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Assessing potential of resistance source for the enhancement of resistance to Maydis leaf blight (*Bipolaris maydis*) in maize (*Zea mays* L.)

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Abstract

Maydis leaf blight caused by *Bipolaris maydis* (*Cochliobolus heterostrophus*) presently has become a major disease of maize, causing considerable losses in productivity. Out of three races C, O and T, race '0' is prevalent in maize tract of India. During last three decades, though considerable breeding research has been carried out to improve the productivity, progress with respect to resistance breeding has been lagging behind with respect to Maydis leaf blight. Work of all these years have led to identification of two resistant source inbred lines namely, CM 104 and CM 105. However, incorporation of maydis resistance from these two sources have been rather discouraging. These two sources though possessed high *per se* resistance, their capacity to transmit their resistant gene have not been very fruitful under different background germplasm. In order to understand the reason behind such behaviour the genetic study based on combining ability was undertaken, using these and two other inbred lines namely CM 119 (susceptible) and CM 206 (moderately resistant). Using four inbred lines of contrasting resistance level in a diallel making system, gene action studies were conducted. Resistance to Maydis leaf blight was found to be predominantly under the influence of additive gene action along with significant contributions from additive x additive epistasis. However, significant role of dominant gene action along with epistasis could not be ruled out entirely.

Key words: Maize, maydis leaf blight, combining ability, additive gene action, dominance, epistatsis

Introduction

Maydis leaf blight caused by *Bipolaris maydis* (Nisikado & Miyake) Shoem. [*Cochliobolus heterostrophus* (Drechs) Drechs] qualifies as a major disease of maize capable of inflicting significant losses in productivity to as high an extent as 41% [1]. This pathogen is known to have polymorphic existence as races C, O and T. Races O and T significantly differ in expression of symptoms produced, cytoplasmic specificity, production of toxins, optimum growth temperature regimes, reproductive rates and in the site of infection in the plants. Though Race T has been detected in India, its distribution and incidence is not widespread whereas Race O has been the most prevalent one.

Host resistance is the most common and the most economical means of controlling this disease of maize. During the last three decades, considerable research efforts have been directed towards the quest for stable resistant sources and their subsequent utilization in the development of high yielding resistant cultivars. Sharma and Payak [2] have identified two inbred lines namely, CM 104 and CM 105 which in a span of 14 years, have been able to sustain resistance to race 0 at a high level with the resistance rating not exceeding 2.0 (in a scale of 1-highly resistant to 5 highly susceptible). In spite of the availability of these two resistance sources namely, CM 104 and CM 105, breeding for resistance using them remains rather inadequate and half baked leading to frustrating results not only with respect to enhancement of resistance status but also to the incorporation of resistance into high yielding commercial entries like hybrids or composites. In the last three decades of research in the All India Coordinated Maize Improvement Project, though several high yielding hybrids and composites have been developed and released, yet the level of resistance to this disease in these cultivars have remained either lower than that of CM 104/CM 105 or have at par. It appears that a dead end has been reached with regard to resistance beyond which all efforts have proved futile.

In the present paper, an attempt has been made to assess the potential of these two resistant inbred lines with respect to their inherent capacity to transmit resistance as well as their amenability to breeding

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manipulations for achieving higher resistance status in derived populations. Based on the result of this study a breeding strategy will be suggested for the most efficient use of these inbred lines in the improvement of resistance as well as yield in derived cultivars.

Materials and methods

Based on several years and multi-location disease nursery screening data, four inbred lines namely, CM 104 (derived from Amarillo Theobromina, Colombia), CM 105 (derived from Peru 330, Peru), CM 119 (derived from R-109 Ht, USA) and CM 206 (derived from SS III, USA) were used in the study. Of these CM 104, CM 105 and CM 206 were categorized as resistant (with resistance rating in the range of 1.6 to less than 2.0) while CM 119 was identified as highly susceptible (with resistance rating exceeding 4.0) using standard artificial inoculation techniques [3]. These four inbred lines were crossed in a diallel mating system giving six all possible combinations (F_1) excluding reciprocals. The F_1 crosses were selfed to give rise to F_2 progenies. Each of the F_1's were crossed with the respective parents to give rise to BC_1 and BC_2 progenies for each F_1 cross. All these materials namely, 4 parental inbreds, 6 F_1 crosses, 6 sets of F_2 progenies, 6 BC_1 and 6 BC_2 progenies were studied in replicated trials (4 replications in each) in diseases nursery conducted in two consecutive years 1996 and 1997 at IARI. The parents, F_1, BC_1 and BC_2 progenies were planted in 4 rows of 5 m length whereas F_2 progenies were planted in 10 rows per replication. All the plants of all the entries were artificially inoculated with *B. maydis* inoculum. Hundred plants per replication were sampled for each of parent, F_1, BC_1 and BC_2 progenies, while for the F_2 progenies, 200 plants per replication were sampled. Data on reaction were recorded on a rating of 1 (highly resistant) to 5 (highly susceptible) as described by Payak and Sharma [4] on per plant basis and then averaged for each replication.

However, in the present paper only parents and F_1's have been used to work out combining ability analysis for disease reaction with dual objective namely (i) to identify inbred parents having maximum potential to transmit resistance i.e. best general combiners for resistance (ii) to assess gross nature of resistance in the inbreds under study for the disease Maydis leaf blight. Since the data were recorded on a rating scale of 1-5, it was subjected to transformation before analysis. Fisher and Yates [5] transformation have been widely used in this kind of data. Nevertheless test of normality was also conducted to confirm the reversion of the rating data to normality.

Analysis of variance by the transformed data was carried out separately for the two years and a combining analysis of the two years data was also carried out (Table 1). The combining ability analysis was carried out using the combined data only, since there was slight variation in the F_1 variances for the years 1996 and 1997 with respect to their statistical significance.

Results and discussion

Table 1 presents the analysis of variance of the two experiments and also for the pooled data. Taking into consideration this pooled data analysis it could be seen that the parental inbred lines, their crosses and subsequent derivates were found to be highly significant at 1% level. The interaction of these entries with environment were also found to be highly significant.

Table 1. ANOVA for design of Experiment

Source	df			MS		
	Pooled	'96	'97	Pooled	1996	1997
Env.	1	-	-	9.22694**	-	-
Rep.wit. env.	6	3	3	0.52931**	0.10009*	–0.9583**
Treatment	27	27	27	2.71035**	2.03267**	0.91118**
Parents	3	3	3	11.69270**	7.83477**	4.20553**
F_1	5	5	5	0.36583**	0.86874**	0.01353
F_2	5	5	5	0.94821**	0.9049**	0.22488**
BC_1	5	5	5	2.66696**	2.08731**	0.7644**
BC_2	5	5	5	2.54763**	1.89775**	0.79296**
Bet. gr.	4	4	4	1.36459**	0.64605**	0.7516**
Trea.× env.	27	-	-	0.23349**	-	-
Par.× env.	3	-	-	0.34761**	-	-
F_1 × env.	5	-	-	0.51643**	-	-
F_2 × env.	5	-	-	0.18156**	-	-
BC_1 × env.	5	-	-	0.18475**	-	-
BC_2 × env.	5	-	-	0.14308**	-	-
Bet. gr × env.	4	-	-	0.03307	-	-
Error	162	81	81	0.02766	0.02534	0.02997

The results of the combining ability analysis are presented in Table 2. It is evident from the table that though both general and specific combining ability variances were highly significant at 1% level, general combining ability variance (*gca*) was 4.85 times larger in magnitude than the specific combining ability variance (*sca*). However, the ratio of *gca* variance to the total

Table 2. ANOVA for combining ability

Source	df	MS
gca	3	0.2632**
sca	6	0.0542*
$\frac{gca \text{ variance}}{(gca + sca) \text{ variance}}$		0.9066
gca × Env.	3	0.9022**
sca × Env.	6	0.2429**
Error	162	0.0043

combining ability variance indicated that general combining ability variance made the major contribution to the total combining ability variance. It, therefore, suggests that resistance to race 0 of Maydis leaf blight is predominantly under the influence of additive gene action which may include additive × additive type of epistasis also. Nevertheless, to a certain extent role of dominance gene action along with epistatic interactions involving dominant genes may also be envisaged as evident from highly significant *sca* variance. Through a precise estimate of the additive, dominance and epistatic components of genetic components cannot be obtained from the relative magnitude of *gca* and *sca* variances, yet it is possible to derive useful conclusions about the genetic architecture of resistance in the material understudy, It may, therefore, be presumed that there is invariable presence of directional dominance with some dominant genes acting in negative direction leading to conferring susceptibility also. Such presumption in fact, have been borne out the generation means analysis carried out with the same data (c.f. paper under publication).

The genetic situation encountered here i.e. dominance as well as epistasis both contributing to resistance along with additive gene effects, creates considerable hindrance in the efficient utilization of additive genes in the enhancement of resistance level by any cyclic breeding procedures. Such genetic situation is not unique as earlier works like Pate and Harvey [6], Burnette and White [7] and Handoo [8] have also reported both additive as well as non-additive gene action involved in resistance.

The pooled analysis also indicated that there existed highly significant interaction of *gca* and *sca* variances with that of environmental variance. Such high magnitude of environmental interaction is not uncommon in case of grain yield but in case of maydis infection the interaction is encountered due to drastic changes in infection intensity caused by variable dry or wet season during the growth period, particularly at knee-high stage of plant. It appears that in the present case dry weather in 1997 resulted in high interaction in the combined analysis data as is also evident for the non-significant F_1 variances.

Table 3 presents the general combining ability effect (*gca*) of the parental inbred lines with respect to resistance. It is interesting to note that resistance is exclusively governed by negative *gca* effect whereas positive *gca* effect confer susceptibility. The parents CM 104, CM 105 and CM 206 exhibited highly significant negative *gca* effects while the parent CM 119 possessed highly significant positive *gca* effects. It may, therefore, be concluded that CM 104, CM 105 and CM 206 not only possessed high magnitude of additive genes with negative effects for resistance but have also the capacity to transmit resistance to the progenies. On contrary, the inbred parent CM 119 possessed higher proportion of additive genes with positive effects that conferred susceptibility to its progenies.

Table 3. *gca* effects of mean disease reaction of parents

Parents	*gca* effects	Rating	Reaction type
CM 104	–0.0792**	1.640	Resistant
CM 105	–0.0785**	1.763	Resistant
CM 119	0.2221**	4.253	Susceptible
CM 206	–0.0658**	1.883	Resistant

Table 4 presents specific combining ability effects of the six F_1 combinations along with their resistance reaction. It was interesting to observe that three out of the six crosses namely, CM 104 × CM 105, CM 104 × CM 206 and CM 105 × CM 206 exhibited negative *sca* effects which however, were highly significant only in the latter two crosses. A perusal of their resistance reaction also indicated that these were the only three crosses which gave resistant reaction.

Table 4. *sca* effects of mean disease reaction of F_1 crosses

Crosses	*sca* effects	Rating	Reaction type
CM 104 × CM 105	–0.0332	1.648	Resistant
CM 104 × CM 119	0.1986**	2.008	Resistant
CM 104 × CM 206	–0.0630**	1.812	Resistant
CM 105 × CM 119	0.2150**	2.018	Resistant
CM 105 × CM 206	–0.2555**	1.822	Resistant
CM 119 × CM 206	0.0830**	2.580	Intermediate

The other three crosses namely, CM 104 × CM 119, CM 105 × CM 119 and CM 119 × CM 206 gave highly significant positive *sca* effects. These crosses showed intermediate resistance to the disease. Such results are commensurate with the expectation of the nature and magnitude of *gca* effects of the parental inbreds along with their resistance reaction *vis-á-vis* *sca* effects of their crosses and their resultant resistance reaction, For instance, all the crosses involving the three resistant inbred lines invariably exhibited not only resistance but also possessed negative estimates of *sca* effects. As expected, all the crosses involving the susceptible parent CM 119 gave highly significant positive estimates of *sca* effects and their resultant resistance was intermediate. It is, therefore, obvious that preponderance of the additive gene with positive effects proportion in CM 119, are mainly governing susceptibility, which when in combination with resistant parent are nullifying the additive gene effects for resistance in the F_1.

In conclusion, it may be highlighted here that though CM 104 and CM 105 have been considered as the two sources of resistance to Maydis leaf blight during the last two decades, their resistant reaction being controlled by additive genes with negative effects appeared to be highly efficient in transferring high level of resistance in a direct crossing programme for hybrid development under this genetic situation. Needless to say that a breeding methodology aimed at increasing the additive genetic component for resistance in these three resistant parents following some sort of recycling procedure would go a long way to not only increase the durable resistance potential *per se* of the inbreds but also their capacity to transmit such resistance to their progenies. This genetic situation in these two parents also augurs well to attain and transmit durable maydis resistance.

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