

GGE Biplot analysis of *Brassica* genotypes for white rust disease severity under aided epiphytotic conditions in India.

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Breeding for disease resistance has been one of the most important objectives in breeding programs aimed at sustainable productivity of a crop. The reaction of a genotype to a pathogen depends upon the genetics of both the host plant as well as the pathogen. Hence, based on the genetics of host-pathogen relationship disease reaction, broadly, can be, in nonspecific genotype by pathogen interaction systems, response of the host to pathogen categorized into two classes i.e. race specific and nonspecific. In race specific, the interaction or compatibility between host genotype and pathogen genotype that determines the disease reaction to develop or not. Moreover, race non-specific resistance is quantitative in nature and is influenced by environmental conditions to a great extent in different geographical locations over the years. Hence reaction of genotypes varies ranging from susceptible to resistance grading under natural conditions termed as horizontal resistance and a wide range of pathogens come under this category. Understanding whether resistance to given pathogen is race-specific or nonspecific is a pre-requisite to selection of breeding strategies and is detected by the presence or absence of crossover interaction between host genotypes and pathogen strains. For this purpose, genotype main effects and genotype by environment interaction (GGE) biplot is the best method for visualizing important crossover interactions. Thus, understanding of *Brassica* genotypes by *Albugo candida* interaction is of vital importance to identify resistant genotypes for specific adaptability viz-a-viz stable performance in spatial and temporal

Material and Methods

The reaction of 13 oilseed *Brassica* genotypes viz., PHR 2, JYM 10, EC 414322, JMM-07-1, JMM-07-2, JGM 901, RRN 604, EC 399299, EC 414324, PBC 9221, Varuna, EC 414299 and GSL 1 was studied under aided epiphytotic conditions under AICRP-RM for three years i.e. 2008, 2009 and 2010 at Ludhiana (Punjab), Hisar (Haryana), Kangra (Himachal Pradesh), Morena (Madhya Pradesh) and Pantnagar (Uttaranchal Pradesh). Data recorded on white rust disease severity were subjected to GGE biplot analysis (Yan and Kang 2003).

Results and Discussion

The results are presented in two sections: section one involves analysis of variance which represents percentage of the total sums of squares accounted for by G, E, and GE interactions over the location under testing; section two exhibits mean performance and stability of genotypes which includes; the interrelationship among genotypes and locations, mean performance of genotypes at different locations, stability of genotypes across the locations, ranking of genotypes based on performance in specific location and across the locations, comparison among the genotypes and "which-won-where" pattern to identify the best genotypes in each environment for thirteen genotypes of *Brassica*.

- 1. Analysis of Variance:** The percentage of the total sums of squares accounted for by G, E, and GE interactions were used as an indicator of variation attributed seed yield (table 1). Variation due to G or GE interactions is a measure of how cultivars respond across environments/locations. The environmental component (years and locations) represents how the genotypes were different across the locations in spatial stability in this study. The total sums of squares were 18.43% for environment, 48.09% for genotype, and 33.48% for the interaction for disease severity. As genotype by environment interaction accounted for 33.48% of the total variation for disease index indicates the presence of crossover interactions due to nonspecific response of genotypes for disease intensity at different locations.

- 2. Mean performance and stability of the genotypes across the locations:**

a) Interrelationship among genotypes and locations

Figure 1 provides the summary of the interrelationships among the environments (locations over years) for different genotype(s) disease severity response at different locations during the years under

study. The lines that connect the biplot origin and the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them. Based on the cosine of angles of location vectors, Morena and Pantnagar locations had different agro-climatic conditions for white rust development compared to rest of the locations. Among the years, 2008 had similar climatic conditions at all locations while 2009 and 2010 had maximum dissimilarity in climatic parameters. The presence of wide obtuse angles i.e. strong negative correlations among the locations is indication of strong cross-over genotype by environment interactions. The vector length of location(s) measures discriminating power of the location for screening the genotypes to the severity of the disease. Thus, Hisar location found to be the best location to identify genotypes sensitive to white rust disease severity as the ideal environment should have both power of discriminating and representativeness for selecting wide adaptive genotypes. Hence, genotypes like EC414324, RM 604, EC 414109 found to be most susceptible while GSL 1, PBC 9221 and EC 414299 resistant to white rust disease.

b) Stability of genotypes across the locations;

The ideal genotype should have both high mean performance coupled with high stability to give wide adaptability in the target region. But this case low mean value is desirable because high value means more susceptibility to disease. The single-arrowed line called average–environment coordination abscissa (or AEA) points to higher mean disease index across the locations. So far stability of resistance is concerned, GSL 1, EC414299 and EC 399299 showed consistent performance at different locations over the years showing wider adaptability. On the other hand, Varuna and JMM 07-2 showed inconsistent behavior w.r.t. disease reaction over the locations and years. Similarly, GSL 1 and PBC 9221 exhibited maximum resistance to white rust at all the locations. However, some of the genotypes viz. JMM 07-2, JYM 10 and EC 399299 exhibited specific adaptability for resistance to white rust at different locations. Genotypes like EC 414324, RM 604, Varuna and EC 414322 exhibited the susceptible reaction at all locations over the years except Varuna at Morena during 2008.

Table 1. Degree of freedom, sums of squares, significance levels and total percentage of total variation of genotype (G), environment (E) and genotype by environment (GE) interaction.

Seed yield per hectare	Source	DF	MS	F	P	SS (%)
	Environment (E)	12	1361.28	20.11	0.00001	60.63
	Genotype (G)	14	447.30	6.61	0.00001	19.92
	GEI	168	436.7	6.52	0.00001	19.45

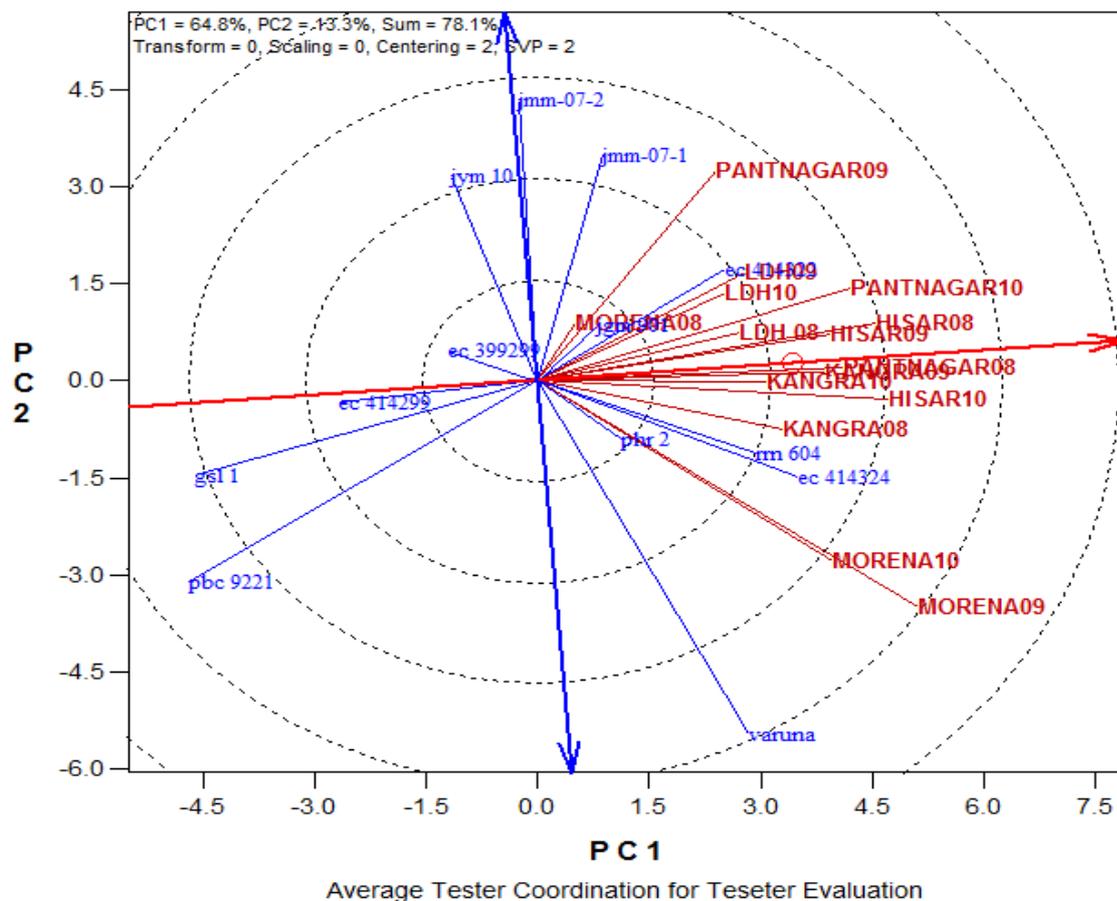


Figure1: Genotypes by locations relationship with respect to white rust disease index.

c) Ranking of genotypes based on performance in specific location and across the locations;

Suppose we want to see the differential response of genotypes Varuna at different locations across years, for this a line will be drawn which passes through the biplot origin and *Varuna* cultivar. *Varuna* found to susceptible at most of the location all over years except Morena (2008) and Pantnagar (2009) where this showed resistance reaction. Similarly only two genotype viz., *GSL 1* and *EC 414299* were free of disease at locations, while rest of the genotypes exhibited mixed reaction with different locations (figures are not given). Similarly we can visualize response of particular locations for disease score among the genotypes. In present investigation, different years viz-a-viz locations gave different ranking of disease score for white disease indicating the clear-cut presence of cross-over interactions (COI), which necessitates exploitation of GEI. It very clear from reversal sensitivity of genotypes to disease index indicating that natural selection had played its role in restructuring genetic make-up of host-pathogenic interaction for specific geographical regions. This means that specific adaptability of genotypes resistance for these locations is entirely different and GEI can be exploited while selecting genotypes for recommendation for cultivation rather than ignoring.

e) Comparison among the genotypes.

The distance between two genotypes approximates the Euclidean distance between them, thus is a measure of dissimilarity among the genotypes. Therefore, *Varuna* and *PHR 2*, *RM 604* and *EC 414324* are quite different in their genetic make-up from *JYM 10*, *JMM 07-1*, *JMM 07-2*. Similarly *GSL1*, *PBC 9226* and *EC414299* from *JGM 901* and *EC 414322* (Figure 1). The biplot origin also represent a "virtual" genotype that assumes the grand mean values and zero contribution additive effect of genotype (G) and multiplicative interactions (GE). The vector length of a genotype of the origin of biplot is due the contribution of G or GE or both. Genotypes those are located near to the biplot origin have little contribution viz., *EC 399299*, *PHR 2* and *JGM 901* to either G or GE and genotypes having longer vectors indicate the contribution of G or GE or both. Therefore, genotypes with the longest vectors are either best (*PBC 9226* & *GSL 1*) or the poorest (*EC 414324*) or most unstable (*Varuna*). The *GSL 1* can be considered as best genotype as its angle very close to ideal

genotype (in opposite direction) coupled with longer vector length. Further angle between vector of a genotype and the AEA partitions the vector length into components of G and GE. A right angle with AEA means that the contribution is due to GE only; an obtuse angle depicts the contribution of G, which leads to lower than average mean performance; and an acute angle again mean the contribution of G but in higher side. Thus Figure1 shows that GSL1, EC414299 and EC399299 showed additive gene for horizontal resistance to white rust which can prove good donors in further genetic improvement programmes. Varuna, JMM 07-2, JMM 07-1 and JYM 10 had non-additive gene action for pathogenecity to white rust. PBC 9221, GSL 1, EC 414299 and EC399299 were very similar in genetic make-up for disease resistance while varuna showed maximum divergence in genetic constitution from these strains.