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Genetics of Bacterial Blight Resistance in Clusterbean

J.V. Singh, M.L. Saini, G.P. Lodhi and R.N. Arora
Department of Plant Breeding,
CCS Haryana Agricultural University, Hisar 125 004, India

Abstract: The gene effects for bacterial blight (*Xanthomonas campestris* pv. *Cyamopsidis*) were studied by using the parental, F_1, F_2, B_1 and B_2 generations in four crosses: HG 75 x RGC 137, HG 75 x Suvidha, Pusa Navbahar x RGC 137 and Pusa Navbahar x Suvidha of clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). The weighted least square analysis of generation mean indicated the presence of non-allelic interactions. The components (d), (h), (i), (j) and (l) were significant in almost all the crosses in both the environmental conditions. Biparental matings in early segregating generations may be useful in generating bacterial blight resistant segregants.

Key words: Clusterbean, *Xanthomonas campestris* pv. *Cyamopsidis*, gene effects, generation mean analysis.

Clusterbean is a drought-hardy arid legume. The productivity of this crop has been low due to many obvious reasons. Although a number of varieties having stable yield have been released for cultivation, these varieties are susceptible to an array of diseases including bacterial blight. The bacterial blight, caused by *Xanthomonas campestris* pv. *Cyamopsidis* is a serious disease of clusterbean (Chand and Gandhi, 1978; Mihai and Alcorn, 1985). The damage due to this disease has been estimated to be around 68% (Srivastava and Rao, 1963; Gandhi, 1984).

The genetic sources with resistance or low level of incidence of bacterial blight have been identified. This would be possible if the nature of gene effects in the material is known. However, no information is so far available on the inheritance of bacterial blight in clusterbean. Present study was, therefore, taken up to estimate the gene effects controlling bacterial blight resistance, deploying generation mean analysis.

Materials and Methods

The experimental material comprised six generations, viz., P_1, P_2, F_1, F_2, B_1 and B_2 of the crosses HG 75 x RGC 137, HG 75 x Suvidha, Pusa Navbahar x RGC 137 and Pusa Navbahar x Suvidha. HG 75 and RGC 137 are resistant to bacterial blight, but Suvidha and Pusa Navbahar are susceptible to it.

The experiment was conducted during 1988-89 in a compact family block design with three replications. In each replication, the parents and F_1s were represented by two rows. Each backcross was accommodated in five rows, whereas, the F_2s were

sown in ten rows. Each row was of 3 m long with a 45 x 15 cm spacing. One non-experimental infector row of a highly susceptible variety CP 42 was also planted, around and in between the experiment, for uniform spread of the disease in the whole experiment. The evaluation was done under uninoculated or natural conditions (E_1) and artificial epiphytotic conditions or inoculated (E_2). Fresh inoculum suspension was prepared by scrapping the culture actively growing for 24 h on nutrient agar medium at 30°C, into the sterile distilled water. This inoculum suspension was adjusted to a standard turbidity (0.1, O.D. at 620 nm) which resulted in inoculum concentration of 6.9×10^6 cells ml^{-1}. This inoculum suspension was sprayed in E_2, 35 days after sowing, as suggested by Gandhi (1984).

The severity of bacterial blight was recorded before and after inoculation on five plants from each parent and F_1, 15 plants from each back cross and 30 plants from F_2 generation of each cross in each replication. The bacterial blight severity (Gandhi, 1984) and disease index (McKinney, 1923) were calculated. Before proceeding to biometrical analysis, the data on per cent bacterial blight severity were subjected to angular transformation (Fisher and Yates, 1957). The joint scaling test (Cavalli, 1952) and generation means analysis (Jinks and Jones, 1958) and perfect fit solution (Mather and Jinks, 1971) were used to estimate the gene effects for bacterial blight reaction.

Results and Discussion

The F_1 mean infection was significantly less than the midparental value in case of HG 75 x RGC 137, HG 75 x Suvidha and Pusa Navbahar x RGC 137, indicating the predominance of resistance over susceptibility, whereas the mean disease intensity of F_1 was higher between Pusa Navbahar x Suvidha. The increase in disease intensity in F_2 compared to F_1 generation was noticed in both the environments for all the crosses except in Pusa Navbahar x Suvidha. This could be due to inbreeding depression for the character studied. The mean values of backcrosses for all the four crosses tended towards their respective recurrent parents.

The calculated x^2 values for three parameter model were highly significant in both the environments indicating the presence of non-allelic interactions in all the crosses. This also showed that the simple additive-dominance model was unable to explain for the total genetic variability in the crosses and thus, warranted the use of six-parameter model. The components (d), (h), (i), (j) and (l) were significant in both environments in the crosses Pusa Navbahar x RGC 137, and Pusa Navbahar x Suvidha (Table 1). The components (d), (h), (i) and (l) were significant in F_1 in cross HG 75 x Suvidha in E_2 and E_1, respectively, whereas, (d), (i), (j) and (l) were significant in cross HG 75 x Suvidha in E_2. This showed that change in environmental conditions and genetic background influenced the estimates of gene effects. It may be noted that the additive (d) and dominance (h) components were significant in all the four crosses in both the environments except for HG 75 x Suvidha in E_2, which revealed the importance

Table 1. Estimation of components of generation means on six parameter model for four crosses in two environments for bacterial blight

Cross	Environments	Gene effects						Type of epistasis
		m	(d)	(h)	(i)	(j)	(l)	
HG 75 x RGC137	E_1	6.62** ± 2.04	1.30** ± 0.11	23.00** ± 5.24	4.20** ± 2.03	2.48** ± 1.48	-22.84** ± 3.32	Dup.
	E_2	14.63** ± 1.82	0.85** ± 0.14	13.47** ± 4.79	-0.86** ± 1.82	1.05 ± 1.40	-16.33** ± 3.06	Dup.
HG 75 x Suvidha	E_1	7.04** ± 3.42	1.88** ± 0.18	24.10** ± 8.65	5.92** ± 3.42	-2.75 ± 2.38	-20.67 ± 5.36	Dup.
	E_2	32.75** ± 2.73	5.54** ± 0.29	-5.08** ± 6.72	-8.44** ± 2.72	-7.99 ± 1.79	-14.09** ± 4.20	-
Pusa Navbahar x RGC 137	E_1	30.38** ± 3.67	7.69** ± 0.15	-54.45** ± 9.46	-19.34** ± 3.67	-11.59** ± 2.68	31.05** ± 5.92	Dup.
	E_2	46.42** ± 2.99	15.57** ± 0.30	-48.30** ± 7.58	-14.78** ± 2.98	-17.92 ± 2.14	31.84** ± 4.72	Dup.
Pusa Navbahar x Suvidha	E_1	13.37** ± 3.90	4.80** ± 0.16	45.93** ± 9.97	11.88** ± 3.90	-15.41 ± 2.78	-26.09 ± 6.19	Dup.
	E_2	14.47** ± 5.39	1.35** ± 0.12	81.19** ± 13.09	26.88** ± 5.39	-31.12** ± 3.32	-46.14** ± 7.90	Dup.

*, ** P=0.05 and 0.01, respectively.

of both fixable and non-fixable gene effects in the inheritance of bacterial blight. Duplicate type of gene interactions were found significant in all the crosses over both the environments except for cross HG 75 x Suvidha in E_2.

Under such situations, it would be difficult for a breeder to evolve genotypes with desired resistance through conventional breeding methods. The only possibility left at present is to go for selective intermating in early segregating generations or mutagenesis of F_1 or F_2 seed which may help in increasing the variation by creating new alleles and/or increasing the range of recombination by breaking the linkages, followed by judicious selection for the trait under consideration.

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