

Plant Germplasm Registration Notice *

180 proposals were received online for the consideration of registration of germplasm for unique/superior traits. The applications were thoroughly screened by the member-secretary, Plant Germplasm Registration Committee (PGRC), and 94 proposals complete in all respects were reviewed by the experts and were presented in the 50th meeting of the PGRC held in virtual mode on June 12, 2023. 67 proposals with unique/novel features belonging to 29 species were recommended for registration by PGRC. The information on registered germplasm is published to disseminate the information to respective crop breeders for utilization of these genetic stocks in their crop improvement programmes. Description of 34 out of the 67 recommended germplasm lines was published in IJGR Vol 39 (Issue no. 1) 2026. Description of the remaining 33 germplasm lines is given below:

1. **WN 657 (IC648611; INGR23035), a finger millet germplasm with longer finger length as per DUS test**

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A total of 38 finger millet [*Eleusine coracana* (L.) Gaertn.] accessions constituted of 25 promising long earhead landraces and thirteen released varieties were evaluated for 12 morphological characters, including grain yield, at three locations in Gujarat, during *kharif* 2019, 2020 and 2021. The pooled data of all locations were used to study the genetic potential of long earhead finger millet genotypes. Moderate genotypic and phenotypic coefficient of variation found for the traits viz., number of fingers per earhead, number of productive tillers per plant, straw yield per plant, grain yield per plant, finger length, harvest index and main earhead indicating ample scope of variation for these traits, allowing further improvement by selection of these traits. High heritability estimates were observed for days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, number of fingers per earhead, main earhead length, finger length, 1000-grain

weight, grain yield per plant, straw yield per plant and harvest index, showing low environmental influence on these traits and presence of additive gene action for these traits. Hence, priority can be given to these traits during selection to get more genetic gains.

Also, on the basis of mean performance over three years at two locations, the genotype 'WN 657' showed long finger length, i.e. 13.13 cm, which is >7 cm (extra-long) as per DUS testing guidelines. This morphological trait, such as the number of fingers per earhead, the main earhead length and the length of finger has direct contributions towards the high grain yield per plant. The best promising finger millet genotypes 'WN-657' for very long finger length with moderate resistance to pests and diseases found during three years of genetic evaluation at three different locations, which can be used as a promising parent in further breeding programmes.

2. **SPV 2813 (IC648612; INGR23036), a sorghum germplasm with longer leaf length and wider leaf width**

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Green fodder yield in sorghum (*Sorghum bicolor* L.) has a significant and strong positive correlation with leaf

area followed by stem girth, plant height, leaf length and number of leaves per plant (Singh *et al.*, 2019).

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Positive and significant association of number of leaves per plant, leaf breadth and dry fodder yield with green fodder yield indicate the importance of these characters during selection for crop improvement program in forage sorghum (Gedam *et al.*, 2015). The significance of brown midrib mutation in sorghum is that it greatly reduces lignification and cell-wall concentration, increases digestibility, and increases voluntary intake of feed by ruminants. Genetic control of the lignification process through use of brown midrib (*bmr*) mutations has offered the most direct and productive approach to reducing lignin concentration and increasing digestibility of sorghum.

SPV 2813 was developed through pedigree method of breeding by crossing between CSV 20 and the *bmr* germplasm line, IS 21891 during *rabi* 2009-10 at the Indian Institute of Millets Research, Hyderabad. CSV 20 is the most popular dual-purpose sorghum variety which was released during 2009 for cultivation in zones I and II in India, while IS 21891 is a brown midrib source carrying the gene *bmr* 8. Agronomically superior derivatives from this cross were selected and

advancement of segregating generations was done.

SPV 2813 is a brown midrib sorghum line with tan pigmentation and days to flower of 83 days. This unique line is superior for longer leaf length (83.1 cm) and longer leaf width (8.39 cm) (Table 1). These identified traits add to the increased forage value of the variety apart from making it more suitable for bio-ethanol production because of increased lignocellulose contents. SPV 2813 is having green fodder yield of 315.6 q/ha and a dry fodder yield of 94.9 q/ha. The other traits like stem girth (4.69 cm), protein (9.03%), total soluble sugars (10.95%) and number of leaves (13) also increase the forage value of this entry.

References

- Gedam SR, DT Deshmukh, MA Sheikh, RB Ghorade and SB Sakhare (2015) Genetic studies on forage sorghum (*Sorghum bicolor* (L.) Moench). *BIOINFOLET-A Quarterly J. Life Sci.* 12: 958-962.
- Singh J, BR Ranwah, L Chaudhary, C Lal, MC Dagla and V Kumar V (2013) Evaluation for genetic variability, correlation and path coefficient analysis in mutant population of forage (*Sorghum bicolor* L.). *Bioscan* 8: 1471-76.

Table 1: Summary data on leaf length and leaf width traits, BMR trial *Kharif* 2020 (AICRP data)

Trait	Location	SPV 2813	CSV 43BMR (C)	CD 5%
Leaf length (cm)	8	83.1	76.8	4.9
Leaf width (cm)	7	8.39	7.81	0.78

3. SPV 2058 (IC648613; INGR23037), a sorghum germplasm with longer leaf length, leaf width and high stem

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Sorghum (*Sorghum bicolor* L.) ranks first among the cereal fodder crops because of its growing ability in low-fertility soil, faster growth habit, higher yield, palatability and nutritious quality. It is preferred over maize and pearl millet for forage because of its better regeneration capacity. Green fodder yield in sorghum has a significant and strong positive correlation with leaf area followed by stem girth, plant height, leaf length and number of leaves per plant (Singh *et al.*, 2019). SPV 2058 is a single-cut forage sorghum genotype with longer leaf length, higher leaf width, higher stem girth and better leaf-stem ratio which are the important characters in an ideal forage sorghum variety. It was developed through pedigree method of breeding by crossing between PC 5 and Indore 12 during *rabi* 2004-

05 at ICAR-Indian Institute of Millets Research, Hyderabad.

SPV 2058 is a tan type plant with good early vigour, stems are thicker with longer leaves and leaf width is also wider conferring more biomass to yield good forage quantity. The forage quality of the line is also good in relation to protein content (8%) and higher IVDMD (51%) values. The green fodder yield (430 q/ha) and dry fodder yield (141.5 q/ha) are superior to the existing check varieties along with higher per day productivity of green fodder yield (5.65 q/ha) and dry fodder yield (1.85 q/ha). SPV 2058 has multiple trait superiority with uniqueness of longer leaf length (85.5 cm), leaf width (7.32 cm), high stem girth (3.07 cm) and leaf: stem ratio (0.41) (Table 1). It recorded the highest

leaf length, leaf breadth and is resistant to Anthracnose and zonate leaf spot. This variety is suitable to be grown as a single-cut forage sorghum variety for rainfed Kharif sorghum growing regions of the country and will be an excellent source of these traits as a donor parent in forage breeding.

Reference

Singh SK, LK Gangwar and Mayank Chaudhary (2019) Studies on character association and path analysis in forage sorghum. *Int. J. Chem. Stud.* 7: 2939-2942.

Table 1: Summary of data for leaf length, leaf width, stem girth and leaf: stem ratio traits of AVT-SC, *kharif* 2012 (AICRP data)

Trait	Genotypes	Zone I (9)	Zone II (6)	All India Avg.	CD 5%
Leaf length	SPV 2058	84.7	86.8	85.5	3.3
	HC 308 (c)	75.1	74	74.7	
	CSV 21F (c)	80.8	77	79.3	
Leaf width	SPV 2058	7.56	6.98	7.32	0.47
	HC 308 (c)	6.82	5.93	6.47	
	CSV 21F (c)	6.58	5.66	6.21	
Leaf: stem ratio	SPV 2058	0.37	0.46	0.41	0.04
	HC 308 (c)	0.28	0.45	0.36	
	CSV 21F (c)	0.3	0.47	0.39	

4. TAKPS 1 (IC648614; INGR23038), a hurda sorghum germplasm with free threshability, excellent fragrance and high hundred tender grain weight

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The special-purpose sorghum (*Sorghum bicolor* L.) can provide a choice to the end users in food enterprises. Green grains of parching sorghum (*Hurda* sorghum) from milk to dough stage are used for consumption as roasted grains. Parching sorghum possesses a pleasant fragrance and more sweetness which make them popular for table purposes. Parching (*Hurda*) sorghum is one of the best alternatives for the value addition of sorghum.

Parching sorghum genotype Sakarimokari was irradiated at BARC, Mumbai. This landrace was gamma irradiated with 300 Gy, using in Gamma chamber (1200 gx) at BARC, Mumbai in order to create genetic variation for the hurda quality parameters to improve hurda yield, hurda quality and earliness. The promising selection Sakarimokari mutant selection number-5-4-1-1 was advanced till M7 generation and finally named as TAKPS 1. Promising mutants along with checks were tested in University Multilocation Trials during Rabi-2018-19 to 2020-21. The sensory evaluation included

colour, size, shape, aroma/flavour, taste and thrashability (Ghorade *et al.*, 2019). The chemical analysis (total sugars and brix) of the hurda was executed according to the standard method of AOAC, 1990.

Free threshability is the prerequisite for the parching of the sorghum genotype. The threshability of TAKPS 1 was in the category of Free threshability while the checks like Gulbhendi, Sakrimokari and Phule Uttara were in the category of Medium threshability. While the check Madhur was also having Free threshability. This genotype recorded high hundred tender grain weight (4.12 g). For the organoleptic trait of Taste, the genotype TAKPS 1 was in the category of Very sweet while the checks like Gulbhendi, Sakrimokari and Phule Uttara were in the category of Medium sweet and Madhur wani was Slightly sweet. For the trait of Fragrance, the genotype TAKPS 1 was in the category of Good while the checks like Gulbhendi and Sakrimokari were in the category of Fair and Phule Uttara and Mahur were in the category of No Aroma.

TAKPS 1 also recorded higher sugar (2.17%) as compared to the checks Gulbhendi (1.96%), Sakrimokari (2.0%), Madhur Wani (2.03% q/ha) and Phule Uttara (1.86% q/ha).

Earliness is a desirable trait in parching sorghum. For days to dough stage, TAKPS 1 recorded fewer days to dough stage of 94.17 days as compared to the checks Gulbhendi (95.17 days), Sakrimokari (102.25 days), Madhur Wani (95.67 days) and Phule Uttara (95.75 days).

Thus, it was concluded from the present study that considering the higher green hurda yield, early maturity along with good threshability and excellent

organoleptic properties, the promising genotype TAKPS 1 needs to be exploited in breeding for improvement of parching traits in rabi sorghum as the donor parent in the crossing programme.

Reference

Ghorade RB, SB Thawari, VV Kalpande, SV Khambalkar and AR Bhuyar (2019) PDKV Hurda Kartiki (WANI 103) a new parching kharif sorghum variety; innovative approach for rural entrepreneurship and empowerment. *J. Multilogic Sci.* Vol. VIII, Special Issue(B): 149-153.

5. TAKPS 3 (IC647559; INGR23039), a hurda sorghum germplasm with earliness, free threshability and excellent fragrance

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The special purpose sorghum (*Sorghum bicolor* L.) can provide choice to the end users in food enterprises. Green grains of parching sorghum (*Hurda* sorghum) from milk to dough stage are used for consumption as roasted grains. Parching sorghum possesses a pleasant fragrance and more sweetness which make them popular for table purpose varieties. It was therefore felt to develop and identify the genotype for hurda purpose of which will give benefit to farmers and consumers too.

The parching sorghum genotype Gulbhendi was irradiated at BARC, Mumbai. This landrace was gamma irradiated with 300 Gy, using in Gamma chamber (1200 gx) at BARC, Mumbai in order to create genetic variation for the hurda quality parameters to improve hurda yield, hurda quality and earliness. The promising selection Gulbhendi Mutant 300 Gy Selection No. -22-2-1-1 was advanced till M7 generation and finally named as TAKPS 3. Promising mutants along with checks were tested in University Multilocation Trials during Rabi-2018-19 to 2020-21. The sensory evaluation included colour, size, shape, aroma/flavour, taste and thrashability (Ghorade *et al.*, 2019). The chemical analysis (total sugars and brix) of the hurda was executed according to the standard method of AOAC, 1990.

For the character green hurda yield, the genotype TAKPS 3 recorded a higher green hurda yield of 40.40 q/ha as compared to the checks Gulbhendi (30.66 q/ha),

Sakrimokari (27.33 q/ha), Madhur Wani (32.51 q/ha) and Phule Uttara (31.64 q/ha). For the trait green fodder yield, the genotype TAKPS 3 recorded a higher green fodder yield of 113.17 q/ha.

Free threshability is the prerequisite for the parching of the sorghum genotype. The threshability of TAKPS 3 was found promising similar to the checks Gulbhendi, Sakrimokari and Phule Uttara.

For the organoleptic traits, TAKPS 3 was superior for almost all the traits. For the organoleptic trait of Taste, the genotype TAKPS 3 was in the category of higher sweetness, while the checks like Gulbhendi, Sakrimokari and Phule Uttara were in the category of Medium sweet and Madhur Wani was slightly sweet. For the trait of Fragrance, the genotype TAKPS 3 was in the category of Good while the checks like Gulbhendi and Sakrimokari were in the category of Fair and Phule Uttara and Mahur were in the category of without Aroma. Sugar content has major role in the sweetness of the parching sorghum. For the character total sugar %, TAKPS 3 recorded higher sugar of 1.99% as compared to the checks Gulbhendi (1.96%), Phule Uttara (1.86% q/ha) and was at par with Sakrimokari (2.0%), Madhur Wani (2.03% q/ha).

Earliness is a desirable trait in parching sorghum. For the character days to 50% flowering TAKPS 3 recorded less days to 50% flowering of 71.42 days as compared to the checks Gulbhendi (73.67 days), Sakrimokari (82.67 days), Mahur Wani (73.92 days) and

Phule Uttara (75.25 days). For days to dough stage, TAKPS 3 recorded less days to dough stage of 92.42 days as compared to the checks Gulbhendi (95.17 days), Sakrimokari (102.25 days), Madhur Wani (95.67 days) and Phule Uttara (95.75 days).

Thus, it was concluded from the present study that considering the higher green hurda yield, early maturity along with desirable threshability and excellent organoleptic properties, the promising

genotype TAKPS 3 needs to be exploited in breeding for improvement of parching traits in rabi sorghum as the donor parent in the crossing programme.

Reference

Ghorade RB, SB Thawari, VV Kalpande, SV Khambalkar and AR Bhuyar (2019) PDKV Hurda Kartiki (WANI 103) a new parching *kharif* sorghum variety; innovative approach for rural entrepreneurship and empowerment. *J. Multilogic in Sci.* Vol. VIII, Special Issue(B): 149-153.

6. AKSV 438 (IC286441; INGR23040), a sorghum germplasm with high zinc and iron content

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Sorghum (*Sorghum bicolor* L.) is one of the cheapest sources of energy and micronutrients, and a vast majority of population in Africa and central India depend on sorghum for their dietary energy and micronutrient requirements. Biofortification of sorghum by increasing mineral micronutrients [especially iron (Fe) and zinc (Zn)] in grain is of widespread interest (Ashok Kumar *et al.*, 2009). Considering this, the sorghum genotype AKSV 440 which was found promising for the higher Zinc (30.61 ppm) and Iron (37.14 ppm) content above the base line. As per the (Ashok Kumar *et al.*, 2013), the base line for Zinc (Zn) = 20 ppm and Iron (Fe) = 30 ppm has been fixed. Everything above the baseline is considered promising for Zinc and Iron content in sorghum.

The *kharif* sorghum genotype AKSV 438 contributed by the Sorghum Research Unit, Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) was analysed during Kharif 2018, 2019, 2020 and 2021. Determination of micronutrients in the sorghum grain sample was done by Di-Acid digestion method and the aliquots of this solution are used for the determination of Zinc and Iron with the help of Atomic Absorption Spectrophotometer (AAS), (Jackson *et al.*, 1967).

For the character Zinc (Zn), the genotype AKSV 438 had a mean value of 30.61 ppm, while the control had low values, *i.e.* PVK 801 (12.80 ppm) and Parbhani Shakti

(16.77 ppm). Similarly, for the character Iron (Fe), the genotype AKSV 438 had a mean value of 37.14 ppm, while the control had low values, *i.e.* PVK 801 (24.40 ppm) and Parbhani Shakti (24.05 ppm).

Besides high Zinc (Zn) and Iron (Fe), the genotype AKSV 438 is also high-yielding. AKSV 438 recorded 32.97 g of grain yield per panicle, while the checks PVK 801 (23.25 g) and Parbhani Shakti (26.61 g) were low-yielding.

Thus, it was concluded from the present study that considering the high zinc and iron along with the higher grain yield per panicle in the genotype AKSV 438, it needs to be exploited in breeding for development of genotypes with better biofortified traits in sorghum as the donor parent in the crossing programme.

References

- Ashok Kumar A, K Anuradha and B Ramaiah (2013) Increasing grain Fe and Zn concentration in sorghum; progress and way forward, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India.
- Ashok Kumar A, BVS Reddy, B Ramaiah, P Sanjana Reddy, KL Sahrawat and HD Upadhyaya (2009) Genetic variability and plant character association of grain Fe and Zn in selected core collections of sorghum germplasm and breeding lines. *J. SAT Agric. Res.* 7: 1-4. (ejournal.icrisat.org).
- Jackson ML (1967) *Soil Chemical Analysis*. Prentice-Hall of India, New Delhi, India.

7. AKSV 440 (EC488403; INGR23041), a sorghum germplasm with high zinc and high iron content

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Sorghum (*Sorghum bicolor* L.) is one of the cheapest sources of energy and micronutrients; and a vast majority of population in Africa and central India depend on sorghum for their dietary energy and micronutrient requirement. Biofortification of sorghum by increasing mineral micronutrients [especially iron (Fe) and zinc (Zn)] in grain is of widespread interest (Ashok Kumar *et al.*, 2009). Considering this, the sorghum genotype AKSV 440 which was found promising for the higher Zinc (29.78 ppm) and Iron (35.51 ppm) content above the base line. As per the (Ashok Kumar *et al.*, 2013) the base line for Zinc (Zn) = 20 ppm and Iron (Fe) = 30 ppm has been fixed. Everything above the base line is considered as promising for Zinc and Iron content in sorghum.

The *kharif* sorghum genotype AKSV 440 contributed by Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) was analyzed during *kharif* 2018, 2019, 2020 and 2021. The testing entries along with the controls PVK 801 and Parbhani Shakti were sown in randomized block design with three replications. Determination of micronutrients in the sorghum grain sample was done by Di-Acid digestion method and the aliquots of this solution are used for the determination of Zinc and Iron with the help of Atomic Absorption Spectrophotometer (AAS), (Jackson *et al.*, 1967).

For the character Zinc (Zn), the genotype AKSV 440 had a mean value of 29.78 ppm, while the control had low values, *i.e.* PVK 801 (12.80 ppm) and Parbhani Shakti (16.77 ppm). While for the character Iron (Fe), the genotype AKSV 440 with the mean value of 35.51 ppm, while the control was with low values, *i.e.* PVK 801 (24.40 ppm) and Parbhani Shakti (24.05 ppm).

Thus, it was concluded from the present study that considering the high zinc and iron in the genotype AKSV 440, it needs to be exploited in breeding for development of genotypes with better biofortified traits in sorghum as the donor parent in the crossing programme. Therefor this genotype needs to be registered with NBPGR as a donor source for enrichment of Zinc (Zn) and Iron (Fe) in *kharif* sorghum.

References

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- Jackson ML (1967) Soil chemical analysis. Prentice-Hall of India, New Delhi, India.

8. SPV 2838 (IC643984; INGR23042), a sorghum germplasm with early flowering and early maturity line

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Sorghum (*Sorghum bicolor* L.) is one of the most important C4 cereal crops cultivated in the arid and semi-arid tropics of the world for its nutritious grain, feed, and recently as a bioenergy crop. In India, sorghum is grown in two main seasons, *kharif* and *rabi*. The requirements for these two seasonal adaptations are quite diverse due to different agroclimatic

conditions. Currently, the area allocated to *kharif* and *rabi* sorghum in the total cropped area is approximately 20% (~1 m ha) and 80% (~3.5 m ha), respectively. Unlike the grain productivity of *kharif* sorghum (~1100 kg/ha), *rabi* sorghum is very low (~700 kg/ha). *Rabi* sorghum is grown in the vast Deccan plateau in residual and receding soil moisture regimes with increasing

temperatures and desiccating winds after flowering. Terminal drought stress is the most critical factor that affects the productivity of *rabi* sorghum grain, the quality of seed and feed.

Breeding for early flowering and maturity is an important strategy to overcome the ill effects of terminal drought. SPV2838 is a BC₃F₄ progeny, developed as an early-flowering and maturing entry in the background of CRS4 by backcross breeding. CRS4 is an important tall variety adapted to *rabi* developed at CRS-IIIMR, Solapur, while B35 is a dwarf source of stay green. The new breeding stock SPV2838 is a tall, early maturing variety evaluated in the All India coordinated project on Sorghum during Rabi 2020 at 19 locations. SPV2838 flowers in 67 days and matures in 110 days compared to the check variety, M35-1, which flowers in 73 days and matures in 115 days. Early flowering and maturity by 6 days is extremely critical for the *rabi*

sorghum under terminal drought stress. M35-1 is the most popular cultivar, occupying 80% of the *rabi* sorghum area and is used as a standard check in the AICRP *rabi* sorghum trials. Therefore, the test entry SPV2838 has been compared against the check, M35-1. SPV2838 ranked first for early flowering at 13 locations out of 19 in AICRP trials at *rabi* locations. Its fodder is 9279 kg/ha with a grain test weight of 3.17 g/100 seeds. Its shoot fly reaction is 19.3% DH compared to M35-1 (23.9% DH). Its charcoal rot index is 16.34, similar to M35-1 (16.87).

SPV2838 can be cultivated in an equivalent way as of M35-1, a popular *rabi* sorghum variety with an advantage of early maturity of one week, which is very crucial in *rabi* season facing terminal drought. SPV2838, with its other matching traits, is extremely useful in the breeding program.

9. NDLA 3116-4 (IC646843; INGR23043), a cotton germplasm with high ginning per cent

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NDLA 3116-4 is a desi cotton (*Gossypium arboreum* L.) advanced breeding line developed from the cross NDLA 2933 × ARBa-79 - 08 through pedigree breeding method and is suitable for cultivation in *khari*f season under rainfed conditions. The line was identified and developed by Acharya N.G. Ranga Agricultural University, Regional Agricultural Research Station (RARS), Nandyal. The proposed entry has a high ginning percentage (40%).

NDLA 3116-4 is a desi cotton with compact type, early maturing, suitable for *khari*f season in cotton-growing districts in Andhra Pradesh. The genotype is having high ginning percentage (40%) coupled with a high seed cotton yield potential (1973 kg/ha). The plant has light green foliage with medium hairiness on the plant, medium palmate leaves with medium hairiness, cream petals with petal spot and with yellow pollen, medium bracts, oval type boll with average boll weight of 2.8 to 3.0 g.

NDLA 3116-4 exhibited a high ginning percentage of 40 and 39.6% in station trials at the Regional

Agricultural Research Station, Nandyal, during 2015-16 and 2016-17, respectively, and in AICRP on Cotton trials showed the ginning percentage of 39.6% (average of six locations) during 2018-19 and 39.9% (average of two locations) during 2019-20. The results from both the RARS, Nandyal and All India Coordinated trials showed the high ginning percentage ability of the genotype NDLA 3116-4

The genotype NDLA 3116-4 also possesses the desirable fibre quality traits, i.e. upper half mean length of 23.2 mm to 24.8 mm, micronaire of 6.2 µg/inch, tenacity of 28.1 g/tex, uniformity index of 82% and elongation percentage of 6.7%. NDLA 3116-4 is a desi cotton genotype suitable for rainfed conditions of cotton-growing areas in Andhra Pradesh.

In view of the above, the cotton entry, NDLA 3116-4 developed from the Regional Agricultural Research Station, Nandyal, (ANGRAU) is recommended for registration with ICAR-NBPGR, New Delhi for its high ginning per cent (40%).

10. CSC-025 (IC648615; INGR23044), a cotton germplasm with salinity stress tolerance

and

11. CSC-057 (IC648616; INGR23045), a cotton germplasm with Salinity stress tolerance

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Cotton is a significant cash crop globally, and its cultivation is alarmingly being shifted to marginal saline agroecosystems. It is a moderately salt-tolerant crop with a threshold salinity level of 7.7 dS/m (Peng *et al.*, 2016). Asiatic diploid cotton (*Gossypium herbaceum* and *Gossypium arboreum*) is the better option in highly saline, arid and semiarid regions of India, as compared to *Gossypium hirsutum* and *Bt* cotton. At ICAR-Central Soil Salinity Research Institute, Regional Research Station (ICAR-CSSRI, RRS), Bharuch, Gujarat, we developed two salt-tolerant cotton (*Gossypium herbaceum* L.) genotypes, CSC-057 and CSC-025. CSC-057 (GShv 451/08 × GBhv 290) and CSC-025 (GShv 297/07 × GBhv 290) are advanced near homozygous breeding lines, developed by the pedigree breeding method and currently in the F8 generation. Based on 4

years evaluation (2017-20) trials (Table 1) conducted on naturally salt affected field (soil salinity ECe 9 dS/m) and micro plots at ICAR-CSSRI, RRS, Bharuch, Gujarat, CSC-057 (5.5) and CSC-025 (9) showed 16% and 90% higher leaf K/Na ratio, respectively as compared to the check variety, G Cot 23 (4.73). CSC-057 (14.65 q/ha) and CSC-025 (16.41 q/ha) also registered 8.1 and 21.1% higher seed cotton yield, respectively, as compared to the salt-tolerant check variety G Cot 23 (13.5 q/ha). Moreover, CSC-057 (2.87g/boll) and CSC-025 (2.98 g/boll) showed 6.5% and 10.6% higher boll weight, respectively, as compared to the check variety, G Cot 23 (2.7 g/boll).

Reference

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Table 1: Performance of CSC-057, CSC-025 and local check, G Cot 23 under salt stress (ECe 9 dS/m)

Genotype	Year of reporting	Seed cotton yield (kg/ha)	Boll weight (g/20 boll)	Leaf K/Na ratio
CSC-057	2017	1717	61	6.9
	2018	1720	58	5.1
	2019	1302	53	4.8
	2020	1121	58	5.2
	mean	1465	57.5	5.5
CSC-025	2017	1892	62	11.7
	2018	1807	60	9.5
	2019	1755	57	7.7
	2020	1110	60	7.1
	mean	1641	59.75	9
Check variety (G Cot 23)	2017	1756	58	5.7
	2018	1396	53	4.9
	2019	1290	50	4.4
	2020	980	55	3.9
	mean	1355.5	54	4.73

12. IC275447 (INGR23046), a chickpea germplasm with ascochyta blight resistance

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Chickpea (*Cicer arietinum* L.) is the second largest pulse crop grown worldwide and Ascochyta blight caused by *Ascochyta rabiei* (Pass.) Labr. is the most devastating disease of the crop in all chickpea growing areas worldwide particularly in areas with cool, humid weather during the growing season. The pathogen *A. rabiei* is highly variable. The resistant sources available are not sufficient, and new needs to be identified from time to time as resistance breakdown in existing chickpea varieties is very frequent due to the fast evolution of new pathotypes of the pathogen. Therefore, this work was undertaken to evaluate the existing chickpea germplasm diversity conserved in the Indian National Genebank against the disease under artificial epiphytotic conditions. A total of 1970 chickpea accessions were screened at two hotspot locations, viz. PAU, Ludhiana and HAREC, CSK HPKV, Dhaulakuan following standard procedures. An artificial standard inoculation procedure was followed for uniform spread of the pathogen (Gayacharan *et al.*, 2020). The promising accessions were further validated against the disease over the years under artificial

epiphytotic conditions in two locations, i.e. PAU, Ludhiana and CSK HPKV, Dhaulakuan. The accession IC275447 was found resistant against the pathogen. The accessions were also found to be resistant in earlier MLE trials done during 2005-06, coordinated by NBPGR; however, this was not published or utilized in breeding programs. IC275447 was found constantly resistant during 2015-16 (disease severity score 3), 2017-18 (disease severity score 2), 2018-19 (disease severity score 2) and 2019-20 (disease severity score 3) at PAU, Ludhiana location. The accession was also screened at HAREC, CSK HPKV, and Dhaulakuan during 2015-16 (disease severity score 2) and 2016-17 (disease severity score 3), and was found resistant. In the screening of germplasm susceptible check varieties, viz. L550 and JG62 were used. The disease severity score for checks was 9 (highly susceptible).

Reference

Gayacharan, U Rani, S Singh, AK Basandrai, VK Rathee, K Tripathi, N Singh, GP Dixit, JC Rana, A Kumar and K Singh (2020) Identification of novel resistant sources for ascochyta blight (*Ascochyta rabiei*) in chickpea. *Plos one* 15(10): e0240589.

13. ICPL 88039A & ICPL 88039B (IC648617 & IC648618; INGR23047), a pigeonpea germplasm with cytoplasmic male sterility and early maturity

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Hybrids based on cytoplasm male sterile (CMS) technology have now emerged as a potential method for significant improvement of pigeonpea [*Cajanus cajan* (L.) Millisp.] productivity in India (Saxena *et al.*, 2016). The efforts of more than three decades R&D of IIPR on the advancement of the CMS technology have led to the development of two early duration

pigeonpea hybrids namely IPH 15-3 and IPH 09-5 for commercial cultivation in the North West Plain Zone of India which comprises Western UP, New Delhi, Haryana, Punjab and Uttarakhand states (<https://seednet.gov.in>). CMS-based hybrid technology requires three components, viz. sterile (A), maintainer (B) and restorer (R) lines. In pigeonpea, of the eight (A1

to A8) different cytoplasm sources available to harness the heterosis, A2 and A4 cytoplasms derived from *Cajanus scarabaeoides* and *Cajanus cajanifolius*, respectively, have been optimized for regular use in hybrid pigeonpea breeding programmes of the country (Bohra *et al.*, 2019 and 2021). The popular early maturing (<150 days) variety ICPL 88039 has been converted as the donor CMS line in the background of A2 cytoplasm (*Cajanus scarabaeoides*). The new CMS lines ICPL 88039A have been converted using standard backcross technique with A₂ cytoplasmic donors (GT 288A). ICPL 88039A is a stable for male sterility and produces completely non-functional pollen grains over the years of sterility testing conducted using field screening and standard Acetocarmine (2%) staining method. The developed new CMS lines, ICPL 88039A have early maturity along with the maintainer and restoration system reported here, which could create novel opportunities for accelerated hybrid breeding in pigeonpea.

The sterility in ICPL 88039A was confirmed by different methods, viz. flower morphology dissection by microscopic study, standard Acetocarmine (2%) staining testing of pollen grains and by using DNA markers confirming the sterility of the genotype. The

cent per cent sterile plants were selected and simultaneously advanced to develop ICPL 88039A. The line ICPL 88039A is an early maturing (140-150 days) indeterminate semi-spreading plant type having a plant height of 170-185 cm and the number of primary branches ranges from 12-16 branches/plant. ICPL 88039A has attained its 50% flowering in 100-105 days. The plant produces yellow colour flowers with sparse streaks and green pods with brown streaks. The seed coat is brown and 100 seeds weigh about 8.9-10 g.

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14. IC140784-P1 (IC648619; INGR23048), a cluster bean germplasm with early maturing determinate growth type and synchronous maturity

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Cluster bean (*Cyamopsis tetragonoloba* L.) is an important drought-tolerant legume cultivated predominantly under rainfed conditions in the arid and semi-arid regions of India. Since the crop is frequently exposed to moisture stress, early maturity is a highly desirable trait that enables plants to escape terminal drought and reduces the risk of crop failure. Most of the improved cultivars popular in the region have a maturity time of 90-95 days after sowing. Due to this, there is always a very high chance of crop failure due to water scarcity. Therefore, any germplasm line having a short duration of maturity will be a useful source of donors in breeding programme as it may escape the dry spell. The availability of diverse genetic resources is essential for developing improved cultivars adapted to such challenging environments (Duvick *et al.*, 1986).

As part of the germplasm characterization and evaluation programme at ICAR-NBPGR Regional Station, Jodhpur, 50 cluster bean accessions collected from Rajasthan, Gujarat, and Maharashtra were evaluated during *kharif* 2020 using an Augmented Block Design with national checks RGC-936 and RGC-1066. During the evaluation, a superior single-plant selection, IC140784P1, was identified from accession IC140784. The selection exhibited desirable traits including early maturity, single-stem growth habit, determinate flowering, all-node pod bearing, and uniform maturity. IC140784P1 initiated flowering 23 days after sowing, attained 50% flowering in 32 days, and matured within 82 days after sowing. This is approximately 10-15 days earlier than the widely cultivated improved varieties that generally mature in

90–95 days. The stability of the early-maturity trait was confirmed through evaluations conducted during Kharif 2021, Summer 2022, and kharif 2022 along with national check varieties.

The identified accession represents a valuable genetic resource for guar improvement. Its determinate and single-stemmed growth habit promotes synchronized maturity, reduces the incidence of black seeds, and improves seed quality (Gopala and Dwivedi *et al.*, 2009). For highest seed yield, the guar plant should have early maturity, a determinate growth type, optimum plant height, all node pod bearing, a high branching number and a high number of clusters per plant, with each cluster having the maximum number of pods (Paroda and Saini *et al.*, 1978). Early-maturing and determinate plant types are particularly

advantageous for drought-prone regions and intensive cropping systems, where shorter crop duration and uniform maturity are essential. Therefore, accession IC140784P1 can serve as an important donor parent in breeding programmes aimed at developing short-duration, climate-resilient, and high-yielding cluster bean cultivars for sustainable production in dryland agriculture.

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15. CAZG-109 (IC648620; INGR23049), a cluster bean germplasm with high test weight, long fleshy pod, glabrous leaves, stem and pods

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Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] a drought hardy legume is an economically important crop of the Indian arid zone. It is globally recognized for the industrially important seed-borne gum besides other multifarious uses in food, feed and fodder. The guar seed is composed of three layers, namely the outer husk (16–18%), the germ (43–46%) and the endosperm (34–40%). The economically important traits like seed weight (test weight $\approx$ 30 g), pod length ($\approx$ 6.0 cm) and seeds per pod ($\approx$ 6) have a very narrow range in seed type varieties (Dadheech *et al.*, 2019). Realizing the paucity of diversity in traits for further improvement of yield and suitable plant type in guar, efforts were made to create variability for seed weight and related traits through mutagenesis.

Seed weight has been recognized as one of the important traits contributing to seed yield in most of the field crops. The test weight of released seed type varieties of guar has been reported to vary around 30–35 g. Though pod length and seed weight either lacked correlation or were negatively correlated to seed yield (Dadheech *et al.*, 2020), a source for large seed and longer pods would be desirable for incorporating in a breeding program with a long-term goal. The two traits show positive correlation with yield per plant among seed type varieties having pod length <6 cm and seed

weight <3.6 g. Thus, there is a possibility of altering linkages in favourable direction. The genotype, CAZG-109, identified for pod length (12.3 cm) and bold seed (test weight 46.8 g) was also evaluated with 5 genotypes varying for the two traits for 4 seasons (Table 1). Pusanavbahar, a vegetable type variety, had maximum test weight (37.4 g) after CAZG-109, while CAZG-102 had minimum (28.8 g). CAZG-109 expressed high values for pod length (12.3 cm), pod width (10.9 mm) and seeds per pod (9.6), hence it could be a desirable donor for improving pod length, seeds per pod and seed weight depending upon linkages with other yield attributing traits, especially pods per plant. Morphologically, the selected genotype CAZG-109 is branched, luxuriant, glabrous having long and thick pods that are suitable for vegetable type as well as seed yield.

References

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Table 1: Pod and seed characteristics of promising genetic stocks–CAZG-109 (Average of 4 seasons)

S.N.	Genetic Stock	Pod length (cm)	Pod width (mm)	Seeds per pod	Test weight (g)
1	CAZG - 102	6.3	7.6	8.6	28.8
2	RGC-936	5.9	7.9	7.4	32.1
3	HG-2-20	6.1	7.4	7.6	36.7
4	RGC-1066	6.1	8.3	8.0	33.8
5	Pusanavbahar	9.9	9.5	9.0	37.4
6	CAZG-109	12.3	10.9	9.6	46.8

16. Improved Pusa Uday-1 (IBL BC2F4) (IC646853; INGR23050), a cucumber germplasm with highly stable tropical gynoecious lines for hybrid breeding and donor for F locus introgression into elite genotype

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Cucumber (*Cucumis sativus* L.) originated in India with a huge diversity in terms of different economically important traits. Most of the commercial cultivars of cucumber in other parts of the world are with F1 hybrids in a gynoecious background, but the contribution of hybrid seed is not more than one-third of total seed replacement in India. However, contribution of the indigenously developed F1 hybrids is not very significant because of the non-availability of gynoecious lines in the background of the tropical genotypes. The gynoecious sex form has been extensively exploited in heterosis breeding for enhancing the productivity of the cucumber worldwide. Most of the gynoecious lines of cucumber are adapted to the temperate regions they are not stable at temperatures >35°C. Gynoecious hybrid cultivars produced by crossing a gynoecious line as female parent have become an integral part of the cucumber improvement programme. In addition to economical hybrid seed production, gynoecious sex expression provided a more concentrated fruit set and early maturity compared to the conventional monoecious × monoecious-based hybrids. Therefore, development of tropical gynoecious lines with stability in sex expression even at temperatures above 40°C is urgently required to develop indigenous F1 hybrids in cucumber and to strengthen the Indian seed industry. The different sex types in cucumber are mainly determined by three major genes F/f, M/m and A/a. The loci F promotes femaleness on the whole plant level, while the gene M determines whether flowers are

unisexual.

The objective of this study was to introgress the F locus into the elite cultivar, Pusa Uday, using the American pickling gynoecious line, Gy421 (EC636513) as a donor. A marker-assisted backcross breeding strategy was adopted for rapid recovery of the recurrent parent along with the donor trait, gynoecy, through foreground and background selection. Two SSR markers (SSR-13251 and SSR- 15516) and one gene-based SCAR marker (CsACS1G) were used for foreground selection of F locus (gynoecy) in 192 developed BC₁F₁ progenies. The identified heterozygote plants were subjected to the selection process. Heterozygote plants for F locus were identified using the co-dominant SSRs along with one SCAR marker. Besides, selection for the plants was done on the basis of the phenotype and only the plants with resemblance to the recurrent parent along with F loci were selected. These plants were selfed to produce the BC₁F₂ and were under gone foreground selection and phenotypic evaluation. The plant #29 from BC₁F₂ population was selected and selfed to develop BC₁F₃ population.

859 markers were used from across the genome of cucumber for background profiling of BC₂F₃ plants, 121 markers found to be polymorphic between donor parents (G421) and recipient parents (Pusa Uday). Background analysis revealed that the recurrent parent genome (RPG) recovery ranged from 69.63 to 78.72% in BC₂F₄ generation. From this BC₁F₃ population, 10 gynoecious plants with more lateral branches (4-5) and

better fruit quality (L:D ratio >3.4) were selected based on the foreground, background and phenotypic selection. The application of MAS with the MABC breeding program accelerated the recovery of the RP genome, reducing the number of generations and the time for incorporating gynoecious gene. The line,

Improved Pusa Uday was selected from IBLs with only female flowers and higher lateral branches, *desi* fruit type resembling Pusa Uday at marketable stage (L:D $\geq$ 3). Hence, this line could be directly utilized or could be utilized in breeding programme to develop gynoecious based F1 hybrid cucumber.

17. IMPU-2 IBL11BC1F4 (IC646854; INGR23051), a cucumber germplasm with Tropical gynoecious line for use in hybrid breeding

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Cucumber (*Cucumis sativus* L.) originated in India with a huge diversity in terms of different economically important traits. Most of the commercial cultivars of cucumber in other parts of the world are with F1 hybrids in a gynoecious background but the contribution of hybrid seed is not more than one-third of total seed replacement in India. However, contribution of the indigenously developed F1 hybrids is not very significant because of non-availability of gynoecious lines in the background of the tropical genotypes. The gynoecious sex form has been extensively exploited in heterosis breeding for enhancing productivity of cucumber worldwide. Most of the gynoecious lines of cucumber are adopted to the temperate regions they are not stable at temperatures >35°C. Gynoecious hybrid cultivars produced by crossing gynoecious line as female parent have become integral part of cucumber improvement programme. In addition to economical hybrid seed production, gynoecious sex expression provided a more concentrated fruit set and early maturity compared to the conventional monoecious $\times$ monoecious based hybrids. Therefore, development of tropical gynoecious lines with stability in sex expression even at temperature above 40°C is urgently required to develop indigenous F1 hybrids in cucumber and strengthen the Indian seed industry. The different sex types in cucumber are mainly determined by three major genes F/f, M/m and A/a. The loci F promotes femaleness on the whole plant level while the gene M determines whether flowers are unisexual.

Introgression of F locus into Pusa Uday was attempted through marker assisted backcross breeding using markers for foreground and background selection using Gy421 (EC636513) as a donor. Two SSR markers (SSR-13251 and SSR-15516) and one gene-based SCAR marker (CsACS1G) were used for

foreground selection of F locus (gynoecy). Heterozygote plants for F locus using these three markers and plants phenotypically matched to recipient parent, Pusa Uday at BC₁F₁ stage. These plants were selfed to produce the BC₁F₂ and were under gone foreground selection and phenotypic evaluation. The phenotypic data of ninety-two plants of the BC₁F₃ population, including yield and its component traits including sex expression, number of lateral branches, fruit length, fruit diameter and L:D ratio were recorded. Sex expression was recorded on individual plants by counting the number of pistillate nodes in the first twenty nodes of the main stem and the total number of lateral branches was also recorded for each plant in the first twenty nodes. Mean fruit L:D ratio per plot was obtained by measuring the length and diameter of 5–10 randomly selected fruits. Out of ninety-two plants in the BC₁F₃ population, phenotypically all the plants showed only female flowers, thirty-six plants showed three lateral branches and fifteen plants showed four lateral branches, whereas fifty-two plants showed an L:D ratio between 3.1 and 4.0. All forty-one inbred backcross lines IBLs (BC₁F₄) were purely gynoecious in sex expression and their fruits were similar to the Pusa Uday type with non-bitter fruits and more than four lateral branches and twenty-eight IBLs had fruit length >15 cm. The maximum fruit length observed was 20.5 cm in IBL12. A total of thirty-five IBLs had average fruit diameter more than 5 cm with the highest average fruit diameter (7.8 cm) recorded in IBL18. Among these lines, only ten IBLs produced fruits with more than 3.0 L:D ratio and the maximum L:D ratio was 4.0 in IBL11. This plant was selected as Improved Pusa Uday-2.

A total of 859 markers were used from across the genome of cucumber for background profiling of BC₁F₃ plants, 121 markers were found to be polymorphic

between donor parents (G421) and recipient parents (Pusa Uday). Background analysis revealed that the recurrent parent genome (RPG) recovery ranged from 60.63% to 78.72% in BC₁F₃ generation. From this BC₁F₃ population, 10 plants were extracted based on the foreground, background and phenotypic selection, which were gynoeious in habit, with more later

branches (4-5) and better fruit quality (L:D ratio >3.4). The line, Improved Pusa Uday-2 was selected from IBLs has complete female flowers and higher lateral branches *desi* fruit type (Pusa Uday) at marketable stage (L:D ≤ 3). Hence, this line could be directly utilized in breeding programme to develop gynoeious based hybrid cucumber.

18. VRSG-7-17 (IC0630886; INGR23052), a sponge gourd germplasm with characteristic basmati aroma

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The flavour and aroma in the food are determined by chemical senses of taste and smell. India is home of several traditional aromatic foods, of which Basmati rice is the most popular. A harmonious aroma blend in the food increases its acceptability and likeability. Apart from Basmati rice, the aroma has been reported as one of the quality characteristics in a variety of crops, fungi, microbes and processed foods. Likewise, consumers' preference for aromatic sponge gourd varieties over non-aromatic varieties has resulted in the high price of aromatic cultivars. *Luffa cylindrica* (L.) Roem (2n=26), as sponge gourd is an important edible vegetable member of the Cucurbitaceae family in the Indian subcontinent. It is suitable for cultivation during the summer and rainy season. Its leaves, flowers and fruits are edible. An aromatic sponge gourd genotype (VRSG-

7-17) has been identified at ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi.

The genotype VRSG 7-17 is a unique line of sponge gourd with characteristic aroma resembling typical aroma of 'Basmati rice' in its fruits, peel and leaves (Table 1). The fruits of this novel sponge gourd genotype (VRSG7-17) also retain special aroma even after cooking and/or boiling at high temperatures.

The inheritance of fruit colour was found to be controlled by a single gene with incomplete dominance. The SPME and GC-MS analysis showed the presence of four compounds hexanal, 1-octen-3-ol, 3-octanone and limonene as dominant volatiles present in this aromatic genotype. This genotype is also tolerant to downy mildew and melon weevil and is less susceptible to leaf miner under field conditions.

Table 1: Morpho-agronomic characters of sponge gourd genotype VRSG7-17

Characters	Genotype VRSG7-17	Characters	Genotype VRSG7-17
Days to first male flower	43 days	Vine length	6.28 meter
Days to first female flower	47 days	Fruit weight	156.5 g
Days to first fruit harvest	55.5 days	Fruit yield/ plant	1.13 Kg
Fruit length	27.46 cm	Number of fruit/plant	3.6
Fruit diameter	3.35 cm	Fruit colour	Light green

19. DRMRIJ 12-26 (IC648622; INGR23053), an Indian mustard germplasm with a novel white rust resistant gene

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White rust caused by *Albugo candida* (Pers. ex Lev.) Kuntze is one of the most devastating diseases of

Crucifers and causes severe losses in Indian mustard (*Brassica juncea*). Symptoms of the disease may appear

at vegetative stage itself and sustain even at flowering stage. Maximum damage is caused by stag head formation due to malformation of flowering buds directly causing the yield losses. Indian germplasm of (*Brassica juncea* L.) has generally been reported to have susceptibility against existing pathogens. Breeding efforts, however, have brought few successes in form of developing resistant cultivars like JM1, Basanti and JM3. One germplasm line BIO YSR (IC443623), has earlier been registered as white rust-resistant genetic stock derived from an exotic source. Genetic studies have revealed dominance of resistance over susceptibility. Resistance to white rust is governed by a single dominant gene.

DRMRIJ 12-26 is an inbred line derived from a cross between KLM227 and EC597313 (exotic germplasm), followed by individual plant selection. Cross was attempted during 2008-09 between KLM227 and EC597313. DRMRIJ 12-26 was induced into AICRP-RM during 2015-16 and had been evaluated continuously for four years during 2015-16, 2016-17, 2017-18 and 2018-19. White rust reaction on leaves was recorded at two different stages, viz. 75 and 100 days after sowing, while staghead formation was recorded at the flowering stage. Candidate strain DRMRIJ 12-26 expressed resistant reaction against white rust at 75 days stage, which was at par with the resistant check BIO YSR during two years of testing at Hisar and one year of testing at Morena centre. Mean Disease index of

DRMRIJ 12-26 was 0.0% in comparison to 32.5% of susceptible check Rohini. Disease reaction against white rust on leaves at 100 days stage was recorded at eight locations, viz. Hisar, Kangra, Kanpur, Pantnagar, Morena, Ludhiana, Sri Ganganagar and New Delhi, which included three hot spots (Kangra, Pantnagar and Morena) (Table 1). On the basis of the mean disease index over all five locations for four years, candidate strain DRMRIJ 12-26 expressed 3.3%, which was better than the resistant check BIO YSR (7.1%) and susceptible check Rohini (28.54%). Observations on staghead formation were recorded at Morena, Sri Ganganagar and Ludhiana, based on mean disease index over three years. DRMRIJ 12-26 had 1.4% disease incidence in comparison to resistant check, BIO YSR (9.9%) and susceptible check Rohini (6.9%). The already reported IP markers, viz. AcB1-A4.1 from Heera and AcB1-A5.1 from Donskaja and WRR candidate gene-specific marker, WR-D from Donskaja have been validated in the concerned strain, DRMRIJ 12-26. It has been found that this genotype does not possess any of the already mapped loci/genes for white rust resistance. This infers that the resistance to WR expressed by DRMRIJ 12-26 is governed by another third/novel gene, which has not been discovered and mapped yet. So, this genotype may be used in developing a mapping population for tagging of that WRR gene in future research endeavours.

Table 1: Mean disease index of candidate strain DRMRIJ 12-26 and check genotypes against white rust pathogen

S. N.	Location	White rust (% WR severity)								
		Disease reaction at 75 days			Disease reaction at 100 days			Staghead formation		
		DRM RIJ 12-26	Bio YSR (Res. C3check)	Rohini (Sus. Check)	DRMRI J 12-26	Bio YSR (Res. Check)	Rohini (Sus. Check)	DRMRI J 12-26	Bio YSR (Res. Check)	Rohini (Sus. Check)
1	Kangra	-	-	-	3.9	14.23	44.83	-	-	-
2	Kanpur	-	-	-	0.0	0.0	31.85	-	-	-
3	Pantnagar	-	-	-	2.8	9.4	27.22	—		
4	Hisar	0.0	0.0	34.15	0.0	0.0	34.75	—		
5	Morena	0.0	0.0	30.9	10.0	8.8	31.18	0.0	9.9	15.2
6	Ludhiana	-	-	-	0.0	-	20.7	0.0	-	0.0
7	Sri Ganganagar	-	-	-	9.6	-	8.9	4.1	-	5.4
8	New Delhi	-	-	-	0.0	-	28.9	—		
	Mean	0.0	0.0	32.53	3.3	7.1	28.54	1.4	9.9	6.9

20. IC384578 (INGR23054), a linseed germplasm with high number of capsules

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Linseed (*Linum usitatissimum* L.) is one of the earliest domesticated crops of the world known for its seed oil and fibre. It is self-pollinated annual crop and has two morphotypes, flax type and linseed type which differ substantially in terms of growth, development and agronomic performance. For linseed type, short height, more branching, high number of capsules and seed weight are desirable traits. Lately, linseed is gaining popularity as nutraceuticals and functional food owing to high omega-3 alpha linolenic acid and other bioactive compounds such as lignans and soluble fibres. Productivity of linseed in India is far below (0.543 tonne/ha) than the world's average (1.053 tonne/ha). Despite the Indian regions (Northwest India) being part of the center of origin (central Asiatic centre) of linseed, there have been limited genetic resources identified for traits of economic and agronomic importance. The number of capsules and primary branches per plant has a positive correlation with yield and, therefore are crucial traits for crop improvement. In this perspective, one germplasm accession, IC0384578 has been identified for high capsule numbers per plant based on

evaluation data of four environments in three consecutive years (*rabi* 2017-18, 2018-19 and 2019-20) at New Delhi (zone 1) (28°38'53.7"N 77°09'05.4"E) and at Akola (zone 3) during *rabi* 2019-20 (20°42'03.2"N 77°01'53.6"E) (Saroha *et al.*, 2022). The average number of capsules recorded in IC0384578 were 280.26 which was significantly higher than in check varieties *Kartika* (242.28) and *Shekhar* (230.3) across multilocation-year trials. In addition, IC384578 also possesses other agronomically important traits such as short plant height (58-67 cm) and high number of primary branches (5-10). The average test seed weight is 6.3 g and yield per plant is 14.5 g.

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21. Jawahar Soybean 20-34 (IC596520; INGR23055), a soybean germplasm with early flowering and early maturity

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Soybean [*Glycine max* (L.) Merr.] is predominantly grown under rainfed conditions in India, where early maturing cultivars are preferred to escape terminal drought and fit into multiple cropping systems. Flowering and maturity in soybean are strongly influenced by photoperiod sensitivity, which is regulated by major maturity genes (*E1*, *E2*, *E3*, and *E4*) (Bernard 1971; Buzzell 1971; Buzzell and Voldeng 1980). Recessive alleles at these loci reduce photoperiod

sensitivity and promote early flowering and maturity, making them valuable targets for soybean improvement in tropical and subtropical environments.

JS 20-34 is an early-maturing soybean variety. In an evaluation of 101 Indian soybean varieties under ambient and extended day length (20 h) conditions, JS 20-34 exhibited one of the lowest levels of photoperiod sensitivity, showing only 29.5% increase in days to flowering under extended day length. This level of

sensitivity was substantially lower than the population mean (51%), indicating its reduced response to changes in photoperiod.

Genotyping using functional marker for major maturity genes revealed that JS 20-34 carries the recessive *e2* allele. Among the 101 varieties examined, only three varieties JS 20-34, PRS 1, and LSb 1, possessed this allele, demonstrating its rarity in Indian soybean. Varieties carrying the recessive *e2* allele exhibited significantly lower photoperiod sensitivity than those possessing the dominant *E2* allele. The presence of the recessive *e2* allele in JS 20-34 is considered a major factor contributing to its early maturity (approximately 87–89 days), making it one of the earliest maturing soybean varieties cultivated in Central India.

The rarity of the recessive *e2* allele in Indian soybean cultivars, combined with the proven adaptation and agronomic performance of JS 20-34,

makes this variety an important genetic resource for soybean breeding. Registration of JS 20-34 as a genetic stock carrying the recessive *e2* allele will facilitate its utilization in marker-assisted breeding programmes aimed at developing early maturing and less photoperiod-sensitive soybean cultivars for diverse agro-ecological regions.

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22. NC-11 (IC205471; INGR23056), a sesame germplasm with tolerance to deficit soil moisture stress

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The sesame (*Sesamum indicum* L.) genotype IC205471 is a local landrace from Himachal Pradesh State, India. The genotype was collected from ICAR-NBPGR, New Delhi, India in the year 2015-16. The genotype IC205471 was evaluated from 2018 to 2019 along with two national checks, i.e., GT-10 and TKG- 22, at ICAR-IIOR Research Farm, Narkhoda, Hyderabad, India (17°15'16" N, 78°18'30" E; 542 meters above sea level) under field conditions. The genotype was tested in two different water regimes, i.e. well-watered (WW) and deficit soil moisture stressed (WS), during four different seasons of 2018 and 2019. The deficit soil moisture stress conditions were imposed from flowering (40-45 days after sowing) to physiological maturity (90-95 days after sowing). The moisture levels in WS plots decreased to 35-40% of available soil moisture, equivalent to -4.5 to -5.0 bars of soil water potential, compared to WW conditions (80% available soil moisture). The soil moisture content was monitored on an hourly basis using field-installed real-time soil sensors (Proximal; SoilSenS, V1.0). The outcome of four-season trials revealed that the genotype IC205471 was a superior performer (20.0 to 38.0% higher seed weight/plant) over two national checks, i.e., GT-10 and TKG-22, particularly under WS

conditions. Further, the genotype was found superior in various morphological, physiological, yield and contributing traits, suggesting tolerant nature of genotype to deficit soil moisture stress conditions (Pandey *et al.*, 2021; Sravanthi *et al.*, 2021). The genotype is moderate-maturing (97-99 days) and medium-height (65-75 cm) in nature. The genotype has an indeterminate growth habit with little hair on the leaves, stem, and capsule. It has basal branching and a single flower at each axil. The flowers are white with violet/purple shading and have alternate leaf and capsule arrangements. The seed coat colour is off-white to light brown. In addition, the genotype IC205471 was also evaluated for root structural and functional traits under well-watered and water stress conditions. It was reported that genotype IC205471 exhibited higher transpiration efficiency, harvest index, and seed yield under water stress conditions. Also, the genotype had higher root length, total root surface area, root volume, root dry weight, and root length density compared to the check GT-10 under water stress conditions (Pasala *et al.*, 2021). Therefore, the genotype IC205471 may be used in sesame crop improvement programmes for the development of varieties adapted to deficit soil moisture stress conditions.

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23. IC626510; GAN/PCT/1212 (INGR23057), an avocado germplasm high Pulp recovery and tolerance to anthracnose

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Avocado (*Persea americana* Mill.) is a native of tropical America. It originated in Mexico and Central America, possibly from more than one wild species. Avocado is the most nutritious among fruits. The pulp is rich in proteins (up to 4%) and fat (up to 30%), but low in carbohydrates. Avocados have been known to maintain good cholesterol while reducing bad cholesterol. Avocado is mainly used fresh, in sandwich filling or in salads. It can also be used in ice creams and milk shakes and the pulp may be preserved by freezing. The Avocado is originated in Central and South American countries. A lion's share of the Avocado production of world, produced in these countries. The world's avocado production was 8.06 million tonnes in 2020. Mexico is the largest producer of Avocado in the world followed by Colombia, Dominican Republic, Peru, Indonesia, Kenya, Brazil, Ethiopia, etc. Mexico supplies 45% of the international avocado market. The avocado market is still growing. Since 2012, the global avocado market has seen a rise, and it is expected to reach a valuation of about 23 million dollars by the end of the year 2027. The production in India is very limited and it is not a commercial avocado plantation. The agro-climatic conditions prevailing in various parts of the country appear to be favourable for bringing more areas under avocado. Avocados are grown scattered in southern tropical states like Tamil Nadu, Kerala, Karnataka, and Maharashtra. Also popular in the

northeastern Himalayan states at elevations if 800-1,600 meters. There are three main production regions of avocado in India, the Kodaikanal area, Ooty area of Tamil Nadu, Gundlupet and Kodagu region of Karnataka and a minor area in North Eastern India. These areas may be producing around 5000 tonnes of avocados every year and the production is increasing rapidly as more and more areas are being brought under cultivation. There are only 2 released varieties of avocado in India and there are needs to identify more promising genotypes to meet the rapidly increasing demand for planting material.

A promising seedling selection (IC626510) was developed by individual plant selection from seeds collected from avocado grown in Madikeri (12.4208° 75.739, 1182 m above MSL) by random selection in 2012. The seedlings were raised and planted at IIHR FGB in 2013. It is a promising genotype with large-sized green fruits, with fruits weighing 243 g. Mean fruit length was 9.15 cm and mean fruit diameter was 8.23 cm with pulp recovery >70%. Mean seed weight was 68g with TSS 4.8 °Brix (Table 1). Fruit colour is light green and flesh colour is creamy white. It is late bearing genotype with pear-shaped fruits and fruit is thin-skinned. Fruit shape is obovate, dark green colour with creamish white flesh colour. It is suitable for fresh fruit purposes.

Table 1: Important features in Avocado accession IC626510

Genotype	Leaf length (cm)	Leaf width (cm)	Fruits plant-1 (no)	Fruit weight (g)	Yield (kg)	Fruit length (cm)	Fruit diameter (cm)	Seed weight (g)	TSS (°Brix)	Pulp recovery	Fruit color	Flesh color
Avocado- 12	10.9	6.32	21	243	5.1	9.15	8.23	68	4.8	72.02	Green	Creamy White

24. CHES R-27 (IC642755; INGR23058), a rambutan germplasm with red colour fruit, free Stone bigger fruit size

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Rambutan (*Nephelium lappaceum* var. *lappaceum* L.) is native to Malaysia and Indonesia and belong family of Sapindaceae. The cultivation of Rambutan is spread over all tropical countries. Indonesia and Malaysia contribute more than 95% of total Rambutan production in the world. In India Rambutan was introduced as a homestead garden in Kerala and slowly it became popular and the area is rapidly increasing in parts of Kerala, Karnataka and Tamil Nadu (Tripathi *et al.*, 2014; 2020). Fruits are used mostly fresh. Rambutan is adapted to a warm tropical climate. It is grown commercially within 12-15° of the equator and grows successfully in a wide range of soils. Several new and underutilized fruits were introduced in India during last few decades. Rambutan is one of the emerging underutilized fruits with high global demand. It is introduced in home garden in some parts of Kerala and Tamil Nadu, and a considerable variability of rambutan is found in these areas. A large collection of rambutan variabilities was made at Central Horticultural Experiment Station (IIHR), Chettalli, Karnataka during 2001-12. Some of the collections (37) of rambutan collected and planted in 2001 were evaluated for growth, flowering and fruiting characters during 2007-12. There was a lot of variability in these collections with respect to fruit, fruit size, fruit colour and fruit quality parameters. The growth data revealed that plant height ranged from 2.90 m in CHESR-24 to 6.30 m in CHESR-28. Plant spread (E-W) was highest in CHESR-28 (5.7 m) and lowest in CHES R-24 (1.25 m). Plant spread (N-S) was highest in CHESR-29 (6.2 m) and lowest in CHES R-24 (1.05 m). The yield data revealed that higher numbers of fruits were harvested from CHESR-26 (2025), whereas CHESR-33 registered the lowest number of fruits (100). The highest yield was recorded in CHESR-26 (48.8 kg) while CHESR-33 registered the minimum yield of 2.77 kg. The highest fruit weight was recorded in CHESR- 27

(44.2 g), whereas CHESR-156 recorded the lowest fruit weight of 16.5 g. Fruit length and breadth were found to be highest in CHESR-27. The lowest fruit length and breadth were recorded in CHESR-156. The highest pulp weight was recorded in CHESR-29 (21.36 g). The highest pulp content was recorded in CHESR-29 (52.47%). The lowest pulp content was recorded in CHESR-8 (37.69%). The highest seed weight was recorded in CHESR-27 (2.69 g), while CHESR-7 recorded the lowest seed weight of 1.66 g. Seed content ranged from 5.92% in CHESR-29 to 11.55% in CHESR-16. TSS content varied from 13.1°B in CHESR-222 to 20.2°B in CHESR-35 and CHESR-138. Titrable acidity was found to be lowest (0.26%) in CHESR-29 and highest (1.00%) in CHESR-222. Ascorbic acid content was estimated to be the highest (63.38 mg/100 g) in CHESR-58 and the lowest was recorded in CHES-28 (29.0 mg/100 g). Among the red colour collections, CHESR-27 was found to be superior to other collections. This line CHESR-27 is an early maturing, promising selection. The trees are medium in size and semi-spreading in nature. The fruit is dark red in colour. Average fruit weight is 40 to 45 g. Fruits are free stone an aril can usually be removed from the seed without attachment to the testa. The arilis are white in colour, thick, firm and dry and sweet (TSS- 17.45°B) with pulp recovery of about 42.18 per cent (Tripathi and Karunakaran *et al.*, 2015).

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25. Lakshamana (IC647019; INGR23059), a tamarind germplasm with big Pod size and high pulp recovery

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Tamarind (*Tamarindus indica* L.) is a well-known commodity of Indian cuisine and has medicinal and industrial uses. It is a nutritious tree crop of widespread occurrence growing on marginal lands in semi-arid and sub-humid tropical climates of India, making it highly valuable in ensuring food security for the rural poor. Given the great potential of this neglected and underutilized species to address global challenges such as hunger, poverty and climate change adaptation, there is a need to revisit research and development priorities in its favour and to develop strategies together with stakeholders to increase its use.

The tamarind germplasm Lakshamana was collected from the field of Shri Laxmannappa in Nandihalli village of Tumkur district, Karnataka. The passport data for this was: latitude 13.52° N, Longitude-76.74° E and 860 m MSL. It was found to be superior with better yield and pod characters compared to local check and registered mean annual yield (4 years from 2016-2020; Table 1) of 251.4 kg/tree as against 165.0 kg/tree in local trees.

'Lakshamana' is a 40-year-old tree and a regular bearer. It commences flowering in September-October, matures in February-March and harvesting can be done

Table 1: Morpho-agronomic traits of 'Lakshamana' in comparison to the local check

S. No.	Trait	Lakshamana	Local
1.	Fruiting season	Feb-March	Feb-March
2.	Pod length (cm)	25.4	13.5
3.	Pod breadth (cm)	3.8	2.36
4.	Number of pods/kg	24	49
5.	Number of seeds/pod	8.2	14.5

in March-April under Tumkur conditions. Healthy grafts are planted at a distance of 5 m × 5m during June-July under Bengaluru conditions. Water requirement is met through drip irrigation (1-2 litres once in 2 weeks in late afternoon), which is sufficient till trees are 5-6-year-old. Weeding is essential in early stages (first 4 years). Intercrops/ cover crops can be grown to control weeds and conserve moisture. FYM is applied at time of planting and yearly as top dressing. When tree starts bearing, 500g of complete fertilizer (NPK) can be applied twice a year at end of rains. Mature, bearing trees can be given 2-3 kg of complete fertilizer. Tamarind trees are largely free of pests and diseases.

26. DLB-10 (IC646865; INGR23060), a lemon basil germplasm with high leaf size

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Lemon basil (*Ocimum × africanum* Lour) also known as lebutulsi. *Ocimum × africanum* is a hybrid between *O. basilicum* L. and *O. americanum* L. The herb is believed to be native to Asia (South-Eastern Asia), Africa, and South America. It is only basil that is used much more in several cuisines due to its rich, varied flavour, ethnobotanical and pharmacological properties. Lemon-scented basil is known for its sweet citrus flavour and fragrance. The highest antimicrobial activities were demonstrated by lemon basil as compared to other *Ocimum* species. The leaves are a good source of vitamin A, C, K, magnesium, iron, copper and calcium. In addition to vitamins and minerals,

lemon basil contains limonene and citral responsible for its flavour and medicinal properties. Aromatic grasses like lemongrass and citronella are perennial in nature and crops are grown commercially up to 5-6 years of plantation; therefore, farmers are hesitant to grow such perennial grass in their fields to avoid long-duration field blockage. Seasonal variations are observed in a very specific manner in a country like India. The lemon basil is a short-duration crop and harvested even in the same season (70-75 days after planting) compared to perennial aromatic grasses. Even farmers are very choosy about such fast-growing and high-yielding crops for harvesting essential oil and

aromatic compounds like citral. Therefore, lemon basil elite 'DLB-10' was found suitable for maximum leaf area (7.45 cm²) and fresh herbage yield (298 q/ha) at full

flowering stage as compared to farmer check (6.66 cm² and 280 q/ha, respectively). Such elite can be promoted for commercial cultivation.

27. DIB-1 (IC646866; INGR23061), a basil germplasm with rich in methyl eugenol

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Genus *Ocimum* derived from "ozo" a Greek word meaning to smell. Basil (*Ocimum basilicum* L.) is the popular name given aromatic herb derived from the Greek word 'Basilica' or 'Dragon' means royal plant. *O. basilicum* originated in Asia, Africa and also grows on some Pacific islands. The basil diversity based on appearance, flavours, fragrances, industrial traits, essential oils and natural pigments provides great opportunities for developing new culinary and industrial crops. This species (Italian basil) having very short history of cultivation and has been cultivated as a commercial crop in a few parts of the globe. With the transformed interest in the world over in herbal drugs and aromatics, species propose an immense scope in developing suitable cultivars for food flavouring purposes. Essential oil extracted from green herbage is a source of biologically active compounds. The aromatic compounds found in the essential oils of basil are mainly the mono-terpenes, sesquiterpenes and phenols with their alcohols, esters, aldehydes, ketones and others. As secondary metabolic products, the essential oil occurs in secondary tissues, glands, trichomes of the flower, leaves and tender stems, and is

usually responsible for characteristic pleasant odours and flavours, which account in large part for their value and determine their uses. Moreover, under covid 19 situation, a complementary trend towards natural products was developed due to negative reports on potential carcinogenic hazards of synthetic aroma chemicals. 'Italian' basil, having large-leafed, robust and lettuce type's leaf are very prominent in the food flavouring industry. Basil, generally used for culinary purposes in Italian and Mediterranean cuisines, actually originated in India. It is used both fresh and dried with vegetables, meat, fish, sauces, stews, dressings, herbal teas, liqueurs, salad, poultry, vinegar and confectionery products, mixed drinks, etc. For this purpose, DIB-1 has a short life cycle (70-75 days) as compared to other basil, upward leaves folding with severe puckering and rich in Methyl Eugenol (30%) share in essential oil. DNA fingerprinting also showed that accession DLB-1, having dissimilarity as compared to DIB-2 and DOB-2 was using ISSR and scot markers. Such an elite could be used to add a unique flavour to pizza, pasta, pesto, sauce, soup, salads, etc.

28. IIHR 17 23 SP 08 (IC642158; INGR23062), a tuberose germplasm with single type flowers and green tinge flower buds; resistance to root knot nematode (*Meloidogyne incognita*) and tolerant to leaf burn disease (*Alternaria polianthi*)

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Tuberose (*Polianthes tuberosa* L.) is a commercially important flower crop cultivated for its extended shelf life and pleasant fragrance. Tuberose is a day-neutral plant that grows well in the tropical climate with the temperature range of 20-35°C. It performs well in loamy to sandy loam soil with a pH of 6.5 to 7.5. It is

propagated vegetatively through bulbs, medium size bulbs of 2.0 to 2.5 cm in diameter are planted with a spacing of 30 cm × 30 cm at a depth of 5.0 cm on the raised beds.

It is highly preferred in the local as well as international markets for garland preparation and

perfumery extraction, respectively. IIHR 17 23SP 08 is developed through the open-pollinated seedling selection from GK-TC-4 at ICAR-Indian Institute of Horticultural Research (ICAR-IIHR), Bengaluru, Karnataka, India. The genetic stock IIHR 17 23SP 08 produces single-type white flowers (RHS colour: NNI55D, white group, Fan 4), flower buds with a green tinge, a greater number of spikes (8.47) and bulbs (8.94) per clump per year. It has resistance to root knot nematode and is tolerant to leaf burn disease under field conditions (Table 1).

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Table 1: Evaluation of tuberose genotype IIHR-23 SP 08 with checks for root knot nematode and leaf burn disease incidence under field conditions

Genotype	Screening for leaf burn disease*	Root knot nematode Screening**
IIHR-23 SP 08	9.79 (18.24)	1.31
Mexican Single	19.20 (26.00)	2.42
ArkaPrajwal	21.33 (27.52)	2.14
GK-TC-4	15.23 (22.98)	1.68
PhuleRajani	23.59 (29.06)	1.53
BidhanUjwal	21.10 (27.36)	1.38
Calcutta Single	13.00 (21.14)	1.51
Sem±	-	0.11
CD (P=0.05)	-	0.34
CV%	-	10.95

*Disease severity scale (Narayanappa and Chandra *et al.*, 1984);

**Gall index (Taylor and Sasser *et al.*, 1978); Figures in parenthesis are *arcsine* transformed values

29. SM/92-338 (IC648625; INGR23063), a potato germplasm with highly resistant to bacterial wilt (*Ralstonia solanacearum*)

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Potato (*Solanum tuberosum* L.) is the third most important food crop globally and a major staple in India (Sood *et al.*, 2022). Being a clonal crop, it attracts many pathogens that affect potato production. Although late blight, viruses, and potato cyst nematode (PCN) affect potato production globally to a major extent (Bhardwaj *et al.*, 2019), bacterial wilt or brown rot (*Ralstonia solanacearum*) has become a major problem in tropical, subtropical and warm temperate zones of the world (Sagar *et al.*, 2014). The pathogen infects more than 400 plant species and is considered a quarantine pest in seed potato production. Despite extensive screening of thousands of potato accessions and related germplasm, highly effective sources of resistance have remained scarce, restricting the development of resistant cultivars.

SM/92-338 is a promising potato germplasm possessing a high level of resistance to bacterial wilt. The clone was developed through a biparental cross between HB/82-372, a breeding line with resistance to late blight and good combining ability, and Kufri

Pukhraj, a widely adapted and popular Indian potato variety. The clone was selected in 1993 from a segregating population based on superior agronomic performance and disease resistance. Subsequent evaluations at Kufri and Modipuram demonstrated stable adaptation and superior yield performance.

The clone was evaluated for bacterial wilt resistance using a rapid in vitro screening protocol and subsequent pot and field assays. During in vitro screening, SM/92-338 remained healthy up to six days after inoculation, whereas the susceptible cultivar Kufri Jyoti collapsed within four days. Similar responses were observed under pot conditions, where SM/92-338 maintained resistance up to 28 days after inoculation, while the susceptible check wilted completely by 13 days. Replicated field testing in bacterial wilt-sick plots further confirmed its high level of resistance under natural disease pressure.

In addition to bacterial wilt resistance, SM/92-338 has shown agronomic superiority and attractive ovoid tubers. The combination of disease resistance, yield

superiority and desirable tuber characteristics makes this germplasm an important genetic resource for potato improvement programmes targeting bacterial wilt-prone regions of India.

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30. ADJVN 01/AAD (IC648626; INGR23064), an arecanut germplasm with noticeably short internodes, dark green leaves, shorter inflorescences and highly fragrant flowers

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Arecanut (*Areca catechu* L.) palm is the predominantly grown crop in the Andaman and Nicobar Islands, next to the Coconut palm, which gives much remuneration to farmers. Characterization of a dwarf arecanut, which was collected and conserved at ICAR-CIARI for palm morphology, revealed that the dwarf type has noticeably short internodes, dense crown with closely arranged leaves and short inflorescences producing bolder nuts. Observations on seedling parameters revealed that more than 80% of the progenies of these dwarf type palms are found to be uniform for seedling traits such as germination, seedling height, number of leaves and collar girth of seedlings. The unique arecanut dwarf accession has immense potential for utilization in breeding for dwarfness in arecanut and has a great opportunity to use for ornamental planting owing to the beautiful appearance of foliage and bunches at an incredibly low height. The palms are observed to produce bunches within 60 cm of height with closely arranged leaf scars. Other unique features, such as compact canopy with shorter, dark green leaves, shorter inflorescences, and highly fragrant flowers, make this dwarf type distinct from the common tall cultivars.

The estimated chali yield of the dwarf arecanut palms ranged from 1.8 kg to 2.8 kg/palm/year. Comparison of 30-year-old tall and this dwarf type palms revealed that the dwarf palms reached a height of 3 to 5.3 m, whereas the tall type palms reached over 15 to 20 m height. A compact block of this dwarf arecanut is established at the Sipighat farm of ICAR-

CIARI. The seed nuts of this unique type were deposited with the National Active Germplasm Site for arecanut, ICAR-CPCRI, Kasaragod, for conservation at the National Gene Bank.

Characterization of a dwarf arecanut AAD-1 was continued, which was collected and conserved at ICAR-CIARI. Observations on seedling parameters revealed that more than 80% of the progenies of these dwarf type palms were uniform for seedling traits such as germination, seedling height, number of leaves and collar girth. The progressive growth rate of AAD-1 seedlings was compared with Samrudhi and Mangala arecanut seedlings. Significantly lower height increment was noticed in AAD-1 in 11 months, whereas number of leaves produced was nonsignificant, indicating the dwarfness of AAD-1 at early seedling stage itself. The AAD-1 seedlings showed 50% lesser height in the initial stages of growth up to 3 to 4-leaf stage and also recorded higher collar girth and produced dark green leaves than Samrudhi and Mangala. Preliminary observations on growth parameters recorded in the compact block of this dwarf arecanut, along with the hybrids using Dwarf with local and the local tall have revealed marked differences in the leaf length, petiole length, leaf lamina and palm height. The hybrid seedlings have exhibited vigorous growth over the dwarf parent. About 200 seed nuts were sown in poly bags nursery for seedling production to establish a new block of dwarf arecanut at the Institute.

31. IIRR-BIO-SB-9 (IC646828; INGR23065), a rice germplasm with tolerance to yellow stem borer

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Yellow stem borer (YSB) is a major pest of rice (*Oryza sativa* L.) and the host plant resistance cannot be exploited due to the unavailability of resistance sources in the rice gene pool. To obtain novel resistant/tolerant sources for YSB, a 10,500 EMS-induced mutant population was developed in the genetic background of Samba Mahsuri (BPT 5204) in collaboration with CSIR-CCMB. After screening of 5000 M₂ families, a mutant line (IIRR-BIO-SB-9) was found to have tolerance to YSB. The selection of the IIRR-BIO-SB-9 was done in M₂ generation after screening every season, selected single tolerant plant in each generation and advancing to M₈ through panicle to row method.

For the estimation of genomic similarity with wild type, a total of 120 SSR markers (selected based on ~1 marker per 5Mb) which were spread uniformly across the twelve linkage groups were used. The results indicated that IIRR-BIO-SB-9 has 95% genomic similarity with wild type (BPT 5204 (Padmakumari *et al.*, 2017). It was evaluated for the agro-morphological variations at the Indian Institute of Rice Research Farm (ICAR-IIRR) and ICRISAT.

The mutagenized population (5000 M₂ lines) were screened for yellow stem borer tolerance in a phased manner at both vegetative and reproductive phases by augmenting the natural pest infestation through artificial releases. Damage was assessed at both dead hearts (symptoms at vegetative phase of rice plant) and white heads (symptoms at reproductive stage) at each

of the crop growth stages on the Standard Evaluation System (IRRI, 2002) SES scale. Evaluation of the M₂ lines, advancement of the promising lines and reconfirmation of the promising lines were carried out simultaneously till M₈ generation and the most promising line IIRR- BIO-SB-9. Further, IIRR-BIO-SB-9 was screened in a stem borer screening trial, a multi-location trial under AICRIP- Entomology Programme for three years (2015-2017). The results indicated that IIRR-BIO-SB-9 exhibited tolerance to YSB.

To identify mutated loci for conferring resistance to YSB, MutMap (NGS-based approach) analysis was performed in resistant and susceptible bulks of the F₂ population derived from SM-92 X BPT 5204. The identification and characterization of mutated loci responsible for YSB tolerance indicated three possible genomic regions (chromosomes -1, 10 & 12) of mutations. The identified mutant line can serve as the best genetic resource in the rice breeding programme, as there were no reports on the existence of high-tolerance-level genetic material in rice. Thus, IIRR- BIO-SB-9 can be used as a donor in rice improvement programmes for YSB tolerance.

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32. BHS 480 (IC646837; INGR23066), a barley germplasm with resistant to all pathotypes of leaf and stem rust at the seedling stage (except for race 11)

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BHS 480 (BBM 803) is a barley (*Hordeum vulgare* L.) line resistant to leaf and stem rust. It has shown seedling resistance against all the prevailing pathotypes of leaf

rust and stem rust (except race 11). BHS 480 (BBM 803) also showed adult plant resistance to stem rust with ACI less than 15, i.e. 5MS (Table 1). This line is developed

following the pedigree method of breeding involving crosses between barley local germplasm BLG 132 and registered barley genetic stock BHS 369 at ICAR-IARI, Regional Station, CHC, Amartara Cottage, Tutikandi Centre, Shimla (H.P.)

BHS 480 (BBM 803) has a semi-spreading growth habit with medium maturity (166 days) under Northern

Hill conditions. The average yield is 3.28 t/ha under rainfed conditions of the Northern Hill Zone of All India Co-ordinated trials 2019-20. The distinguishing features of BHS 480 (BBM 803) are six-rowed, hulled; semi-spreading growth habit; erect flag leaf attitude; green leaves and thousand grain weight of 43 g.

Table 1. Meteorological data from different locations used in the study

Diseases	Condition	Year	Response of Proposed Genetic stock BHS 480 (BBM 803)	Page No.
Leaf Rust (Resistant to brown rust)	NBDSN (Seedling)	2019-20	R (Resistant to all races)	3.28 of Reference (i)
Stem Rust (Resistant to black rust)	NBDSN (APR) NBDSN (Seedling)	2019-20 2019-20	HS=5MS R (Resistant) response to all races (Except for race 11)	3.14 of Reference (i) 3.28 of Reference (i)
Stripe rust (Yellow rust)	IBDSB	2018-19	Yellow rust ACI = 2.7 (Highest Score 5S)	3.7 of reference (ii)

ACI, Average Coefficient of incidence; HS, Highest Score; IBDSN, Initial Barley Disease Screening Nursery; NBDSN, National Barley Disease Screening nursery.

33. CV.WP-14 (IC251385; INGR23067), a blackgram germplasm with high resistance against *Callosobruchus chinensis* L.

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Bruchids (Coleoptera: Bruchinae) cause severe economic losses to stored pulses, and their management has remained challenging as conventional methods often prove ineffective across regions and time. In this context, host plant resistance offers an effective and environmentally friendly solution. Identifying resistant sources in traditional cultivars, landraces, or crop wild relatives (CWRs) and introgressing alien genes into cultivated legumes can diversify and strengthen the genetic base. Several wild legumes, particularly in the *Vigna* subgenus *Ceratotropis*, have been explored for resistance to biotic and abiotic stresses. Bruchid resistance was first identified in wild mungbean accession TC1966 against *Callosobruchus chinensis* and later in other cultivated and wild *Vigna* germplasms. Crosses between resistant wild accessions and cultivated types were attempted to transfer resistance genes (Mariyammal *et al.*, 2019). The susceptible mungbean cultivar VRM (Gg) 1 with the resistant rice bean cultivar TNAU Red, identified several QTLs linked to bruchid resistance. Despite these

advances, studies on diverse genetic resources of wild *Vigna* species and their transfer to cultivated forms remain limited, warranting further research.

India, being the center of diversity for *Vigna*, harbours a rich repository of wild, weedy, and cultivated forms. Gene banks across the country maintain large collections of wild species belonging to the subgenus *Ceratotropis*. However, these remain underexplored for bruchid resistance. To address this gap, the present study screened diverse endemic *Vigna* accessions to identify resistant donors against three prevalent bruchid species in India.

Between 2019–21, 42 wild *Vigna* accessions representing 13 species were evaluated against *C. chinensis*, *C. maculatus*, and *C. analis* at the Storage Entomology Laboratory, Division of Crop Protection, ICAR-Indian Institute of Pulses Research (IIPR), Kanpur. Seeds were sourced from the Germplasm Bank, Division of Crop Improvement, ICAR-IIPR. Qualitative and quantitative seed traits were recorded following NBPGR descriptors to assess their role in resistance. Screening

involved both 'Free-choice' and 'No-choice' tests (Eker *et al.*, 2018), with resistant accessions validated under 'No-choice' conditions. Reactions were categorized based on per cent seed damage (Eker *et al.*, 2018).

Among the accessions, IC251385 of *V. mungo* exhibited complete resistance to *C. chinensis*, recording 0% seed damage in both initial and confirmatory screenings, despite egg deposition averaging 1.7, 0.8, and 1.38 per seed. Correlation studies revealed that seed morphological traits did not significantly influence resistance, suggesting biochemical components in the seed coat and cotyledons play a major role. This accession thus represents an invaluable genetic resource for introgression breeding in mungbean and urdbean. Identification of QTLs associated with bruchid resistance in IC251385 further

strengthens its utility. Deploying these resistance genes through introgression breeding could lead to the development of superior bruchid-resistant cultivars, ensuring sustainable pulse storage and reduced economic losses.

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