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Estimation of Combining Ability for Yield, Yield Related Traits and Fusarium Stalk Rot in New Inbred Lines of Maize (*Zea mays* L.)

Ramakrishnappa Archana [1]*, **H. C. Lohithaswa**[2], **R. Pavan**[2], **Vikram Jeet Singh**[1], **Neethu Mohan**[1], **S. Nanda Kumar**[1], **Sonu**[1] and **B. S. Harshitha**[1]

[1]*Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi -110012, India*
[2]*Department of Genetics and Plant Breeding, College of Agriculture, V. C. Farm, Mandya, UAS-Bangalore, Karnataka -571405, India*

*Corresponding author

A B S T R A C T

Stalk rot in Maize caused by *Fusarium moniliforme* is the most devastating disease of soil-borne in nature, fungicidal control is ineffective. Hence, testing and utilization of genetic resources resistance against pathogens are cost-effective and eco-friendly means of combating the disease. The current study was carried out and combining ability, analysis was performed using a diallel mating design by utilizing 10 newly developed near inbred lines of maize with varying reactions towards Fusarium stalk rot disease. The proportion of GCA to SCA variance showed that dominant and interaction components were abundant in the exhibition of all characters under investigation. The lines CM202, MAI754, 10878, P8, P7 and P9 were found to be the best general combiners for the maximum number of traits with high *gca* effects in the positive direction. Among crosses, MAI754 × MAI766, P13 × MAI754, P9 × P8, P13 × MAI754 and MAI329 × CM202 exhibited highly significant *sca* effects for yield and yield-related attributes. This work led to the investigation of 10 good hybrid combinations with lower *sca* effects towards FSR *viz.*, MAI329 × CM202, 10878 × CM202, P9 × CM202, MAI329 × MAI766, 10878 × MAI329, P13 × MAI754, P9 × MAI754, P8 × 10878, P13 × 10878 and P8 × 31837 which were superior to the commercial checks Hema and Nithyashree, which needs further evaluation at multi locations and multi seasons to identify superior cross combinations for further commercial release.

Introduction

Maize is the third most important cereal food crop in the world and good staple grain in major parts of the globe, with mean annual yield reaching rapidly in comparison with rice or wheat and its desirability as grain is increasing each year as a consequence of its multiple utilities (Troyer, 2006). Maize is one such crop prone to several stresses, particularly diseases caused by biotic agents such as fungi and bacteria. Hence, there is a significant productivity gap between India and the rest of the world (IIMR, New Delhi). Fungal pathogens cause diseases to various parts of the plant *viz.*, leaves, ears, stalks and some

diseases spread by bacteria are among the 65 pathogens that damage maize (Rahul and Singh, 2002). Both fungal and bacterial pathogens cause severe yield loss and reduce the quality of the end product in a congenial environment. Disease-related yield losses in maize have been estimated to be around 9% globally (Oerke, 2005). Due to intensive agriculture, a fungal pathogen, *Fusarium moniliforme* causes Fusarium stalk rot (FSR) is a soil-borne and most serious devastating disease of maize (Silva *et al.,* 2017). Stalk rot occurs after flowering although before physiological maturity, results in a 38 % reduction in overall productivity (AICRP, 2014). Fungicidal treatment of Fusarium stalk rot is ineffective due to its soil-borne infection mechanism. To reduce pathogen-related yield losses with no compromise in higher production to meet burgeoning demands, there is a need to utilise or introduce a vast amount of resistance sources by genetic means to mitigate yield losses (Archana *et al.,* 2019).

Resistance breeding offers a feasible and cost-effective means of combating diseases (Fehr, 1987). As a result, maize germplasm assessment is an important component of maize breeding schemes, where disease resistance screening contributes to yield stability (Archana *et al.,* 2021). Resistance to stalk rot is quantitatively inherited and controlled by several genes with cumulative effects, according to previous studies (Yang *et al.,* 2010; Archana *et al.,* 2019). Thus, knowledge of gene action and the combining ability of newly developed genotypes involved with the production of the resistant reaction are required to develop a cultivar with such a significant degree of resistance to Fusarium stalk rot. To interpret the genetic architecture and pattern of inheritance of traits, many biometrical approaches have been devised (Archana *et al.,* 2021; Archana *et al.,* 2023); one such powerful method is Combining ability analysis, which is used to identify the best general combiners that may be utilised in a hybridization programme to exploit hybrid vigour or to accumulate desirable plus genes (Sprague and Tatum, 1942). This analysis is also useful in unrevealing the genetic makeup of several traits that

provide the plant breeder to plan effective breeding programmes for the future improvement of already available genetic resources (Kempthorne, 1957). Henceforth, an experiment was conducted to quantify the magnitude and nature of combining ability in the newly produced inbred lines of maize to evaluate their capacity to be utilised in exploiting hybrid vigour/ heterosis. The diallel mating design is adopted in the present study to obtain knowledge information regarding the general and specific combining abilities of parents and crosses, respectively.

Materials and Methods

Plant material

Ten inbred lines with varying disease reactions were selected (Table 2) and crosses were made in a half-diallel mating design during *Kharif* 2016.

The resulting 45 single crosses were evaluated for yield; yield related components and FSR during *Rabi* 2016-17 along with the parents and two suitable check varieties *viz*., Hema (NAH 1137) and Nithyashree (NAH 2049) under Randomized Complete Block Design (RCBD) with two replications. Separate experiments were conducted for recording yield observations and screening for artificial disease incidence. For FSR disease screening, research work was carried out under the FSR sick plots (with a high inoculum load) of the University of Agricultural Sciences, Bengaluru (College of Agriculture, V. C. Farm, Mandya). Every single cross was grown in a single row of 4m in length by following a spacing of 60cm between plants and 20cm between two rows and every entry was planted in two rows. To ensure sufficient pathogen inoculum load in the research plot, two suitable susceptible checks for FSR (Hema and Nithyashree) were planted after every 20th row.

Screening under artificial epiphytotic conditions

Artificial inoculation was carried out according to the procedure provided by the Indian Institute of

Maize Research (IIMR), New Delhi, to guarantee consistent disease incidence. Plants that were 45-50 days old were inoculated in the second internode above the soil level, immediately after flowering (Plate1).

About 20-25 days after inoculation, infections appeared in the inoculated plants. The severity and intensity of the disease were measured using the IIMR's 1-9 scoring system (Table1).

Based on disease incidence on maize stalks, the genotypes were grouped into different disease reaction classes (Plate 2) *viz.*, highly resistant genotypes with a score of 1-1.9, resistant class with a disease score of 2-2.9, moderately resistant with an infection score of 3-3.9, moderately susceptible reaction with a score of 4-4.9, susceptible genotypes with a score of 5-5.9 and highly susceptible reaction with a score of 6-9.

Data on Agro-morphological traits

Five plants in each genotype were marked with coloured tags randomly in both replications to record data on the following quantitative and qualitative characters such as the height of the plant (cm), length and diameter of the ear (cm), kernels per row, kernel rows per ear, percentage of shelling, test weight of 100 kernels (g), the yield of the kernel (q/ha) and percentage of Fusarium stalk rot incidence.

All the data was recorded on plants at the right stages of plant development in the prescribed manner. All agronomic packages of practices including irrigation, spacing, fertilization, pest, disease control and weeding of the crop was maintained to reap a good yield.

Statistical Analysis

The data was collected on five random plants for each trait in each entry. The trait means of the 45 half-diallel progenies along with their parents were subjected to method II and model II of Griffing's

(1956) analysis of combining ability. The mean data from each replication was collected to perform a combining ability analysis by using 'WINDOWSTAT' software v 9.1.

Results and Discussion

Combining ability analysis gives information on the genetic nature and inheritance pattern of measurable/quantitative traits and enables the breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes.

The diallel mating design developed by Griffings (1956) is a more general procedure that makes provision for estimating combining ability and also genetic parameters underlying the inheritance pattern

Analysis of variance (ANOVA)

The general ANOVA presented in Table 3, displayed the statistically significant differences in all parents for all the 10 characters under study other than for plant height and shelling percentage.

Whereas, mean squares due to crosses and parents Vs crosses were statistically significant for characters except for the height of the plant, ear and shelling percentage.

The genetic diversity that exists between the parents is high, therefore diverse parents produced heterotic F1 individuals, which confirmed the presence of a sufficient amount of variability in the material used, thus confirming the utilisation of genetic resources in the experiment.

These results further revealed the confirmation for quantifying the combining ability effects of the parents which help choose parents for producing hybrids. The effect of blocks within replication was not significant for any of the traits, suggesting soil homogeneity within the block.

Estimation of combining ability and gene action (variances)

Results revealed that, all the traits considered under study exhibited a higher degree of SCA variance than GCA variance except for the ear height (Table 4). The variance ratio for all studied characters was a value less than one (<unity) displaying the preponderance of nonadditive gene action in the expression of traits, which could be exploited by developing hybrids and alternatively through population improvement programs.

Estimation of General combining ability effects

The difference in the average effect of the allele from the population mean is denoted as *gca* effect. This *gca* effect measures the additive gene effects or additive gene action that prevail among inbreds, this quantification helps in the identification of potential inbred lines for hybrid development programmes (Sprague and Tatum 1942). Only five, out of 10 inbred lines showed superior *gca* effects for grain yield (Table 5). Among them, P9 inbred showed the highest *gca* effect in the positive direction for grain yield and it also exhibited good general combiner for 100-grain weight and FSR disease score. So it can be used as a potential inbred parent line in the exploitation of hybrid vigour in the development of hybrid cultivar with resistance to FSR. The inbred line CM 202 also revealed the highest significant *gca* effect in the positive direction for the height of plant and ear, kernel rows per ear and FSR. Hence, CM202 was considered the best general combiner and used in producing heterotic hybrids with a moderate resistance reaction towards FSR. These results were adequately supported by Pavan *et al.,* (2009); Santiago *et al.,* (2009); Hung and Holland (2012); Hefny *et al.,* (2012); Puttaramanaik (2013) and Anilkumar (2015).

Estimation of Specific combining ability effects of crosses

The deviation of specific cross combination from the *gca* effect of the inbred line involved is *sca* effect of specific cross (Sprague and Tatum, 1942). The hybrids showed a highly significant difference *sca* effects for all the traits under study, which in turn depicted the predominance of non-additive gene action in the control of traits expression of the hybrids (Table 6). The crosses produced in this study involved parents of H×H (high × high), H×L (high × low) and L×L (low × low) combinations. Among 45 single crosses, MAI754 × MAI766 (H×L), P13 × MAI754 (L×H), P9 × P8 (H×L) MAI329 × CM202 (H×H), and P13 × MAI766 (L×L) exhibited highly significant *sca* effects for yield and yield related traits (Table 6).

All the cross combinations revealed the involvement of inbreds ranking low and high general combining capacity therefore there will be a predominance of non-additive gene action in the expression of all the traits. Hence, population improvement programs like recurrent selection for *sca* will be effective in segregating generations for improvement. The involvement of high general combiners in the cross showed the preponderance of additive gene action.

Hence, population improvement programs like recurrent selection for *gca* will be effective. Whereas, hybrids with both inbred lines hybrid produced by involving both with low *gca* revealed the preponderence ofners revealed the significance of over dominance and epistatic gene action in the inheritance of a trait. Hence, population improvement programs like reciprocal recurrent selection or heterosis breeding will be effective.

These results were in agreement with Guerrero *et al.,* (2014); Puttaramanaik (2013) and Anilkumar (2015). The promising crosses MAI329 × CM202 (L×H), P9×P13 (H×L), P13×P7 (L×H) and P13×P8 (L×H) involved low and high combiners which signifies the presence of dominance and epistatic gene action governing FSR resistance. Hence population improvement programs like recurrent selection for *sca* will be effective. These results were adequately supported by Santiago *et al.,* (2009); Hung and Holland (2012) and Hefny *et al.,* (2012).

Table.1 Disease scoring scale: (IIMR, New Delhi; Hooker, 1956)

Disease score	Disease reaction	Symptoms
1-1.9	Highly resistant (HR)	Healthy or slight discolouration at the site of inoculation
2-2.9	Resistance (R)	Up to 50% of the inoculated internode is discoloured
3-3.9	Moderately Resistance (MR)	51-75% of the inoculated internode is discoloured
4-4.9	Moderately susceptible (MS)	76-100% of the inoculated internode is discoloured
5-5.9	Susceptible (S)	Less than 50% discolouration of the adjacent internode
6-6.9	Highly susceptible (HS)	More than 50% discolouration of the adjacent internode
7-7.9	Highly susceptible (HS)	Discolouration of three internodes
8-8.9	Highly susceptible (HS)	Discolouration of four internodes
9-above	Highly susceptible (HS)	Discolouration of five internodes and premature death of plant

Table.2 List of 10 inbred parents along with two standard checks used in diallel analysis with varied disease reactions towards FSR

Sl. No.	Genotype	Disease score	Disease reaction
1	CM202	2.50-3.00	MR
2	MAI766	3.00	MR
3	10878	3.60	MR
4	31837	4.30	MS
5	MAI329	4.00	MS
6	MAI754	4.00	MS
7	P8	5.30	S
8	P7	7.00	HS
9	P9	6.30	HS
10	P13	6.60	HS
11	**Hema (Check)**	**6.20**	**HS**
12	**Nithyashree (Check)**	**5.40**	**S**

Note : P8-VL108867, P7-VL1043, P9-VL109287 and P13-VL1218

Table.3 ANOVA of crosses and their parents for grain yield, its component traits and FSR in maize

Source of variance	Df	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Kernel rows/ear
Blocks within Environments	1	127.72	6.80	0.34	0.16	1.64
Treatments	54	694.42**	234.94 *	6.25 **	2.76***	2.06**
Parents	9	621.38	58.01	6.85 *	2.60**	2.75**
Hybrids	44	229.83	155.94	5.22	2.54***	1.93**
Parents Vs hybrids	1	21793.82***	5302.87**	45.94***	14.05***	1.48
Error	54	355.06	149.01	3.28	0.77	0.95
Total	109	521.09	190.32	4.72	1.77	1.5

* Significant at $P \leq 0.05$, ** Significant at $P \leq 0.01$, *** Significant at $P \leq 0.001$

Table.3 *Contd…*

Source of variance	df	Kernels/row	Shelling %	100 Grain weight (g)	Grain yield (q/ha)	Fusarium Stalk Rot
Blocks within Environments	1	21.47	21.48	1.52	30.85	0.03
Treatments	54	51.01***	64.95	32.57***	840.99***	2.21***
Parents	9	58.76**	89.9	29.34*	595.85***	4.6***
Hybrids	44	36.22*	60.34	28.12**	427.88***	1.67***
Parents Vs hybrids	1	632.69***	43.67	257.65***	21224.16***	4.26***
Error	54	20.72	61.72	13.57	7.75	0.16
Total	109	35.73	62.95	22.87	420.76	1.17

* Significant at P ≤ 0.05, ** Significant at P ≤ 0.01, *** Significant at P ≤ 0.001

Table.4 ANOVA for combining ability for grain yield, its component traits and FSR in maize

Source of variance	GCA	SCA	Error	$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca / \sigma^2 sca$
Df	9	45	54			
Plant height (cm)	366.87 *	343.28 *	177.53	15.78	167.75	0.1
Ear height (cm)	161.72 *	108.62	1.64	0.56	0.45	1.24
Ear length (cm)	8.294 ***	2.086	1.64	7.27	34.07	0.22
Ear girth (cm)	1.25	1.41	0.34	0.08	1.03	0.07
Kernel rows/ear	1.49**	0.94**	0.48	0.09	0.46	0.18
Kernels/row	68.29***	16.95*	10.36	4.83	6.6	0.74
Shelling %	57.51	27.47	30.86	1.22	8.34	0.15
100 Grain weight (g)	21.87**	15.17**	6.78	2.22	3.34	0.66
Grain yield (q/ha)	322.85***	440.02***	3.88	20.56	334.76	0.67
Fusarium stalk rot	2.76***	0.74***	0.07	0.23	0.67	0.32

* Significant at P ≤ 0.05, ** Significant at P ≤ 0.01, *** Significant at P ≤ 0.001

Table.5 Estimates of general combining ability effects of 10 parents for grain yield, its component traits and FSR in maize

Parents	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Kernel rows/ear
CM202	11.19*	6.91**	0	0.43*	0.787***
MAI766	-6.75	-6.18	-2.08	0.1	-0.494
MAI329	3.43	2.83	-0.46	-0.61	-0.05
MAI754	-2.84	0.5	0.14	-0.09	-0.09
10878	-1.91	-3.33	0.21	0.28	0.19
31878	-2.44	2.6	0.15	-0.45	-0.41
P8	3.26	0.44	0.22	-0.1	0.1
P7	4.33	-0.19	0.83*	0.14	0.1
P9	-6.55	-0.59	0.06	0.06	-0.154
P13	-1.62	-2.97	0.95***	0.25	0.05
S Em±	3.65	2.37	0.35	0.17	0.09

* Significant at P ≤ 0.05, ** Significant at P ≤ 0.01, *** Significant at P ≤ 0.001

Table.5 *Contd….*

Parents	Kernels/row	Shelling %	100 Grain weight (g)	Grain yield (q/ha)	Fusarium Stalk Rot
CM202	0.04	-2.55	-1.93	-0.38	-1.04***
MAI766	-5.82	-0.56	1.1	-8.39	-0.08
MAI329	-0.79	0.36	-2.12	-2.77	-0.36***
MAI754	0.3	2.43	0.319	1.73**	-0.15*
10878	1.52	-3.393	1.31	1.33*	0.20**
31878	0.12	2.4	-0.34	-4.72	0.76***
P8	1.23	1.8	1.2	-3.77	0.17*
P7	1.56	2.42	-0.216	7.72***	0.28***
P9	-1.17	0.27	1.62*	7.83***	-0.15
P13	2.98**	-2.45	-0.827	1.42*	0.34***
S Em±	4.83	1.53	1.26	0.54	0.07

* Significant at P ≤ 0.05, ** Significant at P ≤ 0.01, *** Significant at P ≤ 0.001

Table.6 Estimates of specific combining ability effects of 45 crosses for grain yield, its component traits and FSR in maize

Crosses	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Kernel rows per ear
MAI766 ×CM202	-10.79 *	-14.94 **	0.39	-0.17	0.10
MAI329×CM202	20.14 **	9.35 **	4.22 **	1.99 **	1.46 **
MAI754×CM202	13.79 **	6.08	-0.63	-0.03	-0.10
10878×CM202	16.45 **	17.41 **	0.46	0.60 *	-0.03
31878×CM202	1.49	7.29 *	0.98 *	-0.42	0.32
P8×CM202	8.50	10.54 **	0.40	-0.87 **	-1.29 **
P7× CM202	-9.71	-4.29	-1.36 **	-1.23 **	-1.66 **
P13×CM202	10.11 *	10.27 **	-1.34 **	0.32	0.57 *
P9×CM202	10.18 *	7.44 *	-0.13	0.33	-0.02
MAI329×MAI766	8.60	5.26	1.47 **	-0.69 **	-0.77 **
MAI754×MAI766	1.13	6.06	-0.05	-0.25	0.78 **
10878×MAI766	6.99	2.70	-0.62	0.18	-0.10
31878×MAI766	11.83 *	9.17 **	0.08	-0.04	-0.10
P8×MAI766	8.14	4.53	0.17	0.26	-0.21
P7×MAI766	14.77 **	3.15	1.31 **	-1.02 **	-0.39
P13×MAI766	21.14 **	1.65	0.93	1.50 **	1.25 **
P9×MAI766	12.41 *	4.13	-1.01 *	-0.29	0.26
MAI754×MAI329	15.36 **	2.96	-0.42	1.10 **	0.53 *
10878×MAI329	4.61	1.79	-1.53 **	0.43	0.26

31878×MAI329	11.46 *	13.37 **	-0.96 *	0.51 *	0.65 *
P8×MAI329	16.14 **	16.70 **	1.75 **	-0.29	-1.05 **
P7×MAI329	-6.31	2.34	0.24	-1.37 **	-0.24
P13×MAI329	7.86	-0.86	-1.19 *	-1.19 **	-1.65 **
P9×MAI329	4.14	-3.98	0.27	0.06	0.61 *
10878×MAI754	7.97	3.81	-0.43	0.72 **	0.89 **
31878×MAI754	18.12 **	5.99	0.12	-0.15	-0.51 *
P8×MAI754	5.83	9.25 **	-0.74	-1.70 **	-1.02 **
P7×MAI754	3.15	3.07	0.64	0.84 **	2.20 **
P13×MAI745	8.83	4.87	2.22 **	2.24 **	1.04 **
P9×MAI754	9.60	-0.45	0.23	0.65 **	0.25
31878×10878	5.07	3.93	1.86 **	0.62 **	0.42
P8×10878	10.08 *	-3.12	1.19 *	0.62 **	0.51 *
P7×10878	2.21	-4.10	-0.62	1.39 **	0.93 **
P13×10878	19.38 **	8.00 *	2.00 **	1.52 **	-0.24
P9×10878	5.45	0.08	1.27 **	0.73 **	0.38
P8×31878	3.83	-5.24	-0.31	0.95 **	0.11
P7×31878	4.35	2.38	1.63 **	-0.03	0.12
P13×31878	13.18 **	-1.17	-2.35 **	-1.88 **	-1.82 **
P9×31878	2.20	0.36	2.42 **	-0.69 **	0.38
P7×P8	6.26	-2.57	0.22	1.37 **	0.42
P13×P8	-6.16	-8.97 **	1.34 **	0.50 *	0.85 **
P9×P8	-3.69	-0.69	-0.45	1.96 **	0.47
P13×P7	4.57	10.46 **	0.88	-0.63 **	0.87 **
P9×P7	3.94	9.04 **	-1.16 *	0.68 **	-1.32 **
P9×P13	-23.99 **	-5.76	0.31	-1.55 **	-1.68 **
S Em±	4.92	3.19	0.47	0.23	0.26

* Significant at P ≤ 0.05, ** Significant at P ≤ 0.01, *** Significant at P ≤ 0.001

Table.6 *Contd*….

Crosses	Kernels per row	Shelling %	100 grain weight (g)	Fusarium Stalk Rot	Grain yield (q/ha)
MAI766 ×CM202	2.39 *	4.86 *	-1.23	0.64 **	8.30 **
MAI329×CM202	11.58 **	3.46	4.44 **	-1.58 **	31.28 **
MAI754×CM202	-2.03	6.50 **	6.80 **	-0.13	-6.04 **
10878×CM202	4.23 **	2.22	-0.69	-0.36 **	15.54 **
31878×CM202	-0.69	-7.87 **	-2.14 *	0.16	-3.79 **
P8×CM202	1.04	-3.18	0.97	-0.30 **	-2.45 **
P7× CM202	-1.34	-0.41	2.03 *	1.04 **	-1.18
P13×CM202	-2.67 *	5.07 *	-6.99 **	0.22 *	-1.97 **
P9×CM202	-0.62	-7.95 **	2.10 *	1.23 **	30.76 **
MAI329×MAI766	6.38 **	-0.86	0.43	0.12	16.81 **
MAI754×MAI766	-0.68	-0.63	4.52 **	0.52 **	-8.30 **
10878×MAI766	-1.89	-15.35 **	3.03 **	0.41 **	-7.62 **
31878×MAI766	0.30	4.13 *	5.43 **	0.26 *	27.92 **
P8×MAI766	-1.31	0.66	-0.11	0.73 **	2.07 **
P7×MAI766	2.62 *	2.26	-0.05	-0.16	6.67 **
P13×MAI766	-0.02	-3.57	6.48 **	0.29 **	6.40 **
P9×MAI766	-1.26	-0.40	-3.48 **	0.40 **	13.05 **
MAI754×MAI329	-1.61	-3.10	4.34 **	-0.30 **	-2.21 **
10878×MAI329	-2.22	9.26 **	2.61 **	0.60 **	21.32 **
31878×MAI329	-0.33	-1.30	-3.30 **	0.44 **	4.91 **
P8×MAI329	1.86	-9.09 **	0.26	0.43 **	6.11 **
P7×MAI329	1.19	-9.40 **	-1.37	0.12	-10.29 **
P13×MAI329	1.18	-2.23	-0.62	0.70 **	0.09
P9×MAI329	-0.39	3.22	-0.66	0.71 **	-4.96 **
10878×MAI754	-4.01 **	3.21	-6.14 **	1.64 **	-12.16 **
31878×MAI754	3.18 **	5.79 **	4.06 **	0.04	11.17 **
P8×MAI754	-0.03	0.19	-4.78 **	0.05	8.78 **
P7×MAI754	1.70	4.52 *	-0.51	0.69 **	11.06 **
P13×MAI745	6.64 **	1.10	-2.84 **	1.00 **	39.87 **
P9×MAI754	1.82	3.15	2.85 **	-0.12	26.87 **
31878×10878	3.36 **	2.24	2.17 *	-0.22 *	13.05 **
P8×10878	2.96 *	4.05	-0.07	0.70 **	20.74 **
P7×10878	0.49	1.86	0.60	0.76 **	4.14 **
P13×10878	3.95 **	3.82	3.22 **	-0.11	27.67 **

P9×10878	5.80 **	-0.02	-0.99	0.40 **	8.50 **
P8×31878	0.75	2.18	4.73 **	0.52 **	13.81 **
P7×31878	4.08 **	-2.70	4.44 **	-0.35 **	-4.31 **
P13×31878	-0.27	-4.81 *	-2.94 **	-0.16	1.54 *
P9×31878	4.60 **	2.22	-0.29	-0.03	2.78 **
P7×P8	1.57	2.23	2.15 *	-0.71 **	0.21
P13×P8	0.93	3.81	4.17 **	-1.17 **	4.05 **
P9×P8	-1.41	4.83 *	-5.29 **	-1.06 **	-22.73 **
P13×P7	3.66 **	-4.09 *	1.44	-1.31 **	13.32 **
P9×P7	-3.28 **	2.12	3.73 **	-0.93 **	-9.55 **
P9×P13	-1.32	1.37	-0.05	-1.64 **	-6.57 **
S Em±	1.19	2.05	0.96	0.26	0.73

* Significant at P ≤ 0.05, ** Significant at P ≤ 0.01, *** Significant at P ≤ 0.001

Table.7 Overall general combining ability status of parents

Sl. No	Parents	Rank	Status
1	CM202	54	H
2	MAI766	74	L
3	MAI329	70	L
4	MAI754	48	H
5	10878	54	H
6	31837	71	L
7	P8	58	H
8	P7	53	H
9	P9	60	H
10	P13	63	L

Final Norm: 60.5
H: Over all high general combiner
L: Over all low general combiner

Table.8 Overall specific combining ability status of 45 crosses of maize

	CM202 (*H*)	MAI766 (*L*)	MAI329 (*L*)	MAI754 (*H*)	10878 (*H*)	31837 (*L*)	P8 (*H*)	P7 (*H*)	P9 (*H*)	P13 (*L*)
CM202 (*H*)	*	285 (L)	42 (H)	210 (H)	145 (H)	293 (L)	249 (L)	359 (L)	237 (L)	242 (L)
MAI766 (*L*)		*	219 (H)	267 (L)	309 (L)	180 (H)	292 (L)	203 (H)	167 (H)	274 (L)
MAI329 (*L*)			*	214 (H)	245 (L)	250 (L)	229 (H)	326 (L)	329 (L)	281 (L)
MAI754 (*H*)				*	284 (L)	170 (H)	287 (L)	184 (H)	153 (H)	176 (H)
10878 (*H*)					*	155 (H)	192 (H)	245 (L)	106 (H)	207 (H)
31837 (*L*)						*	246 (L)	208 (H)	328 (L)	231 (L)
P8 (*H*)							*	198 (H)	184 (H)	263 (L)
P7 (*H*)								*	169 (H)	250 (L)
P9 (*H*)									*	267 (L)
P13 (*L*)										*

Final norm of hybrids: 230 (*H*): High overall *gca* status of parents   (*L*): Low overall *gca* status of parents
(H): High overall *sca* status   (L): Low overall *sca* status

Plate.1 Syringe method of inoculation and mass multiplication of Fusarium culture on Petri plates

Plate.2 1-9 disease score ratings

Plate.3 Resistance to Fusarium stalk rot in the cross MAI329 × CM202

Overall *gca* status of parents (ranking)

The methods proposed by Arunachalam and Bandopadhya (1979) and modified by Mohan Rao (2001) was used to estimate overall *gca* status of inbred lines of all traits methods advocated by Arunachalam and Bandopadhya (1979) and modified by Mohan Rao (2001) were used to estimate the *gca* inbreds for all character understudy and are presented in Table 7. the results revealed that more than fifty per cent (six) of the inbred lines showed high overall *gca* status inbred exhibited higher overall gca status (H), especially inbred lines CM202 (54) and MAI754 (48) which possesses the highest rank to transfer pass additive genes to the hybrids in the positive direction.

Overall *sca* status of hybrids (ranking)

Estimation of the overall *sca* status for all characters of any specific cross combination is important. Therefore, *sca* status of all the hybrids was estimated for all traits and is presented in Table 8. Based on overall *sca* status, hybrids were grouped into H × H (P1 with high *gca* status × P2 with high *gca* status), H×L (P1 with high *gca* status × P2 with low *gca* status) and L×L (P1 with low *gca* status × P2 with low *gca* status). The results found that out of 45 crosses, 47 per cent of hybrids (21 half-diallel progenies) possessed a high overall *sca* rank. The preponderance of H×L (P1 with high *gca* status × P2

with low *gca* status) or L×H (P1 with low *gca* status × P2 with high *gca* status) hybrid combinations revealed the importance of dominant and epistatic gene action in the expression of all characters thereby promoting the population improvement approach in the subsequent generations of these combinations to select superior inbreds.

Henceforth, two inbreds CM 202 and MAI 766 with the moderately resistant reaction towards FSR could be used as genetic stock in producing hybrid cultivars having good resistance towards FSR with higher additive genetic effects. The hybrid combination, MAI329 × CM202 showed a resistance reaction to FSR (Plate 3) along with a high grain yield that could be evaluated in multilocation trials across the seasons to release as a potential high-yielding hybrid to the commercial release as a new hybrid. Nevertheless, putative markers linked to loci that are responsible for expressing resistance reaction towards Fusarium stalk rot could be identified for effective marker-assisted selection.

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