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Short Communication

STABILITY OF RESISTANCE TO YELLOW MOSAIC VIRUS OVER ENVIRONMENTS IN COWPEA

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The viral diseases alone account for 35-100 percent losses in grain production of cowpea[1]. Among these, cowpea yellow mosaic virus (CYMV) is most serious disease of cowpea. An effective and economical way for the control of this disease is the identification of stable sources of resistance to CYMV and development of resistant cultivars in cowpea. Therefore, the present investigation was carried out to identify the stable sources of resistance.

Ten genotypes with variable reaction to cowpea yellow mosaic virus were grown in a randomized block design with four replications at experimental farms of the University at Hisar and Regional Research Station, Uchani, Karnal during summer and *Kharif* seasons of 1994 and 1995. In order to build up heavy inoculum pressure in the field, one row of highly susceptible genotype (HFC 42-1) was planted after every two test rows in each replication and around the experimental plot. All normal cultural practices were followed except spraying of insecticide to maintain the whitefly population. The disease reaction was graded 0 for resistant and 1 for heavy infestation. Average disease reaction of each genotype was calculated. The analysis of variance for experimental design and the stability parameters were estimated as per standard procedure [2, 3].

The analysis of variance (Table 1) for showed highly significant mean squares for genotypes, environments and genotype × environments interaction. The mean squares due to genotype × environment was further partitioned into components (i) heterogeneity between regression (linear) and (ii) remainder (non-linear). The linear component of G × E interaction was highly significant, whereas non-linear component was non significant which indicated that prediction is possible for CYMV reaction. Based on environmental additive effects for CYMV reaction, Karnal location and summer season were found more favourable for development of disease.

Table 1. Joint regression analysis for yellow mosaic virus reaction in cowpea

Source	d.f.	MS
Genotypes (G)	9	4.686**
Environments (E)	6	0.175**
G × E	54	0.050**
G × E (linear)	9	0.274**
Remainder	45	0.004
Pooled error	189	0.005

Stability parameters viz. mean, regression coefficient and deviation from regression ($\overline{S}^2_{di}$) for disease reaction index of individual genotypes (Table 2) revealed that five genotypes viz. CS 39, CS 55, CS 82, CS 88 and CS 94, had very less mean values for CYMV reaction, and hence these genotypes had resistance to CYMV. Other workers[4] have also identified cowpea genotypes resistant to CYMV. All these five genotypes had negligible 'b' values, which indicated that these genotypes were non-responsive to expression of disease due to changes in the environments. These genotypes had a non significant values of $\overline{S}^2_d$ value. Therefore, these five genotypes were stable for resistance to CYMV. On the contrary genotypes CS 46, ARL 8, ARL 25, GC 2 and HFC 42-1 had much higher values for incidence of CYMV, had higher 'b' values and significant $\overline{S}^2_d$ values and hence these were unstable for resistance to CYMV.

Table 2. Estimates of stability parameters of different genotypes for yellow mosaic virus reaction in cowpea

Genotype\Parameters	Mean	b	S^2_d
CS 39	0.001	0.0002	0.001
CS 46	0.701	3.030*	0.012**
CS 55	0.001	0.0002	0.001
CS 82	0.001	0.0002	0.001
CS 88	0.001	0.0002	0.001
CS 94	0.001	0.0002	0.001
ARL 8	0.828	2.7110**	0.005**
ARL 25	0.128	0.2630	0.004**
GC 2	0.692	3.6180*	0.004**
HFC 42-1	0.968	0.3660	0.001

*, ** Significantly different from zero at 0.05 and 0.01 levels of probability

This study clearly revealed that genotypes as mentioned above viz. CS 39, CS 55, CS 82, CS 88 and CS 94 had stability for CYMV resistance and hence these genotypes may be used in the breeding programme to develop stable resistant cowpea lines to CYMV.

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