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Research Note

Evaluation of pigeonpea [*Cajanus cajan* (L.) Millsp.] hybrids for heterosis, combining ability, wilt and sterility mosaic diseases

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Abstract
An experiment was carried out using three cytoplasmic-genetic male sterile (CGMS) lines as females and four diversified testers as males in a line × tester design. The analysis of variance for combining ability showed that the mean squares due to general and specific combining ability effects indicated involvement of both additive and non additive gene action. The mean sum of squares due to lines × testers and their interactions were highly significant for seed yield and it's component characters further indicated the importance of *sca* variance, and consequently the non-additive genetic variation in the inheritance of these characters are more likely to be improved through heterosis breeding. The *gca* effects of parents revealed that female lineTS-3RA was good general combiners with JKM-197 and ASHA for seed yield and it's direct components. Crosses exhibiting high specific combing ability effects along with their *per se* performance, standard heterosis and gca status of the parents indicated that the cross combinations MARUTI-A x ASHA, WRP-1A x GC-11-39 and TS-3RA x JKM-197 were good specific combiners for seed yield. These parental combinations are being used for exploitation of hybrid vigour.Two hybrids TS-3RA x GRG-2009 and WRP-1A x GRG-2009 were moderately resistant for both the diseases with per cent disease incidence value of 3.57 and 25.00 for *Fusarium* wilt and 16.00 and 15.79 for sterility mosaic disease (SMD) respectively.

Keywords
Pigeonpea, combining ability and heterosis, wilt, SMD

Pigeonpea (*Cajanus cajan* (L.)Millsp.), is an often cross pollinated crop (20 – 70%) with diploid (2n = 2x) chromosome number of 22 and genome size of 1C = 858 Mbp, is a member of the tribe *Phaseoleae*. This tribe is located in the millettioid (tropical) clade within the subfamily *Papilionoideae*, which includes many important legume crop species such as soybean (*Glycine max*), cowpea (*Vigna ungiculata*), common bean (*Phaseolus vulgaris*) and mung bean (*Vigna radiata*).

It is being cultivated as an annual crop in Southern and South Eastern Asia, Eastern Africa, the Caribbean region and South and Central America. It is chiefly grown for its seeds which are consumed either as dry split peas (dhal), providing major source of protein and essential amino acids or as a green vegetable. It's stem is a good source of fuel wood. It is cultivated mainly during *kharif* and suited for dry farming conditions since its roots can tap water reserve in the subsoil zone.

In India, it is one of the very important grain legume and occupies second position in area and production next to chickpea. It is grown in an area of 3.88 m ha with an annual production of 3.17 m tonnes. In Karnataka, pigeonpea occupies second place in area (6.60 Lakh ha) and ranks second in production (3.66 lakh tonnes) with a productivity of 555 kg/ha. (AICRP annual report, 2012-13).

Most of the economic characters like seed yield, number of pods per plant, days to 50 per cent flowering are mostly governed by polygenes and their inheritance is of complex nature. Therefore, before making attempts for improvement of these characters it is essential to know the nature of gene action controlling these quantitative characters. This information will be helpful to breeders in devising appropriate methods of breeding for crop improvement. A review of literature on quantitative genetics of pigeonpea (Saxena and Sharma, 1990) showed that the presence of significant levels of non additive genetic variation for seed yield which could be profitably exploited through heterosis breeding to increase grain yield.

Exploitation of heterosis depends much on general and specific combining ability effects. Combining ability studies are useful in evaluation of the parental lines and their cross combinations, usually this information aids in selection of parents in terms of performance of hybrids and elucidate the nature and magnitude of various types of gene action involved in the expression of quantitative traits. Therefore, present study was undertaken to estimate hybrid vigor, combining ability for seed yield and other traits in pigeonpea using three cytoplasmic genic male sterile lines derived from A_2 cytoplasm and four diverse testers crossed in line x tester design in pigeonpea.

The parental material comprised with three CGMS lines (TS-3RA, WRP-1A and MARUTI-A) used as a females were crossed with four genotypes *viz.* GC-11-39, GRG-2009, ASHA and JKM-197 used as a males in line x tester mating design during *Kharif* 2012-13 and sufficient numbers of hand pollinated seeds were produced and the evaluation experiment was conducted at Pulse Research Institute ARS, Kalaburagi during 2013-14. A total of 12 experimental hybrids, three females and four males along with one check (Maruti) were grown in an RBD design with two replications. Each genotype was sown in two rows of 4.0 meter length with the spacing of 90 x 30 cm between rows and plants respectively.

Observations on five randomly selected competitive plants were recorded for days to 50% flowering, days to maturity, plant height(cm), number of primary & secondary branches/plant, pod bearing length (cm), number of pods/plant, No. of seeds /pods, 100 seed weight (g), seed yield/plant (g) and seed yield/ (kg/ha). The data was subjected to analysis of variance and combining ability using statistic package WINDOSTAT 8.5 developed by Indostat services Hyderabad (India).

Experimental layout for screening *Fusarium* wilt was laid out on national wilt sick plot maintained at Agricultural Research Station, Gulbarga during *kharif* 2013-14 along with wilt susceptible (ICP-2376) and resistant check (MARUTI) varieties. A row length of 4 meters each was maintained with spacing of 75 cm and 30 cm between the rows and plants respectively. The observations on per cent wilt was recorded at flowering (90 days after sowing) and at physiological maturity (150 days after sowing) stage by counting number of dead plants (due to *Fusarium* wilt) among the total number of plants present per genotype and per cent disease was estimated.

Experimental layout for screening sterility mosaic disease (SMD) was laid out at Agricultural Research Station, Bidar. Sterility Mosaic disease pressure was created by maintaining four rows of susceptible check (ICP-8863) all around the plot *i.e* "Infector hedge row technique". Relatively high rainfall coupled with high relative humidity at Bidar favours sterility mosaic disease. Hence, Bidar is considered as hot spot for screening SMD. All the test entries were sown in single rows and susceptible check was sown after every 10th row. Screening of SMD was done during *Kharif* 2013-14, by following "Leaf Stapling Technique" (Nene and Reddy, 1977). SMD infected leaves of test plants at 2-3 leaf stage. As the stapled leaflets from the infected plants get dried, mites from the infected leaves migrate to healthy leaf and inoculates the virus. In all the seasons, plants were scored for incidence of SMD at 15 days interval up to 75 days by counting the healthy plants (no mosaic symptoms) and diseased plants (with mosaic symptoms). Categorization of genotypes for SMD reaction was carried out following the standard scale (Singh *et al.*, 2003) and same is given below.

Per cent disease incidence	**Reaction scale**
0-10 % plants infected	Resistant
10.1 – 30 % plants infected	Moderately resistant
30.1 – 100 % plants infected	Susceptible

Per cent disease incidence (PDI) was estimated using formulae.

$$\text{Per cent disease incidence} = \frac{\text{Number of plants infected in a row}}{\text{Total number of plants in a row}} \times 100$$

The ANOVA for the mean sum of squares for parents showed significant differences for almost all characters studied except primary branches, secondary branches and number of seeds per pods indicating the presence of sufficient variability among parents. The interaction between females x males was significant for days to 50% flowering, days to maturity, number of pods per plant, 100 seed weight, seed yield per plant and seed yield per hectare. The hybrids showed highly significant differences for all the quantitative traits except number of seeds per pods. Parents Vs hybrids also showed significant difference for all the characters except days to maturity, primary branches and pod bearing length (Table 1).

The analysis of variances for combining ability indicated that, mean sum of squares due to females x males interaction were significant for all the traits except days to 50% flowering, primary branches and number of seeds per pods. Thereby it is suggested that the variation of hybrids in respect of seed yield may be strongly influenced by the lines. The mean squares due to lines were larger in magnitude for most of the important yield attributes than those for testers indicating greater diversity amongst the lines as compared to testers (Table-2).

Analysis of variance revealed that the ratio of variance due to *GCA* to *SCA* was less than unity for all the characters except days to 50 % flowering and primary branches (Table-3) indicating that these traits may be under the influence of non additive gene action and these characters are more likely to be improved through heterosis breeding. The above findings are in agreement with the earlier reports of Sunil Kumar *et al.* (2003), Sekhar *et al.* (2004), Sameer Kumar *et al.* (2009), Beekham and Umaharan (2010), Shobha and Balan (2010), Sony Tiwari (2010), Meshram *et al. (*2013*)*, Chethana *et al.* (2013*)* and Yamanura *et al.* (2014).

The analysis of variance for combining ability showed that the mean squares due to general and specific combining ability effects indicated involvement of both additive and non additive gene action. The mean sum of squares due to lines × testers and their interactions were highly significant for seed yield and it's component characters further indicated the importance of *sca* variance, and consequently the non-additive genetic variation in the inheritance of these characters. The trend recorded was in agreement with the findings of Korgade *et al.* (2000), Sunil Kumar *et al.* (2003) and Sekhar *et al.* (2004). Vaghela *et al. (*2009), Sameer Kumar *et al.* (2009), Bharate *et al.* (2011) for seed yield/plant and other important yield attributes *viz.*, pod bearing length, number of pods per plant and 100 seed weight. Preponderance of non-additive genetic variance has been suggested.

The nature and magnitude of combining ability effects help in identifying superior parents and their utilization in breeding programme. Character-wise estimation of *gca* effects of lines and testers is presented in Table- 4. The *gca* effects of parents revealed that female parent TS-3RA was good general combiner with JKM-197 and ASHA for seed yield and it's direct components. The lines TS-3RA and MARUTI-A and testers JKM-197 and GC-11-39 were good general combiners for days to 50 % flowering and days to maturity, lines WRP-1A and TS-3RA and testers ASHA and JKM-197 for plant height, line TS-3RA and tester ASHA for number of branches/plant, line WRP-1A and testers ASHA for pod bearing length and number of pods/plant, lines TS-3RA and WRP-1A and testers GC-11-39 and ASHA for 100 seed weight (Table 4).

The top three crosses exhibiting high specific combing ability effects along with their *per se* performance, standard heterosis and gca status of the parents indicated that the cross combinations MARUTI-A x ASHA, WRP-1A x GC-11-39and TS-3RA x JKM-197 were good specific combiners for seed yield. These parental combinations are being used for exploitation of hybrid vigour. The cross combinations WRP-1A x GC-11-39, WRP-1A x JKM-197and MARUTI-A x JKM-197 were good specific combiners for days to maturity as they were showing highly significant negative *sca* effect this is very much suitable in rainfed condition because it has advantage of escaping terminal moisture stress. The crosses MARUTI-A x GC-11-39, WRP-1A x JKM-197and WRP-1A x ASHA for plant height, MARUTI-A x GC-11-39 for number of primary branches, TS-3RA x JKM-197 for number of secondary branches, MARUTI-A x GC-11-39 for pod bearing length, MARUTI-A x GC-11-39, WRP-1A x ASHA and TS-3RA x JKM-197 for number of pods per plant, MARUTI-A x GC-11-39 for 100 seed weight were found to be useful. The estimates of *sca* effects revealed that 04 experimental hybrids had significant, desirable and positive *sca* effects for seed yield/plant. Among these, three best crosses were selected on the basis of *per se* performance for ascertaining their association with *sca* effects of seed yield per plant and its attributes (Table 5).

Out of three crosses showing high mean and significant positive *sca* effects for seed yield along with their *per se* performance as well as *gca* effects of parents and their significant response to other characters are presented in Table 6. Out of three crosses showing high mean and significant positive *sca* effects for grain yield, crosses TS-3RA x ASHA, WRP-1A x ASHA and TS-3RA x GC-11-39 involved high × high, high × low and low × low *gca* effects of parents respectively. These results were also in conformity with those of Baskaran and Muthiah (2007), Meshram *et al. (*2013*)*, Chethana *et al.* (2013*)* and Yamanura *et al.* (2014). Better performance of hybrids involving high x low or low x low general combiners indicated dominance x dominance (epitasis) type of gene action. The crosses showing high *sca* effects involving one good general combiner indicated additive x dominance type gene interaction which exhibit the high heterotic performance for yield and yield related traits.

Two hybrids s TS-3RA x GRG-2009 and WRP-1A x GRG-2009 were found to be moderately resistant for both the diseases with per cent disease incidence value of 3.57 and 25.00 for *Fusarium* wilt and 16.00 and 15.79 for SMD respectively (Table 7); these findings were in agreement with Sharma *et al.* (2013). The results suggested that the crosses having high mean performance, positive *sca* effects for seed yield and their significant response to other related traits had necessarily involved both or at least one parent as good combiner which could be commercially exploited for heterosis by taking advantage of high degree of natural out crossing in pigeon pea.

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Table 1. Mean sum of squares for parents and hybrids in respect of 11 characters in pigeonpea (*Cajanus cajan* (L.) Millsp.)

SV	DF	DFF	DM	PHT	PB	SB	PBL	NPPP	NSPP	100 SW	YLD/PT	YLD/HA
Replication	1	8.53**	25.29	105.81	5.33	0.08	0.412	46.64	0.47	0.01	0.08	56393.29
Parents	6	614.48**	725.45**	2906.51**	2.58	3.77	370.11**	4765.47**	0.26	1.39**	309.2**	897833.3**
Lines	2	88.66**	240.04*	113.48	0.13	29.40*	15.62	784.01**	.311**	1.95**	180.16*	57129.74
Testers	3	153.94**	499.7**	503.97*	4.99*	8.36	729.20**	4829.62**	0.017	0.19	228.54*	1187169.00**
Lines v/s Testers	1	720.84**	1591.00**	15.15	0.26	0.53	1.81	12535.95**	0.21	3.88**	809.38**	1711234.00**
Crosses	11	64.35**	205.13**	244.98**	18.62**	11.47**	213.48**	1853.95**	0.07	2.17**	1083.15**	523802.5**
Parents v/s Hybrids	1	287.52**	2.83	405.38**	0.01	14.49**	44.19	20957.00**	0.84*	76.48**	252.47*	1897992.00**
Error	18	5.86	11.46	38.71	1.58	1.73	30.77	110.01	0.11	0.22	41.77	41089.60

Table 2. ANOVA for combining ability in respect of 11 characters in pigeonpea (*Cajanus cajan* (L.) Millsp.)

SV	DF	DFF	DM	PHT	PB	SB	PBL	NPPP	NSPP	100 SW	YLD/PT	YLD/HA
Females	2	88.66**	240.04*	113.48	33.75**	29.40*	271.41	45.74	0.311**	6.96**	303.16	912450.60
Males	3	153.94**	499.70**	503.97*	38.17**	8.36	331.98	3846.76	0.02	1.69	905.57	390198.60
Females x Males	6	11.44	46.20**	159.33**	3.80	7.05**	135.18**	1460.27**	0.02	0.82**	1431.94**	461055.00**
Error	11	8.17	9.82	29.93	1.87	1.25	25.25	42.83	0.13	0.19	41.06	55857.18

*, ** – Significant at 5% and 1% levels, respectively

DF = Degree of freedom, DFF = Days to 50% flowering, DM = Days to maturity, PHT = Plant height (cm), PB = No. of Primary branches, SB = No. of Secondary branches, PBL = Pod bearing length (cm), NPPP = No. of pods/ plant, SW = 100-Seed weight (g), SYPP = Seed yield/ plant, SYPH= Seed yield/ha (kg)

Table 3. Variance due to GCA, SCA and their proportion for 11 different characters

Sl. No.	Characters	Variance due to GCA	Variance due to SCA	GCA : SCA proportion
1.	Days to 50 per cent flowering	3.42	1.64	1:0.48
2.	Days to maturity	10.28	18.18	1:1.77
3.	Plant height (cm)	5.54	64.70	1:11.68
4.	Primary branches	0.95	0.96	1:1.01
5.	Secondary branches	0.28	2.90	1:10.36
6.	Pod bearing length (cm)	5.06	54.96	1:10.86
7.	No. of pods/plant	25.47	708.72	1:27.83
8.	No. of seeds /pods	0.0034	0.05	1:15.44
9.	100 seed weight (g)	0.09	0.32	1:3.62
10.	Seed yield/ plant (g)	22.56	695.43	1:30.83
11.	Seed yield/ (kg/ha)	4060.12	202598.91	1:49.90

Table 4. General combining ability effects for parents in respect of 11 characters in pigeonpea (*Cajanus cajan* (L.) Millsp.)

SI. NO.	ENTRIES	DFF	DM	PHT	PB	SB	PBL	NPPP	NSPP	100 SW	YLD/PT	YLD/HA
	LINES											
1	TS-3RA	-2.83 *	-6.08 **	0.89	2.10 **	1.78 **	-6.19 **	-1.88	3.4	0.89 **	-2.62	307.87 **
2	WRP-1A	3.67 **	4.54 **	3.24	-0.1	0.25	5.37 *	2.69	3.1	0.07	7.03 *	53.36
3	MARUTI-A	-0.83	1.54	-4.13	-2.00 **	-2.03 **	0.83	-0.81	3.6	-0.97 **	-4.41	-361.22 **
	TESTERS											
1	GC-11-39	-2.58 *	-7.21 **	-9.42 **	-0.4	-1.02 *	-4.37	-22.25 **	3	0.47 *	0.86	21.41
2	GRG-2009	0.75	-1.88	-5.10 *	-1.30 *	-0.74	-7.29 **	-9.42 **	3.8	-0.52 *	-14.64 **	-349.88 **
3	ASHA	6.75 **	13.29 **	11.24 **	3.66 **	1.61 **	9.41 **	36.31 **	4	0.45 *	-1.55	259.83 *
4	JKM-197	-4.92 **	-4.21 **	3.29	-1.96 **	0.15	2.24	-4.64	3.65	-0.40 *	15.34 **	68.63
	CV	2.38	2.25	3.37	11.50	17.99	13.75	8.03	8.88	4.06	13.50	11.86
	CD @ 5%	5.08	7.10	13.06	2.64	2.76	11.65	22.02	0.69	0.97	13.57	425.68
	CD @ 1%	6.97	9.74	17.91	3.62	3.78	15.97	30.20	0.94	1.34	18.61	583.79

*, ** – Significant at 5% and 1% levels, respectively
DFF = Days to 50 % flowering, DM = Days to maturity, PHT = Plant height (cm), PB = No. of Primary branches, SB = No. of Secondary branches,
PBL = Pod bearing length (cm), NPPP = No. of pods/ plant, SW = 100-Seed weight (g), SYPP = Seed yield/ plant, SYPH = Seed yield/ha (kg)

Table 5. Comparison of top three best crosses on the basis of specific combining ability effects for different characters

Characters	Crosses	SCA effects	GCA effects of Parents and Status			Standard heterosis	*per se*	Significant SCA effects for other traits
			P1	P2	Status			
DFF	WRP-1A x JKM-197	-2.33	3.67	-4.92	H X L	-14.67	96.00	-
	TS-3RA x GRG-2009	-2.00	-2.83	0.75	L X H	-15.11	96.00	NPPP, YPP
	WRP-1A x ASHA	-1.00	3.67	6.75	H X H	-3.11	109.00	NPPP
DM	WRP-1A x GC-11-39	-5.92	4.54	-7.21	H X L	-9.23	148.00	YPP, KGPH
	WRP-1A x JKM-197	-4.04	4.54	-4.21	H X L	-9.54	147.00	-
	MARUTI-A x JKM-197	-2.54	1.54	-4.21	L X L	-10.46	146.00	-
PHT	MARUTI-A x GC-11-39	10.85	-4.13	-9.42	L X L	8.63	184.67	PBL, NPPP, 100SW
	WRP-1A x JKM-197	6.23	3.24	3.29	L X L	17.72	200.13	-
	WRP-1A x ASHA	6.18	-4.13	11.24	L X H	18.04	200.66	SB,YPP, KGPH,
PB	MARUTI-A x GC-11-39	1.45	-2.00	-0.4	L X L	-9.09	10.00	NPPP
SB	TS-3RA x JKM-197	2.09	1.78	0.15	H X L	72.64	11.80	DM, NPPP, YPP
PBL	MARUTI-A x GC-11-39	10.03	0.83	-4.37	L X L	27.96	47.67	PHT, NPPP, 100SW
NPPP	MARUTI-A x GC-11-39	32.59	-0.81	-22.25	L X L	-17.73	122.17	PHT, PBL, 100SW
	WRP-1A x ASHA	17.69	2.69	36.31	L X H	14.02	169.33	-
	TS-3RA x JKM-197	17.56	-1.88	-4.64	L X L	-16.72	123.67	DM, SB, YPP
100SW	MARUTI-A x GC-11-39	0.73	-0.97	0.47	L X H	32.61	12.77	PHT, NPPP, PBL
YLD/PLANT	MARUTI-A x ASHA	34.17	-4.41	-1.55	L X L	89.60	74.10	SB, KGPH
	WRP-1A x GC-11-39	28.63	7.03	0.86	H X L	110.89	82.42	KGPH
	TS-3RA x JKM-197	20.47	-2.62	15.34	L X H	102.34	79.08	DM, SB, NPPP
YLD/HA	WRP-1A x GC-11-39	545.25	53.36	21.41	H X L	-4.27	2499.98	YPP
	MARUTI-A x ASHA	425.58	-361.22	259.83	L X H	34.03	2204.15	SB, YPP

DFF= Days to 50 % flowering, DM= Days to maturity, PHT= Plant height (cm), PB = No. of Primary branches, SB= No. of Secondary branches, PBL = Pod bearing length (cm), NPPP= No. of pods/ plant, SW = 100-Seed weight (g), SYPP= Seed yield/ plant, SYPH= Seed yield/ha (kg), H= High, L= Low

Table 6. Top three crosses based on *per se* for ten yield and yield attributing characters in pigeonpea

Sl. No.	Characters	Crosses	*Per se* performance	*sca* effects	*gca* status of parents	Per cent heterosis over commercial parent	WILT(PDI)	SMD(PDI)
1.	Days to 50% flowering	MARUTI-A x M-197	93.00	-0.83	L x H	-17.33	S(33.50)	S(41.18)
		TS-3RA x GC-11-39	94.00	-0.67	H x H	-16.89	R(5.00)	S(77.14)
		TS-3RA x JKM-197	95.00	3.17	H x H	-15.56	M(17.86)	S(70.00)
2.	Days to maturity	TS-3RA x GC-11-39	138.00	0.58	H x H	-15.08	R(5.00)	S(77.14)
		TS-3RA x GRG-2009	142.00	-1.25	H x L	-12.92	R(3.57)	M(16.00)
		MARUTI-A x GC-11-39	145.00	-0.04	L x H	-10.77	M(18.00)	S(33.33)
3.	Plant height 9cm)	MARUTI-A x ASHA	200.66	6.18	L x H	18.04	S(31.25)	M(28.00)
		WRP-1A x JKM-197	200.13	6.23	L x L	17.72	M(23.81)	S(35.00)
		TS-3RA x ASHA	199.18	-0.32	L x H	17.16	M(13.33)	S(46.67)
4.	No. of Primary branches	TS-3RA x ASHA	15.91	-0.81	H x H	44.68	M(13.33)	S(46.67)
		WRP-1A x ASHA	15.45	0.92	L x H	40.45	M(27.59)	S(50.00)
		TS-3RA x GC-11-39	13.50	0.84	H x L	22.73	R(5.00)	S(77.14)
5.	No. of Secondary branches	TS-3RA x JKM-197	11.80	2.09	H x L	72.64	M(17.86)	S(70.00)
		TS-3RA x ASHA	9.47	1.69	H x H	38.62	M(13.33)	S(46.67)
		WRP-1A x ASHA	9.36	0.28	L x H	36.87	M(27.59)	S(50.00)
6.	Pod bearing length (cm)	WRP-1A x ASHA	56.50	0.55	H x H	28.19	M(27.59)	S(50.00)
		MARUTI-A x ASHA	56.50	5.09	L x H	38.26	S(31.25)	M(28.00)
		WRP-1A x JKM-197	50.83	2.04	H x L	36.44	M(23.81)	S(35.00)
7.	Number of pods per plant	WRP-1A x ASHA	169.33	17.69	L x H	14.02	M(27.59)	S(50.00)
		MARUTI-A x ASHA	155.00	6.86	L x H	4.37	S(31.25)	M(28.00)
8.	100 seed weight (g)	TS-3RA x ASHA	13.99	0.11	H x H	37.75	M(13.33)	S(46.67)
		TS-3RA x GRG-2009	13.47	0.55	H x L	39.82	R(3.57)	M(16.00)
		TS-3RA x GC-11-39	13.27	0.63	H x H	45.33	R(5.00)	S(77.14)
9.	Seed yield per plant (g)	WRP-1A x GC-11-39	82.42	28.63	H x L	110.89	S(34.09)	S(77.78)
		TS-3RA x JKM-197	79.08	20.47	L x H	102.34	M(17.86)	S(70.00)
		MARUTI-A x ASHA	74.10	34.17	L x L	89.60	S(31.25)	M(28.00)
10.	Seed yield (kg/ha)	TS-3RA x ASHA	2687.48	239.81	H x H	93.97	M(13.33)	S(46.67)
		WRP-1A x ASHA	2548.59	292.13	H x L	83.45	M(27.59)	S(50.00)
		TS-3RA x GC-11-39	2499.98	545.25	L x L	49.66	R(5.00)	S(77.14)

Table 7. List of hybrids and parents for *Fusarium* wilt and SMD screening during *Kharif* 2013-14

SI. NO.	CROSS NAME	*FUSARIUM* WILT		STERILITY MOSOIC DISEASE	
		PDI	REACTION	PDI	REACTION
1.	TS-3RA x GC-11-39	5.00	R	77.14	S
2.	TS-3RA x GRG-2009	3.57	R	16.00	MR
3.	TS-3RA x ASHA	13.33	MR	46.67	S
4.	TS-3RA x JKM-197	17.86	MR	70.00	S
5.	WRP-1A x GC-11-39	34.09	S	77.78	S
6.	WRP-1A x GRG-2009	25.00	MR	15.79	MR
7.	WRP-1A x ASHA	27.59	MR	50.00	S
8.	WRP-1A x JKM-197	23.81	MR	35.00	S
9.	MARUTI-A x GC-11-39	18.00	MR	33.33	S
10.	MARUTI-A x GRG-2009	33.25	S	66.67	S
11.	MARUTI-A x ASHA	31.25	S	28.00	MR
12.	MARUTI-A x JKM-197	33.50	S	41.18	S
13.	TS-3RA	16.67	MR	78.57	S
14.	WRP-1A	21.95	MR	35.71	S
15.	MARUTI-A	33.33	S	43.75	S
16.	GC-11-39	52.90	S	68.00	S
17.	GRG-2009	10.00	R	26.70	MR
18.	ASHA	7.20	R	29.90	MR
19.	JKM-197	9.30	R	33.50	S
20.	MARUTI (WRC and SSC)	6.51	R	100	S
21.	ICP-2376(WSC)	92.5	S	78.5	S

WSC: Wilt susceptible check	R: Resistant
WRC: Wilt resistant check	M: Moderately resistant
SSC: SMD susceptible check	S : Susceptible