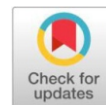


Original Research Article

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Combining ability and hybrid performance in mung bean (*Vigna radiata* (L.) Wilczek) for agronomic traits



Amrish Verma, Shiva Nath, Baudh Bharti*, Javed, Alok Pal, Arvind Patel and Parasram

Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj)-224229, Ayodhya, Uttar Pradesh, India

ABSTRACT

Mungbean, contains 25.0 percent proteins with all essential amino acids, which is almost three times more than that of cereals. High nutritional value, they have restored soil fertility through biological nitrogen fixation. The experimental material comprised of six females, four male parents and their 24 F_1 s developed by crossing Line x Tester mating design. These 24 F_1 hybrids along with 10 parents and three checks were evaluated in a randomized block design with three replications during Kharif 2023 at the Field Experimentation Centre, Genetics and Plant Breeding research farm, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya. The estimates of variances due to general combining ability were higher than The specific combining ability for all the traits except secondary branches per plant, clusters per plant, pods per cluster, pods per plant, and seeds per pod pointed out to be the preponderance of non-additive gene effects in the expression of these characters. Parents HUM 16, VGG 20153 and IPM 02-3 can be considered as a good source of favorable genes for increasing seed yield along with other yield attributes. MML 2552 x IPM 02-3, HUM 16 x VGG 20153, HUM 16 x MH 1142, IPM 1707-1 x IPM 02-3 and TRM 230 x MH 1142. 139 expressed high significant and sca effects as well as high per se performance for seed yield per plant and other traits. HUM 16 x VGG 20153 involved high x high type of general combiners could be due to additive type of gene actions that are fixable in nature, may be exploited further using pedigree method of breeding for the development of pure lines.

Keywords: Combining ability, Line x Tester, Heterosis, predictability ratio, seed yield

INTRODUCTION

Mungbean, scientifically known as *Vigna radiata* (L.) Wilczek, is a self-pollinated diploid plant with a chromosome count of $2n=2x=22$. It possesses one of the smallest genome sizes among legumes, measuring at 579 MB/1C (Arumuganathan and Earle 1991). It has originated from Indian Sub-continent (De candolle 1886, Vavilov 1926 and Zukoveskij 1962). The mung bean (*Vigna radiata* (L.) R. Wilczek) is divided in 3 subgroups: it is cultivated edible mung bean (*Vigna radiata* subsp. *radiata*), and that are two wild subgroups (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*). It contains 25.0 per cent proteins with all essential amino acids, which is almost three times more than that of cereals (Saini *et al.*, 2010). Besides their high nutritional value, they have a unique characteristic of maintaining and restoring soil fertility through biological nitrogen fixation and thus play a vital role in sustainable agriculture (Asthana, 1998). The major constraints in achieving higher yield are lack of exploitable genetic variability, absence of suitable ideotype for different cropping systems, poor harvest index, susceptibility to biotic and abiotic stresses, non-availability of quality seeds of improved varieties, and narrow genetic base due to repeated usage of few parents with a high degree of relatedness in crossing program (Kumar *et al.* 2004). Two parameters normally calculated from such studies include the general combining ability (GCA) and specific combining

ability (SCA). GCA is the average performance of a parent genotype over several cross combinations and is associated with additive gene effects, while SCA reveals the average performance of crosses that perform better and is typically associated with nonadditive gene effects (dominance) (Shiri *et al.* 2010; Darvishzadeh *et al.* 2011).

Heterosis leads to superiority in adaptation, yield, quality, disease resistance, maturity and general vigor over its parents. If the hybrid is superior to mid parent, it is regarded as average heterosis or relative heterosis (Singh and Singh, 2005). The exploitation of the heterosis for commercial purposes is very common in pollinated crops (Priyanka *et al.*, 2008, Ram *et al.*, 2013). The objectives of present investigation were to estimate the heterosis in F_1 hybrids and gca, sca with respective the gene effects for seed yield and its component traits in mung bean though the L x T mating design.

MATERIALS AND METHODS

Plant material and field experiment: The experimental material comprised of six females, four male parents and their 24 F_1 s developed by crossing Line x Tester mating design. These 24 F_1 hybrids along with 10 parents and three checks were evaluated in randomized block design with three replications during Kharif 2023 at the Field Experimentation Centre, Genetics and Plant Breeding, Research Farm, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya. Sowing was done by dibbling the seeds at a distance of 10 cm in rows of 2 m length with row to row spacing of 30 cm. Non-experimental rows were planted around the layout to eliminate border effects. A basal dose of 20 kg N and 40 kg P_2O_5 /ha-1 was applied at sowing time.

*Corresponding Author: **Baudh Bharti**

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All recommended cultural practices and plant protection measures were adopted to raise a good crop. The lines, testers, and check chosen for study along with their characteristic features are listed in (Table. 5). **Quantitative traits:** For recording observations, 5 competitive plants were randomly selected and tagged from each treatment in each replication and the mean value per plant was computed for various yield and its attributing traits viz., plant height, primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pods per plant, seeds per pod, 100 seed weight, biological yield per plant, harvest index, and seed yield per plant. The phenological characters viz., days to 50% flowering and days to maturity were recorded on plot basis.

Statistical analysis: The combining ability analysis was performed for a Line $\times$ Tester mating design as per the method suggested by Kempthorne (1957). The extent of heterosis can be assessed relative to the mid-parent (relative heterosis), the better parent (heterobeltiosis), and a standard parent (standard heterosis). Fonseca and Patterson (1968) Proposed a method that offers a comprehensive approach to estimating these measures of heterosis. All these analyses of various parameters were performed by Windostat version- 9.2.

RESULTS AND DISCUSSION

Combining ability and genetic variances: The ANOVA for the L $\times$ T mating design is summarized in Table 1. Variance due to line showed significant differences for DFF, DM, PH, PBPP, SBPP, HSW, BYPP, HI and SYPP. Mean square due to the tester were highly significant for PH and HSW, while variance due to line $\times$ tester had significant differences for DFF, DM, PH, NPPP, HSW, BYPP, HI and SYPP except PBPP, SBPP, PPC and NSPP. The estimates of variances due to general combining ability were higher than The specific combining ability for all the traits except secondary branches per plant, clusters per plant, pods per cluster, pods per plant, and seeds per pod pointed out to be the preponderance of non-additive gene effects in the expression of these characters. Similar findings were reported by Nath et al. (2017), Hasan et al. (2019), and Kakde et al. (2019). A predictability ratio ($2\sigma^2_{gca} / 2\sigma^2_{gca} + \sigma^2_{sca}$) greater than 0.5 indicates additive gene action, less than 0.5 indicates non-additive gene action, and equal to 0.5 indicates predominance of both additive and non-additive gene action for a character. Whereas predictability ratios were greater than the value of 0.5 for days to 50 % flowering, days to maturity, plant height, primary branches per plant, 100 seed weight, biological yield per plant, and seed yield per plant indicating the predominance of additive gene action for these characters. However, the predictability ratio exhibited less than 0.5 values for rest of the characters indicating the predominance of non-additive gene action.

General combining ability (GCA) effects: The GCA elucidates the average performance of a line in an array of hybrid crosses and it can be used to differentiate the parental lines. In our study, the GCA effect of testers Line 6 (HUM 16) had a negative significant gca effect for DFF. Tester 1 (VGG 20153) had negative for DFF and DM. Both line and tester indicate the earliness. NDM-1, TRM 230 and MML 2552 showed significant and negative effects for days to maturity. TRM 230 was found to be best general combiner for PBPP, SBPP, HSW and BYPP. VGG 20153 (Tester 1) is also a good general combiner for NPPP, NSPP, and SYPP. IPM 02-3 (tester-3) and HUM 16 (Line-6) both parents were found to be

good general combiner for harvest index and seed yield per plant. However, NDM-1, TRM 230 and MML 2552 were poor general combiner for seed yield per plant. None of the parents were exhibited positive and significant gca effects for the CPP and PPC. The above results were supported by similar findings of Rathod et al. (2020) and Sinha et al. (2020). Parents Therefore, parents HUM 16, VGG 20153 and IPM 02-3 can be considered as a good source of favorable genes for increasing seed yield along with other yield attributes. It is evident from these results that high effects for seed yield per plant in these parents were mainly due to important yield contributing characters mentioned above. Therefore, it would be worthwhile to use the above parental lines (HUM 16, VGG 20153 and IPM 02-3) in the hybridization programme for improvement of mung bean.

Specific combining ability (SCA) effects: SCA is mainly associated with non-additive gene action resulting from dominance, dominance and epistatic effects (Su, et al. 2017).

SCA effect reveals deviations in the performance of a certain cross from the performance predicted by the parents' GCA effects, and it is associated with nonadditive gene effects (Musembi et al. 2015). The estimates of effects for yield and yield contributing traits are presented in Table 3. Out of 24 crosses only two crosses namely MML 2552 $\times$ IPM02-3 and HUM 16 $\times$ VGG 20153 exhibited significantly positive sca for seed yield per plant. These results are in conformity with findings of Vaidya et al. (2015), Surasheet et al. (2017), Latha et al. (2018), Zugeet et al. (2018). Significant yield performance in specific crosses was due to the combinations on the basis of their *per se* performance and effects. (Ahmad et al., 2014). The crosses NDM-1 $\times$ IPM02-3, Pusa M23-31 $\times$ IPM12-1, TRM 230 $\times$ IPM02-3, MML 2552 $\times$ IPM02-3, and HUM 16 $\times$ VGG 20153 were exhibited desirable sca effects for days to maturity, TRM 230 $\times$ IPM02-3 for plant height, Pusa M23-31 $\times$ IPM02-3, TRM230 $\times$ MH1142 and MML 2552 $\times$ IPM12-1 for primary branches per plant, TRM 230 $\times$ IPM02-3 for secondary branches per plant, IPM 1707-1 $\times$ IPM02-3 for clusters per plant, IPM 1707-1 $\times$ IPM02-3, IPM 1707-1 $\times$ IPM 12-1, MML 2552 $\times$ IPM02-3, HUM 16 $\times$ VGG 20153 and HUM 16 $\times$ IPM 12-1 for number of pods per plant, TRM 230 $\times$ IPM02-3 and MML 2552 $\times$ IPM12-1 for 100-seed weight and MML 2552 $\times$ IPM02-3 and HUM 16 $\times$ VGG 20153 for biological yield per plant. None of the crosses exhibited such types of combination sca effect significant for day to 50% flowering, number of seeds per pod and harvest index in desirable direction. These results were getting support from the findings Musembi et al. (2015), Singhet al. (2016) and Su et al. (2017). Five promising crosses with desirable sca effects for seed yield per plant along with mean performance, heterosis and gca effects of parents involved in the crosses are listed in Table 4. MML 2552 $\times$ IPM 02-3, HUM 16 $\times$ VGG 20153, HUM 16 $\times$ MH 1142, IPM 1707-1 $\times$ IPM 02-3, and TRM 230 $\times$ MH 1142.

139 expressed high significant and sca effects as well as high *per se* performance for seed yield per plant and other traits. Desirable cross combinations HUM 16 $\times$ VGG 20153 involved high $\times$ high type of general combiners could be due to additive type of gene actions which are fixable in nature; this type of combinations involving high $\times$ high general combiners may be exploited further using the pedigree method of breeding for the development of pure lines. Similar findings were reported Nath et al. (2018). Those crosses had high sca effects involving one good combiner and the other medium or poor. This might be due to epistasis like additive $\times$ dominance type of interaction which is considered as non-fixable genetic components for seed yield contributing traits. This indicated possibility to obtain desirable

transgressive segregants and hybrid vigour from such crosses by adopting cyclic selection or biparental breeding program.

CONCLUSION

Using combining the ability to select parents is an effective approach in hybrid breeding. The current study presented the first report on the combining ability for 13 characters. GCA was significantly different among parents and SCA was also significantly different among crosses. Parents HUM 16,VGG 20153 and IPM 02-3 can be considered as a good source of favorable genes for increasing seed yield along with other yield attributes. MML 2552 x IPM 02-3, HUM 16 x VGG 20153, HUM 16 x MH 1142, IPM 1707-1 x IPM 02-3 and TRM 230 x MH 1142. 139 expressed high significant and sca effects as well as high per se performance for seed yield per plant and other traits. HUM 16 x VGG 20153 involved high x high type of general combiners could be due to additive type of gene actions which are fixable in nature, may be exploited further using pedigree method of breeding for the development of pure lines.

Conflict of interest: All Authors have no conflict of interest.

Table 1. Analysis of variance for combining ability and estimates of genetic variances for 13 characters in L x T mating design in mung bean

Characters	Sources of variation				Genetic variances			
	Lines	Testers	Lines x Testers	Error	σ^2_{gca}	σ^2_{sca}	$\sigma^2_{sca}/\sigma^2_{gca}$	$2\sigma^2_{gca}/2\sigma^2_{gca}+2\sigma^2_{sca}$
d.f	5	3	1	66				
DFF	17.82**	3.88	30.42**	2.97	1.52	-0.44	0.54	1.40
DM	67.15**	2.44	35.55**	3.14	8.07	7.19	0.94	0.53
PH	115.65**	72.22**	131.75**	6.63	20.06	7.83	0.62	0.72
PBPP	0.23**	0.02	0.04	0.02	0.08	0.03	0.64	0.70
SBPP	0.13*	0.08	0.004	0.05	0.01	0.02	1.23	0.40
CPP	0.45	1.00	4.35*	0.69	0.07	0.29	2.06	0.19
PPC	0.98	0.11	0.35	0.71	-0.01	0.26	5.97	-0.03
NPPP	20.48	22.77	254.42**	10.24	6.93	37.92	2.34	0.15
NSPP	0.18	0.30	0.67	0.58	0.05	0.17	1.81	0.23
HSW	2.50**	0.50**	1.18**	0.07	0.12	0.05	0.65	0.70
BYPP	127.11**	6.009	205.91*	48.86	54.36	20.84	0.62	0.72
HI	26.89**	15.07	217.11**	7.62	0.66	-1.26	1.30	-1.11
SYPP	10.02*	0.94	85.18**	3.92	8.11	3.84	0.69	0.67

*,** Significant at 5% and 1% probability levels, respectively, DFF (Days to 50% flowering), DM (Days to maturity), PH (Plant height cm), PBPP (Primary branches per plant), SBPP (Secondary branches per plant), CPP (Clusters per plant), PPC (Pods per cluster), NPPP (Number of pods per plant), NSPP (Number of seeds per pod), HSW (100 seed weight (g)), BYPP (Biological yield per plant g), HI (Harvest index %) and SYPP (Seed yield per plant g)

Table 2. Estimates of general combining ability (GCA) effects of parents (lines and testers) for 13 characters in mung bean

Parents	DFF	DM	PH	PBPP	SBPP	CPP	PPC	NPPP	NSPP	HSW	BYPP	HI	SYPP
Lines/tester													
NDM-1	0.37	-1.43**	-1.50*	0.09	-0.15*	0.13	0.04	1.29	0.02	0.12	0.37	-1.43**	-1.50 *
Pusa M 23-31	0.12	0.98	0.33	-0.01	0.01	-0.11	-0.04	-0.87	-0.30	-0.41**	0.12	0.98	0.33
IPM 1707-1	0.87	2.23**	0.66	-0.11*	-0.03	-0.02	-0.37	-2.54**	-0.22	-0.49**	0.87	2.23**	0.66
TRM 230	1.37**	-3.43**	-2.16**	0.53**	0.23**	-0.02	0.20	-0.70	0.19	0.34**	1.37**	-3.43**	-2.16**
MML 2552	-0.20	-2.01**	-2.25**	-0.21**	-0.06	0.30	0.04	3.62**	0.19	0.33**	-0.20	-2.01**	-2.25**
HUM 16	-2.54**	3.65**	4.91**	-0.29**	-0.001	-0.27	0.12	-0.79	0.11	0.09	-2.54**	3.65**	4.91**
SE (gi)	0.49	0.51	0.74	0.04	0.06	0.24	0.24	0.92	0.22	0.07	2.01	0.79	0.57
SE(gi- gi)	0.70	0.72	1.05	0.06	0.09	0.34	0.34	1.30	0.31	0.11	2.85	1.12	0.80
Tester													
VGG 20153	-0.87*	-1.98**	3.83**	-0.13**	-0.09	0.19	-0.12	2.12**	0.38*	-0.01	-0.87 *	-1.98**	3.83**
MH 1142	0.34	0.29	-4.16**	0.01	0.018	0.02	-0.12	-1.43	-0.22	0.13 *	0.34	0.29	-4.16**
IPM 02-3	0.12	1.51**	1.83**	0.06	0.07	0.25	-0.06	1.18	0.00	0.06	0.12	1.51**	1.83**
IPM 12-1	0.40	0.18	-1.50*	0.05	-0.004	-0.47 *	0.31	-1.87*	-0.16	-0.18**	0.40	0.18	-1.50*
SE (gi)	0.40	0.41	0.60	0.03	0.05	0.19	0.19	0.75	0.17	0.06	1.64	0.65	0.46
SE(gi-gj)	0.57	0.59	0.85	0.05	0.07	0.27	0.28	1.06	0.25	0.09	2.33	0.92	0.66

Table 3. Estimates of specific combining ability (SCA) effects of crosses for 13 characters in Mung bean

Crosses	DFF	DM	PH	PBPP	SBPP	CPP	PPC	NPPP	NSPP	HSW	BYPP	HI	SYPP
NDM-1 x VGG 20153	0.62	2.81 **	0.83	0.06	0.25	-0.02	0.29	0.54	-0.47	0.15	1.36	-1.34	-0.41
NDM-1 x MH1142	0.40	0.20	-1.83	-0.08	-0.16	-0.52	0.62	2.43	-0.19	-0.01	3.04	-1.54	0.23
NDM-1 x IPM02-3	-1.04	-2.34*	1.50	-0.02	-0.05	0.91	-0.76	-0.51	0.25	-0.09	-3.21	2.13	0.08
NDM-1 x IPM12-1	0.01	-0.68	-0.50	0.04	-0.03	-0.36	-0.15	-2.45	0.41	-0.05	-1.19	0.74	0.09
Pusa M23-31 x VGG 20153	-0.12	-1.93	2.00	-0.20*	0.08	0.22	0.04	0.04	-0.13	0.25	1.12	0.17	0.44
Pusa M23-31 x MH1142	0.31	-0.54	-2.33	-0.08	-0.12	0.05	0.04	1.93	-0.52	0.12	0.61	-0.85	-0.10
Pusa M23-31 x IPM02-3	-0.45	5.90**	2.00	0.20*	-0.02	0.16	-0.68	-4.34*	0.58	-0.12	-2.49	0.82	-0.62
Pusa M23-31 x IPM12-1	0.26	-3.43**	-1.66	0.08	0.06	-0.44	0.59	2.37	0.08	-0.25	0.76	-0.14	0.29
IPM 1707-1 x VGG 20153	0.45	1.81	-2.33	0.06	-0.19	-0.86	-0.29	-9.62**	0.44	0.16	-5.87	0.34	-1.95
IPM1707-1 x MH1142	-0.43	0.54	2.00	0.08	0.05	-0.02	-0.95	-6.73**	0.38	0.11	-2.70	0.49	-0.73
IPM 1707-1 x IPM02-3	-0.54	-1.01	1.33	-0.19*	0.09	1.08 *	0.65	12.31**	-0.83	-0.11	5.85	-1.31	1.49
IPM 1707-1 x IPM 12-1	0.51	-1.34	-1.00	0.04	0.04	-0.19	0.59	4.04 *	0.44	-0.16	2.73	0.47	1.20
TRM 230 x VGG 20153	-1.04	-0.18	4.50**	0.12	-0.16	0.13	0.12	2.54	-0.63	-0.04	-3.72	0.90	-0.83
TRM230 x MH1142	0.06	-1.12	1.83	0.27**	0.12	-0.36	0.45	2.09	0.30	-0.09	3.20	0.16	1.30

TRM 230 x IPM02-3	0.62	-3.01**	-7.16**	0.09	0.29*	-0.58	0.06	-0.84	-0.25	0.38*	1.93	-0.23	0.47
TRM 230 x IPM12-1	0.34	4.31**	0.83	-0.49**	-0.25	0.80	-0.65	-3.79*	0.58	-0.24	-1.41	-0.83	-0.93
MML 2552 x VGG 20153	0.87	0.73	-2.75	-0.13	0.06	0.47	-1.04*	0.54	0.69	-0.56**	-1.15	0.32	-0.14
MML2552 x MH 1142	-0.34	0.45	-2.41	-0.08	0.21	0.30	0.29	-0.90	-0.69	0.01	-6.54	0.02	-2.49 *
MML 2552 x IPM02-3	0.54	-2.09*	2.91	-0.02	-0.27*	-0.25	0.90	5.15**	0.41	0.05	10.75 *	-0.34	3.95**
MML 2552 x IPM12-1	-1.06	0.90	2.25	0.24**	0.00	-0.52	-0.15	-4.79*	-0.41	0.50 **	-3.05	0.01	-1.32
HUM 16 x VGG 20153	-0.79	-3.26**	-2.25	0.08	-0.03	0.05	0.87	5.95**	0.11	0.04	8.26 *	-0.40	2.90 *
HUM 16 x MH 1142	-0.01	0.45	2.75	-0.10	-0.11	0.55	-0.45	1.18	0.72	-0.14	2.38	1.71	1.79
HUM 16 x IPM02-3	0.87	2.56*	-0.58	-0.04	-0.03	-1.33**	-0.18	-11.76**	-0.16	-0.10	-12.82 **	-1.07	-5.38**
HUM 16 x IPM 12-1	-0.06	0.23	0.08	0.06	0.17	0.72	-0.23	4.62 *	-0.66	0.20	2.16	-0.24	0.67
SE (Sij – Skl)	1.40	1.44	2.10	0.13	0.18	0.68	0.69	2.61	0.62	0.22	5.70	2.25	1.61
SE (Sij – Sik)	1.86	1.91	2.78	0.17	0.25	0.90	0.91	3.45	0.82	0.29	7.55	2.98	2.13

Table 4. Top ranking crosses for seed yield per plant in Mung bean

Crosses	Heterosis			SCA effects	Perse performance of Crosses	GCA effects		GCA status of parents
	MP	HB	SH (MH 1142)			Line	Tester	
MML 2552 x IPM 02-3	104.05 **	71.04 **	149.49 **	3.95**	27.54	-2.25**	1.83**	L x H
HUM 16 x VGG 20153	90.59 **	71.84 **	123.16 **	2.90*	24.63	4.91**	3.83**	H x H
HUM 16 x MH 1142	66.27 **	47.15 **	91.09 **	1.79	21.09	4.91**	-4.16**	H x L
IPM 1707-1 x IPM 02-3	53.16 **	41.45 **	64.76 **	1.49	18.19	0.66	1.83**	M x H
TRM 230 x MH 1142	61.83 **	37.57 **	96.47 **	1.30	21.69	-2.16**	-4.16**	L x L

* **Significance at 5% and 1% levels of probability respectively, H= High, M=Medium & L= Low

Table 5: List of lines, testers and check used in the present study with their salient features

Genotype	Pedigree	Source of materials	Salient features
Lines			
NDM-1	G65 x UMP 79-34	ANDUA&T (1994)	Dana Dhumil and Disease resistance (yellow mosaic), high yielding
Pusa M 23-31	TM 97-25 x PM 5	IARI New Delhi	High yield, multiple disease resistance
IPM 1707-1	IPM 99-125 x VBG 04-008	IIPR Kanpur	Resistance to MYMV
TRM 230	TMB 24 x Samarat	IGKV, Raipur	High yielding, long pod, Resistant YMD, CLS
MML2552	Mutant of SML 668(50KR)	PAU, Ludhiana	High yielding, Resistance to MYMV
HUM16 (Malaviya Jankalyani)	Pusa bold 1 x HUM 8	BHU (2006)	Big Bright grain, resistance to mung bean yellow mosaic virus (MYMV)
Testers			
VGG 20153	VBN(Gg) 2 x Mash 114	NPRC, Vamban	Resistance to MYMV
MH 1142	Pedigree method	HAU, Hisar (2020)	Non shattering, medium resistance to MYMV, PM & Root rot resistant
IPM 02-3	IPM99-125 X Pusa Bold 2 Pedigree Method	IIPR, Kanpur (2003)	Long Bright grain, Heat resistance with highly resistance to YMD
IPM 12-1	Pedigree Method	IIPR, Kanpur	Resistance to MYMV
Check			
NDM 1	G65 x UMP 79-34	ANDUA&T (1994)	Dana Dhumil & Disease resistance (YMD)
MH 1142	Pedigree Method	HAU, Hisar (2020)	Non-shattering, medium resistance to MYMV, PM & Root rot resistant
IPM512-1 (Soorya)	IPM 99-125 x Co 5 Pedigree Method	IIPR, Kanpur (2020)	Green, shining, medium large size seed, Highly resistant to YMD, CLS and anthracnose

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