Research Article

Evaluation of Popcorn inbred lines for disease severity

Muhammad Noor^{1*}, Hidayat ur Rahman¹ and Muhammad Iqbal²

1. Department of Plant Breeding and Genetics, University of Agriculture, Peshawar, Pakistan.

2. Cereal Crops Research Institute, Pirsabak Nowshera, Khyber Pakhtunkhwa, Pakistan.

*Corresponding author's email: noor_pbg49@yahoo.com

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Abstract

In maize crop maydis leaf blight (MLB) is a sever disease in Pakistan like other countries of the world. Twelve F₁ hybrids were generated in a full diallel mating of four elite popcorn inbred lines. These F₁ hybrids along with parents were evaluated at Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera for combining ability of disease severity. Disease data of four inbred lines with their single cross hybrids were analyzed using GGE Biplot. Both general and specific combining ability (GCA and SCA) were found significant for disease severity. Pop-4 was identified as best general combiner for disease severity, while Pop-1 and Pop-2 were having the maximum projection on average tester coordinate (ATC) Y-axis exhibiting the highest SCA effects for disease severity. These promising inbred lines need further evaluation across different productive environments in larger field trials to confirm their heterotic behavior.

Keywords: MLB; Maize; General combining ability; average tester coordinate.

Introduction

Maize (*Zea mays* L.) is the most important crop after wheat in Pakistan where it was grown on about 0.51 million hectares with a total production of 0.96 million tons and average yield of 1.88 ton ha⁻¹ in a single province Khyber Pakhtunkhwa (KP) [1]. Maize is the primary crop in majority of the farming systems and also staple food of the rural population and poor resource farmers in KP [2]. Although the average yield of maize has dramatically increased in the last decade in Pakistan, an additional increase in yield will be required to meet future needs of the country. Despite its high yield potential, one of the major limiting factors to maize grain yield is its sensitivity to several diseases [3, 4]. Approximately 65 pathogens infect maize [5]. Most of the diseases are

difficult to control since their occurrence is less predictable year to year because they depend very much on the prevailing weather conditions and are also influenced by the variable production environments [6] and [7]. As a result, in favorable seasons with high rainfall, some diseases also become more prevalent and damaging. Most of small-scale farmers cannot afford, in most cases, to control the diseases through the use of pesticides. Southern corn leaf blight (SLB) or may dis leaf blight (MLB) caused by *Helminthosporium maydis* is a serious fungal disease of maize throughout the world where maize is grown under warm, humid conditions [8]. Three races of *C. heterostrophus* known as O, T and C have been described [9, 4, 10]. Race O is considered as the most common race in most

areas where MLB occurs which infects all types of maize and is controlled by nuclear genes. Race T, the cause of 1970's epidemic in North America is specific to maize containing Texas male-sterile cytoplasm (cms-T) and is controlled mainly by cytoplasmic factors. The most prominent difference between race O and T is that race O only attacks leaves while race T attacks all plant parts. Race C is a cms-C cytoplasm-specific race reported only in China. Breeding resistant varieties to maydis leaf blight is the most efficient, economical and sustainable way than chemical control in the long run. Moreover, it also ensures environment safety standards.

Diallel analysis is primary method and has been widely used to determine combining ability, heterotic responses and patterns in maize populations [11, 12]. Combining ability analyses are widely used in maize breeding programs to determine general combining ability (GCA) and specific combining ability (SCA) information of maize germplasm for identification of nature of genes action involved in the expression of quantitative traits, genetic diversity evaluation, suitable parental lines selection for hybridization, heterotic pattern classification, heterosis estimation, and hybrids development [13, 14, 2, 15, 17]. GCA is average performance of a parent in a series of crosses and SCA designates those cases in which certain combinations perform relatively better or worse than would be expected on the basis of average performance of lines involved. The GCA includes additive and additive $\times$ additive variances, while SCA responsible for non-additive genetic variances.

Biplots can also be used for analyzing diallel crosses [18, 19]. Although the GGE biplot methodology was developed for multi-environment trial (MET) data analysis, but they stated that it also applicable to all types of two-way data that assume an entry-by

tester data structure. In MET data, genotypes represent entries and environments are testers. In diallel data, each genotype is both an entry and a tester [19]. The graphical representation in a biplot analysis allowed a rapid and effective overview of GCA and SCA effects of the inbred lines, their performance in crosses, as well as grouping patterns of similar genotypes. The objectives of the present study were to study the combining abilities of 4 maize inbred lines for leaf blight resistance to promote their use by breeders.

Materials and Methods

Four inbred-lines of popcorn were used in this study. These inbred-lines were crossed following a complete diallel fashion to produce single cross (SC) hybrids during spring season 2012. All the SC hybrids (including reciprocals) were evaluated along with parents in randomized complete block design with three replications in the following summer season (July to October, 2012) at Cereal Crops Research Institute, Newshehra, Pakistan. Each plot consisted of two rows with 5 meter length and 0.75 m apart. Two seed per hill were planted which were later thinned to have a population density of 53,333 plants ha⁻¹ at 4-5 leaf stage. Standard cultural practices were applied uniformly at all experimental units. Disease data was recorded on weekly basis in each plot. The plants were visually rated 5 times for percent MLB severity beginning at two weeks post-anthesis [20]. MLB was rated with a 0-5 scale based on leaf's diseased area following [21] procedure, i.e. 0 for no lesion and 5 for heavily blighted leaves. Lines were categorized as 0-1.4 resistant, 1.5-2.4 moderately resistant and 2.5-5.0 susceptible [22]. An arbitrary gradation of 10 classes scale (i.e. 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5 and 5.0) was also used to measure more accurately the disease severity [23].

Results and Discussion

General and specific combining ability

Using GGE Biplot general combining ability (GCA) and specific combining ability (SCA) effects for disease severity of the popcorn inbred lines (entries) were examined by drawing an average tester coordinate (ATC) view for entries. The GCA effect of the entries was approximated by the projection of their markers to the ATC X-axis (the single arrowed line; the direction indicated the positive end) while the SCA of the entries was approximated by the projection of their markers to the ATC Y-axis (double arrowed line) [19]. Significant variation were observed among male parent for disease severity (Table 1). Total variation of 77.5% (40.4 and 37.1% by PC1 and PC2, respectively) was explained by Biplot for disease severity (Fig. 1). Our results were in accordance with that of [24] who observed 76.44% of total variation explained by GGE Biplot for disease severity. As shown in Fig. 1a, Pop-4 has a largest projection onto ATC X-axis exhibiting the highest and positive GCA effect for disease severity. Similarly, Pop-1 also showed higher and positive GCA effects. Whereas, Pop-2 and Pop-5 were located on the left side of the ATC Y-axis (in the opposite direction of ATC X-axis) indicating the lowest and negative GCA effects. The Biplot also displayed the SCA effects of the entries, the vectors length help in ranking the entries as shown in Fig. 1a. Since, the entries Pop-1 and Pop-2 have the largest projections on to the ATC Y-axis exhibiting that they have the highest SCA effects for disease severity. Similarly Pop-4 also showed highest and positive SCA effects. Whereas, entries Pop-5 showed smallest SCA effects (small projections on to ATC Y-axis).

Best double cross hybrid combinations

The polygon view of biplot (Fig. 1b) showed the interaction and best mating partners among entries and testers as mentioned by [25, 19]. As mentioned by Yan & Hunt [19], vertex entries are either the best or the poorest mating partners with some or all of the testers. Vertex entries with largest distances from the origin were more responsive to the change of testers relative to other entries within respective groups. Tester which fall in the same sector share the same best mating partner (i.e. entry at the vertex in that sector) and those fall in different sectors have different best mating partners. The polygon view of biplot showed four sectors with entries Pop-4, Pop-1, Pop-5 and Pop-2 as the vertex entries, and are referred as 1st, 2nd, 3rd and 4th sectors, respectively (Fig 1b). No tester fell in the 3rd and 4th sectors, depicting that the vertex entries (Pop-5 and Pop-2 respectively) of the said sectors were not the best mating partner, with any of the tester, and produced worst combinations. In the 1st sector where Pop-4 is a vertex entry, produced best hybrids with tester POP-1, POP-2 and POP-5. These combinations Pop-4 × POP-2, Pop-4 × POP-1 and Pop-4 × POP-5 showed disease highest degree of severity 9.0, 8.4 and 6.8, respectively (Table 2). A single tester POP-4 fell in 2nd sector, meaning that entry Pop-1 (vertex entry) was the best mating partner for POP-4. Based on original data (Table 3). Maximum resistance of 6.3 to was observed for Pop-2 × POP-4 and Pop-5 × POP-4. The possible reason may be that these crosses were apparently inferior to those that were identified to be superior based on Fig 1b. As mentioned earlier that the biplot explained only 77.5 of the total variation rather than 100%, therefore such contradictions are expected to be raised [19].

Table 1. Analysis of four maize inbred lines and their crosses

SOV	DF	SS	MS	F	P
Rep	2	0.107917	0.053958	0.829242	0.45
Female (F)	3	0.720833	0.240278	1.8185	0.21
Male (M)	3	1.609167	0.536389	4.059566	0.04
F × M	9	1.189167	0.13213	2.030594	0.07
Error	30	1.952083	0.065069		
Total	47	5.579167			

Table 2. Biplot axis scores (X-axis and Y-axis) and eigenvectors (PC1 and PC2) for the entries and testers.

Name	Axis Scores		Eigenvectors	
	X-axis	Y-axis	PC1	PC2
Entries				
Pop-4	0.943	-0.315	0.632	-0.22
Pop-1	-0.584	-1.023	-0.392	-0.715
Pop-2	0.503	0.625	0.337	0.437
Pop-5	-0.861	0.713	-0.577	0.499
Testers				
POP1	0.58	-1.026	0.393	-0.695
POP2	1.13	0.018	0.765	0.012
POP4	-0.466	-1.052	-0.316	-0.713
POP5	0.591	0.141	0.401	0.096

Table 3. Mean values of disease severity of single cross progenies (including reciprocals), and self progenies (diagonal) of four popcorn inbred lines.

Entries	Testers				Entries Mean
	POP1	POP2	POP4	POP5	
Pop-1	<u>8.0</u>	7.5	7.5	6.9	7.5
Pop-2	6.9	<u>8.3</u>	6.3	7.5	7.3
Pop-4	8.4	9.0	<u>6.4</u>	6.8	7.7
Pop-5	6.4	7.5	6.3	<u>6.5</u>	6.7
Testers Mean	7.4	8.1	6.6	6.9

Fig. 1. Biplot based on diallel data of five maize hybrids for grain yield. (A) Average tester ordination view; (B) Polygon view. Codes for genotypes are: POP-1 = ICI-974, POP-2 = Opener, POP-3 = CS-201, POP-4 = CS-222, POP-5 = Pioneer 3025. Genotypes are labeled with uppercase letters when viewed as testers (parents, single crosses) and with lowercase letters when viewed as entries (double crosses)

Fig. 2. Biplot showing relationship among genotypes. (A) Relationship among entries (progenies); (B) Relationship among testers (parents).

Relationship among genotypes

Biplot provide an attractive and informative view of interrelationship among genotypes (Fig. 2) and (Table 2). The lines that connect the biplot origin and the markers of the genotypes are known as vectors. The angle between vectors of two genotypes relates to the correlation coefficient between them, and the linear map to the right of the graph (in degrees) help in explaining the relationship among them [26, 16]. The genotypes having and acute angle will be positively correlated with each other [19]. Strong positive correlation was observed between entries Pop-2 and Pop-4 (Fig 2a). High positive correlation was observed between testers POP2 and POP5. Tester POP2 showed a negatively correlation (angle $> 90^\circ$) with tester POP4 (Fig. 2b).

Conclusion

The GGE biplot concise information about general and specific combining abilities. We identified Pop-4 with the highest and positive GCA effect for disease severity followed by Pop-1. On the other hand Pop-2 and Pop-5 showed lowest and negative GCA effects. The SCA effects reported for Pop-1, Pop-2 and Pop-4, indicated the role of dominant gene, which could be utilized in hybrid development based on this trait.

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