

Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXIInd meeting held on August 17th, 2015 at the ICAR-National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 23 germplasm lines out of 43 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. ANR 38 (IC0613963; INGR15014), a Rice (*Oryza sativa* L.) Germplasm with Open Florets

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Rice (*Oryza sativa* L.) is a self-pollinating and self-fertilizing plant. This behavior is due to cleistogamous nature of rice spikelets which prevents out-crossing with the adjoining plants. This traditional trait is useful to maintain genetic purity, unique identity and homozygosity of rice genotypes. However, the cleistogamous nature is often a constraint in practical hybrid rice breeding wherein wider opening of spikelets or florets is desired to expose stigma to the maximum possible extent to allow landing of maximum number of pollen grains of the intended male parent. Similarly, protruding anthers are desirable in the male parent of the hybrid to shed copious amount of pollen on the targeted female parent or CMS line. External intervention like GA₃ spray application and rope pollination etc are generally followed for achieving higher seed set during hybrid seed production. To facilitate higher pollen shedding by male plant and higher seed set on female (CMS) lines, identification and transfer of "Open florets" trait will be of considerable importance and utility. Though the "Open floret" trait leading to promiscuity in rice is quite scanty, we report its occurrence in a rice germplasm "ANR38" which is collected from the Bay islands (Gautam *et al.*, 2013).

Associated characters and cultivation practices: The ANR 38 rice germplasm is quite tall (185 cm) and photo-sensitive (186 days for maturity from seed to seed) with 6-8 tillers/plant, has long, erect and dark green leaves. It

has strong culm with long panicles (28 cm), medium bold grains with grain length of 8 mm and width of 3.2 mm. It has higher test weight of 1000 grains (28 g) and brown colored lemma. Significant to mention, its florets remain sufficiently open for a longest time. The anthers are considerably protruded outside the spikelets and stigma is well exposed (Anonymous, 2014).

The genetic and molecular basis of open florets have been recently unravelled (Xiao *et al.*, 2014) the presently identified germplasm can be used as a donor for genetic transfer of this trait in both male and female parents of the intended hybrids for achieving higher seed set for the commercial viability and success of the rice hybrids.

References

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- Xiao Y, Y Chen, T Charnikhova, PPJ Mulder, J Heijmans, A Hoogenboom, A Agalou, C Michel, JB Morel, L Dreni, MM Kater, H Bouwmeester, M Wang, Z Zhu and PBF Ouwerkerk (2014) *OsJAR1* is required for JA-regulated floret opening and anther dehiscence in rice. *Plant Mol Biol.* DOI 10.1007/s11103-014-0212-y.

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2. CNH-1102 (IC0611336; INGR15015), a Cotton (*Gossypium hirsutum* L.) Germplasm with High Ginning Outturn

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Cotton is commercially cultivated for its natural fibres called 'lint'. Lint is the most important industrial raw material. Cotton fibers are single-celled outgrowths from individual epidermal cells on the outer integument of the ovules. Certain epidermal cells produce outgrowths that continue to grow or lengthen up to 30 to 40 mm in length, lint hairs of fibre while other cells produce outgrowth similar to fibre but stop growing after attaining short length. These short epidermal hairs are known as fuzz. Cotton fibre development consists of four overlapping stages: fiber initiation, cell elongation, secondary wall deposition, and maturation. Cotton varieties and germplasm lines genetically differ in having relative proportion of long fibres (lint) or short hairs (fuzz). The long fibres after maturation (fibre with increase both in length and thickness, lint), can be easily removed from the seed surface by ginning. Ginning outturn is described as the percentage of lint obtained from a sample of seed cotton and is a useful indicator of the performance of a genotype. Genotypes with high ginning outturn are thus more preferable, because they yield more lint.

CNH-1102, an upland cotton genotype, is a selection developed from a random crossing of three *Gossypium hirsutum* (LRA5166, G. Cot. 10 and Bikaneri Nerma) and one *G. barbadense* (Suvin) genotypes. CNH-1102 is long staple cotton genotype with staple length 26 to 30 mm, fibre strength 20.7 to 24.4 g/tex and high average ginning outturn 40.9%. It is medium tall (90-110 cm), matures in 160-165 days and synchronous in boll bursting. During the evaluation under All India Coordinated Cotton Improvement Project (AICCIP) in 2007-08 and 2008-09, it has shown superiority for ginning outturn percent and fibre quality traits specially fibre strength over rest of the genotypes including best zonal check, Sahana and local check varieties. CNH-1102 has recorded seed cotton yield of 1359-1573 kg/ha.

In all 12 AICCIP trials during 2007-08 and 2008-09, CNH-1102, was identified as the best/ top ranking genotype for ginning outturn and fibre strength. In addition to fibre strength and length, it was also found to be resistant to bacterial leaf blight, tolerant to jassids and has wide adaptability.

CNH1102 recorded highest average GOT of 40.9% that ranged from 37.4 to 44.3%, an increase of above 14.88% over the best zonal check variety Sahana and 9.36 over the local check varieties at 4 locations in the advance South Zone trials of AICCIP in 2008-09. The average fibre strength was 24.0 g/tex with an increase of above 21.2% over the best zonal check variety Sahana and 7.14 over the local check varieties. While the average staple length was 29.0 mm which is higher by 5.5% over the zonal check Sahana and 3.2% over the local check varieties. The strength/length ratio of CNH-1102 was 0.83 indicating its fibre suitability and superiority for high speed spinning in comparison to zonal check Sahana (0.72) and local check (0.79) varieties.

Ginning outturn is one of the most important economic trait and major component of cotton economic lint yield. Cotton ginning outturn is much used measurement in cotton production, marketing and ginneries. Crop growing conditions and location plays major role affecting ginning outturn. However, it has been observed that the ginning outturn is a genetically controlled character. With the advances in molecular markers studies and development of saturated genetic linkage maps, it is understood that several QTLs influence the ginning outturn in cotton. The number of seeds/boll is a component of cotton yield, lint yield (ginning outturn) and fiber quality. Both cultivar and environment contribute to the variation in the number of seeds/boll and also ginning outturn (Hossam, 2010). Ginning outturn is a useful indicator for the performance of a genotype (Waghrare *et al.*, 2009, Joubert *et al.*, 2002). Since cotton lint is considered to be most economic and valued from textile industries and fabrics manufacturing, measurement of lint as an index or proportion helps to identify varieties/genotypes producing more lint.

Fibre quality, specifically fibre strength is the most valued parameter alongwith length considered in yarn spinning and fabric making. Stronger the fibre, least will be the neps and better finish quality of fabrics (Hossam, 2010). Availability of germplasm with combination of both these important traits is rare. Thus, the genotypes

with combination of ginning outturn or lint yield and fibre quality would serve as better genetic stocks for further improvement of both the characters. In addition, the genotype is resistant to bacterial leaf blight disease most severely found in all cotton growing areas, tolerant to jassids and has wide adaptability.

Table 1. Features of CNH 1102

Characters	CNH 1102
Boll weight (g)	3.63 (2.4-5.1)
No. of bolls/plant	25.7(14.1-38)
Seed index (g)	7.85
Ginning Outturn (%)	40.9 (34.9-44.3)
Lint index (g)	5.43
Seed Oil content (%)	17.3
No. of monopodia	1.0
No. of sympodia	20.8
Seed cotton yield (q/ha)	13-20
Days to maturity (days)	160-165
Fibre quality	
Fibre length (at 2.5% SL)	28.3mm (26.2-29.7)
Uniformity ratio	52
Micronaire	3.9 (3.7-4.0)
Maturity (%)	74
Bundle strength (g/tex)	22.4 (20.7-24.4)
Elongation (%)	6.3

3. CNA-1051 (IC0613964; INGR15016), a Cotton (*Gossypium arboreum* L.) Germplasm with Distinct Yellow Top Leaves

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Cotton is an important commercial crop mainly grown for natural fibres and seed oil. It is cultivated in more than 80 countries of the world which include Australia, America, Africa, China, India, Pakistan and Uzbekistan. Among the four cultivated species, diploid species, namely *Gossypium arboreum* and *G. herbaceum*, are mainly cultivated in India, China and Pakistan. South East Asia is considered as the home of *G. arboreum*, possessing wide adaptability and grown on range of soil types and low input conditions. *Desi* cotton varieties are relatively tolerant to biotic (insect pests and diseases) and abiotic stresses (drought and salt stresses), synchronous in maturity and possess consistent fibre properties.

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Waghmare VN, P Ramsundaram, TP Rajendran and MS Kairon (1999) Approaches to increase lint production in cotton (*Gossypium* spp.). *International Seminar on Cotton and its Utilisation in 21st Century*, held at CIRCOT, Mumbai, December 10-12, 1999.

Mutation breeding method is known for creating additional genetic variability and exercising selection for desirable type. Although most of the mutations are usually undesirable, mutations with desirable traits and also the types that did not exist in the gene pool do occur in the population.

G. arboreum variety Y1 was very popular in the Khandesh tract of Central Zone despite its poor yield. Variety Y1 was used for mutation studies. Dry delinted seeds of var. Y1 were subjected to mutagenic treatments of gamma rays (150, 200, 250 and 300 Gy) and 6 hours presoaked seeds in distilled water to ethyl methane sulphonate (0.1, 0.2 and 0.4% for 2 and 4 hours

treatment). The treated seeds were planted in the field, selfed, harvested separately and grown as single plant progenies in M_2 (Waghmare and Koranne, 2000).

A stable virescent chlorophyll mutant with yellow top leaves (3-5 leaves) and remaining normal green leaves were identified in EMS 0.1% (6h) treatment in M_2 . The mutant plant identified in M_2 was raised as single plant progeny in M_3 and it showed complete uniformity for phenotypic traits in M_3 and subsequent generations. The mutant was rigorously evaluated in M_5 generation. Cross between the virescent mutant and control var. Y1 was attempted to study the inheritance of the changed character.

Virescent chlorophyll mutant had average plant height of 114 cm slightly less than that of parent variety Y1. The mutant plant type was similar to parental variety Y1 except yellow leaves (3-5) at the growing top which is a distinguishing and unique trait of this mutant. Boll shape and size, leaves shape and colour and fibre quality traits of mutant were comparable to parental variety Y1. The mutant is unique for its yellow young leaves at the growing top that become normal green with age as plant grows and distinguishable in the population since early seedling stage until cessation of plant growth. After cessation of plant growth, matured top leaves can barely be distinguished from other green leaves on the plant.

Except the morphological features, CNA-1051 has similar economic features as that of parental variety Y1. It matures in 160-165 and is synchronous in boll bursting. Seed cotton yield of this mutant varies from 18 to 65 g/plant and 12-14 q/ha depending on climate and soil types. The ginning outturn which reflects proportion of lint to seed cotton yield is 35.6%. Its fibre characteristic features are as given (Table 1).

The inheritance of changed character has been studied by attempting crosses with parental var. Y1. The F_2 and BC A_1 segregation ratio revealed monogenic recessive gene inheritance of this virescent mutant.

The virescent chlorophyll mutation in CNA-1051 is very unique mutant germplasm; it is stable and has high heritability. The mutant is so distinct that can be identified in early seedling stage until plant maturity. The unique features of this line can be utilized as marker trait. The mutant would also serve the purpose for basic studies on development pathway of chlorophyll in diploid cotton.

Table 1. Features of CNA 1051 – a virescent mutant

Plant height (cm)	114.0
No. of monopodia	1.4
No. of sympodia	17.20
Internode length (cm)	5.23
Average seed cotton yield /plant (g)	12- 14
Average Boll weight (g)	2.56
Ginning Outturn (%)	35.6
Seed Index (g)	5.82
Lint Index (g)	3.22
Staple length (mm)	24.1
Uniformity ratio (%)	50
Micronaire ($\mu\text{g/inch}$)	5.2
Fibre Bundle Strength (g/tex)	21.3
Fibre Maturity (%)	72
Fibre Elongation (%)	4.6

In our view, it is a robust genetic stock with comparable and acceptable fibre quality and economic traits, ginning outturn (35.6%) with yellow growing top leaves feature which makes it a unique mutant or germplasm genetic stock.

Virescent leaves are an important character of plant that may be useful in genetic, physiological studies and breeding in cotton (Song *et al.*, 2012). Virescent mutations occur in a wide range of flowering plants, including cotton (Kohel 1967, 1974 and 1983). Benedict and Kohel (1968) have shown that a virescent cotton mutant shows a high rate of CO_2 assimilation. Further, it is reported that yellow virescent cotton leaves had a high photosynthetic rate, low amount of PEP carboxylase activity (which is typical of most plants possessing a Calvin Cycle, and an absence of lamellar aggregation into grana in the chloroplasts Benedict and Kohel (1970). The virescent mutants in cotton have a decreased amount of chlorophyll and carotenoids but a normal level of ribulose diphosphate carboxylase (Kohel and Benedict 1971). To date, more than 30 virescent and 2 albino mutants have been genetically characterized in the tetraploid cotton species and about 26 virescent nuclear genes have been identified in cotton (Song *et al.*, 1968). CNA 1051 is the first of its kind of virescent mutant being reported and registered as genetic stock in diploid cotton *G. arboreum*. It requires to be further characterized for structural, physiological and functional aspects.

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4. NRC-109 (IC0612435; INGR15017), a Soybean (*Glycine max* L. Merril) for Lipoxygenase-2 Free Soybean with Early Maturity (85 Days)

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The off-flavour associated with soy products is one of the major deterrents in the widespread acceptance of soyfood. This is due to the hexanal compounds released by the catalytic oxidation of polyunsaturated fatty acids in the oil fraction by seed lipoxygenase enzyme. When the seeds are subjected to grinding for making any soy product, lipoxygenase comes in contact with its substrate (polyunsaturated fatty acids) and thereby triggers the catalytic oxidation in the presence of oxygen. In fact, lipoxygenase in soybean seed exists in three isozymic forms – lipoxygenase-1, lipoxygenase-2 and lipoxygenase-3. Presence of each of the isozymes is controlled by single dominant genes, *i.e.* Lx1, Lx2 and Lx3 and their absence is ascribed to the corresponding null alleles (lox1, lox2 and lox3). Soy preparations made from seeds of lipoxygenase-free genotypes are better accepted due to production of low levels of hexanal compounds (Davies *et al.*, 1987). Though lipoxygenases are heat labile, heat inactivation employed at industrial level not only incurs extra cost, but also affects the solubility and functionality of proteins. In India, none of the soybean varieties released so far is free from any of the three lipoxygenases. Lipoxygenase-2 is mainly responsible for generation of off-flavour imparting n-hexanal in soybean products. Genetic removal of lipoxygenase-2 from the seeds has been shown to significantly improve the flavour of soy products. Therefore, bringing lipoxygenase-2-free soybean under cultivation and making the seeds available for soy processors can boost utilization of soybean in food. In view of this pressing need of the soy processing

industry, a breeding programme aimed at the development of lipoxygenase-2-free soybean genotypes was initiated at the Directorate of Soybean Research, Indore.

The authors successfully developed lipoxygenase-2 free genotype INRC109 by crossing Samrat and PI086023. Samrat is a farmers' variety of soybean cultivated widely in Central India. PI086023 is a source of lox2 allele which was procured from the United States Department of Agriculture. Its plant type is agronomically poor and not adaptable to Indian conditions. The crossing programme was carried out up to F7 generation. The selection for null lipoxygenase-2 plants in each generation was made by rapid assay in the seeds, according to Suda *et al.*, (1995). Validation of null lipoxygenase-2 plants in the advanced generations of Samrat × PI086023 was performed using null allele-specific marker recently designed by Shin *et al.*, (2012) from the sequence analysis of lox2 gene (null allele of lipoxygenase-2) of Korean cultivar Jinpumkong 2. DNA amplification using this gene-specific marker was confirmed by deploying it on null allele of lipoxygenase-2 from genotype PI086023 in the present study. For this purpose, genomic DNA extracted from the young leaves of NRC109, NRC110, Samrat (the recipient) and PI086023 (the donor of null allele of lipoxygenase-2) using the CTAB method and used as template for amplification using the primer specific for the null allele of lipoxygenase-2. Amplicons of 769 bp size were observed in NRC109, similar to the donor parent PI086023 and no amplicon was seen in Samrat, the lipoxygenase-2-positive parent. This confirmed the

transfer of null allele of lipoxygenase-2 in NRC109. NRC109 yielded bold seeds with yellow seed coat and brown hilum with 100 seed weight of 16.5g. NRC109 is early maturing (85 days), a character desired by the farmers in Central India, with yield potential of 2.6 tonnes/ha. The germplasm line developed can be very useful in the enhancement of soybean in food uses. This line will be very useful as a source of null lox2 allele in improved agronomic background as pre-breeding line. Besides, this genotype possess the desirable trait of earliness.

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5. CSIR-IHBT-Gr-E-3(HIM Peace) (IC0613966; INGR15018), a Gerbera (*Gerbera jamesoni* Bolus ex Hook. f) for Double Flower Shape, Medium Size (~8 cm Flower Diameter), White Flower Colour (RHS 155D)

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Gerbera (*Gerbera jamesonii*) is an important commercial cut flower of the trade and there is an increasing demand of new types of varieties for export as well as in domestic markets. In this context, with an aim of varietal development, selective breeding of gerbera was done and hybrid F₁ genotype (CSIR-IHBT-Gr-E-3) of gerbera was developed through controlled crossing program and subjected to *in vitro* micro-propagation to achieve quick multiplication. Rooted plantlets were hardened and transferred for cultivation in soil.

Morpho-agronomic characteristics: Characterization of hybrid F₁ genotype under field conditions with respect to floral traits and evaluation for agronomic performance provides evidence about promising gerbera genotype

CSIR-IHBT-Gr-E-3 which has double flower shape of medium size (flower diameter of 7.9 cm) and is white in color (RHS 155D). The genotype has high micro-propagation potential for commercial utilization (Singh *et al.*, 2015).

Associated characters and cultivation practices: In the field experiment conducted during 2013-14 and 2014-15, based on mean performance of hybrid gerbera genotypes with the respective parents, CSIR-IHBT-Gr-E-3 was superior to at least one parental genotype for traits plant spread in a year (cm), leaf length (cm) and leaf width (cm), while it was *at par* to parental genotypes for the other traits (Table 1).

Table 1. Mean performance of gerbera genotypes over two years

S. No.	Source of variation	IHBT-Gr-01		IHBT-Gr-07		CSIR-IHBT-Gr-E-3	
		2013-14	2014-15	2013-14	2014-15	2013-14	2014-15
1.	Leaf number per plant/year	31.25	33.15	32.05	33.05	29.3	31.85
2.	Plant spread (cm)/year	57.75	58.45	48.95	49.45	63.25*	63.8*
3.	Number of suckers per plant/year	2.45	4.45	2.7	6.25	2.75	5.7
4.	Leaf length (cm)	32.55	32.60	23.0	23.75	34.25*	33.425*
5.	Leaf width (cm)	11.55	11.3	7.17	7.075	12.87*	11.975*
6.	Flower number per plant/year	21.15	22.95	17.6	19.55	18.8	21.8
7.	Scape length (cm)	34.6	33.55	50.05	49.05	39.3	40.75
8.	Flower diameter (cm)	8.22	8.25	7.55	7.775	8.05	8.225

*Significant at p = 0.05

Reference

Singh S, Raja Ram, S Kaundal, A Sharma, A Kumar and D Dhyani
 (2015) Field performance and differential response of micro-propagated potential F_1 genotypes of *Gerbera jamesonii*.

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6. CSIR-IHBT-Gr-23 (HIM Glow) (IC0613967; INGR15019), a Gerbera (*Gerbera jamesoni* Bolus ex Hook.f.) for Double Flower Shape. Standard Size (>10 Cm Flower Diameter). Yellow Orange Flower Color (RHS 16C)

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Gerbera (*Gerbera jamesonii*) is an ideal cut flower and ranks fifth among top cut flowers in the international market. New cultivars of gerbera are developed by hybridization of diverse types to create novel genotypes. In this regard, selective breeding of gerbera was done and hybrid F_1 genotype CSIR-IHBT-Gr-23 of gerbera was developed through controlled crossing program and subjected to *in vitro* micro-propagation to achieve quick multiplication. Rooted plantlets were hardened and transferred to sleeves for cultivation in soil.

Morpho-agronomic characteristics: Characterization of hybrid F_1 genotype CSIR-IHBT-Gr-23 under field conditions with respect to floral traits and evaluation for agronomic performance provides evidence about this promising gerbera genotype which has double flower shape of standard size (flower diameter of 10.8 cm) and is yellow orange in color (RHS 16C). The genotype also

has high micro-propagation potential for commercial utilization (Singh *et al.*, 2015).

Associated characters and cultivation practices: In the field experiment conducted during 2013-14 and 2014-15 significant genotypic variations were recorded for the agro-morphological and floral traits based on mean performance of hybrid gerbera genotype with the respective parents; CSIR-IHBT-Gr-23 was superior to at least one parental genotype for traits leaf width (cm), flower number per plant/year and scape length (cm) while it was *at par* to parental genotypes for the other traits.

Reference

Singh S, Raja Ram, S Kaundal, A Sharma, A Kumar and D Dhyani
 (2015) Field performance and differential response of micro-propagated potential F_1 genotypes of *Gerbera jamesonii*.
 American Journal of Experimental Agriculture DOI: 10.9734/AJEA/2016/20653.

Table 1. Mean performance of gerbera genotypes over two years

Source of variation	IHBT-Gr-02		IHBT-Gr-03		23-1	
	2013-14	2014-15	2013-14	2014-15	2013-14	2014-15
Leaf number per plant/year	20.85	23.7	22.75	24.45	25.4	28.65
Plant spread (cm)/year	66.05	66.55	66.25	66.8	65.85	66.55
Number of suckers per plant/year	2.3	4.5	2.45	5.15	2.8	5.75
Leaf length (cm)	37.2	37.3125	36.35	35.6875	38	37.46667
Leaf width (cm)	12.175	11.675	14.675	14.6	16.2*	15.22*
Flower number per plant/year	13.95	16.35	12.75	14.75	23.5*	23.4*
Scape length (cm)	32.8	31.95	32.6	31.5	45.4*	44.75*
Flower diameter (cm)	9.65	9.725	9.35	9.55	10.85	10.75

*Significant at $p = 0.05$

7. WH 1127 (IC0610417; INGR15020), a Wheat (*Triticum aestivum* L.) Germplasm with High Gluten Index (86%)

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The genotype WH 1127 is a selection from a cross RL 6043/4/NAC// PASTOR/3/BABAX. The proposed genotype WH 1127 was evaluated in the Advanced Varietal Trial under timely sown rainfed conditions in the North Western Plain Zone of the country during the year 2012-13. This genotype possessed better quality characters in terms of high gluten index, i.e., 86%.

Morpho-agronomic characteristics: This genotype has semi-erect growth habit dark green foliage and average

plant height of 101 cm. The mean days to heading are about 111 days and maturity is about 153 days under rainfed conditions. Its grain is amber in colour with about 41 g 1000-grain weight. Ear shape is tapering with medium ear density and hairy glumes.

Associated characters cultivation practices: This genotype is suitable for cultivation under timely sown rainfed areas of the NWPZ of the country and resistant to lodging.

8. DHTW-60 (IC036761A; INGR15021), a Wheat (*Triticum aestivum* L.) Germplasm with Heat Tolerance

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Drought and heat are two abiotic stresses which affect wheat yields drastically. In India, nearly 80% wheat is cultivated under irrigated conditions, 66% of it receives only partial (1-2) irrigations, and the remaining 20% is grown under rainfed environments. Heat stress on the other hand is affecting around 13.5 million ha grown under wheat in India (Garg *et al.*, 2013; Sharma *et al.*, 2014). Both drought and heat stress are responsible for 20–30% reduction in grain yield.

Genotype DHTW 60 (IC 36761A) is a unique genotype having tolerance to heat tolerance. It was evaluated for heat stress tolerance under field conditions by timely (non-stress) and late (heat stress) sowing as well as under temperature controlled glass house condition during 2011-12. The mean minimum and maximum temperature during grain growth period was higher by 2.4°C and 2.7°C under late sown field condition compared to timely sown. Under glass house conditions, temperature in one chamber was maintained at ambient whereas in other chamber it was higher by 2.0°C. The genotype registered 2.2% reduction in 1000 grain

weight under high temperature stress condition and heat susceptibility index was 0.20 (Table 1).

Multi location evaluation for heat tolerance at 3 locations: DHTW-60 was evaluated for heat tolerance at three locations; Hisar, Kanpur and Pune during 2012-13. The mean minimum temperature during grain growth period under late sown condition was higher by 1.6 to 3.6°C and mean maximum by 2.0 to 4.3°C. The data pooled over location received 14% reduction in thousand grain weight and 6.6% in grain yield. The Pooled heat susceptibility index was 0.39. Location wise genotype was tolerant to heat stress at Hisar and Kanpur (Table 2).

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Table 1. Data on 1000 grain weight (TGW) and reduction in grain filling duration (GFD), grain weight/spike (GW) and TGW over control under high temperature stress conditions and heat susceptibility index

Genotype	TGW	Reduction (%)			Heat Susceptibility index
		GFD	GW	TGW	
DHTW60 (IC 36761A)	37.0	16.9	9.7	2.2	0.20
HTW 11 (Check)*	38.7	6.0	-0.03	4.39	0.63

*Registered Genetic Stock

Table 2. Heat susceptibility index at different locations

Genotype	Hisar	Kanpur	Pune	Mean
DHTW 60 (IC 36761A)	0.39	0.11	1.10	0.39
HTW 6(Check)*	0.66	1.07	1.23	1.09
HTW 11(Check)*	0.80	0.65	0.85	1.02

*Registered Genetic stock

9. IC536140 (IC0536140; INGR15022), a Wheat (*Triticum aestivum* L.) for Rust Resistance with 3 Minor/APR Genes viz., *Lr34/Sr57/Yr18/Pm38; Lr46/Sr?/Yr29/Pm39* and *Lr67/Sr55/Yr46/Pm46*

and

10. EC573562 (EC573562; INGR15023), a Wheat (*Triticum aestivum* L.) for Rust Resistance with 3 Minor/APR Genes viz., *Lr34/Sr57/Yr18/Pm38; Lr46/Sr?/Yr29/Pm39* and *Lr67/Sr55/Yr46/Pm46*

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Wheat is one of the most important cereal crops for food security and rust diseases (Stem/black rust (caused by *Puccinia graminis* Pers. f. sp. *tritici* Eriks, and Henn.) brown or leaf rust (caused by *Puccinia triticina* Eriks.) and stripe/yellow rust (caused by *Puccinia striiformis* Westend.) continually pose a threat to wheat production at national and international level. Resistant cultivars are the cheapest, most reliable and environmentally safest way to control the rust diseases. Historically, many genes were

deployed to provide resistance to rust diseases. However, most of the rust resistance genes, although initially effective were often short lived due to the ability of the pathogen to become virulent after single step mutations. In wheat breeding programmes, stem, leaf and stripe rust resistance could be achieved through several approaches. Major gene resistance (race specific) is achieved through conventional or backcross approach, or alternatively, breeders could select against race specificity (race non-

specific) and accumulate genes for slow rusting or adult-plant resistance in a cultivar.

Minor genes are the slow-rusting adult plant resistance (APR) type that confers partial resistance in race non-specific manner to one or multiple rust diseases. Slow rusting, race non-specific or partial resistance was defined by Parlevliet (1975). Slow rusting is a type of resistance where disease progresses at a retarded rate, resulting in intermediate to low disease levels against all pathotypes of a pathogen. The concept of race non-specific, horizontal resistance was widely

used by Caldwell (1968) in breeding leaf rust resistant wheat varieties. APR is commonly detected at the post-seedling stage and often as field resistance, but seedling susceptible, although some APR genes are sensitive to varying temperature and light conditions. So far, five rust resistance genes (*Lr34/Sr57/Yr18/Pm38*, *Lr46/Sr?/Yr29/Pm39*, *Lr67/Sr55/Yr46/Pm46*, *Lr68/Sr?/Yr?/Pm?* and *Sr2/Lr27/Yr30/Pm?*) were identified and catalogued as minor genes. These genes are pathotype nonspecific adult plant resistance with pleiotropic association with stem and stripe rust resistance along with powdery mildew.

Table 1. Rust reactions of wheat accessions at different environments in comparison to resistant and susceptible check

Sl. No	Accession No./Checks	Summer - 2011 Wellington		Rabi 2011-12 & Summer- 2012 Wellington			Rabi 2011-12 & Summer - 2012 Wellington					Rabi 2013-14 Shimla		
		Leaf Rust	Stem Rust	I	II	III	17	77A	77-5	77-7	77-8	Stripe rust	Stem rust	Leaf rust
1	IC536140	10MR- MS [#]	F	MR-MS	10 MR- MS	20S	3	X	X	3	3	F	F	F
2	EC573562	10MR- MS	F	MR	5MR	20MR	3	3,3 ⁺	3	X	3,3 ⁺	F	F	F
3	Resistant Check - Diamond Bird (Genetic stock for <i>Lr34</i>)	30MS-S	20MR- MS	10MR- MS	20MR- MS	40MS-S	3 ⁺	3,3 ⁺	3 ⁺	3 ⁺	3,3 ⁺	20S	F	F
4	Resistant Check - Pavon 76 (Genetic stock for <i>Lr46</i>)	40MS-S	40MS-S	10MS-S	20MS-S	40S	3,3 ⁺	3 ⁺	X	3,3 ⁺	3 ⁺	20S	F	F
5	Resistant Check - RL6077 (Genetic stock for <i>Lr67</i>)	30MS-S	40MR- MS	20MR- MS	30MR- MS	40S	3 ⁺	X	3,3 ⁺	3 ⁺	3,3 ⁺	40S	F	F
6	Susceptible check (Agra Local for leaf & stem rust and) A-9-30-1 for stripe rust at Shimla)	80S	60S	40S	80S	100S	3 ⁺	3,3 ⁺	3 ⁺	3,3 ⁺	3 ⁺	80S	F	F

F=Free; R=Resistant; MR=Moderately resistant; MS= Moderately Susceptible; S=Susceptible; T=Traces

Nearly 20,000 wheat accessions conserved by the National Bureau of Plant Genetic Resources (NBPGR), rejuvenated at Indian Agricultural Research Institute (IARI), Regional Station, Wellington through National Off-season nursery facility were initially screened for the presence of leaf tip necrosis (LTN), a phenotypical trait (morphological marker) linked to the APR genes *Lr34+*, *Lr46+* and *Lr67+*. Initially 2,200 accessions were

selected in summer, 2011 which were again screened in rabi, 2011-12 and summer, 2012 at Wellington, of which, 36 wheat accessions which showed prominent necrotic tipping on the leaves and resistant rust reaction in field (Table 1) were subjected to Seedling reaction test (Table 1) and molecular marker analysis. Since this trait (LTN) is environmentally sensitive, use of molecular markers is the reliable option to confirm the presence of these

minor genes. These accessions were again tested for rust diseases at Shimla (Table 1) for stripe rust. Out of the total 36 wheat accessions with LTN when tested with molecular markers (*Lr34* (Lagudah *et al.*, 2006); *Lr46* (Suenaga *et al.*, 2003); *Lr67* (Hiebert *et al.*, 2010)), two lines IC536140 and EC573562 carried all the three APR genes.

At field level, these three accessions showed resistant reaction to stem and stripe rusts, while displayed variable reaction to leaf rust, but within the permissible limit. As expected seedling reaction test showed susceptible reaction, a characteristic feature of minor/APR genes. Pyramiding of these minor genes provide durable and non-specific adult plant resistance. These slow-rusting gene(s) when utilized in combinations in a particular varietal background confer high levels of resistance to leaf, stem and stripe rust and are also expected to be durable. Hence, pyramiding of these minor genes *Lr34+*, *Lr46+* and *Lr67+* are expected to confer resistance that represent an attractive option to breeders for durable multi-pathogen resistance to leaf rust, stripe rust and stem rust.

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11. CNA-407 (NLL-Spotted Petals) (IC0613960; INGR15024), a Cotton (*Gossypium arboreum* L.) Germplasm with Narrow Leaf Lobes, Spotted Petals and Brown Lint

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A brown linted genetic stock, CNA-407 (INGR15024) of *Gossypium arboreum* was developed by pedigree selection. The fiber traits of this genotype are presented in the table.

Economic features and fiber quality traits

Average Seed Cotton Yield/Plant (g)	105.00
Average boll weight (g)	2.30
Ginning Outturn percentage	33.50
Seed Index (g)	7.50
Lint Index (g)	3.90
Staple length (mm)	27.30
Uniformity ratio (%)	51.00
Micronaire ($\mu\text{g/inch}$)	3.80
Fiber Bundle strength (g/tex)	19.80
Fiber maturity (%)	58.00

The stock has following morphological characters taken based on DUS guidelines which include pigmented okra leaf, yellow flower petal with petal spot, yellow pollen colour, pigmented anther filament, red and ovate boll, pitted boll surface, pointed boll tip and light brown seed fuzz colour. Colour fastness of lint was tested as per AATCC test resulting in rating of 5 showing fair stability of colour on washing.

12. CNA-407 (NLL-Spottless Petals) (IC0613961; INGR15025), a Cotton (*Gossypium arboreum* L.) Germplasm with or Narrow Leaf Lobes, Spotless Petals and Brown Lint

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A brown linted genetic stock, CNA-407 (INGR15025) of *Gossypium arboreum* was developed by pedigree selection. The fiber traits of this genotype include 26.8mm staple length, 51% uniformity ratio, 4.6 micronaire, 19.2 g/tex fibre tenacity and 67% fibre maturity coupled with brown colour lint. The stock is characterized by morphological characters such as okra leaf shape, yellow

flower petal without spot, yellow pollen colour, absence of anther filament colouration, red and ovate boll, pitted boll surface, pointed boll tip and light brown seed fuzz colour. Colour fastness of lint was tested as per AATCC test resulting in rating of 5 showing fair stability of colour on washing.

13. IL-13-106 (IC0613360; INGR15026), a Berseem (*Trifolium alexandrinum* L.) Germplasm with Black Seeds and Pentafoliate Leaf

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Berseem (Egyptian clover, *Trifolium alexandrinum* L.) is one of the most important winter season fodder crop. Because of narrow genetic base of the crop, interspecific hybridization using embryo rescue technique was attempted to generate variability and transfer of traits like disease resistance, quality, longevity, yield etc. Several interspecific hybrids of *T. alexandrinum* with different related wild species were developed at Indian Grassland and Fodder Research Institute (Roy *et al.*, 2004; Malaviya *et al.*, 2004; Kaushal *et al.*, 2005). Hybrids of *T. alexandrinum* × *T. apertum* (both parents were yellow seeded and trifoliate) were generated which showed segregation for black seeded and pentafoliate traits in F₂ generation. Selected plants were advanced and by recurrent selection line combining pentafoliate with black seeds (RHS no. black 202A) were developed. Thus, a novel genetic stock, *viz.*, black seeded pentafoliate berseem, was identified. Progeny lines of this novel genetic stock were planted to analyse the stability of these two traits. Progeny lines showed 100% penetrance for both traits while >95% expressivity was observed for pentafoliate trait. Due to black colour the seeds are expected to contain higher tannin content in its seed coat, which may confer better tolerance to pathogens in the early stages

of seedling development. Additionally, the pentafoliate nature is a distinct morphological trait and can be used in breeding programme to enhance productivity and studies in leaves morphogenesis. Further to mention that black (dark tan) seeded pentafoliate berseem has never been reported. In future, it might serve as a marker in various intra and interspecific crosses. This novel genetic stock of berseem with black-seed and pentafoliate leaves could potentially be used for basic studies as well as genetic improvement programme in berseem crop (Anonymous 2013).

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14. SPV-2018 (IC0612063; INGR15027), a Sorghum (*Sorghum bicolor* (L.) Monech.) Germplasm with High Digestibility (IVOMD %), Low Lignin Content and Brown Midrib (*bmr*)

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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. Digestibility of fodder is the most important forage quality parameter which helps in better absorption of the feed taken in by the animal. It is estimated that a 1% increase in digestibility increases milk yield by 5%, resulting in higher income for farmers (Rao and Hall, 2003; Kumaracharyulu *et al.*, 2014).

SPV 2018 was developed through pedigree method of breeding by crossing between SPV 462 and the *bmr* germplasm line, IS 21891 during rabi 2003-04 at Directorate of Sorghum Research, Hyderabad. SPV 462 is a most popular variety which was released as a variety in the states of Tamil Nadu and Andhra Pradesh (PSV 1) 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 from F_3 till F_7 between the period 2004-2007. SPV 2018 is a tan plant with green leaves and brown midrib. Panicle is semi-compact with elliptic shape and medium bold seeds. After stabilization, it was assessed for its yield and quality in station trials during 2007-08 before testing under All India Coordinated Sorghum Improvement Project Trials during 2009 and 2010. Station trial results for IVOMD indicated the superiority of SPV 2018 i.e., (SPV462 \times IS 21891)-3-1-1-1 (52.2%) over the test entries. It was also promising for Relative Fodder Value and was the best among the test entries for this character (Umakanth *et al.*, 2014).

During 2009, SPV 2018 with an IVOMD of 52% had recorded a superiority of 6% for IVOMD (%) over the national check CSV 23 (49%) and local check (49%). During 2010, with an IVOMD of 42.3%, it had recorded a significant superiority of 9% over the national check CSV 23 which has shown 38.7% and 5% over the local check (40.3%). It also had 14% significant superiority for crude protein content and lower lignin content over the national check variety CSV 23.

SPV 2018 offers promise for increased milk yield owing to superior stover quality in terms of low lignin content and higher *in vitro* organic matter digestibility. Apart from its use for increasing milk yields, this line offers promise as a lignocellulosic biofuel feedstock because of higher yield of fermentable sugars during pretreatment and enzymatic saccharification owing to its low lignin content. Earlier studies have indicated that brown midrib mutants significantly increase conversion rate in the lignocellulosic bioenergy process. This variety is suited to be grown under *Kharif* rainfed situation across India.

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15. VRP-147 (IC0598281; INGR15028), a Garden pea (*Pisum sativum* L.) Germplasm with Resistance to Downy Mildew and Rust

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Garden pea is main winter season crop and occupying about 4.6% of total vegetable area and about 2.3 % of total vegetable production. Uttar Pradesh alone contributes about 45.4% of total pea production in India. Diseases such as powdery mildew, downy mildew and rust are the major limiting factors in pea production especially for mid (flowering start 45 DAS) and late duration (flowering start 55 DAS) varieties. The losses in yield in a 100% infected crop by powdery mildew were estimated to be 21-31% in pod number and 26-47% in pod weight. Although these diseases can be controlled very effectively through fungicidal treatment but disease control by chemical means fetch more cost to its production and also it is hazardous to human health and the ecosystem. So, cultivation of resistant varieties is one of the practicable options for the management of the diseases because genetic resistance is safe, reliable, effective and cost-free alternative to ensure a healthy crop. So, keep in mind the above problems, experiment was laid out for screening of available germplasm lines at IIVR against powdery mildew, downy mildew and rust.

During 2008-09, a set of 410 germplasm lines were screened for resistance against powdery mildew, rust and downy mildew. Out of them 85 lines were resistance to powdery mildew and 9 were resistance to rust while five lines (VRP-233, VRP-393, VRP-343, VRP-147 and NO-17) were resistance to both the diseases. However, the incidence of downy mildew was not noticed during the period. Same set of germplasm lines (410) were again sown in 2009-10 under field conditions and observations

were made on selected germplasm lines which comprises of resistance and susceptible for powdery mildew/downy mildew/rust. A high disease pressure was observed in powdery mildew and rust but a moderate level of downy mildew severity was noticed (20-26%). Among the lines screened, VRP-343, VRP-393, NO-17, VRP-147, NO-110 and VRP-233 showed resistance to powdery mildew and rust while VRP-343 and VRP-147 recorded resistance to all three diseases.

On the basis of two year field study, a set of different lines resistance to powdery mildew, rust and downy mildew along with suitable susceptible checks were tested under artificial inoculation conditions during 2012-13 and 2013-14. For artificial inoculation, the spores of all the diseases were collected from pea field in the last week of February and sprayed (approx. 10^6 spores/ml) on all the germplasm lines uniformly in polyhouse. The genotypes VRP-343 and VRP-147 were found resistant for all the three diseases whilst susceptible check showed 100 per cent disease incidence and the results were consistent while comparing previous experiments.

Morpho-agronomic characteristics: VRP-147 is a late maturing genotype. It takes 65-66 days for 50% flowering. Flowering starts after 17.4 nodes. Pod length is 5.5 cm and width is 1.42 cm. Pods are green in colour and slightly curved. Number of pods/plant is 24.5 and 10 pod weight is 44 g and each pod has 6.2 seed. Yield/plant is 98 g and shelling percent is around 47.2. The total sugar is 3.80 %.

16. VRP-343(IC0598280; INGR15029), a Garden Pea (*Pisum sativum* L.) Germplasm with Resistance to Powdery Mildew

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On the basis of two year field study, a set of different lines resistance to powdery mildew, rust and downy mildew along with suitable susceptible checks were tested under artificial inoculation conditions. For artificial inoculation, the spores of all the diseases were collected from pea field in the last week of February and sprayed (approx. 10^6 spores/ml) on all the germplasm lines uniformly in polyhouse. The genotypes VRP-343 and VRP-147 were found resistant for all the three diseases whiles susceptible check showed 100 per cent disease incidence and the results were consistent while comparing previous experiments.

Morpho-agronomic characteristics: VRP-343 is a late maturing genotype. It takes 59-60 days for 50% flowering. Flowering starts after 13.2 nodes. Pod length is 6.10 cm and width is 1.36 cm. Pods are green in colour and slightly curved. Number of pods/plant is 26.4 and 10 pod weight is 42 g and each pod has 6.5 seed. Yield/plant is 110g and shelling percent is around 46.5. The total sugar is 3.15 %.

17. Pune Selection-1 (PS-1) (IC0611690; INGR15030), a Papaya (*Carica papaya* L.) Germplasm with Field Tolerance to *Papaya Ringspot Virus* and Yellow Pulp Colour

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Pune Selection-1 (PS-1) is a near homozygous, yellow fleshed, dioecious papaya (*Carica papaya* L.) line. The line is consistently showing field tolerance to *Papaya ringspot virus* strain papaya (PRSV-P) with good yield (ICAR Report, 2012; AICRP Annual Report, 2013; Datar *et al.*, 2013 and Sharma *et al.*, 2011). The parental material was a segregating land race of papaya named Madhubala. PS-1 was selected from the segregating population in 2009. Since then, it is developed into a line by sib-mating and selection at IARI, Regional Station, Pune.

Morpho-agronomic characteristics: Mean height of the plant is 1.85 meters, mean canopy E-W is 2.45 and N-S 2.25 meters, mean stem girth is 14 cm, leaf shape is palmate type, petiole colour is green. Average time required to flower is 59 days. Petal colour is cream yellow. Average length of the fruiting column is 0.70 meters. Mean number of fruits per plant was 35. Mean fruit

weight is 1336 g. Average yield/plant is 46 Kg. Shape of the fruit is oblong with slight nipple at stylar-end. Mean length of fruit is 24 cm while breadth is 16.5 cm. Flesh colour is yellow (occasionally orange) with average TSS value of 9.3⁰ Brix. The line performed better than both the checks (*C. papaya* cv. Red Lady and Pusa Nanha) under severe PRSV-P pressure.

Associated characters and cultivation practices: PS-1 is having field tolerance to PRSV-P. It shows late and mild PRSV infection. Growth, fruiting characters and incidence of PRSV-P in PS-1 along with two checks of papaya, namely, Red Lady and Pusa Nanha are given in Table 1. Under Pune conditions, it is recommended to plant seedlings having six to eight leaves in spring season (February-March). Since the virus transmitting aphid-vector population is minimal from February to June. Seedlings should be raised in insect-proof polyhouse.

Table 1. Comparison of growth, fruiting characters, yield and PRSV reaction of Pune Selection-1 with local checks (Red Lady and Pusa Nanha)

Variety	PS-1					Red Lady					Pusa Nanha				
	2010-11	2011-12	2012-13	2013-14	Ave.	2010-11	2011-12	2012-13	2013-14	Ave.	2010-11	2011-12	2012-13	2013-14	Ave.
Plant Height (m)	1.88	1.92	1.80	1.78	1.85	1.47	1.60	1.58	1.57	1.56	1.48	1.44	1.25	1.19	1.34
Collar Diameter (cm)	14	14	14	14	14	12	14	14	14	14	13	13	12	12	13
Fruiting Height (cm)	64	75	81	79	75	71	77	81	79	77	56	52	52	46	52
Fruiting Column Length (cm)	84	89	54	51	70	71	62	54	51	60	70	68	47	53	60
Yield (Kg/Pl)	46.9	48.1	40.5	50.1	46.4	18.7	19.2	17.5	13.7	17.3	40.7	39.5	26.4	39.9	36.6
Average Fruit Weight (g)	1283	1366	1361	1334	1336	818	971	948	746	871	1080	1038	1151	1070	1085
Flesh Thickness (cm)	2.72	2.51	3.53	3.00	2.94	2.50	2.88	3.25	2.53	2.79	3.50	3.85	3.75	2.63	3.43
Flesh Colour	Yellow					Red					Yellow				
TSS (°Brix)	9.1	8.4	10.6	9.0	9.3	8.04	8.0	7.5	9.0	8.14	7.5	8.0	7.5	7.5	7.63
PRSV Infection (%)	47.2	44.6	45.5	42.7	45.0	92.3	89.6	84.5	92.6	89.8	62.3	68.3	63.3	61.5	63.8

Being a dioecious line, two seedlings per hill should be planted to maintain higher ratio of productive female plants. Per plant space required is 4.3 to 4.4 square meters that can be achieved by maintaining row to row and plant to plant distance of 2.4m x 1.8 m respectively or by square plantation of 2.1 m x 2.1 m. About 2,300 plants can be accommodated per hectare under both spacings. One square foot FYM, 2 Kg neem seed cake and 1 Kg sterameal should be applied per hill before plantation. Inorganic fertilizers N:P:K at the rate of 300:300:300 g/plant should be applied in four split doses at alternate month. Foliar application of a balance mix of all micronutrients (2g/l) at alternate month along with additional spray of boron (2g/l) at the time of fruit setting, and calcium (2g/l) before fruit ripening is recommended.

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18. IG 91-1100 (IC0612055; INGR15031), a Sugarcane (*Saccharum* Spp.hybrid) Germplasm with Good Seed Setting

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The narrow genetic base of the sugarcane varieties currently under cultivation has posed serious limitations in breaking yield. Past few decades, considerable attention is being given to broaden the genetic base using wild species related to *Saccharum*. The clone IG 91-1100 is polycross hybrid between CoC 772 and *Erianthus* spp which was developed at Sugarcane Breeding Institute, Coimbatore. It was evaluated over the years and identified as one of the potential parents for developing sugarcane varieties with high yield, quality and stress tolerance with good seed set.

Seventeen high yielding clones derived from IG 91-1100 were accepted for pre zonal varietal testing and seven clones were given Co status. Two sugarcane varieties viz., Co 06027 and Co 06030 derived from IG 91-1100 were notified for commercial cultivation under Peninsular and East coast zone respectively during the year 2013. One clone Co 2010-22 having very high yield potential was identified as a biomass type. In addition to high yield and quality, it has also imparted stress tolerance in many Co canes indicating its potential. It has very erect

robust canes, arched leaves and tight clasping leaf sheath. Internodes have heavy wax and big pentagonal buds. It is a regular flowerer with 65 % pollen fertility.

Molecular fingerprinting of 13 recently notified sugarcane varieties for commercial cultivation for Peninsular zone and East coast zone using STMS markers indicated, two varieties viz., Co 06027 and Co 06030 developed by crossing CoC 671 and IG 91-1100 were more diverse than the other varieties (Hemaprabha *et al.*, 2013). The clone IG 91-1100 has produced more seedlings in the crosses compared to other intergenic hybrids involving *Erianthus* and can be used to obtain more seedlings in further crosses. Hence, this clone IG 91-1100 can be used as a potential parent to diversify the sugarcane genetic base as well as sustaining sugarcane productivity.

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19. GU04(28) EO-2 (IC0612056; INGR15032), a Sugarcane (*Saccharum* Spp. hybrid) Germplasm with Regular Flowering, Pollen Fertility of 5.5%

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The narrow genetic base of sugarcane varieties has imposed serious limitations in making a significant improvement in sugarcane productivity. In view of this, attempts are being made at all cane breeding stations to broaden and diversify the genetic base of sugarcane through the introgression of wild relatives. Of late, considerable attention is being given to use *Erianthus* spp. which had high biomass potential and high tolerance to biotic and abiotic stresses. GU04(28)EO-2 is a unique and true intergeneric hybrid between *Erianthus procerus* 'IND 90-776' × *Saccharum officinarum* 'PIO 96-435' which was developed at Sugarcane Breeding Institute, Coimbatore during 2004. It is having intermediate juice brix of 13.92% and sucrose of 8.20%. Evaluation under both drought and normal conditions during 2013-14 had shown that it is relatively drought tolerant.

The true hybridity of clone GU04(28)EO-2 has been confirmed through microsatellite primers and 5srDNA primers. The hybrid had both the fragments of *Saccharum* and *Erianthus*. The plant is morphologically distinct and has erect growth habit with dark green leaves without splits in the internodes. The colour of leaf sheath is purple with medium waxiness without spines. It has unique deltoid ligule with hairiness which is present in *Erianthus* Spp. It has big pentagonal bud and swollen root eyes. It is tolerant to drought and also moderately resistant to red rot. It is a regular flowerer with low pollen fertility of 5.5% and can be used as safe female for introgression. It has *Erianthus* cytoplasm and could serve as a genetic stock for diversifying the genetic base of sugarcane and developing drought tolerant cultivars.

20. GU04(50) RE-16 (IC0612058; INGR15033), a Sugarcane (*Saccharum robustum* × *Erianthus* hybrid) Germplasm with Regular Flowering and Good Seed Set (128 Seedlings)

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Traditionally *Saccharum spontaneum* had been the donor for many important traits in sugarcane. In recent years, considerable attention is given to use *Erianthus* spp. which had been identified as valuable source for many traits such as ratoonability, tolerance to environmental stresses, vigour, disease resistance and potential source for developing energy canes. (Piperidis *et al.*, 2000). Among the different species, *Erianthus arundinaceus* (Rez.) Jeswiet is of specific interest because of the presence of vegetative canes and broad leaves. GU04(50) RE-16 is a true and novel intergeneric hybrid between improved *Saccharum robustum* PIR 00-1100 and

Erianthus arundinaceus IK 76-91 which was developed at Sugarcane Breeding Institute, Coimbatore during 2004. This is the first report about the production of intergeneric hybrids between two wild relatives *viz.*, *S. robustum* and *E. arundinaceus*. It was evaluated for yield and quality traits during 2006-2010. It recorded a mean sucrose of 12.98% with medium purity (74.26%). The true hybridity has been confirmed through cytologically and using *Erianthus* specific markers. It had a somatic chromosome number of $2n=80$ with $n+n$ transmission. The hybrid has semi erect stools with thin cylindrical internodes and heavy wax. It has two rows of root eyes with pentagonal

bud without bud cushion. It has narrow dark green leaves with prominent reddish dewlap. Evaluation of the hybrid GU 04(50) RE-16 for flowering and seed set during 2007-2013 showed that it is a regular flowerer and has produced better seed set compared to other intergeneric hybrids. It can be a donor for genes of value from the wild relatives *Erianthus* and *S. robustum*.

21. GU08 SSH-66 (IC0612060; INGR15034), a Sugarcane (*Saccharum* × *Sorghum* hybrid) Germplasm with High Early Sugar Accumulation

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Intergeneric hybrids between *Saccharum* and *Sorghum* were produced as early as 1929 by Venkatraman to develop early maturing sugarcane varieties. But it was not successful. Four intergeneric hybrids with sorghum cytoplasm were produced by crossing sorghum as female parent with sugarcane (Nair, 1999). All the hybrids resembled sugarcane but lacked vegetative vigour and sugar. Fresh crosses were made between sugarcane and sweet sorghum at Sugarcane Breeding Institute, Coimbatore during 2008 and generated 24 putative hybrids. Among the 24 putative hybrids, nine of them were confirmed as genuine hybrids using SSR markers including GU 08 SSH 66. The hybrids involving sorghum were evaluated for their early sugar accumulation at sugarcane Breeding Institute, Coimbatore for two years during 2010-2011. The results showed that the hybrid GU 08-SSH-66 recorded the highest HR brix of 20.80% at 6th month followed by GU 08-SSH-68 (19.80%). The sugar accumulation was steadily increased in all the hybrids and the hybrid GU 08-SSH 66 had the maximum of 23.5% at 8th month (Mohanraj *et al.*, 2013). Seven intergeneric

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hybrids involving sweet sorghum were also evaluated for red rot under controlled condition testing. Out of which GU 08 SSH 66 was identified as moderately resistant to red rot.

The hybrid had erect stool as well as leaf habit with greenish purple canes and heavy wax. It is medium height with cylindrical internodes and corky patches. Leaf sheath is without hairs and brown dewlap. Bud is small, round without bud grove. Since the intergeneric hybrid GU08 SSH 66 had early high sugar accumulation and red rot resistance it could serve as a diverse source for developing early maturing short duration sugarcane varieties.

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22. 99WL-379 (IC0612061; INGR15035), a Sugarcane (*Saccharum* Spp. hybrid) Germplasm with High Juice Quality Under Water Logged Condition

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99 WL 379 is a high sugar clone developed from cross between Co 7313 (Female parent) with high juice quality, and Co 96011 (Male parent) with waterlogging tolerance from the first selection cycle through a simple recurrent selection scheme. The hybrid is distinct from its female parent for cane thickness and from its male parent for high sucrose content. It is characterized by thick (3.1cm girth) semi erect stem with cylindrical and zigzag arranged internodes. The exposed internode is yellowish green in colour, without ivory and weather marks but with a few shallow cracks. The buds are generally small ovate with apical germ pore and bud cushion but without bud groove. It has open semi-drooping canopy with green coloured lamina. The leaf sheath colour is green with light coating of wax, hard spines and medium loose clasping on the stem.

The clone showed significantly higher juice brix, sucrose % and commercial sugar yield per plot compared to control (Table 1) under waterlogged stress. Excess moisture stress/waterlogging stress is one of the major constraints in sugarcane agriculture. About 2.2 Lakh hectares sugarcane is getting affected by waterlogging

Table 1. Commercial sugar yield and quality traits of 99 WL 379 under waterlogged condition

Character	Average over three years	Percentage improvement over control	
		Co 62175	Co 8231
Juice brix (%)	20.88	10.73	On Par
Sucrose %	18.88	14.6	2.1
Commercial cane sugar (%)	13.3	18%	1.5%
Commercial sugar yield/plot	5.86	2.1%	20.5%
Purity	84.02	6.9%	On par

across the sugarcane growing states in the country (Nair 2012) and this clone can be cultivated under such situation. It also showed high stem nitrogen content (0.493%), a physiological trait highly correlated with waterlogging tolerance with 32% and 24% higher over the standard varieties (Gomathi and Chandran, 2010 and & 2012).

The real potential of this genetic stock is as a parental clone for yield and quality. The clone shows moderate flowering with 40 to 50% pollen fertility and hence has the potential to use as both male and female parent. By using as female parent one hybrid clone (WL 05-499) with high juice quality and sugar yield entered in pre-zonal varietal trial, and as a male parent one hybrid clone identified as Co cane (Co 12015) with high juice quality.

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23. IIHRMGYP-1 (IC0613361; INGR15036), a Marigold (*Tagetes erecta* L.) Germplasm with Petaloid Sterile Flowers; Ability to be Multiplied by Cuttings

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IIHRMGYP-1 is a petaloid male sterile genotype useful for breeding program. Flowers are male sterile consisting of only ray florets with well developed gynoecium and are devoid of disc florets. The genotype can be maintained by vegetative propagation through tip cuttings. With high yielding potential, it has the potential for flower production besides being a valuable genetic stock for hybrid seed production.

Marigold (*Tagetes* spp.) is one of the most popular flowering annuals grown for loose flowers, landscape gardening and pot plants. The flowers are suitable for garlands and floral decorations. Marigold is also widely used as an ingredient for nutraceutical, cosmetic, and pharmaceutical applications. In India, Marigold occupies the first position among flower crops in terms of area covered. As per the estimation of NHB data for the year 2013-14, out of the 255.02 thousand ha. area under flower crops, marigold is covered in an area of 55.89 thousand ha.

Though marigold is being widely used in India, there are not many varieties available and F_1 hybrids are being imported from outside the country and are gaining popularity considering their flower quality and production potential. Identification of male sterile lines is important for exploitation of heterosis and hybrid development. Not much information is available on male sterility in marigold. All the information available about male sterility is limited to apetaloid type of sterility where in flower petals are degenerated (He *et al.*, 2010; Gupta *et al.*, 2013).

Ongoing research program at Indian Institute of Horticulture Research, Bengaluru is focused on development of male sterile lines as a prerequisite for heterosis breeding. Crosses are attempted between plants from wide genetic back ground to create variability and for introgression of characters. Individual plant selection made in the breeding population has resulted in a pool of genetic stocks varying in morphological and reproductive characters. IIHRMGYP-1 is an individual

plant selection from the segregating population resulting from hybridization between MG-87 and MG-32. The parents, MG-87 and MG-32 were heterogeneous and heterozygous population and crossing were attempted between selected plants. From the resulting segregating population, promising progeny plants were selected and multiplied by vegetative propagation followed by clonal selection.

Marigold belongs to Asteraceae family characterized by capitulum inflorescence with peripherally located ray florets and disc florets in the centre. For commercial utility, these inflorescences are considered as flowers and ray and disc florets are considered as petals. Flowers of IIHRMGYP-1 are yellow gold in colour with RHS colour chart No. 12-A in Yellow Group. Distinct features of the genetic stock are its double flowers that are sterile. Sterile flower devoid of petals with all the petals converted to stigma was reported in marigold (He *et al.*, 2010). On the contrary, flowers of novel genetic stock IIHRMGYP-1 developed at IIHR is a petaloid male sterile with double flower type filled with ray florets and are devoid of disc florets and androecium. Plants are of medium height (70 cm), with spreading plant habit and strong branching. All the reported variability in marigold are related to quantitative characters and not much information is available on variability available in sterile types (Singh and Misra 2008; Yuvraj and Dhatt 2014).

In general, marigold varieties are multiplied by seeds and are also amenable for tissue culture (Gupta *et al.*, 2013). We have observed IIHRMGYP-1 having the ability to be propagated by vegetative propagation. We were able to establish a population of IIHRMGYP-1 by tip cuttings and production potential was estimated in replicated trials in comparison with check varieties.

Performance evaluation of IIHRMGYP-1, over three years in replicated trials has revealed it to be having higher production potential compared to the check varieties that includes pure lines of IIHR (IIHRY4 and IIHRY5), a high yielding variety 'Pusa Basanthi' and a commercial

Table 1. Production evaluation of IIHRMGYP-1 in comparison with check genotypes

Genotypes	No of flowers/plant	Flower wt (gms/flower)	Flower yield/plant (gms)
IIHRMYP-1	150.8	6.0	904.8
IIHRMY 4	125.8	5.5	691.9
IIHRMy 5	127.6	5.4	689.0
Pusa Basanthi	119.8	5.2	623.0
F1 Hybrid Gold	118.4	6.4	757.8
c.d@5%	4.3	0.3	249.1
C.V %	6.1	2.9	8.4

hybrid variety 'F₁ Hybrid Gold' (Table 1). IIHRMGYP-1 has the potential for commercial flower production and with its sterile flowers can also be exploited for hybrid seed production.

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