1]*ICAR-Indian Institute of Oil Palm Research, Pedavegi-534450, Andhra Pradesh, India*

[2]*ICAR-CTCRI, Thiruvananthapuram-695017, Kerala, India*

[3]*ICAR-NRC, Banana, Thiruchirapalli-620 102, Tamil Nadu, India*

[4]*ICAR-IIOPR, Regional Station, Palode-695562, Kerala, India*

[*]*Email: Bhagya.HP@icar.gov.in*

Oil palm is very important crop for fulfils the edible oil requirement of our country. As compared to other annual oil yielding crop this is giving more oil yield (5-6 t/ha). Commercial material for farmer cultivation is *Tenera* due to high mesocarp and high oil content. Now a day's demand for the edible oil is increasing and it's very difficult to fulfil by any other oil yielding crops, but there is a chance to reduce the import of oil from other country by increasing the oil palm yield by using elite germplasm material. If yield of the oil palm is increasing, definitely oil yield also will increase. For this we need high yielding *Tenera* genotypes and also low height increment genotypes due to harvesting problem after 15 to 20 year of plantation.

Fertile *Dura* (Female parent) and Sterile *Pisifera* (Male parent) are very important for commercial production of *Tenera* seedlings for commercial plantation. Sterile *Pisifera* population is scarce and we need to develop and maintain in field genebank for pollen collection. For getting *Pisifera* population also need to go for *Tenera* selfing, by selfed bunches, 1:2:1 ratio *Dura, Tenera* and *Pisifera* population will obtain. In this, sterile *Pisifera* can be identified and these can be utilized in breeding programme for commercial Tenera production. Tenera X Pisifera crossing can be made to obtain 1:1 ratio of *Tenera* and *Pisifera* population and by this also we can select sterile *Pisifera* for utilization in breeding programme as male parent. These types of elite *Tenera* genotypes can be directly used in multiplication by tissue culture for getting true to type plants once the tissue culture protocol standardized. This identified genetic stock is having annual height increment of 25.25 cm with high FFB yield of 211.33 kg per palm per year (30.22 t/ha) and high average bunch weight of 23.48 kg/palm/year (Table 1). So elite *Tenera* genotypes can be used in T X T, T X P for production of *Pisifera* and direct multiplication by vegetative method (Tissue culture) for production of uniform saplings.

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Bhagya HP and AnithaP (2021) Identification of elite genotype in germplasm block. ICAR-IIOPR News. 25(2): 3

Table 1: Trait description Accession: IC061001-59 (Pune-2)

Traits	*2015-16*	*2016-17*	*2018-19*	*Average*
Annual height increment (cm)	25.17	25.16	25.20	25.29
Number of bunches	11	11	10.33	9
FFB yield (Kg/palm/year)	274	274.89	253.40	211.33
Average bunch weight (Kg)	24.90	24.99	24.45	23.48
Total Dry matter (kg)	346.46	306.83	319.61	305.55

58. IC0610051-71/TG 9 (IC0610051; INGR21233), an oil palm (*Elaeis guineensis*) germplasm with high yield (261.71kg), more number of bunches (16.66)

Bhagya HP[1*], RK Mathur[1], G Ravichandran[1], P Murugesan[2], K Sunil Kumar[2], D Ramajayam[3], Anitha P[1], B Kalyana Babu[1], G Somasundaram[4] and SN Rahana[4]

[1]*ICAR-Indian Institute of Oil Palm Research, Pedavegi-534450, Andhra Pradesh, India*

[2]*ICAR-CTCRI, Thiruvananthapuram-695017, Kerala, India*

[3]*ICAR-NRC, Banana, Thiruchirapalli-620 102, Tamil Nadu, India*

[4]*ICAR-IIOPR, Regional Station, Palode-695562, Kerala, India*

[*]*Email: Bhagya.HP@icar.gov.in*

Oil palm (*Elaeis guineensis* Jacq.) is monocious and highly cross pollinated crop and in this crop fruit forms are very important and it is having mainly 3 fruit forms *viz. Dura*, *Tenera* and *Pisifera*. *Dura* is mainly used as female parent and pisifera is used as male parent for development of thin shell *Tenera* hybrid for more oil yield and *Tenera* is commercially cultivated variety throughout the world. Dura is mainly used as mother palm in production of hybrid in oil palm breeding programme. In germplasm block we have evaluated and found high yielding dura with37.42 tonnes/ha Fresh Fruit Bunches (FFB) yielding genotype with more number of bunches (16.66) and oil to bunch ratio 20.78 %. As per minimum standards of oil palm mother palm selection these all traits were high and it is elite genotype for development of mother seed garden for improving yield and development of high yielding hybrids. For selection of dura unknown sources should be 18 % oil to bunch ratio and FFB yield should be 220 kg/palm/year (Table 1).

This dura genotype is also having other morphological traits like high TDM (305.55 kg) and average bunch weight (15.73 kg) with bunch index was 0.43. This base material for production of mother dura blocks for production of dwarf *Tenera* hybrids with high FFB yield for commercial production to fulfil the requirement of planting material supply to the farmers field and it will help in fulfil the requirement of edible oil in our country and can reduce the import of oil from other countries. This dwarf trait can be utilized in further breeding programme. This genotype already utililizing in breeding programme for development of dura mother palms.

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Table 1: Trait Description Accession: IC0610051-71(Dura)

Trait	*2015-16*	*2016-17*	*2018-2019*	*Average*
Number of bunches	16	18	16	16.66
FFB yield (kg/palm/year)	238.47	269.48	277.18	261.71
Average Bunch Weight (Kg/palm)	14.90	14.97	17.32	15.73
Bunch Index	0.48	0.45	0.37	0.43
Oil to Bunch ratio	21.73	19.84	20.79	20.78

59. Jor Lab SM-2 (IC0642007; INGR21234), a taro (*Homaelomena aromatica*) germplasm with high rhizome essential oil yield (1.20%dwb) basis

Mohan Lal

CSIR-North East Institute of Science and Technology, Jorhat-785006, Assam, India

*Email: drmohanlal80@gmail.com

Homalomena aromatica Schott., commonly known as 'Sugandhmantri' due to its aromatic nature belongs to the family Araceae (Roy *et al*., 2019). Essential oil of *H. aromatica* has several applications in perfumery, flavour, and pharmaceutical industries. The essential oil of aromatic rhizomatous plants possesses numerous biological activities like larvicidal, nematicidal, anti- inflammatory, antimicrobial, antidepressant, antioxidant, anti-helmintic, etc (Lal *et al*., 2021). Similarly, the rhizome of *H. aromatica* was reported to possess various medicinal properties like anti-inflammatory, analgesic, antiseptic, antidepressant, skin infections, joint pain, sedative, etc (Policegoudra *et al*., 2012; Kehie *et al*., 2017).

The aim and objective of the present study was to identify high and stable essential oil-rich genotype from collected germplasm of *H. aromatica*. During the year 2014, a total of 49 germplasm were collected from different parts of NE India. All the collected germplasm was planted in the year 2015 with three replications in CRBD at the experimental farm of CSIR- NEIST, Jorhat. The same genotypes were again planted during 2017 with the same design. All the agronomical and essential oil data were recorded and analyzed. Based on two crops season (2015-16 and 2017-18) of the selection trial, a new essential oil 1.20% rich strain (RRLJ HA-18) with a high dry rhizome yield of 1454.53 kg/ha/crop season was selected. The identified accession was later renamed as Jor Lab SM-2. The stability of the identified germplasm (RRLJ HA-18) was confirmed by testing in multilocation trial in four different locations for two years i.e., one crop season (2019-2020) along with two check varieties. The stability analysis for the economic character like dry rhizome yield, essential oil% and total essential oil yield/ha showed the high mean value and were stable in all the four locations with β_i=1.05, β_i=1.09, and β_i=1.14 respectively (Table 1a, 1b). The GC/MS profiling of the essential oil extracted from the rhizome of *H. aromatica* revealed linalool (66.27%) major compounds followed by α-cadinol, τ- muurolol, linalool oxide, neointermedeol, and 3-carene as other compounds. The stable germplasm Jor Lab

Table 1(a): Estimation of mean and stability parameters of plant height, number of leaf per plant, leaf width, leaf length, length of rhizome and fresh rhizome genotype (Jor Lab SM-2) of *H. aromatica* in MLT trials

Genotypes	*Plant height (cm)*			*Numberofleaf/plant*			*Leaf width (cm)*			*Leaf length (cm)*			*Length of rhizome (cm)*			*Fresh rhizomeweight/plant (gm)*		
	μ mean	*βi*	*σ^2di*	*μ mean*	*βi*	*σ^2di*	*μ mean*	*βi*	*σ^2di*	*μ mean*	*βi*	*σ^2di*	*μ mean*	*β_i*	*$\sigma^{2}di$*	*μ mean*	*β_i*	*σ^2di*
Jor Lab SM-2	75.41	0.95	-0.47	16.84	1.26***	0.40	20.78	1.05	0.19	28.11	0.79**	0.16	32.38	1.93**	0.18	183.95	0.94	2.26***
Mizoramlocal	72.92	1.01***	0.35***	13.50	1.06***	0.41	20.99	0.65*	-0.13	25.52	1.07***	0.55***	22.95	0.47*	0.61**	149.98	1.08***	2.16***
Tura local	70.81	1.04***	0.36***	12.29	0.68***	0.42	19.99	1.30***	-0.23	24.76	1.14***	0.14	22.41	0.60***	1.06***	125.59	1.08***	1.99***
Population mean	73.05			14.03			20.59			26.13			25.91			153.17		

*Significant at P<0.10, **Significant at P<0.05, *** Significant at P<0.01

Table 1(b): Estimation of mean and stability parameters of dry rhizome recovery, rhizome diameter, fresh rhizome yield, dry rhizome yield, essential oil yield% and total essential oil yield/ha of genotype (Jor Lab SM-2) of *H. aromatica* in MLT trials

Genotypes	*Dry rhizomerecovery (%)*			*Rhizome diameter (cm)*			*Fresh rhizomeyield (kg/ha)*			*Dry rhizome yield (kg/ha)*			*Essential oilyield (%)*			*Total essential oilyield/ha on dry weight basis (kg/ha)*		
	μ mean	*βi*	*σ^2d i*	*μ mean*	*βi*	*σ^2d i*	*μ mean*	*βi*	*σ^2di*	*μ mean*	*βi*	*σ^2di*	*μ mean*	*β_i*	*σ^2di*	*μ mean*	*β_i*	*σ^2di*
Jor Lab SM-2	18.89	0.90	0.64***	5.12	0.58**	0.01	7725.69	0.97	12157.06	1458.86	1.05	85.86	1.20	1.09	0.00	1753.98	1.14	47.07
Mizoram local	17.24	0.93***	0.55***	4.26	1.22***	0.00	6299.06	0.93**	10634.34	1086.83	1.65**	60.95***	0.55	1.35*	0.00	598.95	0.42	525.51*
Turalocal	16.90	1.17***	0.42***	4.12	1.20***	0.02***	5274.57	1.17**	13322.19***	890.64	0.91*	257.60	0.51	1.06***	0.00	452. 69	0.88	646.35***
Population mean	17.68			4.50			6433.11			1145.44			0.75			935.20		

*Significant at P<0.10, **Significant at P<0.05, *** Significant at P<0.01

SM-2 was found to be more than twice superior compared to the check varieties in terms of essential oil yield. All the studied traits of Jor Lab SM-2 were significantly and distinctly higher than the check varieties. As per our knowledge, no essential oil-rich variant of *H. aromatica* is reported so far; therefore, this is the first report on the identification of a superior and stable line of *H. aromatica*.

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60. DBM-4 (IC0642012; INGR21235), a brahmi (*Bacopa monnieri*) germplasm with high Bacoside-A content and API quality parameters

Parmeshwar Lal Saran*, Hiteksha I Damor, Manish Kumar Suthar and Kuldeep singh A. Kalariya

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

*Email: plsdehradun@gmail.com

Jal brahmi (*Bacopa monnieri* L. Pannell) is a creeping, branched succulent perennial herb belonging to family *Plantaginaceae* used in indigenous system of medicine as a nerve tonic and for epilepsy and insanity. Owing to its inherent potential of enhancing memory and vitality, this miracle plant is gaining attention globally for its commercial cultivation. 'DBM-4' is diverse in morphological, qualitative and molecular characters (DMAPR Annual report, 2020). Distinct character like maximum pedicel length (2.80-2.97 cm) was observed as morphological marker as compared to check (Cim Jagriti); Saran *et al*., 2022; Saran and Damor, 2021; DMAPR Annual report 2020). It also contains maximum Bacoside-A (2.64-3.65 % W/W) and Total Bacosides (5.27% w/w) content in dry herbage. Maximum bacoside-A content in DBM-4 (3.65% W/W) and minimum was recorded in CIM Jagriti (1.82% W/W) on dry weight basis (Saran *et al*., 2022; Saran and Damor, 2021; DMAPR Annual report 2020). DBM-4 with the distinct morphological and chemical traits was developed through selection method and conservation carried out at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The herb is the small creeping type prostate with the numerous succulents, glabrous branches. The leaves of herb are oblanceolate, relatively thick, succulent and arranged oppositely on the stem/stolon. Small, actinomorphic flowers are borne in leaf axils, which are whitish purple to medium purple in colour with maximum of flower-stalk length. Further, morphological variation also observed for stolon colour, stolon length and stolon thickness in different accessions of Jal brahmi. Other important quality parameters as per Ayurvedic Pharmacopoeia of India (API) like minimum loss of drying (11.13%W/W), total ash (8.38%W/W), acid soluble ash (0.20%W/W) were higher in DBM-4. At the same time maximum alcohol soluble extractive (14.75% W/W) and water-soluble extractive (28.57% W/W) was observed (Saran *et al.,* 2022).

Jal brahmi grow well in low lying area having poorly drained soils under subtropical area, especially in rice growing regions. It is cultivated through vegetative propagation using soft herbaceous cuttings (Saran and Patel, 2019). In north India, Jal brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperature (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. For planting one-hectare area on an average 3-3.5 quintals herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes are transplanted directly in the field at spacing of 10×10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On an average 130-145 q ha^{-1} dry herbage can be obtained from a multiple harvest (Saran, 2020). The accession DBM-4 was found suitable for commercial cultivation in low-lying rice-wheat cultivation systems and farmers can get approximately Rs. 4.62 lakhs ha^{-1} year^{-1} net return.

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61. DBM-2 (IC0642013; INGR21236), a brahmi (*Bacopa monnieri*) germplasm with Curved/Twisty top leaf of stolon and rich in bacopaside I

Parmeshwar Lal Saran[1*], Hiteksha I Damor[1], Susheel Singh[2], Kuldeepsingh A Kalariya[1] and Manish Kumar Suthar[1]

[1]*ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India*

[2]*Food Quality Testing Laboratory, N.M. College of Agricultural, NAU, Navsari, Gujarat, India*

[*]*Email: plsdehradun@gmail.com*

In India, brahmi has been largely used as a rejuvenating herb for the last 3000 years. In Ayurvedic systems, brahmi is applicable for promoting mental strength (Balya), longevity (Ayushya), life energy (Jivaniya) and Sleep (neendrajan). A distinct morphological character "curved leaf at top of the stolen" and "maximum size or area of basal leaf" identified in DBM-2 (1.653 cm^2) which is minimum in CIM Jagriti (0.736 cm^2) as a morphological marker (Saran et al., 2021; Saran and Damor, 2021). At the same time, the germplasm "DBM-2" reported maximum bacopaside I (1.50% w/w) from total herbage as compared CIM Jagriti (0.65% w/w) using HPLC analysis. DBM-2 with the distinct morphological and chemical traits was developed through selection method and conservation of distinct germplasm at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The Jal brahmi herb is the small creeping type prostate with the numerous succulents, glabrous branches. Different morphological parameters including solitary axillary flowers (five petals) with sessile, succulent and thick leaves grown appositively on stem having different leaf size (Maximum basal leaf area), leaf shape (Oblanceolate), leaf apex (Obtuse) and leaf base (Acuminate type), leaf colour (medium dark green) and flower colour (Purple colour). Further, morphological variation also observed for stolon colour, stolon length, stolon thickness and flower pedicel length in different accessions of Jal brahmi.

Jal brahmi grow well in low lying area having poorly drained soils under subtropical area, especially in rice growing regions. It is cultivated through vegetative propagation using soft herbaceous cuttings (Saran and Patel, 2019). It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level (Saran *et al*., 2022). In north India, Jal brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperature (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. For planting one-hectare area on an average 3-3.5 quintals herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes are transplanted directly in the field at spacing of 10×10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On an average 130-145 q ha^{-1} dry herbage can be obtained from a multiple harvest (Saran, 2020).

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62. DBM-5 (IC0642014; INGR21237), a brahmi (*Bacopa monnieri*) germplasm with Light purple flowers and high Jujubogenin (1.43% w/w) and Bacopaside C (1.29% w/w) content

Parmeshwar Lal Saran[*], Hiteksha I Damor, Kuldeepsingh A Kalariya and Manish Kumar Suthar

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

[*]*Email: plsdehradun@gmail.com*

Bacopa monnieri (L.) Penn. commonly known as 'Neera Brahmi' belongs to the family *Scrophulariaceae* is a perennial, prostrate, and creeping herb that is identified in habitats including wetlands and muddy shores. Jal Brahmi, a nootropic herb being used as a promising agent in the modern Ayurveda system owing to its antioxidant, cholinergic, anti-beta amyloid property. The evaluated germplasm 'DBM-5' varied in morphology, herbage yield, qualitative as well as quantitative parameters. The germplasm has an exceptionally whitish (light purple) flower colour (Purple 76 D; as compared to Voilet 85A in Check as per the RHS colour chart (Saran et al., 2022). The maximum dry herbage yield was recorded in DBM-5 (19.71 t $h^{-1}y^{-1}$) as compared to check (17.55 t $h^{-1}y^{-1}$) variety CIM-jagriti (DMAPR Annual Report, 2020; Saran and Damor, 2021; Saran *et al*., 2022). The growth habit of germplasm is spreading type while check having a semi spreading type branches. The germplasm DBM-5 also contains significantly maximum Jujubogenin (1.43% w/w) and Bacopaside C (1.29% w/w) content as compared to CIM Jagriti (0.35% and 0.56% w/w, respectively). Germplasm DBM-5 having distinct morphological and chemical traits was developed through selection method and conservation of distinct germplasm carried out at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

Jal Brahmi has different morphological parameters including solitary whitish flowers with sessile, oblanceolate, succulent, and relatively thick leaves with larger leaf area, and are arranged oppositely on the stolon. Further, morphological variation was also observed for a number of stolons, stolon length, and stolon thickness in different accessions of Jal Brahmi.

Jal Brahmi performs exceptionally well in poorly drained soils and waterlogged areas under subtropical conditions. Vegetative cuttings are a is suitable propagation technique for commercial cultivation of the Jal Brahmi. It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level (Saran *et al*., 2022). In North India, it can grow in a wide range of temperatures (15–40 °C) and soil pH (5–7.5). It becomes dormant during the winter months except when grown in the vicinity of running water. In the south and central India, it can be grown throughout the year. For planting a one-hectare area on an average 3-3.5 quintals of herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes is transplanted directly in the field at a spacing of 10×10 cm using the plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On average 130-145 q ha^{-1} dry herbage can be obtained from multiple harvests (Saran, 2020). Overall, germplasm was found diverse, unique, and rich in quality herbage for commercial cultivation

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63. DBM-10 (IC0642015; INGR21238), a brahmi (*Bacopa monnieri*) germplasm with maximum number of leaves (760.83) and minimum leaf size (0.47-0.48 cm²)

Parmeshwar Lal Saran*, **Hiteksha I Damor, Manish Kumar Suthar and Kuldeepsingh A Kalariya**

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

Email: plsdehradun@gmail.com

Brahmi (*Bacopa monnieri* L. Pannell) has been identified as a member of the seven important medicinal plants recommended for immediate attention and included in the list of highly endangered medicinal plants of India. It is also known as '*Herpestis monnieri*', 'Jal brahmi', 'water hyssop', 'Neera-brahmi', and 'Jalanimba'. Morphological distinct characters especially a maximum number of leaves (760.83) with minimum leaf size or least leaf area was observed in DBM-10 (0.47-0.48 cm^2) as compared to CIM Jagriti (465.83 and 0.55-0.60 cm^2), respectively (DMAPR Report 2020; Saran *et al*., 2021; Saran and Damor, 2021). At the same time the germplasm "DBM-10" reported diversity for a maximum number of leaves with minimum leaf size after 55 days of transplanting and at full flowering (Saran *et al*., 2021). DBM-10 with the unique morphological traits and yield associated traits was developed through selection method and conservation of distinct germplasm at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The herb can be grown up to a height of 40 cm with 10-35 cm long branches. It is a tender herb having various branches with rooting at all nodes. The leaves are sessile, entire, opposite, simple, fleshy, and obscurely veined. Leaves are oblanceolate in shape with 2 cm long and 3 mm broad. In summer fruits and flowers are seems. It has normally light purple-colored flowers.

Jal Brahmi grows well in low-lying areas having poorly drained-water logged soils under subtropical climatic conditions. Normally it is propagated through stem cuttings. It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level (Saran *et al*., 2022). In north India, Jal Brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperature (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. The leaves under shade conditions made efficient use of the less intense irradiation reaching up to them like *rauvolfia*, patchouli, turmeric, Shatavari, and Brahmi (Saran *et al*., 2019). For planting a one-hectare area on an average 3-3.5 quintals of herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes is transplanted directly in the well prepared FYM-rich field at a spacing of 10×10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. The herbage portion including stem and leaves are harvested and shade dried. On average 130-145 q ha^{-1} dry herbage can be obtained from a multiple harvest (Saran, 2020).

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64. DBM-13 (IC0642016; INGR21239), a morphotype brahmi (*Bacopa monnieri*) having light green leaf colour, purplish white flower color and low chlorophyll content (0.74-1.07 mg g^{-1})

Parmeshwar Lal Saran*, Hiteksha I Damor, Kuldeepsingh A Kalariya and Manish Kumar Suthar

ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand-387310, Gujarat, India

**Email: plsdehradun@gmail.com*

Jal Brahmi (*Bacopa monnieri* (L.) Wettst. is an important prostrate herb belonging to the family *Platanaceae*. It is a diverse family comprising approximately 90 genera and 1900 species. It is precious as a revitalizing herb and used by Ayurvedic practitioners for nearly 3000 years ago. This miracle herb has the inherent potential of enhancing memory and vitality, therefore, gaining attention for its commercial cultivation globally (Saran and Patel, 2019) and required to understand the existing genetic variability for successful retrieval. DBM-13 accession of *B. monnieri* has been identified for variation in morphological characters *viz*., light green leaf colour (Yellow Green 146B) and purplish-white flower colour (Purple 76B petal with Violet 84C petal veins colour), while check has Green N137C (leaf) and Violet 85A (flower colors) using RHS colour chart in DBM-13 (Saran *et al*., 2021). For total chlorophyll content, accessions DBM-13 showed the lowest total chlorophyll content (0.74- 1.07 mg g^{-1}) compared to check (0.92-1.50 mg g^{-1}) and among all the studied accessions (Saran *et al*., 2021). DBM-13 with the distinct light green colour leaves with the lowest chlorophyll content was identified and developed through selection method and conservation of distinct germplasm at the ICAR-Directorate of Medicinal and Aromatic Plants Research (DMAPR), Anand, Gujarat.

The Jal brahmi herb is the small creeping type prostate with numerous succulents, glabrous branches. Different morphological parameters including solitary axillary flowers with 0.5 cm to 4.0 cm pedicels length, small-tubular, five-petaled flowers are white-purple in colour. Leaves are sessile, succulent, and thick grown appositively on 40-45 cm long stem with different leaf shape (Obovate), leaf apex (Rounded) and leaf base (Acuminate type). The fruit is oval and sharp at the apex, while seeds are oblong and pale-colored.

The perennial herb performs exceptionally well in poorly drained soils and water-logged areas. Near-neutral, clayey loam to clayey soils is best suited for its growth. It is commonly found in marshy habitats throughout the country up to 1320 m in height from sea level. It is cultivated through vegetative mass propagation using soft herbaceous cuttings. In north India, Jal Brahmi can grow in a wide range of temperatures (15-40 °C) and soil pH (5-7.5) at temperatures (30-40°C) and humidity (65-80%). In south India, it can be grown throughout the year. For planting a one-hectare area on an average 3-3.5 quintals of herbage are required. The whole plant is cut into small divisions to about 4-5 cm long, each with two-three nodes is transplanted directly in the well-prepared FYM-rich field at a spacing of 10×10 cm using plastering method during the month of July-August to get maximum herbage yield (Saran and Patel, 2019). Flood irrigation is provided quickly just after planting. On average 130-145 q ha^{-1} dry herbage can be obtained from multiple harvests (Saran, 2020).

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65. Jor Lab CL-1 (IC0642017; INGR21240), a turmeric (*Curcuma longa*) germplasm with high leaf essential oil (1.2%)

Mohan Lal

CSIR-North East Institute of Science and Technology, Jorhat-785006, Assam, India

Email: drmohanlal80@gmail.com

Curcuma longa, which belongs to the family Zingeberaceae, is an important crop plant having important medicinal properties. India is a leading producer of turmeric. The commercially available material (i.e. turmeric powder) in Europe is obtained mainly from India and somewhat from other south eastern Asian countries (Murugananthi *et al*., 2008). The essential oil is the one that provides the *C. longa* rhizome a particular spicy and aromatic flavour with its distinctive chemical composition (Saiz, 2014; Luthra *et al*., 2001). It is reported to possess potential applications in the agri-food industry, such as antimicrobial, weedicide and as food preservative agent (Ibáñez and Blázquez, 2021). The essential oil of this species is rich in various valuable chemical compounds, which are useful for pharmaceutical, industrial as well as food purposes. In this present investigation, a total of 352 germplasm of *C. longa* germplasm were collected from different regions of India, from 2014 to 2016 and planted in RBD design at CSIR-NEIST Jorhat Assam during March, 2016. After two year of the evaluation trial a high leaf essential oil rich germplasm was identified and named as Jor Lab CL-1. To identify the constituents, extraction of leaf essential oil was done using hydro- distillation and GC/MS analysis. The identified germplasm was planted in multi-location trial, along with the standard check variety during the year 2019. The average leaf essential oil yield of the newly identified germplasm in the five different locations was 1.20%, which is much higher as compared to the check variety that showed essential oil yield of 0.60%. This selected germplasm also showed better agronomical traits in comparison to the check variety as it has an average of 96cm of plant height, 5 number of tillers per plant, 44cm of leaf length, 29% dry rhizome recovery, and fresh rhizome yield of 17.9t/ha. This new identified line was named as "Jor Lab CL –1" and is suitable for commercial cultivation and essential oil production.

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66. IC-625596 (IC0625596; INGR21241), a ber (*Ziziphus mauritiana*) germplasm with small proportion of stone (7%) and excellent blend of high T.S.S. (17-18 (°B), acidity (0.35 %) and Vitamin C (51.2 mg/100 gm). Superior in taste and fruit weight (23 gm) compared to stone less landrace (INGR No. 19100)

Vijay Singh Meena[1*], Rakesh Bhardwaj[1], RR Sharma[2], Manoj Mahawar[3], VK Sharma[4] and Kuldeep Singh[4]
[1]*ICAR-NBPGR Regional Station, Jodhpur-342001, Rajasthan, India*
[2]*ICAR-CIPHET, Abohar-152117, Punjab, India*
[3]*ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India*
[4]*ICAR-National Bureau of Plant Genetic Resources, Pusa Campus-110012, New Delhi, India*
**Email: vijay.meena1@icar.gov.in*

Ber (*Zizyphus mauritiana*. L) is an indigenous fruit crop grown extensively in arid and semi-arid part of india. Presently, its cultivation is gaining popularity across the country because of its low maintenance cost, ability to grow in saline and drought condition, high nutrition value and high yield and money returns. But, bigger size of stone is major hindrance for its processing. Less proportion of stone is trait of interest and prime need of breeder for improvement of this Fruit crop. Hence 12 germplasm (Banarashi Karka, Umran, Chhuhara, Gola, Kaithili, Seb, Jogia, Saharanpur narnaul, Katha Phal, aliganj, Delhli local and IC0625596) of ber maintained at Exp. Station Issapur farm, ICAR-NBPGR, New Delhi were evaluated during 2017-18, 2018-19, 2019-20 and 2020-21 for superior fruit characteristics and chemical analysis under randomized block design (RBD).

A germplasm IC0625596 found promising in term of least stone/ kernel length (2.66 cm) and width (0.6 cm). This accession attained maturity during February with average stone weight (0.63 gm) that is only 7 % compared to more than 20 percent in other genotype. Fruit were oblong in shape with smooth surface and turn greenish yellow at the time of maturity. Fruit was soft with apex as broadly pointed and pulp colour was white. The pulp to stone ratio found (21.15) which is highly desirable for breeding purpose. It has excellent blend of T.S.S. of 17 (°B) and acidity (0.35 %) which makes it tasty and juicy over stone less landrace of ber (INGR No. 19100) that consist very small fruits (1-2 gm) which gives gumminess feeling after eating. This accession rich in Vitamin C in (51.2 mg/100 gm), total phenolic content found (201.5 mg GAE/100gm) and antioxidant activity expressed as AOX (11.5μmol trolor/gm).

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67. CZCM-2001 (IC642018; INGR21242), a carissa (*Carissa carandas*) germplasm with multiple flowering/fruiting in a year

PR Meghwal and Akath Singh
ICAR-Central Arid Zone Research Institute, Jodhpur-342003, Rajasthan, India
**Email: PR.Meghwal@icar.gov.in*

Karonda (*Carissa carandas* L.) is an Indigenous underutilized fruit plant with high phyto-therapeutic and nutritive value. It is a multipurpose plant with ability to grow and sustain in diverse agro-ecological conditions including arid and semi-arid regions. A unique genotype i.e. CZCM-2001 has been identified at Central Arid Zone Research Institute, Jodhpur. It bears flowers and fruits thrice in a year as against single flowering/ fruiting season in other accessions and popular varieties. It may be of more valued due to higher fruit yield and ornamental purposes round the year. The genotype was identified during long term evaluation of karonda germplasm. It is a selection from seedling population of the parent materials originally collected from one of the home gardens in Jodhpur city of Rajasthan state. In subsequent years, true to type plants were multiplied from single selected plant by air layering where the same trait was confirmed subsequent years.

The data on vegetative growth and fruit yield were recorded in CZCM-2001along with other accessions and a released variety Pant Manohar (Table1). Since, karonda is basically a spreading bush, there was not much variation in plant height but significant differences in canopy area and fruit yield were recorded with highest value in CZCM-2001. Because of multiple fruiting, the cumulative fruit yield in CZCM-2001 was higher by 25 to 68 % over the fruit yield of

Table 1: Vegetative growth and fruit yield of CZCM-2001 and other genotypes/variety (7th year onwards)

Genotype	*Plant height (m)*	*Canopy area (m^2)*	*Fruit yield (kg plant^{-1})*				
			2012	*2013*	*2014*	*2015*	*Mean*
CZCM-2001	3.06	7.45	25.60	29.8	26.5	30.1	28.25
CZCM-2021	2.56	6.73	15.52	17.3	16.8	17.5	16.78
CZCM-2022	2.38	5.14	22.2	21.4	22.8	23.7	22.52
CZCM-2031	3.15	6.76	18.20	20.1	22.6	21.2	20.50
Pant Manohar	2.82	6.92	16.80	18.3	23.5	20.2	19.70
CD(p=0.05)	NS	2.1	3.2	3.7	4.6	4.45	

Table 2: Flowering and fruiting pattern and fruit characteristics in CZCM-1 and other varieties/genotypes of karonda

Genotypes	*Flowering time*	*Fruit maturity time*	*Mean fruit weight (g)*	*Fruit length (cm)*	*Fruit girth (cm)*	*No. of seeds/fruit*
CZCM-2001	March-April	June-July	3.50	2.12	1.52	5.10
	July-August	September-October	3.10	2.07	1.65	4.40
	October-November	December-January	3.20	2.18	1.69	4.50
CZCM-2012	March-April	July-August	2.96	2.30	1.83	3.60
CZCM-2021	March-April	July-August	2.76	1.93	1.60	6.60
CZCM-2022	March-April	July-August	4.18	2.25	1.91	4.90
CZCM-2031	March-April	July-August	4.21	2.26	1.96	5.40
Pant Manohar	March-April	July-August	3.34	2.15	1.71	3.50

other genotypes/Pant Manohar which can be attributed to higher canopy area and multiple fruiting. The variation in vegetative growth and fruit yield among different genotypes confirms the earlier publication on karonda (Meghwal *et al*.,2014 and Meghwal, 2018).

The data on flowering/fruiting frequencies and fruit morpho-physico characteristics (Table 2) of CZMCM-2001 along with other genotypes indicated that except CZCM-2001, all other genotypes had single flowering/ fruiting habit while CZCM-2001 gave flowering/ fruiting three times in a years as depicted Table 2.

The species responds well to air layering for multiplication of cent per cent true to type plant. However, for large scale propagation seeds from ripened fruits can be used for propagation which should be sown immediately after extraction. The planting can be done in July-August or during February-March in blocks or in hedge row for live fencing. Spacing may differ from 3 to 5 meters either way while about 2 m between the plants is kept in hedge. Bearing bushes usually do not require pruning, however, to give desired shape, additional twigs are pruned. Diseased or broken twigs are also need to be removed. Old hedges may be headed back to induce new growth. Karonda once established do not require much water as it behaves as xerophytic plant. New plantations need to be irrigated at every weekly and fortnightly interval in summer in winter season respectively. Irrigation in April and June is helpful for survival of the plants for longer duration. There are no major diseases and pests on karonda except die back and anthracnose which sometimes attack the foliage of the plants. The anthracnose can be controlled by spraying with Blitxo-50 or Fytolon @ 2 g/litre water while dieback can be kept under check by spraying Benomyl @ 0.2%.

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