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Heterosis studies for grain mould resistance parameters in Sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract
The present investigation entitled "Grain mould resistance studies in sorghum (*Sorghum bicolor* (L.) Moench)" was carried out to estimate the amount of heterosis and heterobeltiosis, for selection of potential crosses and to ascertain the nature of gene action operating in inheritance of some important quantitative characters associated with grain mould resistance. In the present study, a set of 10 x 10 diallel consisting of F_1 & F_2 progenies, along with their parents were evaluated to study the inheritance of some mould resistance traits and to identify useful crosses. The highest estimates of heterobeltiosis were upto-80.00 per cent for field grade score, -67.74 per cent for threshed grade score, 41.84 per cent for grain hardness, 11.88 per cent for grain density, 36.10 per cent for germination, -77.95 per cent for glume coverage, -44.94 per cent for water absorption capacity, -81.01 for fungal load of *Fusarium* spp., -85.39 for *Curvularia* spp. and -85.31 for fungal load of other spp.

Keywords: grain mould, heterosis, sorghum, threshed grade score

Introduction
Sorghum (*Sorghum bicolor* (L.) Moench) is an important cereal crop in India. It is one of the main staple food for the world's poorest and most food insecure people across the semi arid tropics (DSR Vision 2030) [4]. In India the major sorghum growing state is Maharashtra which contributes 49.14 per cent of area and 42.07 per cent production and other sorghum growing states are Karnataka, Tamil Nadu, Andhra Pradesh, Rajasthan and Madhya Pradesh. In Maharashtra, sorghum is grown in the districts *viz*., Solapur, Beed, Parbhani, Osmanabad and Latur with an area of 28.58 lakh hectares, production of 25.07 lakh tonnes and productivity of 1971 kg/ha. Sorghum belongs to natural order Poaceae, tribe Andropogenae, Sorghum bicolor includes the annual sorghum with ten pairs of chromosomes (2n=20). Grain mould is an important biotic constraint of sorghum and seriously compromises the grain yield and quality grains obtainable from improved cultivars. Grain mould occurs throughout the humid tropical and subtropical climates particularly when improved, short- and medium-duration cultivars that mature before the end of the rains are grown (Bandyopadhyay *et al*.1988) [3]. Heterosis or hybrid vigour is the increased or decreased vigour growth, fitness or yield of a hybrid over the parental values, resulting from the crossing of genetically unlike organisms. Heterosis has positive association with specific combining ability (sca) variance.

Material and Methods
The present field study was undertaken at Sorghum research station, Vasantrao Naik Marathwada Agricultural University, Parbhani (Maharashtra) during *rabi* season 2015-16 The experimental material comprised of 10 divergent parents and their 45 F_1 hybrids in half-diallel fashion. The Randomized block design was used with three replication and the plant spacing within a row was 15 cm and row to row spacing was 45 cm. Recommended package of practices were followed to raise the good crop. The data were recorded on five competitive fertile plants for field grade score, threshed grade score, grain hardness, grain density, germination percentage, glume coverage percentage, water absorption capacity, fungal load *of Fusarium* spp., Fungal load of *Curvularia* spp. and fungal load of other mould spp. Fonesca and Patterson (1968) described the methods of analysis for heterosis.

Results and Discussion

The mean square for ten characters of F_1 crosses under study are presented in Table 1. It is seen from Table 1 that, mean squares due to replication were non-significant for all the characters germination percentage, water absorption capacity and fungal load of *fusarium spp*. Treatment differences were highly significant for all the traits studied. Further partitioning of treatment variance into components *viz*., parents, hybrids and parents vs hybrids revealed that parents significantly differed among themselves for all the characters. Similarly, hybrids also showed highly significant differences for all the traits. Whereas, the parents vs hybrids comparison was significant for all the characters except germination percentage. It may, thus be concluded that the parents included in this investigation possessed sufficient variability for the characters studied.

Heterosis is a genetic expression of the beneficial effects of hybridization. Heterosis in common use, represents per cent increase or decrease in mean value of hybrid over mid (H_1) or better parental value (Heterobeltiosis, H_2) or Standard heterosis (H_3). Heterosis has been of great interest to plant and animal breeders, so also to the geneticist since long time. (Table 2.)

For field grade score, heterosis in desired direction (negatively significant) was exhibited by 16 crosses and heterobeltiosis by 33 crosses Out of 45 hybrids, 44 hybrids exhibited significant negative heterosis (desirable) for field grade score over the standard check PVK 801. Only one cross exhibited negative non-significant standard heterosis i.e. MS 296B x PVK 801 (-16%). For threshed grade score, heterosis in desired direction (negatively significant) was exhibited by 19 crosses, however, negative non-significant heterosis was registered by 9 crosses and 34 crosses recorded heterobeltiosis in desired (negative and significant) direction. Standard heterosis for threshed grade score ranged from -54.55 per cent to 136.36 per cent over the standard check PVK 801. Out of 45 hybrids, three hybrids exhibited significant negative standard heterosis (desirable) for threshed grade score over the check. Similar findings have also been reported by Nimbalkar (2001) [7].

For grain hardness, desirable and significant heterosis were exhibited by 19 crosses and their range varies from 1.30 to 54.87 per cent over mid parent. Desirable heterobeltiosis exhibited by ten crosses in this character. Standard heterosis ranged from -37.04 to 50.79 per cent. Patil (1982) [9] and Ghorade (1995) [5] reported positive heterosis for grain hardness, indicating in general the trend of more crushing strength. The significant desirable heterosis for grain density was exhibited by 12 crosses. Thus, positive trend was observed for this character. Significant desirable heterobeltiosis exhibited by four crosses. Standard heterosis ranged from -9.41 to 10.22 per cent for this character. Positive heterosis for grain density was also reported by Nagur and Murty (1970) [6], Patil (1982) [9] and Ghorade (1995) [5].

For germination percentage, the range of positive heterosis was from 2.59 to 48.37 per cent and 22 hybrids recorded significantly superior germination percentage, However, the range of positive heterobeltiosis was 0.65 from 36.10 per cent. Out of 45 hybrids, 35 hybrids exhibited significant positive standard heterosis (desirable) for germination percentage over the check. Patil (1982) [9], Ghorade (1995) [5] and Agarkar (2000) [1] reported positive heterosis indicating increase in germination percentage. The range of desirable heterosis for glume coverage was -3.71 to -75.25 per cent over mid parent and from -2.99 to -77.95 per cent over better parent. Heterosis per cent recorded negative trend over mid and better parent for this character. Out of 45 hybrids, only one hybrids exhibited significant negative standard heterosis (desirable) for glume coverage over the check *viz*. PMS 71B x PMS 42B. Very limited information is available in literature for this character. Ghorade (1995) [5] and Ashok kumar *et al*. (2008) [2] reported similar results for glume coverage percentage. Majority of the hybrids were showing significant and negative heterosis for water absorption capacity. Heterobeltiosis in desired direction (negative and significant) was exhibited by 38 crosses. Standard heterosis for water absorption capacity ranged from -42.01 per cent to 34.70 per cent over the standard checks PVK 801. Out of 45 hybrids, 23 hybrids exhibited significant negative standard heterosis (desirable) for water absorption capacity over the check. Negative heterosis for water absorption capacity was also reported by Bandyopadhyay *et al*. (1988) [3] and Ghorade (1995) [5].

For fungal load of *Fusarium* spp., desirable heterosis i.e. significantly negative heterosis was exhibited by 30 hybrids. The range of required (negative) heterosis was observed from -3.28 to -77.34 per cent. Desirable significant heterobeltiosis for this character ranged from -0.09 to -81.21 per cent. Thirty nine crosses exhibited negative and significant heterobeltiosis indicating negative trend for this character. Standard heterosis for fungal load due to *Fusarium* species ranged from -76.36 per cent to 65.10 per cent over the standard checks PVK 801. Out of 45 hybrids, 26 hybrids exhibited significant negative standard heterosis. Negative heterosis for fungal load of Fusarium spp. was also recorded by Narayana and Prasad (1983), Ghorade (1995) [5] and Agarkar (2000) [1]. For fungal load of *Curvularia* spp., seventeen hybrids recorded significant and negative heterosis and seven hybrids recorded significant positive heterosis. Heterobeltiosis ranged from -1.06 to -85.39 per cent and 24 hybrids recorded negative and significant heterobeltiosis for this character. Standard heterosis for fungal load of *Curvularia* spp.ranged from -75.62 per cent to 116.96 per cent over the standard check PVK 801. Out of 45 hybrids, eight hybrids exhibited significant negative standard heterosis. Heterosis for fungal load of *Curvularia* spp. was also recorded by Narayana and Prasad (1983), Ghorade (1995) [5] and Agarkar (2000) [1] and Reddy *et al*. (2011) [10].

For fungal load of other mould spp., 38 hybrids recorded significant negative heterosis which ranged from -21.75 to -84.29 per cent and negative trend was observed for this character. Heterobeltiosis ranged from -4.26 to -85.31 per cent and 37 hybrids recorded negative significant heterobeltiosis for this character. Out of 45 hybrids, 39 hybrids exhibited significant negative standard heterosis (desirable) for fungal load of other mould spp. over the check. Negative heterosis for fungal load of other spp. was also recorded by Narayana and Prasad (1983) Ghorade (1995) [5] and Agarkar (2000) [1] and Reddy *et al*. (2011) [10].

Germination is a result of number of component traits associated with grain mould resistance. It may therefore, be desirable to consider the extent of heterosis for different traits along with the germination percentage. Heterotic crosses showing substantial and significant heterobeltiosis for germination percentage along with their expression for other characters over mid and better parents are indicated in crosses MS 296B x PVK 801, MS 296B x I 26, I 26 x PVK 801, GNM 14-7 x I 26, AKGMR 110 x PVK 801, GNM 14-7 x MS 296B, B 58586 x MS 296B, I 26 x PMS 71B, AKGMR 110 x IS 14332. From the data of heterosis and heterobeltiosis for germination percentage, it is observed that hybrids with

high magnitude of heterosis or heterobeltiosis have not necessarily showed better *perse* performance or vice versa. Hence, selection of superior crosses should necessarily be based not only on magnitude of heterosis but also on actual performance of hybrids for germination percentage, so that appropriate selection can be made without errors.

Table 1: Analysis of Variance of parents and F_1 hybrids in 10 x 10 diallel of sorghum

Sr. No.	Characters	Source					
		Replication	Treatments	Parents	F_1 hybrids	Parents Vs. F_1 hybrids	Error
Degrees of freedom		2	54	9	44	1	108
1	Threshed grade score	1.71	11.83**	25.49**	9.06**	10.42*	0.96
2	Grain hardness (kg/cm^2)	0.21	4.93**	3.69**	5.24**	2.60**	0.19
3	Grain density (g/ml)	0.003	0.014**	0.02**	0.012**	0.002	0.0019
4	Germination percentage	98.53*	319.60**	447.68**	278.45**	977.53**	25.72
5	Glume coverage (%)	2.38	602.85**	823.70**	570.75**	27.90	18.37
6	Water absorption capacity (g)	0.003**	0.051**	0.031**	0.049**	0.28**	0.0006
7	Fungal load of *Fusarium* spp. (%)	5.44*	98.19**	86.50**	99.47**	147.30**	1.52
8	Fungal load of *Curvularia* spp. (%)	16.75	113.32**	70.97**	122.68**	82.27*	8.63
9	Fungal load of Other mold spp. (%)	0.80	64.15**	21.17**	61.56**	564.81**	3.26

* Significant at 5% level and ** Significant at 1% level

Table 2: Average Heterosis (H_1), Heterobeltiosis (H_2) and standard heterosis (H_3) for 10 X 10 diallel set.

Sr. No.	F_1 crosses	Field grade score			Threshed grade score			Grain hardness (kg/cm2)		
		H_1	H_2	H_3	H_1	H_2	H_3	H_1	H_2	H_3
1	GNM14-7XAKGMR110	-23.81	-38.46	-68.00 **	8.33	-18.75	18.18	2.61	-4	14.29 *
2	GNM-14-7X B 58586	-33.33	-53.85 *	-76.00 **	10	-31.25 *	0	9.62 *	3.64	20.63 **
3	GNM14-7 X MS 296B	-68.42 **	-76.00 **	-76.00 **	-42.86 **	-53.85 **	9.09	-16.40 **	-19.39 **	-16.40 **
4	GNM14-7 X I26	-55.56 **	-65.22 **	-68.00 **	-50.00 **	-58.33 **	-9.09	54.87 **	41.84 **	47.09 **
5	GNM14-7 X PMS74B	-37.50 *	-47.37 **	-60.00 **	-31.58 **	-40.91 **	18.18	-4.26	-5.91	1.06
6	GNM14-7 X PMS71B	-27.78	-43.48 **	-48.00 **	-23.81 *	-38.46 **	45.45 *	40.88 **	14.29 *	18.52 **
7	GNM14-7 X PMS42B	-54.84 **	-61.11 **	-72.00 **	-26.32 *	-36.36 **	27.27	20.80 **	18.72 **	27.51 **
8	GNM14-7 X PVK801	56.52 *	38.46	-28.00 *	55.56 **	31.25 *	90.91 **	29.35 **	27.04 **	31.75 **
9	GNM14-7 X IS14332	5.26	-23.08	-60.00 **	4.76	-31.25 *	0	31.18 **	19.83 **	50.26 **
10	AKGMR110X B58586	-7.69	-25	-76.00 **	33.33	0	-27.27	-11.46 **	-12.44 *	4.23
11	AKGMR110XMS296B	-21.21	-48.00 **	-48.00 **	5.88	-30.77 **	63.64 **	5.65	-4.44	13.76 *
12	AKGMR110 X I26	-29.03	-52.17 **	-56.00 **	-18.75	-45.83 **	18.18	14.43 **	-1.33	17.46 **
13	AKGMR110XPMS74B	11.11	-21.05	-40.00 **	20	-18.18	63.64 **	-11.68 **	-16.00 **	0
14	AKGMR110XPMS71B	-9.68	-39.13 **	-44.00 **	23.53	-19.23 *	90.91 **	-19.88 **	-38.22 **	-26.46 **
15	AKGMR110XPMS42B	-23.08	-44.44 **	-60.00 **	-33.33 *	-54.55 **	-9.09	-18.69 **	-22.67 **	-7.94
16	AKGMR110XPVK801	44.44	30	-48.00 **	68.42 **	45.45 *	45.45 *	-5.8	-13.33 **	3.17
17	AKGMR110XIS14332	42.86	25	-60.00 **	100.00 **	62.50 *	18.18	-9.09 *	-11.39 *	11.11
18	B58586XMS 296B	-66.67 **	-80.00 **	-80.00 **	-60.00 **	-76.92 **	-45.45 *	14.43 **	4.55	21.69 **
19	B58586 X I26	-57.14 **	-73.91 **	-76.00 **	-35.71 *	-62.50 **	-18.18	-37.86 **	-45.91 **	-37.04 **
20	B58586 X PMS74B	-16.67	-47.37 **	-60.00 **	7.69	-36.36 **	27.27	-16.78 **	-20.00 **	-6.88
21	B58586 X PMS71B	-50.00 **	-69.57 **	-72.00 **	-46.67 **	-69.23 **	-27.27	15.79 **	-10.00 *	4.76
22	B58586 X PMS42B	-13.04	-44.44 **	-60.00 **	-7.69	-45.45 **	9.09	-13.95 **	-17.27 **	-3.7
23	B58586 X PVK801	-46.67	-60.00 *	-84.00 **	-33.33	-54.55 *	-54.55 *	17.85 **	9.55	27.51 **
24	B58586 X IS-14332	27.27	16.67	-72.00 **	100.00 *	80	-18.18	-19.04 **	-21.94 **	-2.12
25	MS 296B X I26	-29.17 **	-32.00 **	-32.00 **	-16	-19.23 *	90.91 **	-0.29	-5.49	-8.99
26	MS 296B X PMS74B	-13.64	-24.00 *	-24.00 *	-12.5	-19.23 *	90.91 **	-30.91 **	-34.48 **	-29.63 **
27	MS 296B X PMS71B	-20.83	-24.00 *	-24.00 *	-11.54	-11.54	109.09 **	9.21	-8.79	-12.17 *
28	MS 296B X PMS42B	-16.28	-28.00 *	-28.00 *	-20.83 *	-26.92 **	72.73 **	1.3	-3.94	3.17
29	MS 296B X PVK801	20	-16	-16	40.54 **	0	136.36 **	-3.5	-5.29	-5.29
30	MS 296B X IS14332	-54.84 **	-72.00 **	-72.00 **	-48.39 **	-69.23 **	-27.27	-34.13 **	-41.77 **	-26.98 **
31	I 26 X PMS74B	-28.57 *	-34.78 **	-40.00 **	-17.39	-20.83 *	72.73 **	15.85 **	4.43	12.17 *
32	I 26 X PMS71B	-34.78 **	-34.78 **	-40.00 **	-32.00 **	-34.62 **	54.55 *	37.54 **	20.25 **	3.7
33	I 26 X PMS42B	-36.59 **	-43.48 **	-48.00 **	-26.09 **	-29.17 **	54.55 *	37.16 **	23.65 **	32.80 **
34	I 26 X PVK801	3.03	-26.09 *	-32.00 **	25.71 *	-8.33	100.00 **	22.73 **	14.29 *	14.29 *
35	I 26 X IS14332	-24.14	-52.17 **	-56.00 **	-10.34	-45.83 **	18.18	10.00 *	-7.17	16.40 **
36	PMS74B X PMS 71B	-52.38 **	-56.52 **	-60.00 **	-41.67 **	-46.15 **	27.27	12.62 *	-9.85	-3.17
37	PMS74B X PMS42B	-8.11	-10.53	-32.00 **	-22.73 *	-22.73 *	54.55 *	-3.45	-3.45	3.7
38	PMS74B X PVK801	-31.03	-47.37 **	-60.00 **	-51.52 **	-63.64 **	-27.27	21.94 **	17.73 **	26.46 **
39	PMS74B X IS14332	28	-15.79	-36.00 **	48.15 **	-9.09	81.82 **	5	-2.53	22.22 **
40	PMS71B X PMS42B	-26.83 *	-34.78 **	-40.00 **	-33.33 **	-38.46 **	45.45 *	-2.77	-22.17 **	-16.40 **
41	PMS71B X PVK801	-9.09	-34.78 **	-40.00 **	-2.7	-30.77 **	63.64 **	6.75	-12.17 *	-12.17 *
42	PMS71B X IS14332	-65.52 **	-78.26 **	-80.00 **	-67.74 **	-80.77 **	-54.55 *	41.50 **	7.17	34.39 **
43	PMS42B X PVK801	-50.00 **	-61.11 **	-72.00 **	-39.39 **	-54.55 **	-9.09	45.41 **	40.39 **	50.79 **
44	PMS42B X IS14332	0	-33.33 *	-52.00 **	3.7	-36.36 **	27.27	16.82 **	8.44	35.98 **
45	PVK801X IS14332	125.00 **	80.00 **	-28.00 *	162.50 **	90.91 **	90.91 **	-14.55 **	-23.21 **	-3.7
	SE(d)±	0.829	0.957	0.957	0.693	0.800	0.800	0.311	0.359	0.359
	CD at 5%	1.671	1.930	1.930	1.397	1.614	1.614	0.627	0.724	0.724
	CD at 1%	2.175	2.511	-20	1.818	2.099	2.099	0.816	0.942	0.942

* Significant at 5 per cent H_1 Heterosis over mean of parents

** Significant at 1 per cent H_2 Heterosis over mean of better parents, H_3 Heterosis over mean of standard ckeck

Continue

Sr. No.	F1 crosses	Grain density (g/ml)			Germination (%)			Glume coverage (%)		
		H1	H2	H3	H1	H2	H3	H1	H2	H3
1	GNM14-7XAKGMR110	8.99 **	7.30 *	2.69	17.81 *	10.93	34.43 **	-56.31 **	-57.82 **	-4.74
2	GNM-14-7X B 58586	1.21	-5.3	0.81	-5.49	-13.11	25.51 **	-21.44 **	-41.11 **	148.00 **
3	GNM14-7 X MS 296B	6.00 *	2.15	2.15	37.38 **	15.28	39.69 **	-42.02 **	-56.91 **	-9.39
4	GNM14-7 X I26	10.98 **	10.66 **	3.23	40.88 **	10.2	33.54 **	-51.50 **	-58.62 **	-12.99
5	GNM14-7 X PMS74B	5.13	0.8	1.88	27.19 **	24.14 **	50.43 **	-22.96 *	-41.65 **	22.7
6	GNM14-7 X PMS71B	3.98	-4.16	5.38	9.8	8.02	35.28 **	-12.08	-31.14 **	44.78 *
7	GNM14-7 X PMS42B	5.55 *	-1.02	4.84	10.74	0.65	49.16 **	-21.49 *	-32.31 **	42.33 *
8	GNM14-7 X PVK801	-6.00 *	-9.41 **	-9.41 **	12.81	2.95	24.75 *	-5.87	-30.55 **	46.03 *
9	GNM14-7 X IS14332	15.40 **	11.88 **	3.76	16.92 **	4.85	60.12 **	-34.49 **	-48.51 **	8.26
10	AKGMR110X B58586	8.78 **	3.28	9.95 **	-8.34	-20.21 **	15.25	4.17	-19.99 **	236.95 **
11	AKGMR110XMS296B	1.65	-0.54	-0.54	-0.9	-12.39	-6.24	44.76 **	5.17	137.50 **
12	AKGMR110 X I26	0.43	-0.84	-5.11	27.78 **	4.72	12.08	8.65	-9.95	103.36 **
13	AKGMR110XPMS74B	4.92	2.13	3.23	24.96 **	20.44 *	38.95 **	-45.09 **	-59.39 **	-8.28
14	AKGMR110XPMS71B	-8.50 **	-14.43 **	-5.91 *	16.50 *	8.03	35.30 **	-43.40 **	-56.78 **	-2.39
15	AKGMR110XPMS42B	-4.27	-8.88 **	-3.49	-3.41	-16.83 **	23.25 *	-39.57 **	-49.40 **	14.25
16	AKGMR110XPVK801	4.67	2.42	2.42	40.72 **	36.10 **	45.67 **	-22.44 *	-44.05 **	26.35
17	AKGMR110XIS14332	1.76	-2.81	-6.99 *	30.71 **	11.16	69.76 **	-18.47	-37.52 **	41.08
18	B58586XMS 296B	-8.85 **	-11.62 **	-5.91 *	36.44 **	7.04	54.62 **	-12.06	-45.35 **	130.17 **
19	B58586 X I26	10.36 **	3.54	10.22 **	4.73	-22.83 **	11.46	16.14 *	-21.45 **	230.80 **
20	B58586 X PMS74B	-9.59 **	-11.87 **	-6.18 *	-1.64	-11.54	27.77 **	-8.6	-42.55 **	141.93 **
21	B58586 X PMS71B	-3.35	-4.89	4.57	12.26	4.8	51.37 **	16.70 *	-25.15 **	215.22 **
22	B58586 X PMS42B	0.51	0.25	6.72 *	2.59	1.29	50.11 **	-27.28 **	-50.49 **	108.52 **
23	B58586 X PVK801	-5.47 *	-8.33 **	-2.42	4.33	-11.72	27.51 **	30.92 **	-19.00 **	241.12 **
24	B58586 X IS-14332	-5.56 *	-14.14 **	-8.60 **	-25.82 **	-27.83 **	10.22	-34.14 **	-57.67 **	78.27 **
25	MS 296B X I26	2.64	-0.81	-0.81	42.55 **	30.60 **	7.34	-27.81	-39.04 **	-9.45
26	MS 296B X PMS74B	7.49 **	6.91 *	8.06 **	-28.84 **	-39.07 **	-29.71 **	10.81	7.76	16.67
27	MS 296B X PMS71B	-5.25 *	-9.54 **	-0.54	-27.07 **	-39.60 **	-24.36 *	83.71 **	70.78 **	103.36 **
28	MS 296B X PMS42B	4.44	1.52	7.53 *	5.95	-17.64 **	22.05 *	76.20 **	47.27 **	124.34 **
29	MS 296B X PVK801	-4.03	-4.03	-4.03	48.37 **	35.16 **	35.16 **	26.57	25.14	28.03
30	MS 296B X IS14332	2.59	-4.03	-4.03	-27.09 **	-43.93 **	-14.36	-30.2	-35.41 *	-22.32
31	I 26 X PMS74B	-1.8	-5.59	-4.57	15.72	-7.83	6.33	59.46 **	37.84 **	104.75 **
32	I 26 X PMS71B	-4.76	-11.98 **	-3.23	33.75 **	3.4	29.50 **	-19.95	-27.89	7.12
33	I 26 X PMS42B	5.26 *	-1.02	4.84	29.23 **	-5.56	39.95 **	-12.76	-13.85	31.24
34	I 26 X PVK801	5.98 *	2.42	2.42	42.10 **	19.66 *	19.66 *	-31.86 *	-42.99 **	-15.32
35	I 26 X IS14332	3.73	0.29	-6.45 *	24.53 **	-9.85	37.69 **	-20.9	-28.43 *	6.31
36	PMS74B X PMS 71B	-5.48 *	-9.29 **	-0.27	7.59	3.35	29.43 **	184.04 **	171.14 **	222.87 **
37	PMS74B X PMS42B	-4.68	-6.85 *	-1.34	16.75 **	3.82	53.85 **	126.64 **	93.86 **	195.31 **
38	PMS74B X PVK801	-0.8	-1.33	-0.27	14.66	7.02	23.47 *	119.63 **	111.25 **	128.71 **
39	PMS74B X IS14332	8.29 **	0.8	1.88	-5.25	-16.84 **	27.00 **	2.1	-2.99	16.67
40	PMS71B X PMS42B	-12.08 **	-13.69 **	-5.11	9.37	0.9	49.52 **	-75.25 **	-77.95 **	-66.41 **
41	PMS71B X PVK801	-9.60 **	-13.69 **	-5.11	27.95 **	15.06	44.10 **	-13.04	-20.01	-4.74
42	PMS71B X IS14332	0.41	-10.02 **	-1.08	16.60 **	6.11	62.05 **	-21.39	-21.78	-5.93
43	PMS42B X PVK801	4.44	1.52	7.53 *	23.60 **	3.5	53.38 **	9.85	-9.02	38.59
44	PMS42B X IS14332	8.36 **	-1.27	4.57	2.76	1.24	54.62 **	-3.71	-13.85	31.24
45	PVK801X IS14332	-2.01	-8.33 **	-8.33 **	15.05 *	-4.81	45.38 **	-17.78	-24.71	-9.45
	SE(d)+	0.031	0.036	0.036	3.586	4.140	4.140	3.031	3.500	3.500
	CD at 5%	0.062	0.072	0.072	7.227	8.345	8.345	6.109	7.054	7.054
	CD at 1%	0.081	0.094	0.094	9.403	10.858	10.858	7.948	9.178	9.178

* Significant at 5 per cent H_1 Heterosis over mean of parents

** Significant at 1 per cent H_2 Heterosis over mean of better parents, H_3 Heterosis over mean of standard ckeck

Continue

Sr. No.	F1 crosses	Water absorption capacity (g)			Fungal load of Fusarium spp. (%)			Fungal load of Curvularia spp. (%)		
		H1	H2	H3	H1	H2	H3	H1	H2	H3
1	GNM14-7XAKGMR110	-4.91	-4.91	-2.74	-76.72 **	-79.21 **	-76.36 **	18.13	-7.21	21.91
2	GNM-14-7X B 58586	-4.56	-11.16 **	-9.13 **	-11.59	-42.57 **	-34.69 **	-2.75	-13.23	14
3	GNM14-7 X MS 296B	-25.87 **	-31.84 **	-16.89 **	-44.34 **	-50.76 **	-27.20 **	-35.47 **	-42.33 **	-3.78
4	GNM14-7 X I26	-23.28 **	-23.79 **	-21.00 **	-23.43 **	-28.06 **	-18.19 *	-43.84 **	-47.93 **	-19.91
5	GNM14-7 X PMS74B	-6.96 **	-16.13 **	6.85 *	-30.20 **	-35.43 **	-13.64	-20.81	-26.95 *	13.57
6	GNM14-7 X PMS71B	1.85	-5.70 *	13.24 **	15.70 **	10.27	38.39 **	-30.15 **	-37.03 **	3.03
7	GNM14-7 X PMS42B	-22.20 **	-26.10 **	-15.98 **	24.80 **	9.43	65.10 **	-61.34 **	-66.94 **	-38.86 *
8	GNM14-7 X PVK801	-7.45 **	-8.48 **	-6.39 *	-44.47 **	-47.82 **	-40.66 **	32.59 *	16.75	53.39 **
9	GNM14-7 X IS14332	-25.85 **	-32.14 **	-30.59 **	-31.81 **	-55.70 **	-49.63 **	92.00 **	56.46 **	105.56 **
10	AKGMR110X B58586	-11.75 **	-17.86 **	-15.98 **	25.31 *	-13.5	-22.68 **	29.84	12.16	15.6

11	AKGMR110XMS296B	-12.42 **	-19.48 **	-1.83	3.63	-16.86 **	22.91 **	12.19	-18.68	35.67
12	AKGMR110 X I26	9.53 **	8.81 **	12.79 **	-42.05 **	-45.12 **	-45.13 **	33.02 *	-1.06	52.20 **
13	AKGMR110XPMS74B	-22.86 **	-30.47 **	-11.42 **	-33.40 **	-44.45 **	-25.70 **	-49.60 **	-62.64 **	-41.92 *
14	AKGMR110XPMS71B	-8.83 **	-15.59 **	1.37	-48.93 **	-56.28 **	-45.13 **	23.61	-9.86	47.48 *
15	AKGMR110XPMS42B	-5.71 *	-10.44 **	1.83	-12.99 *	-30.72 **	4.52	23.35	-13.31	60.31 **
16	AKGMR110XPVK801	-27.77 **	-28.57 **	-26.94 **	77.74 **	68.30 **	68.30 **	-19.57	-29.62	-29.62
17	AKGMR110XIS14332	-30.24 **	-36.16 **	-34.70 **	13.13	-21.91 *	-30.20 **	97.06 **	87.84 **	55.44 **
18	B58586XMS 296B	-24.35 **	-34.83 **	-20.55 **	-64.20 **	-77.98 **	-67.45 **	48.19 **	19.86	99.97 **
19	B58586 X I26	-25.71 **	-31.28 **	-28.77 **	-38.11 **	-58.53 **	-58.54 **	20.67	0.76	54.99 **
20	B58586 X PMS74B	-14.83 **	-27.96 **	-8.22 **	-23.93 **	-52.29 **	-36.19 **	-0.77	-17.5	28.27
21	B58586 X PMS71B	-8.33 **	-20.53 **	-4.57	-68.49 **	-79.97 **	-74.86 **	62.71 **	32.60 **	116.96 **
22	B58586 X PMS42B	-31.22 **	-38.96 **	-30.59 **	-50.31 **	-69.55 **	-54.07 **	-14.25	-33.23 **	23.48
23	B58586 X PVK801	-19.42 **	-24.20 **	-24.20 **	118.12 **	46.16 **	46.16 **	-24.6	-25.72	-23.45
24	B58586 X IS-14332	-32.98 **	-34.20 **	-42.01 **	338.95 **	338.95 **	49.34 **	-62.27 **	-65.99 **	-64.95 **
25	MS 296B X I26	2.02	-5.62 *	15.07 **	-3.28	-18.94 **	19.84 *	-74.30 **	-75.30 **	-58.80 **
26	MS 296B X PMS74B	-19.05 **	-20.79 **	0.91	13.87 **	8.44	60.32 **	-72.53 **	-73.47 **	-55.74 **
27	MS 296B X PMS71B	-1.51	-2.25	19.18 **	8.1	-0.07	47.74 **	-42.38 **	-42.93 **	-4.79
28	MS 296B X PMS42B	14.34 **	10.49 **	34.70 **	-59.27 **	-59.67 **	-39.16 **	15.63	9.97	103.38 **
29	MS 296B X PVK801	1.65	-7.49 **	12.79 **	-77.34 **	-81.01 **	-71.92 **	-42.62 **	-54.12 **	-23.45
30	MS 296B X IS14332	-35.10 **	-44.94 **	-32.88 **	62.44 **	-0.09	47.71 **	-80.46 **	-85.39 **	-75.62 **
31	I 26 X PMS74B	-10.67 **	-19.00 **	3.2	-50.50 **	-56.75 **	-42.16 **	19.59	18.95	84.93 **
32	I 26 X PMS71B	5.31 *	-1.9	17.81 **	-5.93	-15.50 *	6.04	-57.61 **	-58.87 **	-32.71
33	I 26 X PMS42B	-9.24 **	-13.25 **	-1.37	-56.25 **	-63.63 **	-45.13 **	-31.75 **	-37.49 **	15.6
34	I 26 X PVK801	4.93	3.08	6.85 *	-74.86 **	-74.86 **	-74.86 **	-21.29	-35.06 **	-0.11
35	I 26 X IS14332	-8.47 **	-16.74 **	-13.70 **	-55.85 **	-70.41 **	-70.42 **	80.56 **	38.85 **	113.57 **
36	PMS74B X PMS 71B	-40.96 **	-42.65 **	-26.94 **	-29.89 **	-32.05 **	-9.12	-38.36 **	-39.89 **	-1.65
37	PMS74B X PMS42B	-21.59 **	-25.81 **	-5.48	-26.55 **	-30.72 **	4.52	-10.56	-17.69	52.22 **
38	PMS74B X PVK801	-36.95 **	-43.73 **	-28.31 **	-78.49 **	-81.21 **	-74.86 **	-13.17	-28.66 *	10.91
39	PMS74B X IS14332	-3.23	-19.35 **	2.74	-57.65 **	-73.44 **	-64.48 **	13.01	-13.42	34.6
40	PMS71B X PMS42B	-18.75 **	-20.91 **	-5.02	-16.62 **	-23.63 **	15.22	-30.97 **	-34.95 **	20.31
41	PMS71B X PVK801	-9.54 **	-17.11 **	-0.46	-44.71 **	-50.33 **	-37.66 **	9.37	-11.89	44.16 *
42	PMS71B X IS14332	-35.41 **	-44.87 **	-33.79 **	-34.96 **	-58.67 **	-48.13 **	24.87	-5.99	53.82 **
43	PMS42B X PVK801	-31.20 **	-35.34 **	-26.48 **	-26.33 **	-38.75 **	-7.59	-9.61	-30.37 **	28.77
44	PMS42B X IS14332	-6.21 *	-18.07 **	-6.85 *	61.63 **	-0.96	49.42 **	-68.08 **	-76.90 **	-57.28 **
45	PVK801X IS14332	24.94 **	15.53 **	15.53 **	104.05 **	36.73 **	36.73 **	-59.95 **	-63.40 **	-63.40 **
	SE(d)+	0.018	0.021	0.021	0.872	1.007	1.007	2.077	2.399	2.399
	CD at 5%	0.036	0.042	0.042	1.758	2.030	2.030	4.187	4.835	4.835
	CD at 1%	0.048	0.055	0.055	2.287	2.641	2.641	5.448	6.291	6.291

* Significant at 5 per cent H_1 Heterosis over mean of parents

** Significant at 1 per cent H_2 Heterosis over mean of better parents, H_3 Heterosis over mean of standard ckeck

Continue

Sr. No.	F_1 crosses	Fungal load of other mould spp. (%)		
		H_1	H_2	H_3
1	GNM14-7XAKGMR110	-44.88 **	-50.15 **	-53.58 **
2	GNM-14-7X B 58586	9.94	-17.35	-23.04 *
3	GNM14-7 X MS 296B	-62.72 **	-65.34 **	-62.46 **
4	GNM14-7 X I26	-31.37 **	-33.29 **	-34.20 **
5	GNM14-7 X PMS74B	-36.21 **	-39.49 **	-43.66 **
6	GNM14-7 X PMS71B	-65.72 **	-66.98 **	-69.25 **
7	GNM14-7 X PMS42B	-64.08 **	-64.09 **	-66.54 **
8	GNM14-7 X PVK801	-34.64 **	-36.89 **	-36.89 **
9	GNM14-7 X IS14332	-45.14 **	-53.99 **	-57.16 **
10	AKGMR110X B58586	63.66 **	32.77 *	0
11	AKGMR110XMS296B	-72.36 **	-76.57 **	-74.62 **
12	AKGMR110 X I26	-59.97 **	-64.70 **	-65.19 **
13	AKGMR110XPMS74B	-71.42 **	-72.83 **	-77.31 **
14	AKGMR110XPMS71B	-45.30 **	-48.77 **	-55.80 **
15	AKGMR110XPMS42B	-55.52 **	-59.77 **	-62.53 **
16	AKGMR110XPVK801	-83.25 **	-85.31 **	-85.31 **
17	AKGMR110XIS14332	-38.06 **	-43.09 **	-57.13 **
18	B58586XMS 296B	-44.76 **	-60.42 **	-57.13 **
19	B58586 X I26	52.70 **	12.64	11.09
20	B58586 X PMS74B	59.75 **	24.71	4.16
21	B58586 X PMS71B	-69.88 **	-76.75 **	-79.94 **
22	B58586 X PMS42B	-71.39 **	-78.50 **	-79.97 **
23	B58586 X PVK801	-48.94 **	-62.50 **	-62.50 **
24	B58586 X IS-14332	9.85	-4.26	-39.60 **

25	MS 296B X I26	-31.13 **	-34.21 **	-28.74 **
26	MS 296B X PMS74B	-74.90 **	-77.78 **	-75.93 **
27	MS 296B X PMS71B	-61.46 **	-65.38 **	-62.50 **
28	MS 296B X PMS42B	-64.12 **	-66.63 **	-63.86 **
29	MS 296B X PVK801	-84.29 **	-84.89 **	-83.63 **
30	MS 296B X IS14332	31.48 **	4.03	12.68
31	I 26 X PMS74B	-21.75 *	-27.75 **	-28.74 **
32	I 26 X PMS71B	-53.63 **	-56.53 **	-57.13 **
33	I 26 X PMS42B	55.61 **	51.30 **	49.22 **
34	I 26 X PVK801	-40.57 **	-40.98 **	-40.98 **
35	I 26 X IS14332	-30.32 **	-42.87 **	-43.66 **
36	PMS74B X PMS 71B	-76.38 **	-76.75 **	-79.94 **
37	PMS74B X PMS42B	51.16 **	43.33 **	33.53 **
38	PMS74B X PVK801	-57.63 **	-61.13 **	-61.13 **
39	PMS74B X IS14332	-52.51 **	-58.32 **	-65.19 **
40	PMS71B X PMS42B	-75.77 **	-76.67 **	-78.26 **
41	PMS71B X PVK801	-82.43 **	-83.63 **	-83.63 **
42	PMS71B X IS14332	-31.78 **	-40.95 **	-49.05 **
43	PMS42B X PVK801	-75.08 **	-75.93 **	-75.93 **
44	PMS42B X IS14332	-26.18 *	-38.10 **	-42.33 **
45	PVK801X IS14332	-27.56 *	-40.93 **	-40.93 **
	SE(d)+	1.277	1.475	1.475
	CD at 5%	2.575	2.973	2.973
	CD at 1%	3.350	3.869	3.869

* Significant at 5 per cent H1 Heterosis over mean of parents

** Significant at 1 per cent, H2 Heterosis over mean of better parents & H3 Standard parents

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