Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXIIIrd meeting held on December 7th, 2015 at the ICAR-National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 30 germplasm lines out of 68 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. Mainagali (IC0390780; INGR15037), Rice (*Oryza sativa* L.) Germplasm with Long Sterile Glume

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Chhattisgarh has a wide variability of rice germplasm. Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur maintains a huge collection of 23,250 rice germplasm accessions. The registered germplasm Mainagali (IC0390780, INGR15037) with long sterile glume was collected from Dharmjaigarh Block of Raigarh District of Chhattisgarh.

Morpho-agronomic characteristics: The lemma palea colour of registered germplasm is brown and kernel colour is white with long slender grains. Its spikelets look like flying birds.

Associated characters and cultivation practices: In this accession spikelets are found with long sterile glumes. Length of sterile glume is nearer to lemma length. Long sterile glumes prevent infestation of insect pests in spikelets. This accession is planted normally in mid land condition of Chhattisgarh Plains.

References

Accession register year 1971-74, part I p. 269.

Pandey RL, NK Motiramani, AK Sarawgi, RK Verma, SB Verulkar, D Sharma, GR Sahu, VS Trimurthy and BC Shukla (2008). Catalogue on Indigenous Rice (*Oryza sativa* L.) Germplasm of Chhattisgarh and Madhya Pradesh Part-II (Eds.) ASRAS Sastri, SS Rao and RN Sharma. IGKV Raipur (C.G.):307 p.

Morphological descriptions and mean agronomic traits are presented below

Characteristics	Mainagali (IC0390780, INGR15037)
Basal leaf sheath colour (BLSC)	Green
Leaf blade colour (LBC)	Green
Collar colour (CC)	Green
Auricle colour (AC)	Light Green
Culm internode colour (CmlC)	Green
Apiculous colour (ApC)	Light Green
Stigma colour (SgC)	White
Awning (An)	Absent
Days to maturity (DM)	132.5
Plant height (PH) cm	161.7
Tiller No. (Til No.)	5.5
Lemma palea colour (LmPC)	Brown
Seed coat colour (ScC)	White
100 grain weight (TW) gm	3.31
Grain length (GRL) mm	9.0
Grain breadth (GRB) mm	2.9
Grain ratio (L/B)	3.1
Grain type	Long Slender

Note: Quantitative data given based on the mean of 4 years.

Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi–110012.

2. Nariyal Phool (IC0390772; INGR15038), a Rice (*Oryza sativa* L.) Germplasm with Clustered Spikelets in the Range of 2-10

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Chhattisgarh is blessed with a wide variability of rice germplasm accessions. IGKV, Raipur has a huge collection of 23,250 rice germplasm accessions. The registered germplasm Nariyal Phool **(**IC0390772, INGR15038) with clustered spikelets was collected from Saraipali block of Mahasamund district of Chhattisgarh.

Morpho- agronomic characteristics: The lemma palea colour of the germplasm is gold and gold furrows on straw and kernel colour is white and translucent. Due to clustering habit, spikelets look like the flower of coconut, so it is called Nariyal Phool by local inhabitants.

Associated characters and cultivated practices: In this accession clustering of spikelet recorded in broad range i.e. 2 to 10 grains amongst all clustered accessions available in IGKV rice germplasm. Whereas, clustering of 3 grains was found in large frequency (35.4%) followed by 4 grains (20%). A minimum frequency of clustering observed was 10 grains (2.55%). This germplasm accession is cultivated in low land condition of Chhattisgarh Plains.

Morphological description and mean agronomic traits are presented below

Characteristics	Nariyal Phool (IC 0390772, INGR 15038)
Basal leaf sheath colour (BLSC)	Green
Leaf blade colour (LBC)	Green
Collar colour (CC)	Green
Auricle colour (AC)	Light Green
Culm internode colour (CmlC)	Green
Apiculous colour (ApC)	Light Green
Stigma colour (SgC)	White
Awning (An)	Absent
Days to maturity (DM)	145.8
Plant height (PH) cm	138.6
Tiller No. (Til No.)	10.7
Lemma palea colour (LmPC)	Gold and gold furrows on straw
Seed coat colour (ScC)	White
100 grain weight (TW) gm	1.91
Grain length (GRL) mm	8.4
Grain breadth (GRB) mm	2.4
Grain L/B ratio	3.5
Grain type	Medium Slender

Note: Quantitative data given based on the mean of 4 years.

References

Sahu GR, RK Rao, JK Tiwari and AK Sarawgi (2014) Clustering Pattern in some indigenous Rice accessions from C.G. *Indian J. Plant Genet. Resour.* **27:** 225-229.

Sarawgi AK, GR Sahu, R Verma, SB Verulkar, S Nair, S Bhandarkar, RRSaxena and D Sharma (2012) A Catalogue of Unique Rice Germplasm Collection from Chhattisgarh. *IGKV/Pub*/2012/18: 57 p.

Pandey RL, NK Motiramani, AK Sarawgi, RK Verma, SB Verulkar, D Sharma, GR Sahu, VS Trimurthy and BC Shukla (2008) Catalogue on Indigenous Rice (*Oryza sativa* L.) Germplasm of Chhattisgarh and Madhya Pradesh Part-II (Eds.) ASRAS Sastri, SS Rao and RN Sharma. IGKV Raipur (C.G.): p. 307.

3. KBRL77-1 (IC0616061; INGR15039), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. KBRL 57, a Karnal bunt (KB) free wheat stock was developed from a cross between Aldan and H567.71, both lines are resistant to the disease (Bala *et al.,* 2015). This stock was used as a donor to introgress the KB resistance into PBW 343, the famous wheat cultivar of India. The introgression was done using conventional backcrossing method along with artificial inoculations with KB fungus. KBRL 77-1 is one such line developed through this introgression.

Morpho-agronomic characteristics: The parental lines PBW 343 and KBRL 57 and the germplasm KBRL 77-1 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980).The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in table 1a & 1b.

Associated characters and cultivation practices: The germplasm KBRL 77-1 is highly resistant to Karnal bunt disease of wheat. KBRL 77-1 is also high yielding and agronomically desirable. With limited sources of resistance to KB, KBRL 77-1 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): MS Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

Aujla SS, Grewal AS and I Sharma (1980) A screening technique for Karnal bunt disease of wheat. *Crop Improv.* **7:** 145-146.

Bala R, Satish Kumar, Bains NS and I Sharma (2015) Development of disease resistant bread wheat (*Triticum aestivum*) line in background of PBW 343 and genetics of Karnal bunt-free trait. *Indian Phytopath.***68**: 42-44.

Table 1a. KB infection and yield data of KBRL 77-1 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 77-1	KBRL 57/*6PBW 343	92	146	114	63	46
KBRL 57	Donor Parent	97	149	123	54	46
PBW 343	Recipient parent	93	142	134	55	43

Table 1b. Agronomic characteristics of KBRL 77-1 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 77-1	KBRL 57/*6PBW 343	0.8	0.4	0.5	0.5	51.6	44.9	52.3	49.6
KBRL 57	Donor Parent	0.0	0.0	0.3	0.1	41.3	39.2	41.3	40.6
PBW 343	Recipient parent	15.3	11.4	19.7	15.5	43.5	39.8	44.2	42.5

4. KBRL 78-2 (IC0616062; INGR15040), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High 1000 Grain Weight

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 78-2 is one such line developed utilizing Aldan as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and Aldan and the germplasm KBRL 78-2 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 78-2 and the parents

		KB infection (%)				Yield (q/ha)			
Name	Pedigree	2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 78-2	ALDAN/*6WH 542	1.7	1.7	2.0	**1.8**	51.2	49.6	46.8	**49.2**
ALDAN	Donor Parent	3.2	0.8	1.6	**1.9**	35.0	34.0	32.5	**33.8**
WH 542	Recipient parent	42.1	37.9	46.4	**42.1**	47.3	44.7	45.3	**45.8**

Table 1b. Agronomic characteristics of KBRL 78-2 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/ meter	Grains per spike	1000-grains weight
KBRL 78-2	ALDAN/*6WH 542	94	148	114	63	51
ALDAN	Donor Parent	101	150	103	45	49
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 78-2 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics and high 1000 grains weight of 51 g. With limited sources of resistance to KB, KBRL 78-2 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous(2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): MS Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

Aujla SS, AS Grewal and I Sharma (1980) A screening technique for Karnal bunt disease of wheat. *Crop Improv.* **7:** 145-146.

Bala R, I Sharma and NS Bains (2011) Genetic analysis of Karnal bunt (*Tilletia indica* Mitra) in near isogenic lines of bread Wheat (*Triticum aestivum L.). J. Wheat Res.***3**: 59-62.

Kaur A, MA Joshi and I Sharma (2011) Genetics of Karnal bunt resistence in a new set of bread wheat lines. *Crop Improv.* **38**: 38-44.

Sharma I, NS Bains, K Singh and GS Nanda (2005) Additive genes at nine loci govern Karnal bunt resistance in a set of common wheat cultivars. *Euphytica* **142:** 3071-3078.

5. KBRL 79-2 (IC0616063; INGR15041), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High Number of Tillers/m

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.,* 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.,* 2011). KBRL 79-2 is one such line developed utilizing CMH 77.308 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and CMH 77.308 and the germplasm KBRL 79-2 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 79-2 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 79-2	CMH 77.308/*6 WH 542	2.5	2.3	1.9	2.2	49.7	51.3	52.6	51.2
CMH 77.308	Donor Parent	1.9	3.2	2.4	2.5	32.0	36.0	38.0	35.3
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 79-2 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/ meter	Grains per spike	1000-grains weight
KBRL 79-2	CMH 77.308/*6WH 542	97	137	146	57	53
CMH 77.308	Donor Parent	103	149	92	43	46
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 79-2 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics and high number of tillers per meter. With limited sources of resistance to KB, KBRL 79-2 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): M S Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

Aujla SS, AS Grewal and I Sharma (1980) A screening technique for Karnal bunt disease of wheat. *Crop Improv.* **7:** 145-146.

Bala R, I Sharma and NS Bains (2011) Genetic analysis of Karnal bunt (*Tilletia indica Mitra*) in near isogenic lines of bread Wheat (*Triticum aestivum L.*). *J. Wheat Res.* **3**: 59-62.

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Sharma I, NS Bains, K Singh and GS Nanda (2005) Additive genes at nine loci govern Karnal bunt resistance in a set of common wheat cultivars. *Euphytica* **142:** 3071-3078.

6. KBRL 80-3 (IC0616064; INGR15042), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High Number of Grains/Spike

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al*., 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 80-3 is one such line developed utilizing H 567.71 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and H 567.71 and the germplasm KBRL 80-3 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a.KB infection and yield data of KBRL 80-3 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 80-3	H 567.71/*6WH 542	1.3	2.6	1.4	1.8	42.6	45.2	46.8	44.9
H 567.71	Donor Parent	3.0	1.9	2.8	2.6	36.2	32.1	31.6	33.3
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 80-3 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 80-3	H 567.71/*6WH 542	96	147	123	70	50
H 567.71	Donor Parent	105	146	104	46	45
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 80-3 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics and high number of grains per spike. With limited sources of resistance to KB, KBRL 80-3 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): M S Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

Aujla SS, AS Grewal and I Sharma (1980) A screening technique for Karnal bunt disease of wheat. *Crop Improv.* **7**:145-146.

Bala R, I Sharma and NS Bains (2011) Genetic analysis of Karnal bunt (*Tilletia indica* Mitra) in near isogenic lines of bread Wheat (*Triticum aestivum L.). J. Wheat Res.***3**:59-62.

Kaur A, MA Joshi and I Sharma (2011) Genetics of Karnal bunt resistence in a new set of bread wheat lines. *Crop Improv.* **38**:38-44.

Sharma I, NS Bains, K Singh and GS Nanda (2005) Additive genes at nine loci govern Karnal bunt resistance in a set of common wheat cultivars. *Euphytica* **142:**3071-3078.

7. KBRL 81-1 (IC0616065; INGR15043), a Wheat (*Triticum aestivum)* Germplasm with Karnal Bunt Resistance

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.,* 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in the derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 81-1 is one such line developed utilizing HD 29 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and HD 29 and the germplasm KBRL 81-1 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 81-1 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 81-1	HD 29/*6WH 542	3.4	2.9	4.7	3.6	54.3	44.8	49.2	49.4
HD 29	Donor Parent	4.1	2.8	3.9	3.6	31.0	34.8	38.1	34.6
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 81-1 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 81-1	HD 29/*6WH 542	89	148	116	58	45
HD 29	Donor Parent	96	145	106	48	42
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 81-1 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics. With limited sources of resistance to KB, KBRL 81-1 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): M S Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

Aujla SS, AS Grewal and I Sharma (1980) A screening technique for Karnal bunt disease of wheat. *Crop Improv.* **7:** 145-146.

Bala R, I Sharma and NS Bains (2011) Genetic analysis of Karnal bunt (*Tilletia indica Mitra*)in near isogenic lines of bread Wheat (*Triticum aestivum* L.). *J. Wheat Res.* **3**:59-62.

Kaur A, MA Joshi and I Sharma (2011) Genetics of Karnal bunt resistence in a new set of bread wheat lines. *Crop Improv.* **38**:38-44.

Sharma I, NS Bains, K Singh and GS Nanda (2005) Additive genes at nine loci govern Karnal bunt resistance in a set of common wheat cultivars. *Euphytica* **142:**3071-3078.

8. KBRL82-2 (IC0616066; INGR15044), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High Number of Tillers/m

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in the derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 82-2 is one such line developed utilizing HP 1531 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and HP 1531 and the germplasm KBRL 82-2 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 82-2 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 82-2	HP 1531/*6WH 542	2.1	3.6	4.5	3.4	52.7	47.6	49.9	50.1
HP 1531	Donor Parent	2.8	1.7	3.1	2.5	29.1	34.5	33.7	32.4
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 82-2 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 82-2	HP 1531/*6WH 542	91	139	143	54	47
HP 1531	Donor Parent	107	147	107	49	49
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 82-2 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics including high number of tillers per meter. With limited sources of resistance to KB, KBRL 82-2 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

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9. KBRL 83-3 (IC0616067; INGR15045), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High 1000 Grains Weight

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Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in the derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 83-3 is one such line developed utilizing W 485 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and W 485 and the germplasm KBRL 83-3 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 83-3 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 83-3	W 485/*6WH 542	3.6	1.5	2.7	2.6	51.3	51.6	49.3	50.7
W 485	Donor Parent	2.4	3.4	3.3	3.0	36.1	37.0	35.6	36.2
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 83-3 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 83-3	W 485/*6WH 542	89	149	142	54	49
W 485	Donor Parent	99	149	116	45	49
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 83-3 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics including high 1000 grains weight. With limited sources of resistance to KB, KBRL 83-3 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

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10. PAU16055 (IC0616571; INGR15046), a Wheat (*Triticum aestivum* L.) Germplasm with Leaf Rust and Stripe Rust Resistance Genes Lr57 and Yr40

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An *Aegilops geniculata* ($U^gU^gM^gM^g$) accession PAU3547 was crossed with a leaf rust and stripe rust susceptible *T. aestivum* cv. WL711 and disomic substitution lines with 5M chromosome of *Ae. geniculata* substituted for 5D of wheat {DS5D(5M)} were developed through restricted backcrossing and selfing. These substitution lines were resistant to leaf rust and stripe rust and have been registered as INGR03018. For the reduction of the linkage drag, one of the substitution lines was crossed with a Chinese Spring stock carrying inhibitor for *Ph1* locus (CSPh^I) and resulting F_1 was crossed to WL711. Leaf rust and stripe rust resistant introgression lines (ILs) were developed by induced homoeologous chromosome pairing between wheat chromosome 5D and $5M^g$ of *Aegilops geniculata* (UM). Characterization of rust resistant homozygous ILs with Genomic *in situ* hybridization (GISH) method using *Aegilops comosa* (M) DNA as probe identified an IL PAU16055 (syn. T598) having small introgression on the short arm of wheat chromosome 5D. The IL PAU16055 showed complete resistance to the most prevalent pathotypes of leaf rust and stripe rust in India. Molecular mapping using physically mapped RFLP probes revealed that the alien introgression in PAU16055 conferring resistance to leaf rust and stripe rust comprised less than 25% of the short arm of wheat chromosome 5D (Kuraparthy *et al.,* 2007).

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11. PAU16057 (IC0616573; INGR15047), a Wheat (*Triticum aestivum* L.) Germplasm with New leaf Rust and Stripe Rust Resistance Genes

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Aegilops umbellulata acc. 3732 was found to be an excellent source of resistance to major wheat diseases including leaf rust and stripe rust. An amphiploid *Ae. umbellulata* acc. 3732 and *Triticum durum* cv. 'WH890' was crossed with Chinese Spring Ph^I to induce homoeologous pairing between *Ae. umbellulata* and wheat chromosomes. The F_1 was crossed to the susceptible *Triticum aestivum* cv. 'WL711' and leaf rust and stripe rust resistant plants were selected among the backcross progenies. Homozygous lines were selected and screened against six *Puccinia triticna* and four *Puccinia striiformis* f. sp. *tritici* pathotypes at the seedling stage and a mixture of prevalent pathotypes of both rust pathogens at the adult plant stage. Depending on the rust reactions and allelism tests, the introgression lines with new seedling leaf rust and stripe rust resistance genes were identified. Introgression line PAU16057 carries two new genes - one for leaf rust resistance and one for stripe rust resistance introgressed into wheat from *Ae. umbellulata* (Chhuneja *et al.,* 2008). This introgression with no apparent linkage drag is being used in the wheat breeding programme. A marker *Lr57-Yr40_caps16* is the closest linked marker which is being used for marker assisted selection of these genes. Leaf rust and stripe rust resistance genes in PAU16057 have been designated as *Lr76* and *Yr70*, respectively (Bansal *et al.*, 2016).

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12. PAU16058 (IC0616574; INGR15048), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

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Aegilops peregrina (syn *Aegilops variabilis*) 2n=4x=28, a tetraploid non progenitor species of wheat with UUSS genome. It has been found to be a useful source for resistance to stripe rust and leaf rust, making this species an important source to transfer useful genes. *Ae. peregrina* acc. pau 3519, was crossed with Chinese Spring stock, CS (*Ph*^{1}), carrying an inhibitor of *Ph*^{I} locus for the induction of homoeologous pairing. The resultant F_1 plants were crossed with rust susceptible *T. aestivum* cv. WL711(NN), which has *kr* (crossability) alleles. All BC_1 plants were screened at the seedling stage and adult plant stage against leaf rust and stripe rust. The plants resistant to both the rusts were backcrossed to WL711 (NN) to recover the recurrent genotype. Some selected BC_2F_1plants were selfed to BC_2F_4introgression lines. Homozygous wheat-*Ae. peregrina* ILs *viz.* PAU16058 with 2n=42 chromosomes was selected for a donor stock for transfer of leaf rust and stripe rust resistance to elite wheat backgrounds.Molecular mapping using F_2 population between PAU16058 and WL711 mapped stripe rust resistance gene *YrP* at a distance of 6.7cM from three co-localized markers (*Xgwm234, 5DS_276,* and *5DS_159*) while leaf rust resistance gene *LrP* was mapped at distance of 1.1cM from *YrP* towards distal end of chromosome 5D.

13. PAU16059 (IC0617118; INGR15049), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

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The diploid 'A' genome progenitor gene pool of wheat, comprising three closely related species *T. monococcum*, *T. boeoticum* and*T. urartu*, harbours useful genes for many economically important traits including resistance to different diseases. *T. monococcum* accession. PAU14087 and *T. Boeoticum* accession PAU5088 are highly resistant to leaf rust and stripe rust and RIL population generated from these two accessions segregated for resistance to leaf rust and stripe rust. One of the RILs designated as RIL101 wascrossed to susceptible *T. durum* parent, N59 and F_1 further crossed and backcrossed with hexaploidwheat cultivar WL711 led to the development of leaf rust and stripe rust resistant introgression lines (Singh *et al.,* 2007). Segregating populations from these introgression lines have been evaluated in field and glass house for leaf rust and stripe rust resistance and one gene for leaf rust and two genes for stripe rust resistance have been identified. The leaf rust resistance gene from *T. monococcum LrTm* has been mapped on wheat chromosome 6A. Two stripe rust resistance genes one each from *T. monococcum* and *T. boeoticum* were mapped on chromosome 2A and 5A in the RIL population derived from *T. boeoticum/T. monococcum* cross (Chhuneja *et al.,* 2008). One of the QTL designated as *QYrTm.pau-2A* maps in the 3.6 cM region between the SSR markers *Xwmc407* and *Xwmc170*. Other QTL on chromosome 5A designated as *QYrTm-5A* mapped in 8.9 cM region between the markers *Xbarc151* and *Xcfd12* on the long arm. The introgression lines with leaf rust and stripe rust resistance are bing used to transfer these genes to elite wheat backgrounds.

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14. PAU16060 (IC0616575; INGR15050), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

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A leaf rust and stripe rust resistant accession of diploid non-progenitor species with CC genome, namely *Aegilops caudata* L. acc. PAU#3556, was crossed with *Triticum durum* cv. WH868 and an amphiploid was synthesized which was further crossed with a Chinese Spring stock, CS (*Ph*^{1}), carrying an inhibitor for *Ph1* locus, for the induction of homoeologous pairing. The F_1 plants were crossed with a leaf rust and stripe rust susceptible cultivar WL711 for transferring leaf and stripe rust resistance genes to bread wheat. Homozygous F_8 introgression line PAU16060 with 2n=42, was developed with high level of resistance to both leaf rust and stripe rust. It was crossed with wheat cv. PBW343 and BC-RIL population developed. The population segregated for single seedling leaf rust resistance gene and an adult plant stripe rust resistance genes. The genetic mapping using SSRs located leaf rust resistance on short arm of wheat chromosome 5D (Riar *et al.*, 2012). Further genetic analysis using markers from wheat survey sequence (IWGSC 2014) mapped stripe rust resistance locus, temporarily designated as *YrAc*, at the distal most end of 5DS linked with a group of four co-located SSRs and two RGA-STS markers at a distance of 5.3cM. Leaf rust resistance *LrAc* mapped at a distance of 9.0cM from the *YrAc* and at 2.8cM from RGA-STS marker *Ta5DS_2737450* (Toor *et al.*, 2016). PAU16060 and derived BC-RILs are being used for transfer of these genes to elite wheat backgrounds using marker assisted selection.

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15. PAU16062 (IC0616577; INGR15051), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

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An *Aegilops geniculata* accession 3547 was crossed with a susceptible *T. aestivum* cv. WL711 and disomic substitution lines with 5M chromosome of *Ae. geniculata* substituted for 5D of wheat {DS5D(5M)} were developed through restricted backcrossing and selfing. These substitution lines were resistant to leaf rust and stripe rust and have been registered as INGR03018. For the reduction of the linkage drag, one of the substitution lines was crossed with a Chinese Spring stock carrying inhibitor for *Ph1* locus (CS*Ph*^{I}) and F_1 was crossed to WL711. Leaf rust and stripe rust resistant introgression lines were developed by induced homoeologous chromosome pairing between wheat chromosome 5D and 5M^{g} of *Aegilops geniculata* (UM). Characterization of rust resistant homozygous introgression lines using genomic *in situ* hybridization with *Aegilops comosa* (M) DNA as probe identified an introgression line T756 (PAU16062) with cytologically undetectable introgression. The introgression line PAU16062 showed complete resistance to the most prevalent pathotypes of leaf rust and stripe rust in India. Molecular mapping revealed that cryptic alien introgression conferring resistance to leaf rust and stripe rust comprised less than 5% of the short arm of wheat chromosome 5D. Genetic mapping with an F_2 population of PAU16062 demonstrated the monogenic and dominant inheritance of resistance to both diseases. Two diagnostic RFLP markers, previously mapped on chromosome arm 5DS, co-segregated with the rust resistance in the F_2 population. The unique map location of the resistant introgression on chromosome 5DS suggested that the leaf rust and stripe rust resistance genes were new and were designated *Lr57* and *Yr40*(Kuraparthy *et al*., 2007). A STS marker *Lr57-Yr40_caps16* has been found to co-segregate with these genes and is being used for marker assisted transfer of *Lr57* and *Yr40* to elite wheat backgrounds.

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16. PBW703 (IC0616578; INGR15052), a Wheat (*Triticum aestivum* L.) Gene Pyramided Line Carrying Leaf Rust Resistance Genes *Lr*24 and *Lr*28 and Stripe Rust Resistance Genes *Yr*10 and *Yr*15

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High productivity and wide adaptation rendered wheat variety PBW 343 an excellent target for incorporation of rust resistance genes through marker assisted selection (MAS). PBW 343, (one of the 'Attila' sibs from CIMMYT, Mexico) was released by Punjab Agricultural University in 1995 for timely sown, irrigated conditions of North Western Plains Zone (NWPZ). After a reign of more than a decade as a mega variety grown on more than 7 million hectares, PBW 343 succumbed to highly virulent stripe rust race, 78S84, which led to its exit from cultivation in this zone. Earlier it had succumbed to new leaf rust strains belonging to 'race 77 complex'. MAS generated near isogenic lines in PBW 343 background with leaf rust resistance genes *Lr*24 and *Lr*28 had been developed previously (Chhuneja *et al.,* 2005) and a high yielding version named as BWL 9250 was identified for further crosses. BWL9250 was crossed and backcrossed to two different genetic stocks, Avocet 6*/*Yr10* and Avocet 6*/*Yr15* individually for incorporation of the highly effective stripe rust resistance genes *Yr*10 and *Yr*15. Both individual backcross selected progenies (BC_2F_1) were subjected to MAS and identified positive plants were involved in convergent crosses to pyramid the four genes viz., *Lr*24-*Lr*28-*Yr*10-*Yr*15. Genes *Lr*24, *Lr*28 are present on chromosomes 3DL and 4AL respectively while *Yr*10 and *Yr*15 are present on 1BS and have accessions of *Agropyron elongatum* (Syn. *Thinopyrum ponticum*), *Triticum speltoides*, *Triticum spelta* and *Triticum dicoccoides* respectively as their original sources (McIntosh *et al.,* 1995). Markers *Xwmc313*, *scs-73*$_{719}$*-1(SCAR)*, *Xbarc* 8 and *Xpsp*3000 (http://maswheat.ucdavis.edu, http://wheat.pw.usda.gov/cgi-bin/graingenes) were employed for marker assisted selectionof genes *Lr*28, *Lr*24, *Yr*15 and *Yr*10 respectively. A large set of lines was carried to homozygosity with extensive use of off-season location in Lahaul-Spiti (HP) and molecular marker assays for the rust resistance genes. Two outstanding derivatives PBW 698 and PBW 703 were nominated for all India coordinated wheat trials under irrigated regime for timely sown and late sown conditions respectively. PBW 703 was confirmed to be positive for all the four genes with least detriment to the recipient parent attributes and was thus chosen for registration as a stock.

Morpho-agronomic characteristics: PBW 703 is 100 cm tall, with 116 tillers per metre row length and 17 spikelets per spike. It took 99 days to flower (50%) and yielded 52.9 q/ha under timely sown conditions. In contrast to PBW 343, PBW 703 has red glume colour (tightly linked to *Yr*10 gene). PBW 703 was evaluated in NIVT (National Initial Varietal Trial) in 2012-13 at eight locations under late-sown, irrigated conditions. It was promoted to AVT (Advanced Varietal Trial) carried out at 17 locations in NWPZ during 2013-14, whose summary of results is given below:

AVT I -late sown, irrigated conditions	PBW 703	WH 1021	HD 3059	PBW590	PBW343	C.D.
Yield (Q/ha)	46.9	40.3	48.6	40.0	-	0.8
Average coeff. of stripe rust infection	1.3	19.9	4.7	31.5	58.9	-
Average coeff. of leaf rust infection	0.0	11.0	0.2	5.0	8.1	-

Associated characters and cultivation practices: PBW 703 showed complete resistance to two widely prevalent stripe rust races 78S84 and 46S119 and two major leaf rust races 77-5 and 104-4 at seedling as well as adult plant stage. PBW 703 is agronomically competitive, carries four effective rust resistance genes and can be of great significance as a parental line in wheat breeding programmes of the country.

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17. DWR 30 (IC0616068; INGR15053), a Barley (*Hordeum vulgare L.)* Germplasm with High Beta Glucan Content in Grain

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With the changing lifestyles and increasing urbanization, the diseases like coronary heart disease, diabetes *etc*. are on the rise in India. One of the ways suggested to control these diseases is changes in the dietary habits. Besides this in past few years it has been shown that inclusion of nutraceuticals such as soluble dietary fibres can help in controlling the blood cholesterol and glucose levels besides providing benefits to gut health. Cereals, specifically, the barley and oats possess higher amounts (3-7%) of one such dietary fibre called beta glucan. The mixed linkage (1-3; 1-4) beta glucans have been shown to lower postprandial blood glucose and lower the LDL cholesterol and thus help in reducing the risk of heart diseases and type-2 diabetes (Sullivan *et al*., 2013) and is approved in many countries as health benefitting soluble fibre. Screening of germplasm lines and varieties for higher grain beta glucan lines was started at the ICAR-IIWBR, Karnal and the germplasm line DWR30 (hulled barley) has been identified with higher beta glucan content (>6.0 % dwb). The genotype can serve as a good material for basic scientific studies regarding biochemical and genetic factors controlling beta glucan content in the barley grains being grown under sub-tropical climates of India where grain filling period is too short as compared to temperate climates. Further the genotype can also be used for food barley improvement programme, wherein barleys with higher beta glucan content can be very useful from health point of view.

After initial screening at ICAR-IIWBR, Karnal, DWR 30 was evaluated at seven locations (Karnal, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2012-13 and at eight locations (Karnal, Durgapura, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2013-14 for different grain quality traits and average values are given in Table 1 and Table 2.

Table 1. Mean performance (mean of seven locations) of genotypes with high beta glucan content during *rabi* 2012-13

Genotype	Beta Glucan (% dwb)	Protein (% dwb)	Bold grain (%)	Thin grain (%)	1000 grain wt (g)
DWR30	6.9	12.1	74.2	2.5	49.3
DWRUB73 (c)	5.8	13.0	74.8	3.6	49.5
RD2668 (c)	5.7	11.9	62.2	5.4	40.5
BHS352 (c)*	6.5	12.8	14.2	48.2	29.7
HBL276 (c)*	6.0	14.0	20.7	44.1	29.4

Source: AICW&BIP – Barley Network (2012-13)*Husk less barley

Table 2. Mean performance (mean of eight locations) of genotypes with high beta glucan content during *rabi* 2013-14

Genotype	Beta Glucan (% dwb)	Protein (% dwb)	Bold grain (%)	Thin grain (%)	1000 grain wt (g)
DWR30	7.4	12.3	65.0	6.0	48.3
DWRUB73 (c)	5.7	12.7	83.0	4.9	49.8
RD2668 (c)	6.0	12.3	62.9	7.9	41.1
BHS352 (c)*	6.4	14.3	14.1	57.9	32.3
HBL276 (c)*	5.4	15.3	6.6	62.5	25.9

Source: AICW&BIP – Barley Network (2013-14) *Husk less barley

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18. BK 1127 (IC06160298; INGR15054), a Barley (*Hordeum vulgare L.*) Germplasm with High Thousand Grain Weight and Protein Content

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Grain number and thousand-grain weight (TGW) are considered to be the most important grain yield components in case of cereal crops including barley. Thousand grain weight is considered as an important parameter in case of two-row barleys as higher thousand grain weight is important contributing factor in addition to the higher tillering capacity for yield compensation as compared to six rowed varieties. Furthermore, the TGW trait is widely used as a standard indicator for grain development and quality and presently is limiting factor for six row barley in India. At ICAR-IIWBR, Karnal, BK 1127, has been identified having high mean thousand grain weight (mean value > 50.0 g) during two crop seasons over different diverse locations. This genotype can serve as useful material for genetics studies and developing improved barley cultivars for higher thousand grain weight in barley.

There is renewed interest in the barley grain since last few years due to its health benefits and it is expected that in coming years the consumption of food barley may increase (Baik and Ullrich, 2008). Therefore, the genotypes of barley are also being screened for higher protein content without compromising the grain boldness. Genotype BK 1127 has higher protein content (mean value of > 14.0% dwb) also. BK 1127 by combining the higher protein and high thousand grain weight, can prove useful source of nutritional traits for the future food barley improvement programme in the country.

After initial screening at ICAR-IIWBR, Karnal, BK 1127 was evaluated at seven locations (Karnal, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2012-13 and at eight locations (Karnal, Durgapura, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2013-14 for grain quality traits, including the bold seeded checks of two row barley and mean values of different traits are presented in Table 1 and 2.

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Table 1. Mean performance (mean of seven locations) of genotypes with high thousand grain weight during *rabi* 2012-13

Genotype	1000 grain wt (g)	Protein (% dwb)	Bold grain (>2.5mm) (%)	Thin grain (<2.2 mm) (%)
BK 1127	53.6	14.6	94.8	1.0
DWR 91 ©	35.1	12.3	69.6	7.3
DWRUB 52 ©	44.3	11.6	82.5	2.4

Source: AICW&BIP – Barley Network (2012-13)

Table 2. Mean performance (mean of eight locations) of genotypes with high thousand grain weight during *rabi* 2013-14

Genotype	1000 grain wt (g)	Protein (% dwb)	Bold grain (>2.5mm) (%)	Thin grain (<2.2 mm)(%)
BK 1127	59.8	14.4	86.9	1.3
DWR 28 (c)	50.8	12.8	91.1	2.0
DWRUB 52 (c)	46.3	10.2	85.6	3.1
DWRB 92 (c)	50.2	13.5	84.5	5.3
BH 902 (c)*	42.1	11.1	85.6	5.3

Source: AICW&BIP – Barley Network (2013-14) *Six rowed barley

19. SRP#75 (IC0616375; INGR15055), a Self-Compatible Obligate Sexual Guinea Grass (*Panicum maxicum* Jacq.*)* Line

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Guinea grass (*Panicum maximum* Jacq.) is a high yielding perennial multicut forage grass, widely grown in tropical and sub-tropical countries. Tetraploid cytotypes (2n=4x=32) with obligate apomictic mode of reproduction are most predominant (Savidan 1981, Jain *et al.,* 2003). Breeding through hybridization approach is restricted in these grasses owing to apomixis, and thus a large part of potential variability goes untapped (Savidan 2000). Identification and utilization of sexual lines in otherwise apomictic crops has great potential in generating desirable variability for genetical and breeding studies. However, availability of obligate sexual lines in guinea grass is highly limited both nationally and internationally. Moreover, most of the obligate sexual lines are generally weak and self-incompatible, and do not set seed on self-pollination. To our knowledge, no sexual line in guinea grass is registered in India. It thus becomes imperative to identify and utilize sexual lines in guinea grass. Additionally, obligate sexual line with self compatible and vigourous morphology would be added advantage in their selection as one of the parents.

A segregating population (represented by more than 85 progenies) was generated from a cross between an exotic self-incompatible sexual line (SPM92) and an obligate apomictic variety (Riversdale), and was characterized for mode of reproduction (sexual, apomictic or facultative) utilizing methyl salicylate mediated cleared whole ovule mounts observed under differential interference contrast microscope following Kaushal *et al.* (2008). Self-compatibility was tested by subjecting panicles to forced self pollination in pollination bags. Amongst the progenies, a rare self-compatible obligate sexual plant viz., SRP#75 was identified. This plant (SRP#75) generated all sexual embryo-sacs (ES), with no multiple ES and less aborted ES (19%), was self-compatible, vigourous, perennial, multicut and vegetatively propagated, thus making it highly suitable to be utilized as female parent in hybridization programme in guinea grass genetics and breeding experiments.

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20. L-4704 (IC0616579; INGR15056), a Lentil (*Lens culinaris* subsp. *culinaris*) Germplasm with High Grain Iron and Zinc

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The cultivated lentil is an ancient crop originated somewhere in the 'Fertile Crescent'. All Lens species are self-pollinated annual diploids with 2n = 2x = 14 chromosomes having haploid genome size of 4063 Mbp (Arumuganathan and Earle, 1991). It is cultivated in as many as 52 countries across the world with an area and production of 4.08 million ha and 4.36 million t, respectively (FAO, 2013). Its wide-spread cultivation owes to its ability to produce a high quality protein in drought-prone marginal environments. In India, lentil is cultivated on 1.48 million ha area with production and productivity of 0.98 mt and 660 kg ha^{-1}, respectively. Micronutrient malnutrition affects more than two billion people worldwide. Particularly vulnerable are women and preschool children in south Asia, Africa and Latin America. Micronutrient malnutrition has been addressed through food fortification, dietary supplementation and biofortification of staple crops, but to date such programs have had limited success. Sustainable solutions to malnutrition in general, including micronutrient malnutrition, calls for better linking food systems with the dietary needs of people. The biofortification approach holds great promise for improving the nutritional, health, and socioeconomic status of people around the world. Lentils are rich in minerals: Se (500–2500 µg kg^{-1}), Fe (60–80 mg kg^{-1}), Zn (44–54 mg kg^{-1}), and with very low concentration of phytic acid (6–8 mg g^{-1}) and high in ascorbic acid. (Casey Johnson *et al*., 2013). L 4704 is unique because of it is rich in Iron and Zinc, 136.91 mg/kg and 71.69 mg/kg of seed respectively. It was developed at Division of Genetics, IARI, and New Delhi by pedigree method of selection from cross between L 4149 × L 4076 parents.

Morpho-agromonic characters: Morpho-agromonic characters of line L 4704 are its height ranges 40-44 cm with erect plant type with days to 50% flowering ranges from 70-74. It reaches to physiological maturity around 130 to 135 days. The 100 seed weight of L 4704 is 2.5 grams. Seed testa colour is brown and pattern of seed testa is dotted in nature along with orange red cotyledon. The harvest index ranges between 31-33 %. Number of pods per plant rages between 160-165 with a single plant yield of 6.0 to 6.5 gms. Multilocation data on yield in NHZ (1098 kg/ha), NWPZ (1063kg/ha) and in NEPZ (1072 kg/ha) and 100 seed weight (gm) NHZ (3.1 gm) NWPZ (2.9 gm) and NEPZ (3.4 gm) (ACRIP on MULLaRP *Rabi* report – 2010). Uniqueness of this line for having high grin Fe 136.91 mg/kg seed and Zn 71.69 mg/kg seed (reference).

Associated characters and cultivated practices: This line is moderately resistant to resistant root knot nematode (*Meloidogyne inconita*) and nematode M *javanica*. Land should be prepared by one ploughing and two harrowing. Lentil is grown in *rabi* season. Sowing time in October – November in *rabi*. Seed rate is 35-40 kg/ha. Spacing is 30 x 10 cm. Seeds are treated fungicide, insecticide and with rhizobium culture before sowing. Sowing is done by drilling or broadcasting method. One weeding and two hoeing are done for control of weeds. Manuring: 3 to 5 tons FYM and DAP 100 kg/ha. Generally, lentil is grown as unirrigated crop in the residual soil moisture but irrigation at pod development stage helps in getting more yield.

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21. Chilli Queen Sima (IC0615423; INGR15057), a Chilli (*Capsicum annum)* Germplasm with Tall Plant and High Capsaicin Content. SHU (Scoville Heat Unit) Red Fruit 274500 and Green Fruit 259500

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22. CS 1100-1-2-2-3 (IC0511389; INGR15058), an Indian mustard (*Brassica juncea* (L.) Czern. Germplasm with Suitable for Salt Affected Soils of Indo-Gangetic Plains

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

Consistent breeding efforts at ICAR-Central Soil Salinity Research Institute (ICAR-CSSRI), Karnal resulted in the development of an improved salt tolerant genotype CS 1100-1-2-2-3 by crossing two salt tolerant genotypes CS 52 and CS 609-B10 (CS 52: a highly salt tolerant variety; CS 609-B10: a high yielding (Seed and oil) salt tolerant genotype, both developed at ICAR-Central Soil Salinity Research Institute, Karnal). Pedigree method was followed for selection and evaluation of germplasm in salt affected soils for high seed yield and tolerance to soil salinity conditions.

Morpho-agronomic characteristics: On the basis of three year (2012-13 to 2014-15) trials conducted for saline/alkaline conditions in AICRP on Rapeseed and Mustard, CS 1100-1-2-2-3 provided mean seed yield of 2090 kg/ha which was 23% higher than yields of two checks i.e. CS 54 (1707 kg/ha) and Kranti (1704 kg/ha). It also provided 26-28% higher oil yield (798 kg/ha) than CS 54 (620.5 kg/ha) and Kranti (633.5 kg/ha). This strain matures, on an average, in 138 days and takes 59 days to flower. The strain attains the height of approximately 175 cm; main shoot length (89) and 1000 seed weight (5g) (Table 1).

Associated characters and cultivated practices: CS 1100-1-2-2-3also showed resistance to Alternaria blight under natural conditions compared to check Rohini and salt tolerant variety CS 54. Alterneria blight severity in pods was at par with checks. Further, it also showed much lesser incidence of white rust, powdery mildew, downy mildew and sclerotinia rot compared to check Rohini. Under artificial conditions also, similar performance was recorded. Against mustard aphid, data of 24 trails showed lesser average aphid infestation index (AAI)

Table 1. Multi-location performance on important traits like yield and yield components [Locations: Salinity [Agra (ECiw 12 dS/m) Karnal (ECe 10.7 dS/m), Hisar (ECe 10.6 dS/m)]; Alkalinity: Karnal (pH 9.3) and Lucknow (pH 9.4)]

Parameters	Year of testing	Proposed genotype CS 1100-1-2-2-3	Check 1 CS 54 (NC)	Check 2 Kranti (NC)
Mean Seed Yield (Kg/ha)	2012-13	2168	1923	1841
	2013-14	2053	1649	1770
	2014-15	2049	1550	1502
	Mean	2090	1707	1704
Per cent increase (+) or decrease (-) over checks	2012-13		+12.74	+17.76
	2013-14		+24.50	+15.99
	2014-15		+32.19	+36.42
	Mean		+23.14	+23.39
Mean Oil Yield (Kg/ha)	2012-13	- #	- #	- #
	2013-14	789	639	683
	2014-15	807	602	584
	Mean	798	620.5	633.5
Per cent increase (+) or decrease (-) over checks	2012-13		-	-
	2013-14		+23.47	+15.52
	2014-15		+34.05	+38.18
	Mean		+28.76	+26.85
Plant height (cm)	2012-13	170	164	176
	2013-14	170	172	175
	2014-15	186	170	170
	Mean	175	169	174
Main shoot length (cm)	2012-13	87	90	98
	2013-14	88	87	94
	2014-15	92	87	81
	Mean	89	88	91
1000 Seed weight (g)	2012-13	5	5	4
	2013-14	6	4	5
	2014-15	5	5	4
	Mean	5	5	4

[Source – AICRP on R&M Annual Report 2012-13 (Page PB 73, Table 2.3.30), 2013-14 (Page PB 81, Table 2.3.31) and 2014-15 (Page PB 75, Table 2.3.33)]. # During the year 2012-13, data on Oil Yield were not reported.

compared to checks CS 54, Kranti, Rohini and Varuna. CS 1100-1-2-2-3 responded favorably to the additional doses of fertilizer (N: P: K). Further 100% Recommended dose of fertilizer was found suitable for this genotype. Looking to its seed and oil yields and disease resistance, CS 1100-1-2-2-3is being proposed for identification for salt affected soils conditions (saline and alkaline) of *Rabi* season in the states of Haryana, Punjab and Uttar Pradesh.

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23. JEX/A 785 (IC0616582; INGR15059), a Potato (*Solanum tuberosum L.)* Germplasm Suitable for Cold Chipping and Resistance to Cold Induced Sweeting

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Potato is a semi-perishable commodity and has to be consumed within a short period of time, or is required to be shifted to the cold store for round the year availability. Unfortunately, during cold storage potato undergoes an undesirable phenomenon known as cold-induced sweetening where the rate of conversion of starch to reducing sugars is accelerated (van Es and Hartmans, 1987). It also results in lowering the quality of processed products due to an unwanted brown colouration in potato chips and crisps (Edwards *et al*., 2002). The source for cold chipping and resistance to cold induced sweetening are hard to find. In search of sources for cold chipping and resistance to cold induce sweetening primitive cultivated Andigena group (148 accessions) germplasm were evaluated from 2006-2008 (Marwaha *et al.*, 2008). This resulted in identifying JEX/A 785 as a useful source for resistance to cold induced sweetening and cold chipping. JEX/A-785 produced good chip colour after reconditioning at 20°C for 4 weeks of potatoes cold stored for 6 months and was identified as most suitable for cold chipping. This unique and rare trait of JEX/A 785 of producing light coloured acceptable chip colour after withdrawal of tuber material from cold store was also verified in 2009 at Jalandhar and Shimla. This accession can be used as parents for the development of indigenous cold chipping varieties. JEX/A 785 also possess resistance to cold induced sweetening as it even just after withdrawal from cold store contained lower levels of total sugars (including reducing sugar and sucrose) than the prescribed limit (>1.25% on fresh weight) which imparts sweet taste in table potatoes.

Morpho-agronomic Characteristics

Tubers of JEX/A 785 are round shape, whitish cream skin, small sized with shallow eyes and cream flesh colour. The flower is blue-violet in colour. Plant is tall with red brown as secondary stem colour which is highly scattered throughout. Anthocyanin colouration of rachis is present. Leaflets are ovate in shape. The yield performance of JEX/A 785 is lower than commercial Indian processing varieties Kufri Chipsona-1 and Kufri Chipsona-3.

Associated Characters and Cultivated Practices

This accession is susceptible to late blight and early blight diseases. It can be grown in Indian sub-tropical plains in autumn crop season.

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24. LBRIL-102 (IC0611477; INGR15060), a Wheat (*Triticum aestivum)* Germplasm with Spot Blotch Resistant

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Spot blotch or *Helminthosporium* Leaf Blight (HLB) caused by *Bipolaris sorokiniana*, is one of the major biotic constraint to wheat production in Africa, South America, warm wheat growing regions of South Asia and particularly to Indian subcontinent, affecting the livelihood of small scale farmers, who depend on the wheat cultivation (Duveiller *et al.,* 2005). Improvement of host resistance against leaf blight, widening the genetic base of the model genotypes through introduction of new alleles for HLB resistance is one of the major activities at Indian Institute of Wheat and Barley Research, Karnal to meet the challenge. The cross was made between most susceptible Indian genotype Sonalika (II53.388/AN//YT54/N10B/3/LR/4/B4946.A.4.18.2.1Y/Y53//3/Y50) and highly resistant Brazilian genotype BH 1146 (Fronteira/Mentana//Ponta Grossa 1). The 220 recombinant inbred lines (RILs) developed from this cross in F_{9-10} generation, were phenotypically evaluated for spot blotch during crop season 2012-14 under high disease pressure at two hot spot locations (Coochbehar and Kalyani) in eastern India and also at IIWBR, Karnal under field and epiphytotic conditions in polyhouse (3 replications). Phenotypic data was recorded on double digit scale (taking disease reaction of top two leaves, flag and flag-1) at dough stage. The promising line LBRIL102 showed spot blotch resistance (Table 1) consistently across the locations and over the two years (Singh *etal.,* 2014). Disease resistance was improved in LBRIL 102 over its donor parent BH 1146.

Morpho-agronomic characters: The duration of days to heading and days to maturityhas increased but the plant height has significantly reduced as compared to the resistant check BH 1146. The average thousand kernel weight (TKW) of LBRIL 102 was 42.0 g which is on par with the best check BH 1146 having TKW 43.0 g. Disease resistance was improved without compromising the yield.

Associated characters and cultivation practices: Besides HLB, the proposed genotype was also rust resistant in all the environments. Diagnostic markers reported earlier *Xgwm*371 (Kumar *et al.,* 2010) and SSRs-*Xbarc59*, *Xbarc*232were also used to validate the promising line for spot blotch resistant (Singh *et al*., 2014).

Table1. LB score of LBRIL102 as compared to checks at four environments of India

	Karnal		Kalyani		Coochbehar		Polyhouse	
	2012-13	2013-14	2012-13	2013-14	2012-13	2013-14	2012-13	2013-14
LBRIL 102	02	02	02	03	13	13	13	13
SONALIKA (C)	79	79	89	89	89	89	99	99
BH1146 (C)	13	13	24	24	24	13	35	24

(C)-check

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25. HGMS-20 (IC0617407; INGR15061), a Cotton (*Gossypium hirsutum* L.) Germplasm Suitable as Parent to Produce Hybrid Seed with Less Cost

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It is a genetic male sterile line of *Gossypium hirsutum* designated as HGMS 20. Its male sterility is governed by a single recessive gene. This line is a cross between a genetic male sterile (HGMS 1) and GAK 32 a male parent. The female line HGMS 1 has genetic male sterility characteristic along with cream petal and cream pollen colour, normal cup shaped leaves, whereas male parent GAK 32 has cream petal and yellow anthers with petal spot. Repeated backcrossing of heterozygote (male) with the homozygote recessive (female) resulted in the development of HGMS 20 line. This genetic male sterile line has been developed by SS Siwach, RS Sangwan, Omender Sangwan, SR Pundir, Somveer and Ashish Jain from Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The progeny of this line produces 50 per cent male fertile and 50 per cent male sterile plants. HGMS 20 has normal, medium broad cup shaped leaves. Its flower has cream petal and yellow anther colour with petal spot inside the petal base. This line also has good fibre quality i.e. 2.5% span length (27.1 mm), fibre strength (22.4 g/tex), micronaire value (4.6) and uniformity ratio (51 %).

26. HGMS-21 (IC0610389; INGR15062), a Cotton (*Gossypium hirsutum L.*) Germplasm Suitable as Parent to Produce Hybrid Seed with Less Cost

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It is a genetic male sterile line of *Gossypium hirsutum* designated as HGMS 21. Its male sterility is governed by a single recessive gene. This line is a cross between a genetic male sterile (HGMS 1) and Super okra a male parent. The female line HGMS 1 has genetic male sterility characteristic along with cream petal and cream pollen colour, normal cup shaped leaves, whereas male parent Super okra has cream petal and yellow anthers with deep leaf lobes. Repeated backcrossing of heterozygote (male) with the homozygote recessive (female) resulted in the development of HGMS 21 line. This genetic male sterile line has been developed by SS Siwach, RS Sangwan, Omender Sangwan, SR Pundir, Somveer and Ashish Jain from Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The progeny of this line produces 50 per cent male fertile and 50 per cent male sterile plants. HGMS 21 has okra type leaves. Its flower has yellow petal and cream anther. This line also has good fibre quality i.e. 2.5 % span length (26.1 mm), fibre strength (20.8 g/tex), micronaire value (5.0) and uniformity ratio (51 %).

27. MS SLA 9 & SLB 9 (IC0612149 & IC0612150; INGR15063), a Sorghum (*Sorghum bicolor*) MS Line with Bold Seed and Panicle

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Rabi sorghum is grown over a total area of 5.6 million hectares mainly in the states of Maharashtra, Karnataka, Telangana and Andhra Pradesh with average productivity of 819 kgs/ha. Hybrid vigour and its commercial exploitation have paid rich dividends in *kharif* sorghum, but less impact in *rabi* sorghum. In *Rabi,* this could be realized only when the sterile and restorer lines having the seasonal adaptability and desired combining ability are identified and used in the development of *rabi* sorghum hybrids. In order to develop new parental lines with diversity and broaden the genetic base in *rabi* materials, 161 indigenous and 159 exotic lines were used for identifying maintainer and restorer gene reactions on A1 cytoplasm. New MS lines with diverse genetic base were derived.

The male sterile line SLA-9 & SLB-9 was developed at Centre on *Rabi* Sorghum (Indian Institute of Millets Research), Solapur. Male sterile line SLA-9 was developed from a cross between *rabi* MS line 104B and SPV 1538 during *Rabi* 2000. The F2 population was raised in Rabi 2001 and 27 agronomically superior derivatives were advanced. The selections were reduced to 5 lines in F4. Superior cross derivatives were test crossed for identification of lines with maintainer genes and sterile were further advanced to BC5. One agronomically superior male sterile line having good combining ability and *rabi* traits was developed as MS SLA-9 male sterile line. The pedigree of MS SLA-9 & SLB-9: 104 B × SPV 1538 (104B = 296B × Swati, 296B = IS 3922 × Karad local, Swati = SPV86 × M35-1, SPV 1538 = Selection from Phul Mallige, Chandakpur village, Aland taluk, Gulbarga district, Karnataka).

Entry	Days to 50% flower	Plant height (cm)	Grain yield / plant (g)	100 seed weight (g)	Panicle length (cm)	Panicle width (cm)	Branches / panicle	Charcoal Rot (%)
SLB 8	72	185	68	2.8	18	4	46	19.6
SLB 9	71	173	77	4.4	24	6	53	14.3
SLB 10	70	163	63	3.0	16	5	63	27.5
SLB 11	74	196	75	2.7	15	6	69	17.8
SLB 12	73	188	69	2.7	15	4	33	18.2
SLB 19	75	183	81	3.7	24	6	94	16.6
SLB 25	73	172	59	3.3	19	6	61	22.7
SLB 29	69	185	78	3.3	12	6	71	19.4
SLB 36	64	187	66	3.6	16	7	60	27.5
SLB 39	65	180	71	3.0	13	7	65	17.1
SLB 45	69	230	64	4.1	13	6	59	25.4
SLB 46	67	201	70	3.2	15	6	64	26.1
SLB 49	73	205	65	3.0	16	7	70	28.3
104B (C)	76	160	58	3.7	20	5	67	34.2
CD at 5 %	3.88	8.09	5.66	0.25	3.12	1.02	13.65	5.46
C.V.%	5.0	11.2	27.6	17.4	23.5	18.5	23.4	24.9

Morpho-agronomic characteristics: A total of 14 B lines were evaluated in *rabi* seasons of 2006-07 and 2007-08 at Centre on *Rabi* Sorghum (IIMR), Solapur. Theses parental lines were compared with the checks 104B, parental line of commercial rabi hybrid CSH 15R. Performance of 14 B lines indicated that SLB-9 flowered in 71 days compared to check 104B (76 days). Panicle length was more in case of SLB-9 (24 cm). The MS SLA-9 was superior by 32.7% and 42.6% over the check 104B for grain yield and charcoal rot, respectively. Thus, MS SLA-9 & SLB-9 is diverse and superior in grain yield.

Associated characters and cultivation practices: It is bold seeded and also tolerant to drought. It has superior grain quality (seed shape, color and luster) than the check 104B. The MS line is having good general and specific combining ability for high grain yield. It offers better resistance to charcoal rot and possesses better grain quality. This diverse parental line SLA-9 is suited to *Rabi* season and can be directly used for the development of commercial *rabi* hybrids.

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28. MS SLA 29 & SLB 29 (IC0612157 &IC0612158; INGR15064), a Sorghum (*Sorghum bicolor)* MS Line with Compact Head

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Rabi sorghum is grown over a total area of 5.6 million hectares mainly in the states of Maharashtra, Karnataka, Telangana and Andhra Pradesh with average productivity of 819 kgs/ha. Hybrid vigour and its commercial exploitation have paid rich dividends in *kharif* sorghum, but less impact in rabi sorghum. In *Rabi*, this could be realized only when the sterile and restorer lines having the seasonal adaptability and desired combining ability are identified and used in the development of *rabi* sorghum hybrids. In order to develop new parental lines with diversity and broaden the genetic base in *rabi* materials, 161 indigenous and 159 exotic lines were used for identifying maintainer and restorer gene reactions on A1 cytoplasm. New MS lines with diverse genetic base were derived. Male sterile line MS SLA-29 was developed from a cross between *rabi* MS line 104B and Selection from IS 3420-2-1 during *Rabi* 2000. The F2 population was raised in *Rabi* 2001 and 41 agronomically superior derivatives were advanced. The selections were reduced to 7 lines in F4. Superior cross derivatives were test crossed for identification of lines with maintainer genes and sterile were further advanced to BC5. One agronomically superior male sterile line having good combining ability and *rabi* traits was developed as MS SLA-29 male sterile line. The pedigree of MS SLA-29 & SLB-29 is 104B × IS 3420 (104B = 296B × Swati, 296B = IS 3922 × Karad local, Swati = SPV86 × M35-1, IS 3420 = Local landrace from Parbhani, Maharashtra).

Morpho-agronomic characteristics: A total of 14 B lines were evaluated in *rabi* seasons of 2006-07 and 2007-08 at Centre on *Rabi* Sorghum (IIMR), Solapur.

Entry	Days to 50% flower	Plant height (cm)	Grain yield / plant (g)	100 seed weight (g)	Panicle length (cm)	Panicle width (cm)	Branches / panicle	Charcoal Rot (%)
SLB 8	72	185	68	2.8	18	4	46	19.6
SLB 9	71	173	77	4.4	24	6	53	14.3
SLB 10	70	163	63	3.0	16	5	63	27.5
SLB 11	74	196	75	2.7	15	6	69	17.8
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SLB 29	69	185	78	3.3	12	6	71	19.4
SLB 36	64	187	66	3.6	16	7	60	27.5
SLB 39	65	180	71	3.0	13	7	65	17.1
SLB 45	69	230	64	4.1	13	6	59	25.4
SLB 46	67	201	70	3.2	15	6	64	26.1
SLB 49	73	205	65	3.0	16	7	70	28.3
104B (C)	76	160	58	3.7	20	5	67	34.2
CD at 5 %	3.88	8.09	5.66	0.25	3.12	1.02	13.65	5.46
C.V.%	5.0	11.2	27.6	17.4	23.5	18.5	23.4	24.9

Theses parental lines were compared with the checks 104B, parental line of commercial *rabi* hybrid CSH 15R. Performance of 14 B lines indicated that SLB-29 flowered in 69 days compared to check 104B (76 days). Panicle length was compact (12 cm) with more branches (71) than 104B (67). The MS SLA-29 was superior by 34.4% and 43.2% over the check 104B for grain yield and charcoal rot, respectively. Thus, MS line SLAS-29 is early with compact head, high yield and more branches. Thus, MS SLA-29 & SLB-29 is early, diverse and superior in grain yield.

Associated characters and cultivated practices: It is bold seeded and also tolerant to drought. It has superior grain quality (seed shape, color and luster) than the check 104B. MS line is diverse, early and superior in grain yield and tolerance to charcoal rot. The MS line is having good general and specific combining ability for high grain yield. It offers better resistance to charcoal rot and possesses better grain quality. This diverse parental line is suited to Rabi season and can be directly used for the development of commercial *rabi* sorghum hybrids.

References

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29. JCR/PLB 299 (IC0341862; INGR15065), a Kidneybean (*Phaselous vulgaris)* Germplasm with Resistant to Anthracnose (*Colletotrichum lindmuthianum)*

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Common bean (*Phaseolus vulgaris* L.) also known as *rajmash* is one of the most important legumes grown all over the world including India particularly in the hilly regions. The crop is predisposed to the attack of various pathogens like fungal, bacterial and viral during humid environments throughout the growing season. Bean anthracnose is a serious seed born disease and early infection during growing period of susceptible cultivar leads to heavy yield losses. The pathogen possess high degree of pathogenic variability and >100 races of *C. lindemuthianum* have been identified worldwide. Management of this disease can be done by using certified seed, crop rotation, seeds and foliar treatment with fungicides and genetically resistant varieties. Among these, use of genetically resistant varieties is most effective, least expensive and easy to adopt by marginal farmer and resource poor farmers. Germplasm comprising 99 accessions was evaluated at two hot spots i.e. Shimla and Palampur and also under artificial epiphytotic conditions at Palampur against 4 races of *C. lindemuthianum* viz., 03, 515, 598 and 529. Germinated seed dip method of inoculation was used for evaluation of resistance. The disease reaction was recorded after 6 days by using 0-5 point scale. Accession IC0341862 was found resistant to all the four races. Additional features of this accessions include bush type plant growth habit, deep pink flower colour, white seed colour, pod length (11.80 cm), no. of pods (18.00), no. of seeds (6.00) and 100 seed weight (22.04 g).

30. DRMR-541-44 (IC0598624; INGR15066), an Indian Mustard (*Brassica juncea* L.) Germplasm with Drought Tolerant under Rainfed Condition

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DRMR 541-44, an Indian mustard (*Brassica juncea* L.) genotype derived from inter specific hybridization between *Brassica juncea* and *Brassica carinata* was studied during 2010-11 along with 20 germplasm for morpho-physiological and biochemical characters under irrigated and rainfed condition in RCBD with 3 replications. DRMR 541-44 recorded less decrease in seed yield and more seed yield under rainfed condition as compared to other genotypes. The carbohydrate content decreased under rainfed condition whereas free proline increased significantly. The increase in free proline under stress condition might be attributed to one of the defence mechanism of plant to drought situation. The high seed yield of DRMR 541-44 under rainfed condition could be due to high plant dry weight and carbohydrate accumulation. (DRMR Annual Report, 2011-12).DRMR 541-44 was also tested for physiological basis of drought tolerance with 15 other strains under AICRP (RM) programme-2011-12 at Ludhiana, Bharatpur and Kanpur centers. The different strains were sown in paired rows under irrigated and rainfed conditions in 3 replications under RCBD factorial design. DRMR 541-44 showed < 1 DSI and higher seed yield than the check RH 819 at Bharatpur and Kanpur centers. It also showed < 10% reduction (even less than check RH 819) in RWC under drought condition. (AICRP RM Annual Progress Report, 2012). Thirteen B. *juncea* genotypes/ germplasm were further studied for their different morpho-physiological characters under irrigated and drought condition during 2011-12. There were 2 rows each of 5m long for each genotype. The spacing between rows and within plant was kept 30 and 10cm respectively. The experiment was planned in randomized complete block design with three replications under rain out shelter.

The physiological characters investigated under irrigated and drought situation showed appreciable variation at both the phenotypic and genotypic level. DRMR 541-44 showed higher tolerance index and higher photosynthesis under drought situation along with other genotypes. Water potential measured at flowering stage showed increase potential under drought condition and the proposed strain DRMR 541-44 along with other genotypes recorded high water potential as compared to others genotypes. Seed yield recorded on per plant basis showed significant decrease under drought condition over the irrigated condition. After significant decrease, maximum seed yield was recorded in DRMR 541-44. On the other hand, maximum tolerance index was observed in DRMR 541-44 even higher than the check RH 819. Thus on the basis of photosynthesis, leaf water potential, high water use efficiency, and yield DRMR 541-44 germplasm were identified as promising ones.

(DRMR Annual Report, 2012-13). DRMR 541-44 was evaluated along with check variety RH 819 and other 40 genotypes for assessing drought tolerance through physiological parameters during 2013-14 under AICRP RM physiological trials at Kanpur and Ludhiana. Proposed strain recorded consistently <10% reduction in terms of Relative water content (RWC %), SPAD Chlorophyll, seeds/siliquae and 1000 seed weight when genotype was grown under irrigated (IR) and rain fed (RF) conditions at both the centres (AICRP RM Annual Progress Report 2014). DRMR 541-44 was evaluated along with check variety RB 50 and RH 406 and other 31 genotypes for assessing drought tolerance during 2014-15 under AICRP RM physiological trials. Proposed strain recorded DSI value less than 1 at all the four locations i.e. Kanpur, Hisar, Bharatpur and Ludhiana which indicates its drought tolerance. Further, DRMR 541-44 exhibited less than 10% reduction in harvest index (%) and oil content as compared to checks. Reduction in Relative water content (RWC %) and SPAD Chlorophyll values was also minimum (<20%). (AICRP RM Annual Progress Report 2015).

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