Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXXIVth meeting held on June 30th, 2021 at the ICAR-National Bureau of Plant Genetic Resources, New Delhi. A total of 43 proposals were received for registration. Out of that, 24 proposals were considered for registration. Finally, 21 applications covering nine crop species were approved for registration. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer (s) / author (s) is / are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. Introgression line IL 274 (IC0637547; INGR21091), a rice (*Oryza sativa* L.) germplasm for bacterial blight resistance.

Kuldeep Singh, Kumari Neelam*, Yogesh Vikal, Dharminder Bhatia, JS Lore and GS Mangat

Punjab Agricultural University, Ludhiana, Punjab-141004, India

*Email: kneelam@pau.edu

Bacterial blight, caused by Xanthomonas oryzae pv. oryzae, is one of the major constraints of rice productivity in Southeast Asia (Mew 1987; Chen et al. 2011). Here, we want to register an introgression line IL 274, derived from Oryza glaberrima accession IRGC 102600B with novel bacterial blight resistance gene xa-45(t) (Neelam et al., 2020). The inheritance studies in F₂ and F₂₃ populations of a cross involving Pusa44 and IL274 revealed the presence of single recessive locus controlling resistance to the Xanthomonas pathotype seven. The QTL mapping identified a major locus on the long arm of rice chromosome 8 with a LOD score of 33.22 between the SNP markers C8.26737175 and C8.26818765. The peak marker, C8.26810477, explains 49.8% of the total phenotypic variance and was positioned at 202.90 cM on the linkage map. This major locus spans 80 kb region on Nipponbare reference genome IRGSP-1.0 and contains 9 candidate genes. A co-segregating STS marker was developed from the LOC_Os08g42410 for efficient transfer of this novel gene to elite cultivars.

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

auricles, pubescence of leaf blade surface and anthocyanin coloration of lemma apex are absent.

Associated characters and cultivation Practices: The genetic stock IL274 has bacterial blight resistance against all the ten prevalent *Xanthomonas* pathotypes of Punjab and Northern states of India. The genetic stock carries bacterial blight resistance gene *xa-45* (*t*) from *Oryza glaberrimma* accession IRGC102600b on the long arm of chromosome 8 of rice.

References

Chen S, Liu X, Zeng, L, Ouyang D, Yang J, Zhu X (2011) Genetic analysis and molecular mapping of a novel recessive gene Theor. Appl. Genet. **122:** 1331https://doi.org/10.1007/s00122-011-1534-7

Mew T W (1987). Current status of future prospects of research on bacterial blight of rice. *Annu. Rev. Phytopathol.* **25:** 359–382. https://doi.org/10.1146/annurev.py.25.090187.002043

Neelam, K., Mahajan, R., Gupta, V. *et al.* High-resolution genetic mapping of a novel bacterial blight resistance gene xa-45(t) identified from *Oryza glaberrima* and transferred to *Oryza sativa*. *Theor. Appl. Genet.* **133:** 689–705 (2020). *https://doi.org/10.1007/s00122-019-03501-2*.

Table 1: Frequency of resistant and susceptible plants in F_2 and F_{23} populations and Chi squareanalysis

	Number of plan	ts				
Population	Resistant	Segregating	Susceptible	Total	X_c^2	X_t^2
F ₂	91	-	221	312	2.57	$x^2 (0.05,1) = 3.84$
F _{2:3}	74	158	80	312	0.27	x^2 (0.75, 2) = 0.57

^{*}Edited by: Anju Mahendru Singh and Anjali Kak, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012.

^{*}Acknowledgement is due to Arup Das for providing technical assistance in compilation.

2. Minatik Charang (ARC 10075); IC0597237 (IC0597237; INGR21092), a rice (*Oryza sativa* L.), germplasm with high grain protein content (12–14%).

Torit Baran Bagchi^{*1}, Krishnendu Chattopadhyay¹, Bishnu Charan Marndi¹, Awadhesh Kumar¹, Lotan Kumar Bose¹, Padmini Swain¹, BC Patra¹, SG Sharma² and Ruchi Bansal²

ARC 10075 with high grain protein content (13-16%) was identified from the genetic stock of the Assam Rice Collections (ARC) of the CRRI (NRRI) Rice Gene Bank. Three glutelin bands were highly expressed in the high-protein cultivar. They showed higher activity of nitrate reductase (NR) and glutamic dehydrogenase (GDH) at seedling stage (one-week-old) and maximum tillering stage (three weekold)(DARE/ICAR Annual Report 2011-12). It was found that this germplasm does contain an average 12.03% with a range of 10.43% - 15.27% grain protein as tested over the years and different environments (Table 1). Nitrate reductase (NR) and Nitrite reductase (NiR) activity was found to be higher for ARC 10075 as compared to low protein counterpart (ICAR-NRRI Annual Report 2019). It was also found with higher free amino acids (0.26%), methionine (0.082%), Lysine (0.049%) and Tryptophan (0.063%) (Mohanty et al. 2011). The fractions of different soluble protein in this germplasm are 0.434%, 1.415%, 0.443% and 12.864% of albumins, globulins, prolamins and glutelins, respectively (Chattopadhyay et. al. 2019a). The yield of this germplasm was 2.45 t/ha. The average maturity duration was found medium (130 days). It has tall (140cm) plant type and the grain type is medium slender. It is having high head rice recovery (61%), high alkali spreading value (7) and medium amylose content (24.6%) (ICAR-NRRI Annual Report 2013-14). A consistent QTL for grain protein content (*qGPC1.1*) and two QTLs for single grain protein content (*qSGPC2.1*, *qSGPC7.1*) were detected using backcross derived population from ARC 10075/Naveen (Chattopadhyay *et al.* 2019b). The first high protein rice variety of India, CR Dhan 310 was developed using this donor, ARC 10075.

Justification

This valuable rice germplasm was found stable in high seed protein content (12%) over the years and environments. This donor was also utilized in development of first high protein rice variety of India, CR Dhan 310 (10% protein content).

Table 1: Evaluation of ARC 10075 for grain protein content under multi- environmental condition

SI. No.	Year of evaluation	Season	Grain protein content related information	References
1	2008	Wet season	15.27% grain protein content in brownrice	DARE/ICAR Annual Report 2011-12; Mohanty <i>et al.</i> 2011
2	2010	Wet season	10.43% grain protein content in polished rice with 220.24g proteinyield/plant	Chattopadhyay et al,2011
3	2011	Wet season	11% grain protein content in polished rice	Chattopadhyay <i>et al.</i> 2018
4	2013	Wet season	12.8% protein content	ICAR-NRRI Annual Report, 2013-14
5	2014-15	Rabi season	13.00 % grain protein content and wasricher in nearly all amino acids as compared to check, Naveen.	ICAR-NRRI Annual Report, 2014-15, https://icar-nrri.in/wp- content/ uploads/2018/06 /2014-15.pdf
6	2014	Rabi season	10.80% in milled rice	Chattopadhyay <i>et al.</i> 2019a
7	2014	Wet season	10.88% in milled rice	Chattopadhyay <i>et al.</i> 2019a
8	2019	Wet season	Nitrate reductase (NR) and Nitrite reductase (NiR) activity was found to be higher for ARC 10075	ICAR-NRRI Annualreport 2019.
	Average		12.03% grain protein content over the environm	nents
	Range		10.43- 15.27%	

¹ICAR-National Rice Research Institute, Cuttack, Odisha-753006, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India

^{*}Email: torit.crijaf09@gmail.com

Moreover, consistent QTLs for grain protein contents were detected using this germplasm.

References

Chattopadhyay K, Das A and Das SP (2011) Grain protein content and genetic diversity of rice in north eastern India. *Oryza* **48(1):** 73-75.

Chattopadhyay K, Sharma SG, Bagchi TB, Molla K A, Sarkar S, Marndi BC, Sarkar A, Dash K and Singh ON (2018) Development of recombinant high yielding lines with improved protein content in rice (*Oryza sativa* L.) *J. Agric. Sci.* 1–17. https://doi. org/10.1017/ S0021859618000230.

Chattopadhyay K, Sharma SG, Bagchi TB, Mohanty B, Sardar SS, Sarkar S and Singh ON (2019a) High-protein rice in high-

yielding background, cv. Naveen. *Curr. Sci.***117(10):** 1722-1726. Chattopadhyay K, Behera L, Bagchi TB, Sardar SS, Moharana N, Patra NR, ChakrabortiM, Das A, Marndi BC, Sarkar A, Ngangkham U, Chakraborty K, Bose LK, Sarkar S, RayS, Sharma SG (2019b) Detection of stable QTLs for grain protein content in rice (*Oryza sativa* L.) employing high throughput phenotyping and genotyping platforms. *Sci. Rep.* **9(1):** 1-16.

DARE/ICAR Annual Report 2011-12

ICAR-NRRI Annual Report, 2013-14

ICAR-NRRI Annual Report, 2014-15, https://icar-nrri.in/wp-content/uploads/2018/06/2014-15

ICAR-NRRI Annual Report 2019.

Mohanty A, Marndi BC, Sharma SG and Das A (2011) Biochemical characterization oftwo high protein rice cultivars from Assam rice collections. *Oryza*. **48(2):** 171-174.

3. Phougak (D82) (IC0639794; INGR21093), a rice (*Oryza sativa* L.) germplasm for tolerance to sheath blight. Resistance to neck blast. resistance to leaf blast.

Jyothi Badri¹*, V Prakasam¹, RM Sundaram¹, MS Prasad¹, GS Laha¹, VP Bhadana², LV Subba Rao¹ and C Priyanka¹

¹ICAR-Indian Institute of Rice Research, Hyderabad, Telangana-500030, India

Rice is an important staple food for more than half of the global population. Rice production is constrained by several biotic and abiotic stresses and sheath blight (ShB) is one of the major devastating disease and responsible for 70% of yield losses and quality degradation. ShB is caused by necrotrophic soil born pathogen *Rhizoctonia solani* AG-1 IA which affects sheath, leaf and panicle. It produces water soaked brown color oval shaped lesions on sheath, irregular lesion on leaf and produces sclerotia during unfavourable conditions. So far, no immune sources to sheath blight have been identified throughout the world. Use of chemical fungicides for ShB disease management not only has an

adverse impact on the ecology, environment but it also stresses the pathogen to develop virulentraces.

Landraces from north eastern part of the country along with wild introgression lines, tropical japonica accessions, mutants, elite cultivars totalling about 1500 were evaluated for sheath blight resistance in 2012 and the genotypes identified as resistant/moderately resistant were further tested both under glass house and field conditions in the subsequent years (2013 and 2014) and seasons (Both *Kharif* and *Rabi*). Based on three years of testing, Phougak, a north eastern landrace with a unique characteristic of clustered panicle was found withconsistent tolerance reaction against

Table1: Disease reaction among rice germplasm under artificial inoculation during 2012 to 2020

		<u> </u>							
S.No	K-2012(F)	R-2013(GH)	K-2013(F)	R-2014(GH)	K-2014(F)	K-2017(F)	K-2018(F)	K-2019(F)	K-2020(F)
Tetep	3	3	3	3	3	3	5	5	3
Phougak	3	3	3	3	3	3	3	3	3
IR-50	9	9	9	9	9	9	9	9	9
Maritchatpi	5	3	5	7	7	NT	NT	NT	NT
TJP-19	3	3	5	7	5	NT	NT	NT	NT
TJP-28	5	3	5	7	7	NT	NT	NT	NT
Remi	3	5	3	5	7	NT	NT	NT	NT
APMS 6B	3	5	5	5	7	NT	NT	NT	NT
495	3	5	5	7	5	NT	NT	NT	NT
APMS-6B	3	5	5	5	7	NT	NT	NT	NT
ARC 6605	5	5	5	7	5	NT	NT	NT	NT
BG-380-2	5	5	5	7	3	NT	NT	NT	NT

NT-Not tested; F-Field; GH-Glass House

²ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, Jharkhand-834010, India

^{*}Email: jyothirishik@gmail.com

sheath blight disease (Dey et al., 2016; Dey et al., 2019; Dey et al., 2020) and its disease reaction under repeated artificial screening in field condition for the past 6 monsoon seasons viz., Kharif-2012, Rabi-2013, Kharif-2013, Rabi-2014 and Kharif-2014 is presented in (Table 1).

Considering its promising performance against sheath blight over the seasons and years, Phougak was evaluated in donor screening nurseries (DSN) of AICRIP during 2019. Sheath blight screening under artificial inoculation conditions was taken up at 16 locations and Phougak showed a disease susceptibility index (*dsi*) of 1.0 at four locations viz., Bankura, Moncampu, Pantnagar and Titabar, a *dsi* of 3.0 at Raipur and 5.0 at remaining locations with an overall mean *dsi* of 4.3 for 9 locations where LSI >4.0 (Table 2.

In addition to its resistance reaction to sheath blight, Phougak was also found promising against leaf blast and neck blast in DSN of AICRIP 2019. Of the 14 locations under artificial screening, Phougak recorded a *dsi* of 1.0 at Rewa, 2.0 at 3 locations *viz.*, Gangavati, Mandya, and Ranchi, a *dsi* of 3.0 at 4 locations *viz.*, IIRR, Malan, Rajendranagar and Bankura and a *dsi* of 4.0-5.0 at remaining 6 locations. A

mean *dsi* of 3.78 was shown by Phougak for 9 locations with LSI>4.0 under artificial inoculation conditions. Natural field screening against leaf blast at 13 locations indicated *dsi* of 1.0 at Rewa, 2.0 at Jagitial, Gangavati and RNC, 3.0 at Almora, Umiam, IMP and Pattambi, 4.0 at Upper Shillong, Ponnampet and Jagdalpur and 5.0 at Mugad and Hazaribhag with a mean *dsi* of 3.71 for 7 locations where LSI>4.0. Multi-location screening both under natural and artificial screening conditions indicated resistance to leaf blast. Screening of Phougak in UBN at ICAR-IIRR confirmed resistance to blast.

Neck blast screening under natural conditions was taken up at 10 locations and Phougak scored a mean *dsi* of 3.3 for 4 locations with a LSI >5.4 and at individual locations, it recorded a *dsi* of 1.0 at Mandya, 2.0 at Umiam, 3.0 at Imphal and 5.0 at remaining 4 locations.

Field and glasshouse screening in multiple years/seasons and multi-location testing under AICRIP-DSN indicated tolerance to sheath blight and resistance to both leaf blast and neck blast in Phougak. In view of its consistent promising performance against sheath blight, leaf blast and neck blast, Phougak was deployed in crosses with elite susceptible cultivars like Swarna, Improved Samba Mahsuri

Table 2: Sheath blight disease reaction in donor screening nursery (DSN) of AICRIP during 2019 under artificial screening conditions

Entry	MND	GNV	LDN	IIRR	СТК	MSD	PTB	ADT	NDL	CHP	RPR	BNK	MNC	PTN	PNT	SI	TTB*
LSI	7.7	7.5	7.0	6.9	6.8	6.8	6.8	6.4	5.7	5.5	5.3	4.8	4.6	4.5	4.4		3.6
Phoghak	5	7	7	5	5	5	5	5	3	5	3	1	1	7	1	4.3	1
T(N)1	9	9	7	9	7	7	9	9	7	7	7	7	7	7	5	7.5	-
IR-50	9	5	7	9	5	7	7	7	7	5	9	7	5	4	5	6.5	-
Tetep	1	3	5	5	3	5	5	3	5	5	3	3	0	5	5	3.7	-

^{*}Titabar with LSI < 4.0 was not included in the calculation of DSI for sheath blight.

Table 3: Reaction against Leaf blast in donor screening nursery (DSN) of AICRIP during 2019 under artificial screening conditions

Entry	MND	LNV	NLR	KJT	GNV	NWG	IIRR	MLN	RNR	SI
LSI	6.4	6.0	5.7	5.4	5.4	5.1	5.0	4.8	4.4	
Phougak	2	5	6	4	2	6	3	3	3	3.78
Tetep	5	2	4	4	3	3	1	1	3	2.89
HR-12	9	9	6	7	9	8	9	7	9	8.11
TN-1	9	9	7	4	9	7	9	8	9	7.89
IR-64	8	9	5	4	7	5	3	8	7	6.22

Table 4: Reaction against Leaf blast in donor screening nursery (DSN) of AICRIP during 2019 under natural field conditions

Entry	ALM	JGT	HZB	GGT	UMM	USG	PNP	SI
LSI	6.4	5.5	5.4	5.3	4.9	4.6	4.0	
Phougak	3	2	5	5	3	4	4	3.71
Tetep	3	8	1	5	2	5	3	3.85
HR-12	9	6	8	5	-	9	3	6.67
TN-1	9	5	7	5	-	4	3	5.5
IR-64	7	2	3	5	8	3	2	4.29

Table 5: Reaction against neck blast in donor screening nursery (DSN) of AICRIP during 2019 under natural field conditions

Entry	JGT	LNV	UMM	MND	SI
LSI	6.0	5.7	5.7	5.4	
Phougak	5	5	2	1	3.3
HR-12	7	9	-	9	8.3
IR-64	3	9	9	5	6.5
TN-1	5	9	-	7	7.0
Tetep	7	1	3	1	3.0

and Samba Mahsuri and populations are being developed (Tables 3-5).

References

- Bhaktavatsalam G, Satyanarayana K, Reddy APK, John VT (1978). Evaluation of sheathblight resistance in rice. *Int. Rice Res. Newsl* **3:** 9–10.
- IRRI (2004). Standard evaluation system for rice. International Rice Research Institute, Los Banos, Manila.
- Laha GS, Madhav MS, Prakasam V, Jyothi Badri, Ladha Lakshmi (2018-2019). Incentivizing Research in Agriculture: Research Highlights, PP34-35.
- Prakasam V, Ladhalakshmi D, Laha GS, Krishnaveni D, Sheshu Madhav M, Jyothi Badri, Srinivas Prasad M and Viraktamath BC (2013). Sheath blight of rice and its management. Technical Bulletin No.72. Directorate of Rice Research (ICAR),

- Rajendranagar, Hyderabad-500 030, A.P., India. pp. 56.
- Prakasam V, Priyanka C, Ravindra Khale, Jyothi Badri, Lydia Ch, Ladha Lakshmi, Laha GS, Prasad MS, Sundaram RM (2020). Comprehensive patho-phenotyping and molecular mapping of RIL population of Wazuhophek/Improved Samba Masuri against sheath blight of rice. 7th International Conference on "Phytopathology in Achieving UN Sustainable Development Goals" during January 16-20 at IARI, New Delhi, India, P 283
- Susmita Dey, Badri J, Prakasam V, Bhadana VP, Eswari KB, Laha GS, Priyanka C, Aku R and Ram T. (2016). Identification and agromorphological characterization of rice genotypes resistant to sheath blight. *Australas*. *Plant Pathol.*, **45**: 145-153.
- Susmita Dey, Jyothi Badri, Eswari KB and Prakasam V (2020) Diversity analysis for yield traits and sheath blight resistance in rice genotypes. *Electron. J. Plant Breed.*, **11(1):** 66-64.

4. DT-RIL110 (IC0638868; INGR21094), a wheat (*Triticum aestivum* L.) germplasm with drought tolerance.

Sonia Sheoran*, Gyanendra Singh, BS Tyagi, Sindhu Sareen, Rinki, PC Mishra and GP Singh

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

*Email: Sonia.Sheoran@icar.gov.in

The current climatic conditions pose serious threat to wheat production in the form of abiotic stress conditions. Among abiotic stresses, drought stress is of major concern, causing significant yield loss globally. Efforts are underway to mitigate the drought through breeding resilient wheat varieties. The wheat genotype DT-RIL110 was identified as a drought tolerant genotype based on physiological trait characterization.

The genotype DT-RIL110 was developed from the cross Dharwar Dry/DPW621-50 at ICAR-Indian Institute of Wheat & Barley Research (ICAR-IIWBR), Karnal. The parental line DPW621-50 is high yielding genotype released for timely sown irrigated conditions of the NWPZ whereas Dharwar Dry is a well-established drought tolerant Indian genotype (Kirigwi et al., 2007). The parental adaptability to endure in the stress condition has been combined in wheatgenotype DT-RIL110. It was phenotyped for two years under drought in rain out shelter (ROS) at Karnal (2016-18) and in rainfed conditions at Powerkheda (2016-17) and Karnal (2018-19) where it showed promising performance for drought stress tolerance as indicated by very low drought susceptibility index (0.48) score (Table 1).

Therefore, this promising genotype (DT-RIL110) was also evaluated under AICRP on Wheat and Barley, 32nd Drought Tolerance Screening Nursery (DTSN) along with 5 checks

(DBW 110, C306, K1317, MP3288 and NI5439) at 06 centres (2019-20). The proposed entry DT-RIL110 showed highest tolerance to drought stress with DSI of 0.74 and lowest reduction in yield (18.68%) as compared to five checks in pooled data of 06 drought stress locations (Dharwad, Junagarh, Indore, Kanpur, Bardoli, and Hisar), covering major wheat growing zones (Table 2). This indicated suitability of DT-RIL110 under rainfed environment. DT-RIL110 was also superior to the check varieties for days to heading (DH), days to maturity (DM), plant height(PH), grain filling duration (GFD), grain number per spike (GN/S) and biomass (BM) (Table 2) in pooled data of DTSN conducted at 6 locations.

DH-days to heading, DM-days to maturity, GFD-grain filling duration; PH-plant height; GW/S-grain weight per spike; BM-biomass

It may be concluded that the genotype DT-RIL110 may be used as potential source to be utilized in wheat breeding programmes to develop drought tolerant bread wheat varieties.

Reference

Kirigwi FM, M Van Ginkel, G Brown-Guedira, BS Gill, GM Paulsen, AK Fritz (2007) Markersassociated with a QTL for grain yield in wheat under drought. *Mol. Breed.* **20:** 401–413.

5. pau16071 (IC0638869; INGR21095), a wheat (*Triticum aestivum* L.) germplasm pau16071 with leaf rust resistance (LrT) and gluconess (IwT).

Satinder Kaur, Achla Sharma, Puja Srivastva and Parveen Chhuneja*

Punjab Agricultural University, Ludhiana, Punjab-141004, India

*Email: pchhuneja@pau.edu

The growing and cultivating resistant wheat crop varieties is important in order to meet the demands of the growing population and minimizing the yield losses. The three rust diseases viz stem rust (Puccinia graminis f. sp. tritici), leaf rust (Puccinia triticina), and stripe or yellow rust (Puccinia striiformis f. sp. tritici) (Aboukhaddour et al. 2020; Krattinger et al. 2009; Wellings 2011) create a never ending challenges for wheat improvent. Species belonging to the genus Aegilops L. are important sources of genetic material for expanding genetic variability of cultivated bread wheat. Aegilops tauschii, the D genome donor of wheat, is an invaluable source of genetic variability, which can be utilized for broadening the wheat gene pool. Evaluation of wild *Triticum* and *Aegilops species* at the Punjab Agricultural University, Ludhiana, India has led to the identification of several Aegilops species including Ae. tauschii as very good sources of resistance to many diseases including leaf rust and stripe rust (Chhuneja et al., 2010).

An accession of *Ae. tauschii* named pau 14195 found to be resistant to mixture of leaf rust races in field and was non-glaucous. Testing at seedling and adut plant stage reveled the rust resistance to be all stage resistance (ASR). Non-Glaucousness found in *Ae. tauschii* is a visual trait, which

is related to greyish or whitish appearance on the leaves, sheaths, glumes and stems in wheat. This appearance is due to epicuticular wax exudates produced by the plant. Cuticular wax deposits are known to reduce the loss of water due to transpiration and hence increasing drought tolerance in plants (Riederer and Schreiber 2001). This accession of Ae. tauschii was crossed with T. durum cultivar PBW114 and the F₁ so obtained was crossed with hexaploid wheat WH542. The double F1 was again backcrossed twice with WH542 to obtain BC₃F₁ Triticum durum cv. PBW114/ Ae. tauschii acc. pau14195//4*T. aestivum cv. WH542. Linked leaf rust resistance and non-glaucousness genes from Ae. tauschii to cultivated wheat variety WH542 were mapped. Inheritance studies was done on F₂ population from a BC₃ plant derived from the cross Triticum durum cv. PBW114/ Ae. tauschii acc. pau14195//4*T. aestivum cv. WH542 against leaf rust race 77-5 at seedling stage and against mixture of leaf rust races at adult plant stage. The rust data revealed monogenicdominant inheritance for both the traits of rust resistance and non-glaucousness. The leaf rust resistance and the non-glaucousness gene were tentatively named LrT and IwT, respectively. SSR markers Xbarc124, Xqdm5, Xqdm35, Xcfd51 and EST-derived markers Xcau96 and

Table 1: Drought susceptibility index (DSI) under drought stress (pooled over four environments)

Genotype	Karnal * (2016-17)	Powarkheda (2016-17)	Karnal * 2017-18	Karnal 2018-19	Pooled Data
DT-RIL110	0.47	-0.01	0.65	0.79	0.48
Dharwar Dry ©	-0.06	0.9	0.78	0.91	0.63
AKAW3717 ©	1.02	0.91	0.98	0.83	0.94
C306 ©	0.95	0.89	0.87	0.99	0.93
DPW621-50	1.63	1.3	1.36	1.02	1.33

^{*}ROS-Rain out shelter

Table 2: Pooled analysis of DSI and agro-morphological traits of DTSN genotypes during 2019-20

Trait	Test Genotype	Checks				
	DT-RIL110	DBW110 ©	C306 ©	K1317©	MP3288©	NI5439©
Pooled DSI	0.745	0.81	0.833	0.954	1.36	1.44
Yield % reduction	18.68	20.36	20.88	23.9	33.97	36.19
DH	64	74	71	67	68	71
DM	111	114	115	115	112	115
GFD	47	40	44	44	44	44
PH	72	81.3	93.4	89	84.6	85.3
GW/S	1.74	1.75	1.58	2.3	1.95	1.65
BM (g)	1862	1769	1734	1771	1507	1679

Xte6 on chromosome 2DS were linked with both genes. Chromosomal assignments of the genes were confirmed by testing linked SSR markers on Chinese Spring nullitetrasomics lines. SSR markers Xcau96 (1.6 cM) and Xbarc124 (0.6cM) flanked LrT and Xgdm35 (4.1 cM) and Xte6 (2.5 cM) flanked non-glaucousness gene. LrT and IwT showed a recombination distance of 3.4 cM. Hence, IwT can be used as an easy to score morphological marker of LrT during its transfer to other glaucous backgrounds.

References

Aboukhaddour R, Fetch T, McCallum B D, Harding M W, Beres B L and Graf R J (2020) Wheat diseases on the prairies: A Canadian

story. Plant Pathol. J. (October 2019): 1-15.

Chhuneja P, Garg T, Kumar R, Kaur S, Sharma A, Bains NS, Ahuja M, Dhaliwal HS and Singh K (2010) Evaluation of Aegilops tauschii Coss. germplasm for agromorphological traits and genetic diversity using SSR loci. *Indian J. Genet.* **70:** 328–338.

Krattinger S G, Lagudah E S, Spielmeyer W, Singh R P, Huerta-espino J, Mcfadden H, Bossolini E, Selter L L and Keller B (2009) Pathogens in *Wheat sci. (80-)* **323(February):** 1360–1363.

Riederer M and Schreiber L (2001) Protecting against water loss: analysis of the barrier properties of plant cuticles. Journal of Experimental Botany **52:** 2023–2032.

Wellings CR (2011) Global status of stripe rust: A review of historical and current threats. **179(1):** 129–141.

6. pau 16068 (IC0638873; INGR21096), a wheat (*Triticum aestivum* L.) germplasm with resistance to powdry mildew and two powdry mildew resistance genes PmTb7A.1 and PmTbA.2 mapped on chromosome 7AL.

Parveen Chhuneja*, Kuldeep Singh and Satinder kaur Punjab Agricultural University, Ludhiana, Punjab-141004, India *Email: pchhuneja@pau.edu

Powdery mildew (PM), caused by Blumeria graminis f. sp. tritici, is one of the important wheat diseases, worldwide. A number of PM resistance genes have been identified from cultivated wheat and its wild relatives. So far more than 82 PM resistance genes/alleles have been identified at 50 loci (Pm1-Pm53, Pm18- Pm1c, Pm22 - Pm1e, Pm23 - Pm4c, Pm31 -Pm21) in wheat and its wild relatives (McIntosh et al 2013). Of the 50 loci, 11 have been mapped on the A genome, 26 on the B genome and 13 on the D genome of wheat. Twentyseven these genes/alleles have been transferred into wheat from wild species (Peterson et al 2015, Xiao et al 2013). In India, PM is prevalent in the northern and southern hill zones causing serious yield losses whereas in north western plains zone (NWPZ) of India, which constitutes the most productive wheat growing region, PM appears sporadically but causing significant yield losses (Singh et al 2009).

T. boeoticum, (2n = 2x = 14, AA), a close relative of the A genome donor of wheat, harbours useful variability for many agronomically important traits including resistance to diseases (Feldman and Sears 1981, Singh et al 2007). We identified *T. boeoticum* acc. pau5088 having two PM resistance genes, designated as PmTb7A.1 and PmTb7A.2, and mapped on chromosome 7AL approximately 48cM apart. Two resistance gene analogue (RGA)-STS markers Ta7AL-4556232 and 7AL-4426363 were identified to be linked to the PmTb7A.1 and PmTb7A.2, at a distance of 0.6cM and 6.0cM, respectively. Following marker assisted selection (MAS), the two genes were transferred to *T. aestivum* using T. durum as bridging species. As many as 12,317 florets of F1 of the cross T. durum /T. boeoticum were pollinated with T. aestivum lines PBW343-IL and PBW621 to produce 61 and 65 seeds, respectively, of three-way F₁. Theresulting F₁s of the cross T. durum/T. boeoticum// T. aestivum were

screened with markerflanking both the PM resistance genes PmTb7A.1 and PmTb7A.2 (foreground selection) and the selected plants were backcrossed to generate BC1F1. Marker assisted selection was carried bothin BC1F1 and the BC2F1 generations. Introgression of alien chromatin in BC2F1 plants varied from 15.4 - 62.9 percent. Out of more than 110 BC₂F₁ plants showing introgression for markers linked to the two PM resistance genes, 40 agronomically desirable plants were selected for background selection for the carrier chromosome to identify the plants with minimum of the alien introgression. Cytological analysis showed that most plants have chromosome number ranging from 40-42. The BC₂F₂ plants homozygous for the two genes have been identified. These will be crossed to generate lines combining both the PM resistance genes but withminimal of the alien introgression. The PM resistance gene PmTb7A.1 maps in a region very close to Sr22, a stem rust resistance gene effective against the race Ug99. Analysis of selected plants with markers linked to Sr22 showed introgression of Sr22 from T. boeoticum in several BC2F1 plants. Thus, in addition to PM resistance, these progenies might also carry resistance to stem rust race Ug99.

References

McIntosh RA, Dubcovsky J, Rogers WJ, Morris C, Appels R, Xia XC (2013) Catalogue of gene symbols forwheat: 2014 supplement. Available: http://www.shigen.nig.ac.jp/wheat/komugi/genes/macgene/supplement2013.pdf.

Petersen S, Lyerly JH, Worthington ML, Parks WR, Cowger C, Marshall DS, et al. (2015). Mapping of powdery mildew resistance gene Pm53 introgressed from Aegilops speltoides into soft red winter wheat. *Theor. Appl. Genet.* **128:** 303–312. doi: 10.1007/s00122-014-2430-8 PMID: 25425170

Xiao M, Song F, Jiao J, Wang X, Xu H, Li H (2013) Identification of

the gene Pm47 on chromosome 7BS conferring resistance to powdery mildew in the Chinese wheat landrace Hongyanglazi. *Theor. Appl. Genet.* **126:** 1397–1403. *doi:* 10.1007/s00122-013-2060-6 PMID: 23429903

Singh DP, Sharma AK, Singh D, Rana SK, Singh KP, Srivastava K, et al. (2009) Resistance to powdery mildew in Indian wheat. Pl Dis Res: 24: 942.

Feldman M, Sears ER (1981) The wild gene resources of wheat. *Sci* Am **244:** 98–109.Feld

Singh K, Ghai M, Garg M, Chhuneja P, Kaur P, Schnurbusch T, et al (2007b) An integrated molecular linkage map of diploid wheat based on a *Triticum boeoticum* X T. monococcumRIL population. *Theor. Appl. Genet.* **115:** 301–312. PMID: 17565482

7. IC252458 (IC252458; INGR21097), a wheat (*Triticum aestivum* L.) germplasm with three minor/adult plant rust resistance genes (APR) for leaf rust.

Vikas VK*1, Sundeep Kumar², BS Phogat², AK Sharma³, MS Saharan⁴, Amit Kumar Singh², Jyoti Kumari², Rakesh Singh², Sherry R Jacob², M Sivasamy¹, P Jayaprakash¹, JP Jaiswal⁵, Deepsikha⁵, SP Singh⁶, IK Kalappanavar², SS Vaish³, PC Mishra⁰ and GP Singh³

¹ICAR-IARI Regional Station, Wellington, Tamil Nadu-643231, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India

³ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana-132001, India

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

⁵Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand-263145, India

6 Narendra Deva University of Agriculture and Technology, Faizabad, Uttar Pradesh-224229, India

⁷University of Agricultural Sciences, Dharwad, Karnataka-580005, India

⁸Banaras Hindu University, Varanasi-221005, Uttar Pradesh-560065, India

⁹Zonal Agricultural Research Station (JNKVV), Powarkheda, Madhya Pradesh-461110, India

*Email: vkvikaswtn@gmail.com

Leaf rust (Puccinia triticina Eriks.) is a fungal disease of wheat (Triticum aestivum L.), which causes considerable yield loss. Adult plant resistance (APR) is one of the most sustainableapproaches to control leaf rust. A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of minor/adult plant rust resistance genes (APR) for leaf rust at phenotypic and genotypic level. Field phenotyping was carried out across ten different locations viz., Pantnagar (Uttarakhand), Ludhiana (Punjab), Karnal (Haryana), Varanasi (Uttar Pradesh), Kumarganj (Uttar Pradesh), Vijapur (Gujarat), Powarkheda (Madhya Pradesh), Pune (Maharashtra), Dharwad (Karnataka) and Wellington (Tamilnadu) for two years, followed by molecular screening, to detect thepresence of APR genes, Lr34+, Lr46+, Lr67+ and Lr68 in Indian wheat germplasm. In field screening, 190 wheat accessions were selected from 6,319 accessions based on leaf tip necrosis (LTN), disease severity and the average coefficient of infection. APR genes are also associated with leaf tip necrosis (LTN), a phenotypical marker that is linked or pleiotropic with these genes [14]. LTN appears on the flag leaves when plants are grown in fields (Lagudah et al., 2006). Molecular screening of 190 wheat accessions revealed that 73% of the accessions possessed known APR genes either as single or as a combination of two or three genes. Furthermore, 49 accessions possessing two and three APR genes were evaluated for yield stability across four different viz., Pantnagar, Varanasi, Powarkheda and Pune, using additive main effects and multiplicative interaction (AMMI) model (Kumar et al., 2019).

Among the nine wheat accessions identified with the presence of three APR genes, wheat accession, IC252458 showed the presence of three adult plant leaf rust resistance genes, Lr34+ (Lr34/Sr57/Yr18/Pm38/Ltn1), Lr46+ (Lr46/Sr58/ Yr29/Pm39/Ltn2) and Lr67+ (Lr67/Yr46/Sr55/Pm46/Ltn3). Accession, IC252458 displayed resistance reaction (0) in all the locations with average coefficient of Infection (ACI) of 0.0. Moreover, APR genes have pleiotropic association with stem and stripe rust resistance along with powdery mildew which is an added advantage. Synergistic combination of minor rust resistance genes made the accession resistance to the prevailing leaf rust pathotypes in India (Singh et al., 1992). APR genes are pathotype non-specific resistance based on horizontal type of resistance mechanism. Development of new pathotype(s) is slow/remote compared to major gene resistance which leads to durable resistance. So, the germplasm could be vital source for imparting durable rust resistance in wheat.

References

Lagudah ES, H Mc Fadden, RP Singh, J Huerta-Espino, HS Bariana and W Spielmeyer (2006)Molecular genetic characterization of the *Lr34/Yr18* slow rusting resistance gene region in wheat. *Theor. Appl. Genet.* **114:** 21-30.

Kumar S, BS Phogat, VK Vikas, AK Sharma, MS Saharan, AK Singh *et al.* (2019) Mining ofIndian wheat germplasm collection for adult plant resistance to leaf rust. *PLoS One* **14(3):** e0213468

Singh RP, S Rajaram (1992) Genetics of adult plant resistance to leaf rust in 'Frontana' andthree CIMMYT wheats. *Genome* **35:** 24-31.

8. IC290150 (IC290150; INGR21098), a wheat (*Triticum aestivum* L.) germplasm with three minor/adult plant rust resistance genes (APR) for leaf rust.

Vikas VK*1, Sundeep Kumar², BS Phogat², AK Sharma³, MS Saharan⁴, Amit Kumar Singh², Jyoti Kumari², Rakesh Singh², Sherry R Jacob², M Sivasamy¹, P Jayaprakash¹, JP Jaiswal⁵, Deepsikha⁵, SP Singh⁶, IK Kalappanavar², SS Vaish⁶, PC Mishra⁶ and GP Singh³

¹ICAR-IARI Regional Station, Wellington, Tamil Nadu-643231, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India

³ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana-132001, India

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

⁵Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand-263145, India

⁶Narendra Deva University of Agriculture and Technology, Faizabad, Uttar Pradesh-224229, India

⁷University of Agricultural Sciences, Dharwad, Karnataka-580005, India

⁸Banaras Hindu University, Varanasi-221005, Uttar Pradesh-560065, India

⁹Zonal Agricultural Research Station (JNKVV), Powarkheda, Madhya Pradesh-461110, India

*Email: vkvikaswtn@gmail.com

Leaf rust (*Puccinia triticina* Eriks.) is a fungal disease of wheat (*Triticum aestivum* L.), which causes considerable yield loss. Adult plant resistance (APR) is one of the most sustainable approaches to manage leaf rust. APR is best expressed at the adult plant stage wherein resistance is conferred by multiple additive genes possessing quantitative inheritance. Since APR is generally governed by multiple additive genes, it is not subjected to the "boom and bust cycle" of disease epidemics. Therefore, APR is considered more durable than all stage resistance (ASR) or seedling resistance or race-specific resistance, which is governed by a major gene providing hypersensitive response (HR).

A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of minor/adult plant rust resistance genes (APR) for leaf rustat phenotypic and genotypic level. Field phenotyping was carried out across ten different locations viz., Pantnagar (Uttarakhand), Ludhiana (Punjab), Karnal (Haryana), Varanasi (Uttar Pradesh), Kumarganj (Uttar Pradesh), Vijapur (Gujarat), Powarkheda (Madhya Pradesh), Pune (Maharashtra), Dharwad (Karnataka) and Wellington (Tamilnadu) for two years, followed by molecular screening, to detect the presence of APR genes, Lr34+, Lr46+, Lr67+ and Lr68 in Indian wheat germplasm. In field screening, 190 wheat accessions were selected from 6,319 accessions based on leaf tip necrosis (LTN), disease severity and the average coefficient of infection. APR genes are also associated with leaf tip necrosis (LTN), a phenotypical marker that is linked or pleiotropic with these genes. LTN appears on the flag leaves when plants are grown in fields (Lagudah et al., 2006). Molecular screening of 190 wheat accessions revealed that 73% of the accessions possessed known APR genes either as single or as acombination of two or three genes (Kumar et al., 2019). Among the nine wheat accessions identified with the presence of three APR genes, wheat accession, IC290150 showed the presence of three adult plant leaf rust resistance genes, Lr34+ (Lr34/Sr57/Yr18/Pm38/Ltn1), Lr67+ (Lr67/Yr46/ Sr55/Pm46/Ltn3) and Lr68. Accession, IC290150displayed resistance reaction (5R) in all the locations with average coefficient of Infection (ACI) of 0.7. Moreover, APR genes have pleiotropic association with stem and stripe rust resistance along with powdery mildew which is an added advantage. Synergistic combination of minor rust resistance genes made the accession resistance to the prevailing leaf rust pathotypes in India (Singh et al., 1992). APR genes are pathotype non-specific resistance based on horizontal type of resistance mechanism. Development of new pathotype(s) is slow/remote compared to major gene resistance which leads to durable resistance. Resistance based on APR genes, in the background of high yielding cultivars, is expected to provide a high level of race non-specific resistance, which is durable. So, the germplasm could be vital source for imparting durable rust resistance in wheat.

References

Kumar S, BS Phogat, VK Vikas, AK Sharma, MS Saharan, AK Singh et al. (2019) Mining of Indian wheatgermplasm collection for adult plant resistance to leaf rust. *PLoS One* **14(3)**: e0213468

Lagudah ES, H Mc Fadden, RP Singh, J Huerta-Espino, HS Bariana and W Spielmeyer (2006)Molecular genetic characterization of the *Lr34/Yr18* slow rusting resistance gene region in wheat. *Theor. Appl. Genet.* **114:** 21-30.

Singh RP, S Rajaram (1992) Genetics of adult plant resistance to leaf rust in 'Frontana' and three CIMMYT wheats. *Genome* **35:** 24-31.

9. IC279875 (IC279875; INGR21099), a wheat (*Triticum aestivum* L.) germplasm with two minor/adult plant rust resistance genes (APR) for leaf rust.

Vikas VK*1, Sundeep Kumar², BS Phogat², AK Sharma³, MS Saharan⁴, Amit Kumar Singh², Jyoti Kumari², Rakesh Singh², Sherry R Jacob², M Sivasamy¹, P Jayaprakash¹, JP Jaiswal⁵, Deepsikha⁵, SP Singh⁶, IK Kalappanavar², SS Vaish⁶, PC Mishra⁶ and GP Singh³

¹ICAR-IARI Regional Station, Wellington, Tamil Nadu-643231, India

²ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110012, India

³ICAR-Indian Institute of Wheat & Barley Research, Karnal, Haryana-132001, India

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

⁵Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand-263145, India

6 Narendra Deva University of Agriculture and Technology, Faizabad, Uttar Pradesh-224229, India

⁷University of Agricultural Sciences, Dharwad, Karnataka-580005, India

⁸Banaras Hindu University, Varanasi-221005, Uttar Pradesh-560065, India

⁹Zonal Agricultural Research Station (JNKVV), Powarkheda, Madhya Pradesh-461110, India

*Email: vkvikaswtn@gmail.com

Leaf rust (*Puccinia triticina* Eriks.) is a fungal disease of wheat (*Triticum aestivum* L.), which causes considerable yield loss. Adult plant resistance (APR) is one of the most sustainable approaches to control leaf rust. APR is best expressed at the adult plant stage wherein resistance is conferred by multiple additive genes possessing quantitative inheritance. Since APR is generally governed by multiple additive genes, it is not subjected to the "boom and bust cycle" of disease epidemics. Therefore, APR is considered more durable than all stage resistance (ASR) or seedling resistance or race-specific resistance, which is governed by a major gene providing hypersensitive response (HR).

A comprehensive germplasm evaluation study of wheat accessions conserved in the Indian National Genebank was conducted to identify sources of minor/adult plant rust resistance genes (APR) for leaf rustat phenotypic and genotypic level. Field phenotyping was carried out across ten different locations viz., Pantnagar (Uttarakhand), Ludhiana (Punjab), Karnal (Haryana), Varanasi (Uttar Pradesh), Kumarganj (Uttar Pradesh), Vijapur (Gujarat), Powarkheda (Madhya Pradesh), Pune (Maharashtra), Dharwad (Karnataka) and Wellington (Tamilnadu) for two years, followed by molecular screening, to detect the presence of APR genes, Lr34+, Lr46+, Lr67+ and Lr68 in Indian wheat germplasm. In field screening, 190 wheat accessions were selected from 6,319 accessions based on leaf tip necrosis (LTN), disease severity and the average coefficient of infection. APR genes are also associated with leaf tip necrosis (LTN), a phenotypical marker that is linked or pleiotropic with these genes. LTN appears on the flag leaves when plants are grown in fields (Lagudah et al., 2006). Molecular screening of 190 wheat accessions revealed that 73% of the accessions possessed known APR genes either as single or as acombination of two or three genes. (Kumar et al., 2019).

Among the nine wheat accessions identified with the presence of three APR genes, wheat accession, IC279875 showed the presence of two adult plant leaf rust resistance genes, Lr34+ (Lr34/Sr57/Yr18/Pm38/Ltn1) and Lr68. Accession, IC279875 displayed resistance reaction (0) in all the locations with average coefficient of Infection (ACI) of 0.0. Moreover, APR genes have pleiotropic association with stem and stripe rust resistance along with powdery mildew which is an added advantage. Synergistic combination of minor rust resistance genes made the accession resistance to the prevailing leaf rust pathotypes in India (Singh et al., 1992). APR genes are pathotype non-specific resistance basedon horizontal type of resistance mechanism. Development of new pathotype(s) is slow/remote compared to major gene resistance which leads to durable resistance. Resistance based on APR genes, in the background of high yielding cultivars, is expected to provide a high level of race nonspecific resistance, which is durable. So, the germplasm could be vital source for imparting durable rust resistance in wheat.

References

Kumar S, BS Phogat, VK Vikas, AK Sharma, MS Saharan, AK Singh et al. (2019) Mining of Indian wheatgermplasm collection for adult plant resistance to leaf rust. *PLoS One* **14(3):** e0213468

Lagudah ES, H Mc Fadden, RP Singh, J Huerta-Espino, HS Bariana and W Spielmeyer (2006)Molecular genetic characterization of the *Lr34/Yr18* slow rusting resistance gene region in wheat. *Theor. Appl. Genet.* **114:** 21-30.

Singh RP, S Rajaram (1992) Genetics of adult plant resistance to leaf rust in 'Frontana' and three CIMMYT wheats. *Genome* **35:** 24-31.

328

10. DWRB 206 (DWRNB 17) (IC0638874; INGR21100), a barley (*Hordeum vulgare* L.) germplasm with resistant to stripe rust at APR under artificial inoculation in naked barley.

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

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

*Email: Jogendra.singh2@icar.gov.in

DWRB206 (DWRNB17) is a six-row hulless barley genotype, selected from exotic (INBYT-(2013)-20, ICARDA) breeding material (ZIGZIG/4/TOCTE//HIGO/LINO/3/PETUNIA1). DWRB206 was evaluated for agro-morphological traits at ICAR-IIWBR, Hisar and for disease reaction (stripe rust at 5) locations) during 2016-17 in Initial Barley Disease Screening Nursery (IBDSN) under artificial epiphytotic conditions. The genotype shown higher resistance against stripe rust (ACI=3.0 HS 10S) at adult plant stage (Table 1). The check cultivars as well as infector showed high susceptible reaction against stripe rust. The genotype was again screened for stripe rust at 6 locations in National Barley Disease Screening Nursery (NBDSN) during 2018-19. DWRB206 exhibited resistance to stripe rust with ACI=5.6 and HS=10S only, while the huskless checks Karan16 and NDB943 were highly susceptible.

Agro-morphological and quality traits

DWRB206 flowers in 95 days and matures in 127 days. Its average plant height is 111 cm and has 109 tillers/meter. The average spike length is 8.0 cm with 68 grains per spike and thousand grain weight of 36.5g. The genotype had 61.3 kg/hl test weight and protein content 12.9%.

References

Anonymous (2017). Progress report of AICRP on Wheat and Barley 2016-17, Barley Improvement. Eds. AS Kharub, Chuni

Table 1: Disease reaction of DWRB206 (DWRNB17) in IBDSN (2016-17) and NBDSN (2018-19)

Genotype	Stripe rust r	Stripe rust reaction							
	IBDSN (201	6-17)	NBDSN (2018-19)					
	ACI	HS	ACI	HS					
DWRB206 (DWRNB17)	3.0	105	5.6	105					
Karan16	NT	NT	46.6	60S					
NDB 943	NT	NT	66.6	100S					
Infector	84	100S	83.3	100S					

ACI= average coefficient of infection, HS= highest score across all locations

Lal, Dinesh Kumar, Jogendra Singh, Lokendra Kumar, Anil Khippal, Vishnu Kumar, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal, India pp. 3.2-3.14.

Anonymous (2019). Progress report of AICRP on Wheat and Barley 2018-19, Barley Improvement. Eds. AS Kharub, Chuni Lal, Dinesh Kumar, Jogendra Singh, Vishnu Kumar, Amit Kumar Sharma, Anil Khippal, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal, India pp. 3.13-3.14.

11. BCLA11-6 (IC0638875; INGR21101), a barley (*Hordeum vulgare* L.) germplasm with corn leaf aphid resistance genotype.

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

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

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

BCLA11-6 is a six-row barley genotype, developed from a cross between BCU390/Alfa93 in institutional barley breeding program at IIWBR, Karnal in barley network program and fixed up to F9 generation. This genotype was found resistant for corn leaf aphid under epiphytotic and natural infection conditions. BCLA11-6 was screened for five consecutive years (2014-19) in especially designed structure in net house under high load of Corn leaf aphid (CLA) inoculum (Table 1). The genotype was consistently found resistant for CLA during 2014-19. It was then contributed to the multilocation testing under AICRP Wheat and Barley in

NBDSN in 2019-20 under natural hot spot condition (Table 2). BCLA11-6 has shown average resistance (1.7) in 2019-20 at two locations and almost similar resistance score (1.67) during 2014-19 at IIWBR, Karnal on a 1 to 5 scale where 1 is immune and 5 is highly susceptible. The genotype was evaluated for agro-morphological traits at ICAR-IIWBR, Karnal during 2018-20.

Agro-morphological and quality traits: BCLA11-6 flowers in 95 days and matures in 145 days. Its average plant height is 159 cm. The flag leaf waxiness is present (low) and spike

Table 1: Screening of BCLA11-6 against foliar aphids under epiphytotic conditions during 2014-19 at ICAR-IIWBR, Karnal

	Location:	karnal										
	2014-15		2015-16		2016-17		2017-18		2018-2019		Average o	ffiveyears
Entry no.	Average number of aphids/tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Overall average number of aphids/ tiller	Grade
BCLA11-6	1.61	*R	1.63	R	1.81	R	1.69	R	1.63	R	1.67	R
Alfa –93 (Suscepti ble Check)	117.57	**HS	119.03	HS	129.63	HS	114.13	HS	111.32	HS	118.33	HS

^{*}Resistant; **Highly Susceptible

Table 2: Screening of BCLA11-6 against foliar aphids under natural hot spot conditions during 2019-20 in coordination trial at Karnal and Kanpur

Entry No.	Kanpur					Karnal		Overall	Overall			
	Date of ok	oservation		Av.	HS	Date of ob	Date of observation			Highest	Av. score	HS
	05.02.20	12.02.20	19.02.20	score		03.02.20	17.02.20	02.03.20	score	score		
BCLA 11-6	1	2	1	1.3	2	2	2	2	2.0	2	1.7	2
Alfa - 93	5	5	5	5.0	5	5	5	5	5.0	2	5.0	5

waxiness is absent. Leaf width is broad, spike length is medium. Auricle pigmentation is absent. The thousand grain weight is 42.5g.

References

Anonymous (2020). Progress Report of AICRP on Wheat & Barley 2019-20, Barley Improvement. Eds: RPS Verma, AS Kharub, Chuni Lal, Dinesh Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Sudheer Kumar, SC Bhardwaj, Poonam

Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh. ICAR-Indian Institute of Wheat andBarley Research, Karnal, India. P. 215

Rekha Malik, Poonam Jasrotia, Surendra Singh1, Rajendra Kumar, Ajit Singh Kharub and RPS Verma (2019). Identification of promising barley genotypes with aphid resistance. Wheat and Barley Newsletter, ICAR-IIWBR, Karnal. July-Dec, 2019: 19-20.

12. BCLA3 (IC0638876; INGR21102), a barley (*Hordeum vulgare* L.) germplasm with corn leaf aphid resistance genotype.

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

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

BCLA3 is a two-row barley genotype, developed from a cross between EB921/Alfa93 in institutional barley breeding program at IIWBR, Karnal in barley network program and fixed up to F9 generation. Thisgenotype was found resistant for corn leaf aphid under epiphytotic and natural infection conditions. BCLA3 was screened for five consecutive years (2014-19) in especially designed structure in net house under high load of Corn leaf aphid (CLA) inoculums. The genotype was consistently found resistant for CLA during 2014-19. It

was then contributed to the multilocation testing under AICRP Wheat and Barley in NBDSN in 2019-20 under natural hot spot conditions. BCLA3 has shown average resistance (1.7) in 2019-20 at two locations and almost similar resistance score (1.60) during 2014-19 at IIWBR, Karnal on a1 to 5 scale where 1 is immune and 5 is highly susceptible. The genotype was evaluated for agro-morphological traits at ICAR-IIWBR, Karnal during 2018-20.

^{*}Email: rekha.malik@icar.gov.in

Table 1: Screening of BCLA3 against foliar aphids under epiphytotic conditions during 2014-19 at ICAR-IIWBR, Karnal

Entryno.	Location: karnal											
	2014-15		2015-16		2016-17		2017-18		2018-2019)	Average o	f five years
	Average numberof aphids/t iller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Average number of aphids/ tiller during the season	Grade	Overall average number of aphids/ tiller	Grade
BCLA3	1.47	*R	1.68	R	1.75	R	1.56	R	1.54	R	1.60	R
Alfa –93 (Suscep ŧible Check)	117.57	**HS	119.03	HS	129.63	HS	114.13	HS	111.32	HS	118.33	HS

^{*}Resistant; **Highly Susceptible

Table 2: Screening of BCLA3 against foliar aphids under natural hot spot conditions during 2019- 20 in coordination trial at Karnal and Kanpur

Entry No.	Kanp	Kanpur					Karnal					
	Date	of obser	vation			Date of observation				ıre	score	
	05.02.20	12.02.20	19.02.20	Av. score	HS	03.02.20	17.02.20	02.03.20	Av. score	Highest scc	Overall Av.	Overall HS
BCLA3	1	2	1	1.3	2	2	2	2	2.0	2	1.7	2
Alfa - 93	5	5	5	5.0	5	5	5	5	5.0	2	5.0	5

Agro-morphological and quality traits

BCLA3 flowers in 99 days and matures in 146 days. Its average plant height is 124 cm. The flag leaf waxiness is present (low) and spike waxiness is absent. Leaf width and spike length is medium. Auricle pigmentation is present. The thousand grain weight is 44.0q.

References

Anonymous (2020). Progress Report of AICRP on Wheat & Barley 2019-20, Barley Improvement. Eds: RPS Verma, AS Kharub,

Chuni Lal, Dinesh Kumar, Jogendra Singh, Amit Kumar Sharma, Anil Khippal, Sudheer Kumar, SC Bhardwaj, Poonam Jasrotia, Rekha Malik, Ajay Verma, Satyavir Singh and GP Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal, India. P. 215

Rekha Malik, Poonam Jasrotia, Surendra Singh1, Rajendra Kumar, Ajit Singh Kharub and RPS Verma (2019). Identification of promising barley genotypes with aphid resistance. *Wheat and Barley Newsletter*, ICAR-IIWBR, Karnal. July-Dec, 2019:19-20.

13. IC340947 (IC0340947; INGR21103), a french bean (*Phaseolus vulgaris* L.) germplasm resistant to BCMV disease.

Basavaraja T*1, Manjunatha L1, Mohar Singh2, Rahul Chandora2, Shiv Sewak1 and NP Singh1

¹ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh-208024, India.

²ICAR-NBPGR Regional Station, Shimla, Himachal Pradesh-171004, India.

*Email: Basavaraja.T@icar.gov.in

Rajmash/Common bean (*Phaseolus vulgaris* L.; 2n = 2x = 22) is also known by kidney bean, French bean, Snap bean and dry bean etc. It is one of the most vital and highly relished pulse crop used for direct human consumption globally and is an important component of subsistence agriculture (Broughton *et al.*, 2003). Therefore, rajmash is regardedas "Grain of hope". In India, rajmash mainly produced by resource-poor farmers,

small and marginal land holding farmers in the traditional production system that include rotation with vegetables and intercropping of climbing/ pole type varieties with grain amaranth, potato and maize during *Kharif* season in North Eastern Hilly (NEH) region. While, it grown as a sole crop by using bush types varieties during *rabi* season in northern plain and central India. It is growing under

diverse geographical location in which crop may expose to varied climatic condition. However, crop was prone to many diseases, among them Bean common mosaic virus (BCMV) is one of the most destructive diseases of common bean, it is mainly transmitted by vector Aphid and having seed borne nature. The virus belongs to genus *Potyvirus* of family *Potyviridae* and in India, BCMV is of regular recurrence in North- western Himalayas with disease incidence ranging from 0.5 to 77.0 % (Sharma *et al.* 1998; Kapil *et al.* (2011)). Thus, the prevalence of BCMV disease has posed a serious threat for dry bean production in rajmash growing areas of Himachal Pradesh, Jammu & Kashmir, Sikkim, Uttar Pradesh and Uttarkhand. Hence, Identification of stable BCMV resistant donors is crucial in Rajmash/Common bean improvement programme.

Pedigree

During rabi 2015-16, 2016-17, 2017-18 and 2018-19 a set of 300 germplasm accessions were evaluated for agronomic traits and BCMV disease screening under natural epiphytotic condition at IIPR, Kanpur by using BCMV resistant checks as Arun & Amber while, susceptible check as Jawala, Uday and IC341339. Disease scoring was done at three stages of crop growth viz., 45 DAS, 65 DAS and 90 DAS (Pathologist assistance involved). In these experiments, both agronomic and morphological data were recorded and based on BCMV percent disease incidence (PDI) data revealed that germplasm accession viz., IC340947 and IC360831 were highly resistant against BCMV disease as they recorded 0.00% PDI over four consecutive seasons and Kharif rajmash is a highly remunerative pulse crop in hilly tract of Himachal Pradesh but BCMV disease is a major obstacle for grain production. During Kharif 2017 and 2018, a set of selected promising germplasm accession were screened against BCMV disease under natural field condition at NBPGR, Regional station, Shimla by using BCMV resistant checks as Arun & Amber while, susceptible check as Jawala and Uday. Based on agronomic traits and BCMV disease reaction scale the germplasm accession viz., IC340947 and IC360831 were superior to check varieties and highly resistant against BCMV disease as they recorded 0.00% PDI. In addition to that, during rabi 2019-20 a set of selected promising germplasm accessions were screened against BCMV disease both under field and lab condition through sap inoculation method, similarly above experiments both agronomic and BCMV disease reaction was recorded at three different stages of crop growth. Likewise, previous experiments the germplasm accessions such as IC340947 and IC360831 were highly consistent and noticed highly resistant reaction against BCMV disease and stable across the location and seasons. Therefore, these donors being already utilized in disease breeding programme of Common bean. The germplasm identification committee under the chairmanship of Director, ICAR-IIPR visited the field on 09.03.2020 and examined the BCMV resistant donor in all aspects and GIC committee recommended for submission of germplasm registration proposal for unique germplasm identification.

Morpho-agronomic Characteristics

IC340947: it is having very good plant vigour at early plant stages of crop growth and It has adventitious root system, plant growth habit is bush (determinate) type, green stem pigmentation, the dark green leaves grow alternately on the stems, days to 50% flowering attaining at 75 days, flower colour bears light pink, leaflet shape is ovate-lanceolate, pod colour is pale green and pod shape is slightly curved, pod length is 14.23 cm and physiological maturity attaining at 140 days. It gives seed yield about 22quintal/ha.

Associated characters and cultivated practices

Rajmash grows well in areas where medium rainfall occurs, but not suited to the humid condition. Soil pH should be in the range of 5.5 - 6.0 to obtain maximum yield. The raimash + potato intercropping found quite profitable and efficient in irrigated areas. In hills, it is grown as a Kharif crop where as in plain grown as rabi crop. Seed rate varies with seed size. Bold seeded varieties with a test weight of 350-450 g need 120-140 kg seed/ha, while in small seeded varieties, it varies from 70-100 kg/ha and spacing for Kharif (Hills) - 45-50 cm x 8-10 cm while, Rabi & Spring - 40 cm x 10 cm (irrigated); 30 cm x 10 cm (Rain fed). For enhanced productivity, application of 90-120 kg N ha-1 has been found optimum. Half of the nitrogen should be applied as basal during sowing and rest half as top dressing after first irrigation and application of 60-80 kg P2O5/ha will give better yield. It requires 2 to 3 irrigations in NEPZ, Irrigation at 25 days after sowing is most critical followed by irrigation at 75 days after sowing. The crop matures in 125-130 days. A well-managed crop can easily give 20-25qtls/ha yields.

Reference

Sharma OP, Sharma PN, Sharma PK (1998) Comparative occurrence and distribution patternof French bean mosaic in Himachal Pradesh. *Himachal J Agric. Res.* **24:** 165–171.

Kapil R, Sharma P, Sharma SK, Sharma OP, Sharma OP, Dhar JB, Sharma PN (2011) Pathogenic and molecular variability in Bean common mosaic virus infecting common bean in India. *Arch. Phytopathol. Plant Prot.* **44:** 1081–1092.

Broughton WJ, Hernandez G, Blair M, Beebe S, Gepts P, & J. Vanderleyden, (2003) Bean (*Phaseolus* spp.)-model food legumes. *Plant Soil*, **252:** 55–128.

14. IPM 604-1-7 (IC0639796; INGR21104), a mung bean (*Vigna radiata* L.) germplasm with yellow seed coat colour and early maturity (55 days).

Aditya Pratap, Basavaraja T*, Revanappa SB, Sanjeev Gupta and NP Singh

ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh-208024, India.

*Email: Basavaraja.T@icar.gov.in

Mungbean is a preferred grain legume finding an important place in local cuisine in different parts of the Indian subcontinent. Variable preferences with respect to its grain size, seed coat color (green or yellow) and seed coat luster (shiny or dull) based on cooking type, aroma and taste have been reported from different parts. While most of the consumers prefer shiny green grains, yellow grains are preferred in parts of West Bengal and also a few pockets in Bangladesh and Sri Lanka. Yellow seeded traditional mungbean cultivars are known to be associated with a peculiar aroma after boiling and owing to their organoleptic properties fetch a premium price. However, cultivation area of yellow mungbeans could not expand much due to the associated limitations viz., indeterminate growth habit, asynchronous flowering, high susceptibility to yellow mosaic disease and long crop duration in contrast to the modern high yielding, synchronous and stress resistant mungbean cultivars. This improved mungbean genotype was developed to meet the demand of consumers and farmers who prefer yellow seeds mungbean.

Pedigree

To improve the yellow mungbean cultivars and increase their adaptation, an initiative was taken to improve the local cultivars of Sona Mung through breeding. 3 elite cultivars viz., IPM 99- 125, IPM 02-3, PDM 139 were crossed with a local landrace of Sona Mung collected from Malda District of West Bengal. All the crosses were advanced till F_7 between 2009-16 following pedigree method of breeding and single plant selections were done in each generation F_2 onwards for golden yellow seed coat colour besides other desired traits viz., erect plant type, resistance to yellow mosaic disease, early and synchronous maturity (<70 days) and a wider adaptability to different cropping systems. Finally, the superior fixed lines lines were evaluated in preliminary yield and station trials and 5 outstanding golden yellow seeded lines viz., IPM 604-1-1, IPM 604-1-2, IPM 604-1-6, IPM

604-1-7 and IPM 604-01-8 were identified from the cross IPM 99-125 x Sona Mung. Among these, the genotype IPM604-1-7 performed significantly better then the best check and therefore, was nominated for multilocation evaluationin All India Coordinated Research programme on MULLaRP (AICRP-MULLaRP) in 2019. Currently, this genotype is in advanced stage of evaluation and is expected to be identified and released as superior golden yellow cultivar of mungbean.

Morpho-agronomic Characteristics

IPM 604-1-7 is characterized by determinate, erect and upright plants. The seedlings have green hypocotyls which develop into green stem at vegetative stage. Stem and leaf pubescence is intermediate with medium green leaves. The flower colour is light yellow and the pods at maturity are tan and are slightly curved at the apex. Each pod bears 10-12 seeds. The seeds are oval in shape and are bright yellow in colour. This genotype is an early maturing genotype with <55days maturity. The average seed yield is12-14q/ha.

Cultivation practices

It is suitable for Spring/Summer and kharif seasons and well adapted to fertile, sandy loam soils with good internal drainage and a pH in the range of 6.3 and 7.2. It requires slightly acidic soilfor best growth. Sowing should be done in 22 x 7 cm. Nitrogen fertilizer is usually not required at higher dose in mungbean as this crop fixes a good amount of nitrogen at its own. Phosphate fertilizer is usually required at higher amount in irrigated crops or on severely P-deficient soils.

Once released, this will be a unique genotype to offer the farmers the advantages of golden yellow mungbean cultivar with better disease resistance, wider adaptability and a host of other positive traits and therefore, will help in improving their socio-economic condition.

15. S-208 (IC0638877; INGR21105), a cabbage (*Brassica oleracea* var. *capitata*) germplasm with self-incompatibility (SI), flat compact head and shorter stalk length.

Chander Parkash^{1*}, Sandeep Kumar¹, Shyam Sundar Dey² and Reeta Bhatia²

¹ICAR-IARI Regional Station, Katrain, Himachal Pradesh-175102, India

²ICAR-Indian Agricultural Research Institute, Pusa, New Delhi-110012, India

*Email: cp1968@gmail.com

Cabbage occupies the most important position among the *Brassica* vegetable crops, which are cultivated in temperate

to tropical climatic conditions throughout the world including India (Singh et al., 2009). In cabbage, F1 hybrids

are advantageous since they are very early with uniform maturity and yields better quality heads. They also have resistance to many insect-pests, diseases and tolerance to unfavourable weather conditions. But in India, >95% of the F1 hybrid seed of cabbage is being imported or supplied by the private sector (Koundinya and Kumar, 2014) and seed is sold at very high prices to the farmers. Therefore, there is an immense need to breed high yielding quality cabbage hybrids from public sector in the country, so that their seeds can be made available to the farmers at reasonable prices. The genetic phenomenon of self- incompatibility (SI) has been widely used for commercialization of hybrid seed production in cabbage (Mohanty and Prusti, 2002). The major benefit of SI system is that we can produce hybrid seed by utilizing two self-incompatible lines as parents having dissimilar homozygous S alleles (Kucera et al., 2006). Therefore, a self-incompatible (SI) line, S-208 was developed at ICAR-IARI Regional station Katrain through single plant selection from Pusa Drumhead, anopen pollinated variety of cabbage.

Agro-morphological characteristics

The line, S-208 has compact flattish green coloured heads with average weight of 1.19 kg and shorter stalk length

(0.45 cm). It has very strong self-incompatibility reaction. Hence, hybridity of the hybrids developed by using this line is 100%. Moreover, it has very good combining ability for its use in hybrid breeding. For hybrid seed production it is recommended to follow a planting ratio of 2:1 with fertile male parental line. Hence, this genotype would be instrumental in developing indigenous cabbage hybrids in India.

References

Koundinya AVV and Kumar PP. (2014). Indian vegetable seeds industry: status and challenges. *Intl. J. Plant Animal Environ. Sci.* **4(4):** 62-69.

Kucera V, Chytilova V, Vyvadilova M and Klima M. (2006). Hybrid breeding of cauliflower using self-incompatibility and cytoplasmic male sterility. *Horti. Sci.* **33(4):** 148-152.

Mohanty BK and Prusti AM. (2002). Hybrid vegetable technology-a review. *Agri. Rev.* **23(3):** 149-164.

Singh BK, Sharma SR and Singh B. (2009). Combining ability for superoxide dismutase, peroxidase and catalase enzymes in cabbage head (*Brassica oleracea* var. *capitata* L.). *Sci. Hortic.* **122(2):** 195-199.

16. S-681 (IC0638878; INGR21106), a cabbage (*Brassica oleracea* var. *capitata*) germplasm with self-incompatibility, round and very compact head, smaller plant spread and height with minimum number of non-wrapper leaves.

Chander Parkash^{1*}, Sandeep Kumar¹, Shyam Sundar Dey² and Reeta Bhatia²

¹ICAR-IARI Regional Station, Katrain, Himachal Pradesh-175102, India

²ICAR-Indian Agricultural Research Institute, Pusa, New Delhi-110012, India

*Email: cp1968@gmail.com

Cabbage occupies the most important position among the Brassica vegetable crops, which are cultivated in temperate to tropical climatic conditions throughout the world including India (Singh et al., 2009). In cabbage, F1 hybrids are advantageous since they are very early with uniform maturity and yields better quality heads. They also have resistance to many insect-pests, diseases and tolerance to unfavourable weather conditions. But in India, >95% of the F1 hybrid seed of cabbage is being imported or supplied by the private sector (Koundinya and Kumar, 2014) and seed is sold at very high prices to the farmers. Therefore, there is an immense need to breed high yielding quality cabbage hybrids from public sector in the country, so that their seeds can be made available to the farmers at reasonable prices. The genetic phenomenon of self- incompatibility (SI) has been widely used for commercialization of hybrid seed production in cabbage (Mohanty and Prusti, 2002). The major benefit of SI system is that we can produce hybrid seed by utilizing two self-incompatible lines as parents having dissimilar homozygous S alleles (Kucera et al., 2006). Therefore, a self-incompatible (SI) line, S-681 was developed at ICAR-IARI Regional station Katrain through single plant selection from Golden Acre, an open pollinated variety of cabbage.

Agro-morphological characteristics

The line, S-681 has round and very compact green coloured heads with average weight of 0.92 kg and smaller plant spread (39.27 cm) and height (16.50 cm) with minimum number of non-wrapper leaves (9.67). It has very strong self-incompatibility reaction. Hence, hybridity of the hybrids developed by using this line is 100%. Moreover, it has very good combining ability for its use in hybrid breeding. For hybrid seed production it is recommended to follow a planting ratio of 2:1 with fertile male parental line. Hence, this genotype would be instrumental in developing indigenous cabbage hybrids in India.

References

Koundinya AVV and Kumar PP. (2014). Indian vegetable seeds industry: status and challenges. Intl. J Plant Animal Environ Sci. 4(4): 62-69. Kucera V, Chytilova V, Vyvadilova M and Klima M. (2006). Hybrid breeding of cauliflower using self-incompatibility and cytoplasmic male sterility. *Horti. Sci.* **33(4):** 148- 152.

Mohanty BK and Prusti AM. (2002). Hybrid vegetable technology-a review. *Agri. Rev.* **23(3):** 149-164.

Singh BK, Sharma SR and Singh B. (2009). Combining ability for superoxide dismutase, peroxidase and catalase enzymes in cabbage head (*Brassica oleracea* var. *capitata* L.). *Scientia Horticulturae* **122(2):** 195-199.

17. IPC-21 (DPC-21) (IC0638879; INGR21107), a castor (*Ricinus communis* L.) germplasm pistillate line with good combining ability.

C Lavanya*, G Balakishen, B Usha Kiran, KT Ramya, T Manjunatha, S Senthilvel, P Duraimurugan and M Santhalakshmi Prasad

ICAR-Indian Institute of Oilseeds Research, Hyderabad, Telangana-500030, India.

*Email: c.lavanya@icar.gov.in

IPC-21 (DPC-21), an Stype pistillate line is developed through intra varietal hybridization involving DPC-9 {(VP-1 x (Bhagya x CO-1)} and DCS-45 (163-1 x 99-2) followed by pedigree method of selection and generation advancement of pistillate (female) plants. IPC-21 is of normal plant type with elongated internodes, divergent branching, flat leaves unlike other dwarf pistillate lines viz., SKP-84 and M-574 (Table 1). It has long, conical, heavy spike, both morphologically and genetically distinct to other registered pistillate lines like DPC-9 (INGR01009) and IPC-15 (INGR19017) (Ushakiran and Lavanya, 2016). It is also a good combiner for seed yield, early maturity, effective primary spike length, 100 seed weight and oil content and recommended for development of castor hybrids (Ramya et al. 2018, Lavanya et al., 2018). The utility of IPC-21 in development of hybrids is established through development of an experimental hybrid viz., DCH-1720 (IPC-21 (DPC-21) x DCS-107), a high yielding, wilt resistant hybrid (Lavanya et al., 2018). It is tested in coordinated trials for three years and recorded 6-10 % increase over the best hybrid checks, DCH-519 and DCH-177 (Lavanya et al., 2018).

Screening for leafhopper resistance using infester row method in multi-location trials for two years indicated, IPC-21 (DPC-21) is resistant to leafhopper with a hopper burn grade of 0-1 compared to hopper burn of 4 in susceptible check. IPC-21 is also physiologically efficient with high early vigor (0.47 g/pl), bold seed size (31g/100 seeds), high TDM at 35 DAS (15.3 g/pl), at harvest (357.2 g/plant) and high seed yield (84.1g/ plant) (ICAR-IIOR Annual Report, 2014-15, 2015-16). IPC-21 is resistant to wilt (<10%) compared to the susceptible check, JI-35 (98 %) in National Screening nursery for wilt (NSNW) at IIOR and SK Nagar (Santalakshmi *et al.*, 2016). In a trial on evaluation of 15 new pistillate lines for seed yield

Table 1: Unique morphological traits of IPC-21 (DPC-21)

S. No.	Characteristic	IPC-21 (DPC-21)	SKP-84 (IC-537353)	M-574 (143 of 2020)*
1.	Plant type	Normal	Dwarf	Dwarf
2.	Type of internodes	Elongated	Condensed	Condensed
3.	Leaf lascination	Flat	Cup shaped	Cup shaped
4.	Branching pattern	Divergent	Convergent	Convergent
5.	Stem color	Green	Mahogany	Green
6	Bloom	Double	Triple	Triple

^{*}Registered as extant variety by PPV&FRA

and yield components during rabi 2017-18, in a RBD of three replications, DPC-21 recorded 31% yield increase over the best check, M-574 (551 kg/ha) and 47% oil content. Effective primary spike length is also long (74 cm) compared to the three checks with short to medium long primary spikes (32-56 cm) (Lavanya *et al.*, 2020).

References

Lavanya C, Manjunatha T and S Senthilvel (2020) Evaluation of new castor pistillate lines for agro-morphological characters and sex expression in different seasons. *J. Oilseeds Res.* **37:** 19-21.

Ramya KT, Mukesh Patel, Manjunatha T and C Lavanya (2018) Identification of best combiners for development of castor hybrids under irrigated conditions. *Elect. J. Pl. Breed.* **9(1):** 387-391. ISSN 0975-928X 387. *DOI: 10.5958/0975 928X.2018.00046.7.*

Santalakshmi MP, Bharathi E, Lavanya C and AJ Prabakharan (2016)
Parental lines and advanced breeding material of castor resistant to wilt disease. Ind. Phytopath. **69(4):** 721-723.

Ushakiran B and C Lavanya (2016) Genetic diversity in castor (*Ricinus communis* L.) pistillate lines using EST-SSR markers. *J. Oilseeds Res.* **33(3):** 189-192.

18. DFR C-1 (IC0638881; INGR21108), a chrysanthemum (*Chrysanthemum morifolium* L.), germplasm with spatulate florets and long peduncle (8–12 cm).

Tarak Nath Saha^{1*}, Ganesh B Kadam¹, P Naveen Kumar¹, Gunjeet Kumar², Late Puja Rai², DVS Raju³, Shilpashree KG¹, Ramesh Kumar¹ and KV Prasad¹

¹ICAR-Directorate of Floricultural Research, Shivajinagar, Pune 411005, Maharashtra, India

Chrysanthemum (*Chrysanthemum morifolium* Ramat.) is one of the most widely cultivated garden flowers with diverse and beautiful range of flower colours and forms, and range of height (Swaroop *et al.*, 2008). These characters make it highly suitable for pot culture, bedding purposes and for production of loose flowers for use in garland making, in worship and for decoration purposes (Bala, 2015). It belongs to the family Asteraceae and is an herbaceous short day flowering plant which generally blooms during autumnwinter. In India, chrysanthemum is cultivated extensively in almost all parts of the country either for loose or cut flower; pot-mums, in beddings or for gardening/landscaping purposes.

The chrysanthemum new genetic stock/variety, DFR C-1 (OPCh 16-5-1213) was developed through half-sib selection using PAU D-1 as one of the parent at New Delhi and evaluated at Pune, Maharashtra. (ICAR-Directorate of Floricultural Research was shifted from New Delhi (latitude of 28.6423° N, longitude of 77.1524° E and altitude of 228 MSL) to Pune (latitude of 18.5204° N, longitude of 73.8567° E and altitude of 560 MSL on the western margin of the Deccan plateau in the year 2014). The plants (DFR C-1) produces pink colour flower unlike the parent (PAU D-1) which is white in colour.

Morpho-Agronomic Characteristics

The plants are erect (78.12 cm height) and spreading with sturdy/robust stems, with good number of branches (8 and 16.80 average nos. of primary and secondary branches, respectively). The variety takes about 92-96 days for bud initiation and another 10-12 daysfor flower opening (Table 1). The flowering continues upto 1-2 months. The plant bears attractive pink coloured (RHS colour 64D-Red purple group) double type flowers. The quality of flowers improves in cooler/ winter areas. One month after flowering, the old flower stalks are removed to encourage suckering.

Associated Characters and Cultivated Practices

The variety DFR C-1 (OPCh 16-5-1213) produces pink colour double type flowers. The florets are spatulate in shape. The flowers are placed on long peduncle (8-12 cm), it can therefore be used in table bunch. On an average, each plant produces 154.36 numbers of flowers with average size of 6.22 cm. The field life of flower is about 9.33 days whereas shelf lifeis 3-4 days. As the flowers are double, it can be well used for loose flower, beds and border purpose. It produces prolific suckers after flowering is over.

It is easily cultivated by terminal rooted cuttings as well as suckers. The rooted cuttings (5-7 cm) are prepared during

Table 1: Performance of the Identified Variety 'DFR C-1' (OPCh 16-5-1213) over Parent 'PAU D1'

S.N.	Character	2017-18	2018-19	2019-20	Mean	
5.14.	Character	DFR C 1	DFR C 1	DFR C 1	DFR C 1	PAU D 1
1.	Plant height (cm)	67.53	82.16	84.66	78.12	83.34
2.	Plant Spread (cm)	48.73	78.54	80.54	69.27	64.52
3.	No. of Primary branches/plant	8	7.8	8.2	8.00	4
4.	No. of Secondary branches/plant	13	18.4	19	16.80	12.33
5.	Days to bud initiation	97.67	92.4	95.2	95.09	74.00
6.	Days to flower opening	100	102.4	108.2	103.53	90.00
7.	No. of flowers per plant	114.67	174.8	173.6	154.36	62.33
8.	Flower diameter (cm)	6.27	5.74	6.64	6.22	4.30
9.	Individual weight of flowers(g)	-	-	-	2.6	-
10.	Field life of flowers (days)	-	9.2	9.4	9.3	-
11.	Shelf/ vase life (days)	-		-	3-4	-

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

³ICAR-DFR Regional Station, Kadiyam, Andhra Pradesh-533125, India

^{*}Email: tnsaha1981@gmail.com

June- July and can be transplanted during July-August. Flowering commences from November-December and continues upto January. The plant prefers mild climatic condition and can be grown on a wide range of soil. However, it prefers deep friable soil rich in organic content having good water holding capacity and pH around 6.0-7.0. NPK@ 125:120: 125 kg/ha along with FYM (20-25t/ha) is recommended for good growth and flowering.

References

Bala M (2015) Evaluation of chrysanthemum (*Chrysanthemum morifolium* Ramat.) genotypes for morphological traits. *J. Hortl. Sci.* **10(2):** 242-244.

Swaroop K, KV Prasad and DVS Raju (2008) Evaluation of chrysanthemum (*Dendranthema grandiflora* Tzvelev.) germplasm in winter season under Delhi conditions. *J. Orn. Hort.* **11:** 58-61.

19. DFR C-2 (IC0638882; INGR21109), a chrysanthemum (*Chrysanthemum morifolium* L.), germplasm with cream white, ligulate type fragrant flowers.

Tarak Nath Saha^{1*}, Ganesh B Kadam¹, P Naveen Kumar¹, Gunjeet Kumar², Late Puja Rai², Girish KS¹, DVS Raju³, Shilpashree KG¹, Ramesh Kumar¹ and KV Prasad¹

¹ICAR-Directorate of Floricultural Research, Shivajinagar, Pune, Maharashtra-411005, India

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

³ICAR-DFR Regional Station, Kadiyam, Andhra Pradesh-533125, India

*Email: tnsaha1981@gmail.com

Chrysanthemum (*Chrysanthemum morifolium* Ramat.) is one of the most widely cultivated garden flowers with diverse and beautiful range of colours, shades, widely variable flower shapes and range of height (Swaroop *et al.*, 2008). These characters make it highly suitable for pot culture, bedding purposes and for production of loose flowers for use in garland making, inworship and for decoration purposes (Bala, 2015). It belongs to the family Asteraceae and is an herbaceous short day flowering plant which generally blooms during autumn-winter. In India, chrysanthemum is cultivated extensively in almost all parts of the country either forloose or cut flower; pot-mums, in beddings or for gardening/landscaping purposes.

The chrysanthemum variety DFR C-2 (OPCh 9-4-1011) was developed through half-sib selection method using PAU D-1 as one of the parent at New Delhi and evaluated

at Pune, Maharashtra. (ICAR- Directorate of Floricultural Research was shifted from New Delhi (latitude of 28.6423° N, longitude of 77.1524° E and altitude of 228 MSL) to Pune (latitude of 18.5204° N, longitude of 73.8567° E and altitude of 560 MSL on the western margin of the Deccan plateau in the year 2014).

Morpho-Agronomic Characteristics

Plants are erect (65.87 cm height) and very spreading (17.33 and 31.04 average numbers of primary and secondary branches, respectively). The average leaf length is 7-9 cm andwidth 4-6 cm. Also the internodal distance is 2.3-4.5 cm which makes the plant tall. The plant bears good number of flowers per plant (166.33 nos.) which makes it suitable for garden as well as loose flower production. The average flower size is 5.66 cm with 3-4 days

Table 1: Performance of the Identified Variety 'DFR C-2' (OPCh 9-4-1011) over Parent 'PAU D1'

S.N.	Character	2017-18	2018-19	2019-20	Mean	
3.11.	Character	DFR C 2	DFR C 2	DFR C 2	DFR C 2	PAU D 1
1.	Plant height (cm)	65.93	65.08	6.66	65.87	83.34
2.	Plant Spread (cm)	55.9	70.22	69.42	65.18	64.52
3.	No. of Primary branches/plant	17	18.2	16.8	17.33	4
4.	No. of Secondary branches/plant	30.33	31.2	31.6	31.04	12.33
5.	Days to bud initiation	96	92.6	94.6	94.40	74.00
6.	Days to flower opening	102	108.8	109.8	106.87	90.00
7.	No. of flowers per plant	181	172	157.8	170.27	62.33
8.	Flower diameter (cm)	6.83	4.82	5.34	5.66	4.30
9.	Individual weight of flowers(g)	-	-	-	1.1	-
10.	Field life of flowers (days)	-	9	6.2	9.1	-
11.	Shelf/ vase life (days)	-		-	3-4	-

of shelf life and 8-9 days of field life (Table 1). The plant bears cream white coloured (RHS NN155B, White Group) semi-double type flowers.

Associated Characters and Cultivated Practices: The plant takes about 102-109 days for flower opening and the flowering continues upto 1-2 months. It bears semi-double type flowers with ligulate shape florets. The flowers possess mild fragrance and attract more number of honey bees compared to other cultivars. It makes them suitable for garden decoration, loose flower production and also for pot-culture (with staking). It produces prolific suckers after flowering is over.

It is easily cultivated by terminal rooted cuttings as well as suckers. The rooted cuttings (5-7 cm) are prepared during June- July and can be transplanted during July-August.

Flowering commences from November-December and continues upto January. The plant prefers mild climatic condition and can be grown on a wide range of soils. However, it prefers deep friable soil rich in organic content having good water holding capacity and pH around 6.0-7.0. NPK@ 125:120: 125 kg/ha along with FYM (20-25t/ha) is recommended for good growth and flowering.

References

Bala M (2015) Evaluation of chrysanthemum (*Chrysanthemum morifolium* Ramat.) genotypes for morphological traits. *J. Hortl. Sci.* **10(2):** 242-244.

Swaroop K, KV Prasad and DVS Raju (2008) Evaluation of chrysanthemum (*Dendranthema grandiflora* Tzvelev.) germplasm in winter season under Delhi conditions. *J. Orn. Hort.* **11:** 58-61.

20. DFR C-3 (IC0638883; INGR21110), a chrysanthemum (*Chrysanthemum morifolium* L.) germplasm suitable for pot mums and garden decoration.

Tarak Nath Saha^{1*}, Ganesh B Kadam¹, P Naveen Kumar¹, Gunjeet Kumar², Late Puja Rai², Girish KS¹, DVS Raju³, Shilpashree KG¹, Ramesh Kumar¹ and KV Prasad¹

¹ICAR-Directorate of Floricultural Research, Shivajinagar, Pune, Maharashtra-411005, India

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

³ICAR-DFR Regional Station, Kadiyam, Andhra Pradesh-533125, India

*Email: tnsaha1981@gmail.com

Chrysanthemum (*Chrysanthemum morifolium* Ramat.) is one of the most beautiful flowering plants, commercially grown in different parts of the world for loose flower, cut flower and potted ornamentals. It is a herbaceous short day flowering plant which generally blooms during autumn-winter. It belongs to the family Asteraceae. In India it is commercially cultivated in Andhra Pradesh, Haryana, Karnataka, Maharashtra, Punjab, Telangana, Tamil Nadu, Uttar Pradesh, West Bengal and many other states. More than 2000 cultivars are reported all over theworld and about 1000 from India (Kumar *et al.*, 2019).

The chrysanthemum variety DFR C-3 (OPCh 26-7-1314) was developed through half-sib selection using PAU A-64 as one of the parent at New Delhi and evaluated at Pune, Maharashtra. (ICAR–Directorate of Floricultural Research was shifted from New Delhi (latitude of 28.6423° N, longitude of 77.1524° E and altitude of 228 MSL) to Pune (latitude of 18.5204° N, longitude of 73.8567° E and altitude of 560 MSL on the western margin of the Deccan plateau in the year 2014). The plants produce yellow colour flower unlike the parent which produces purple colour flowers.

Table 1: Performance of the Identified Variety 'DFR C-3' (OPCh 26-7-1314)

S. No.	Character	2017-18	2018-19	2019-20	Mean
1.	Plant height (cm)	52.1	55.96	56.3	54.79
2.	Plant Spread (cm)	43.53	64.72	63.74	57.33
3.	No. of Primary branches/ plant	6	6.4	9.2	7.20
4.	No. of Secondary branches/ plant	10	14	13.4	12.47
5.	Days to bud initiation	115	101.2	101.2	105.80
6.	Days to flower opening	123.67	108.8	108	113.49
7.	No. of flowers per plant	166.33	163	169.2	166.18
8.	Flower diameter (cm)	5.8	5.46	5.22	5.49
9.	Individual weight of flowers (g)	-	-	-	1.15
10.	Field life of flowers (days)	-	9	7.8	8.4
11.	Shelf/ vase life (days)	-		-	2-3

Morpho-Agronomic Characteristics

The plants are spreading (57.33cm), medium in height (54.79cm) with good branching (7.20 and 12.47 Average numbers of primary and secondary branches, respectively). The plant appears in a dome shape during flowering. The plant gives an appearance of leaflessness during flowering. The average flower size is 5.49 cm and the field life of flower is about 8.4 days. The petals are ligulate in shape. The plant bears attractive yellow coloured (RHS colour 7C- Yellow group) single type flowers. The quality of flowers improves in cooler/ winter areas. One month after flowering the old flower stalks are removed to encourage suckering.

Associated Characters and Cultivated Practices

The plant takes about 101-115 days for bud initiation and takes another 7-10 days for flower opening. The plant bears yellow colour single type flowers and the florets are ligulate in shape. The plant bears 163-169 numbers of flowers per plant with an average size of 5.49 cm. The field life of the flower is 7-8 days. The plants appear in dome shape during flowering and are very attractive. During peak flowering, the

plant gives an appearance of leaflessness. It is very much suitable for pot culture and can be of great demand for urban dwellings. It produces prolific suckers after flowering is over.

It is easily cultivated by terminal rooted cuttings as well as suckers. The rooted cuttings (5-7 cm) are prepared during June-July and can be transplanted during July-August. Flowering commences from November-December and continues upto January. The plant prefers mild climatic conditions and can be grown on a wide range of soils. However, it prefers deep friable soil rich in organic content having good water holding capacity and pH around 6.0-7.0. NPK@ 125:120: 125 kg/ha along with FYM (20-25t/ha) is recommended for good growth and flowering.

Reference

Kumar Rajiv, LC De and P Baiswar (2019) Production of Chrysanthemum Under Greenhouse Condition. In: MTC on Advanced Technologies for Production of Commercial Flower Crops under Greenhouse Conditions, NRCO Sikkim, pp 40-44.

21. N/9-42 (IC0638884; INGR21111), a potato (*Solanum tuberosum* L.) germplasm with better nitrogen use efficiency.

Raj Kumar*1 and Manoj Kumar2

ICAR-Central Potato Research Institute, Research Station, Jalandhar, Punjab-144026, India

Efficient use of nitrogen (N) is important as the recovery of N in plants is less than 50 %. Development of N use efficient cultivars can reduce input cost for the farmers and can also help in preventing environmental degradation. In India Potato is grown under diverse agro-climatic conditions. Farmers cannot afford high doses of fertilizers. Keeping this in view a line N/9-42 was bred at Central Potato Research Station, Jalandhar that can give comparatively higher yield at relatively lower N availability.

Morpho-agronomic Characteristics

Tubers of N/9-42 are oval shape, white skin, with shallow eye depth and yellow flesh colour. The flower corolla colour is white. Foliage is semi-compact and plant tall. Leaflets are ovate. Sprout colour is white-green. N/9-42 is a high yielding line with very good N use efficiency as it produce yield betterthan popular varieties at lower doses of N. After initial evaluation at Central Potato Research Station, Jalandhar, it was tested for tuber yield for 2 crop

Table 1: Tuber yield of hybrid/cultivars

	Yield (t/h	Yield (t/l	Yield (t/ha) at N dose (kg/ha) during 2016-2017							
Hybrid/cultivar	0	80	160	240	Mean	12.1	24.2	30.6	31.2	24.5
N/9-42	24.7	33.2	41.2	44.2	35.8	13.3	22.9	25.0	28.1	22.3
Kufri Pukhraj	22.2	27.3	32.7	36.6	29.7	10.6	18.8	24.2	25.0	19.7
Kufri Gaurav	21.6	30.6	33.6	33.2	29.7					2.07
CD(5%) Genotype					3.25					N/A
CD (5%) Genotype x dose					N/A					

^{*}ICAR-CPRI-Regional Station, Modipuram, Uttar Pradesh-250110, India

^{*}Email: rajcprs@hotmail.com

Table 2: Agronomic use efficiency (kg tuber/kg N applied) of hybrid/Cultivars

	_	c use efficien a) during 201	,	kg N) at N	Agronomic use efficiency (kg tuber/kgN) at N dose (kg/ha) During 2016-2017			
Hybrid/cultivar	80	160	240	Mean	80	160	240	Mean
N/9-42	106.489	102.824	81.222	96.845	151.25	115.445	79.648	115.448
Kufri Pukhraj	82.127	69.903	63.185	71.738	118.981	72.908	61.725	84.538
Kufri Gaurav	111.701	74.766	48.14	78.202	102.264	84.618	59.69	82.191
CD(5%) Genotype				16.46				26.45
CD (5%) Genotype x dose				N/A				N/A

seasons at ICAR-Central Potato Research Institute Campus Modipuram from 2015 to 2017. The trial was laid out with four applied nitrogen doses i.e. 0, 80, 160 and 240 kg/ha. In both the crop seasons yield of N/9-42 averaged over four doses was significantly better than popular N use efficient cultivars Kufri Pukhraj and Kufri Gaurav (Tables 1

and 2). The agronomic N use efficiency of N/9-42 was also significantly better than control varieties in both 2015-2016 and 2016-2017 crop seasons (Tables 1 and 2).

this accession is medium maturing and moderately resistant to late blight and disease.