SHORT COMMUNICATION

Components of Genetic Variances, Heritability and Genetic Advance in Maize Lines for Resistance to Northern Corn Leaf Blight in North-west Himalayas

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The study on components of variances, genetic advance and heritability of northern corn leaf blight (turcicum leaf blight) was conducted at VPKAS, Almora during 1999-2001. Four susceptible (CM 128, V 327, V 128 and V 17) and two resistant inbred lines (V 335 and V 13) and their 15 F_1s, 15 F_2s, 15 BC_1s and 15 BC_2s, were generated for study of components of variances, genetic advance and heritability. Additive genetic variance (D), dominance (H) and environmental variance (E) were more in environment E_1 than in environment E_2 in most of the crosses which showed the importance of additive as well as non-additive components and also environmental variance. The broad and narrow sense heritability varied from cross to cross. However, their magnitude was higher in E_1 than E_2. The higher magnitudes of heritability estimates in E_1 were encouraging as it offered viable scope for selection in this environment. The estimates also revealed greater scope of genetic advance in E_1, nevertheless, high genetic advance expressed as percentage of mean were evident for turcicum leaf blight in both environments. The results showed that all types of gene effects *viz*., additive, dominance and epistasis were operating in the crosses in controlling resistance to turcicum leaf blight.

Key Words: Components of variances, Genetic advance, Heritability, Northern corn leaf blight

Turcicum leaf blight (*Helminthosporium turcicum* Pass or *Exserohilum turcicum*) of maize, also known as northern corn leaf blight is the major foliar disease of maize in the plains of India and in Himalayan region, especially Jammu and Kashmir, Himachal Pradesh, Uttaranchal, Sikkim, Meghalaya, Tripura and Assam. The production of the maize in North-west Himalayas (Kumaun hills) of India is low as compared to the other areas of the country. Northern corn leaf blight is the major cause of low yield and may cause 28 to 91% yield losses of maize (Pant *et al.*, 2000; Singh *et al.*, 2004). Most of the maize cultivars, particularly early maturing, have been found highly susceptible.

Success of any crop improvement programme depends on the nature and magnitude of genetic variability available in the crop. The effectiveness of selection largely depends on the degree of heritability and genetic advance for traits under study. The present study was therefore undertaken to investigate heritability and genetic advance for turcicum leaf blight to formulate appropriate breeding strategies for development of high yielding, early maturing and disease resistant maize cultivars suitable for the hilly areas. To reduce the loss from turcicum leaf blight through selecting early maturing resistant maize material, an attempt has been made to access the variability in present material of maize.

Four susceptible (CM 128, V 327, V 17 and V 128) and two resistant (V 335 and V 13) inbred lines were used to develop the F_1 crosses and their segregating generations. These lines, evolved under hilly environment were selected on the basis of their disease reaction and early maturity. These susceptible and resistant lines were crossed in all possible combinations (excluding reciprocals) to get 15 F_1 crosses during *Rabi* (Post-monsoon), 1998-99 at Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS). During *Kharif* (Monsoon), 1999, 15 BC_1s and 15 BC_2s were made along with the advancement of F_1 generation by bulk pollinations to obtain 15 F_2s. The 66 populations comprising 15 F_1s, 15 F_2s, 15 BC_1s, 15 BC_2s and 6 parents were grown in a complete randomized block design during *Kharif* 2000 (E_1) at the Experimental Farm of VPKAS, Almora and during *Rabi* 2000–01 (E_2) at Sihora Farm, Rudrapur, with two replications. Row-to-row spacing of 60 cm and plant-to-plant of 25 cm was maintained at both the locations. Recommended fertilizer dose of 160 Kg N, 60 Kg P_2O_5 and 40 Kg K_2O was applied to the crop at both the locations.

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Components of Variances for Reaction to Turcicum Leaf Blight: Additive (D), dominance (H) and environmental (E) components of variances were worked out following Mather (1949) and the estimates are presented in Table 1. Additive effects were higher in E_1 than E_2 in 10 crosses, *viz*., CM 128 × V 327, CM 128 × V 13, CM 128 × V 128, CM 128 × V 17, V 327 × V 335, V 327 × V 128, V 327 x V 17, V 335 × V 13, V 335 × V 128 and V 128 × V 17. The dominance effects were higher in E_1 than E_2 for 10 crosses and were lower in 5 crosses, *viz*., V 327 × V 13, V 335× V 13, V 335 × V 17, V 13 × V 128 and V 13 × V 17**.** The environmental effects were also higher in E_1 than in E_2 for all the crosses, except in 2 crosses, CM 128 × V 327 and V 13 × V 17. The additive effects were higher in E_1 by 1.0 time, 3.3 times in 5 crosses, by 7.0 to 9.8 times in two crosses, by 19.5 and 19.6 times in two crosses and by 32.5 times in one cross CM 128 × V 17. Thus in environment $E_{1,}$ 10 crosses showed higher magnitude of additive gene effects than in E_2. Like-wise the magnitude of dominance component was higher in E_1 than E_2 by 1.0 to 3.0 times in 10 crosses and was higher in E_2 by 1.1 to 3.5 times and by 21.5 times in one cross V 13 × V 128. Similarly the environmental component was higher in E_1 by 1.2 to 3.2 times in 13 crosses and was higher in E_2 by 1.1 to 1.3 times. On the basis of pooled analysis the magnitude of estimates of dominance component was higher than the additive component for all the crosses. These results indicated that both additive and dominant genetic variance were important in the inheritance of resistance to turcicum leaf blight. The magnitude of additive, dominance and environmental variances was higher in E_1 than in E_2. The ratio $(H/D)^{1/2}$ was more than 1.00 for all crosses in E_1, and in pooled data and in 13 crosses in E_2 indicating over dominance for the trait. Only two crosses, namely CM 128 × V 128 and V 13 × V 128 in E_2 showed the above ratio below 1.00 indicating partial dominance. In a similar study Sharma *et al*. (2003) found that the resistance to maydis leaf blight was controlled by additive gene effects and inbreds CM 104, CM 105 and CM 206 were highly efficient in transferring resistance to their progenies.

Heritability and Genetic Advance for Reaction to Turcicum Leaf Blight: Estimates of heritability broad sense (bs) as well as narrow sense (ns) and genetic advance for turcicum leaf blight in 15 maize crosses in two environments are presented in Table 2. The estimates differed in two environments as well as for different crosses. The heritability (bs) in 15 crosses ranged from 35.42 to 84.44% in E_1, 44.69 to 73.38% in E_2 and 39.03 to 64.99% on the basis of pooled analysis. The estimates of heritability (bs) were higher in 8 crosses in E_1 and in 7 crosses in E_2. The heritability (ns) ranged from 4.0 to 50.0% in E_1, 1.91 to 46.80% in E_2 and 3.40 to 68.60% in pooled data. Estimates of heritability (ns) were higher in E_1 than in E_2 in 10 crosses. The broad sense estimates were high to very high in both the environments, while narrow sense estimates ranged from very low to high in two environments. Furthermore, the estimates of both broad and narrow sense heritability varied in most of the crosses. Such variation was, however, more for heritability (ns) as compared to heritability (bs). Lerner (1958) has also reported that the heritability of a character may vary from one cross to another due to the extent of genetic

Table 1. Estimates of D, H and E components for reaction to turcicum leaf blight in E_1, E_2 and pooled data

Crosses	Additive effects (D)			Dominance effects (H)			Environmental effects (E)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
CM 128 × V 327	0.0469	0.0416	0.0187	0.1800	0.1316	0.1512	0.0528	0.0586	0.0288
CM 128 × V 335	0.0321	0.0725	0.0049	0.5179	0.3163	0.1522	0.1129	0.0347	0.0311
CM 128 × V 13	0.0242	0.0152	0.0416	0.2379	0.1471	0.1363	0.052	0.0361	0.0371
CM 128 × V 128	1.2035	0.0613	0.0416	0.856	0.2854	0.1363	0.0714	0.0376	0.0364
CM 128 × V 17	0.0423	0.0013	0.0416	0.3721	0.2061	0.1363	0.0592	0.0345	0.0333
V 327 × V 335	0.0704	0.0036	0.019	0.3483	0.192	0.0679	0.0787	0.0445	0.0283
V 327 × V 13	0.0638	0.1327	0.0681	0.4879	0.7834	0.2775	0.0755	0.047	0.035
V 327 × V 128	0.1402	0.0532	0.0136	0.3029	0.3022	0.176	0.0792	0.0481	0.0378
V 327 × V 17	0.064	0.0194	0.0397	0.3867	0.1416	0.1871	0.0817	0.0525	0.0291
V 335 × V 13	0.0354	0.0272	0.0429	0.3142	0.3498	0.1286	0.0929	0.0551	0.0289
V 335 × V 128	0.0279	0.004	0.0055	0.1562	0.1274	0.0771	0.0881	0.0406	0.0258
V 335 × V 17	0.0171	0.0898	0.0025	0.2025	0.4334	0.113	0.0767	0.0657	0.0271
V 13 × V 128	0.1742	0.4196	0.0874	0.0475	1.0226	0.3191	0.0752	0.0414	0.0276
V 13 × V 17	0.0102	0.3887	0.1151	0.3029	1.0575	0.3846	0.0574	0.075	0.0323
V 128 × V 17	0.0994	0.0101	0.0194	0.2387	0.1473	0.1677	0.0559	0.0393	0.0206

Table 2. Estimates of heritability and genetic advance for reaction to *turcicum* leaf blight in E_1, E_2 and pooled data

Crosses	Heritability broad sense (hbs)			Heritability narrow sense (hns)			Genetic Advance (GA)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
CM 128 × V 327	56.43	48.37	49.67	19.33	18.34	16.30	10.14	08.85	05.70
CM 128 × V 335	50.11	55.26	55.60	07.10	46.80	03.40	04.90	19.90	01.41
CM 128 × V 13	47.69	44.69	59.66	12.20	11.70	22.62	05.50	04.10	10.92
CM 128 × V 128	84.44	52.03	60.12	31.07	39.10	22.79	16.81	16.30	11.00
CM 128 × V 17	65.85	60.18	62.22	12.20	10.78	23.59	08.49	00.37	11.39
V 327 × V 335	39.74	52.81	48.34	27.00	01.91	17.31	12.70	00.88	05.80
V 327 × V 13	54.42	73.38	50.22	19.20	37.60	48.40	11.90	27.90	18.80
V 327 × V 128	64.81	50.46	57.32	31.16	27.40	07.69	24.51	12.50	03.57
V 327 × V 17	44.2	46.23	48.01	21.90	09.94	35.40	11.40	04.35	12.00
V 335 × V 13	50.89	64.71	64.99	09.36	08.71	26.02	05.98	05.70	12.41
V 335 × V 128	37.57	45.48	39.03	09.89	02.69	06.60	04.69	01.02	01.70
V 335 × V 17	35.42	49.16	52.08	07.20	34.80	02.22	03.00	18.00	00.79
V 13 ×V 128	56.82	52.52	56.65	50.00	40.40	68.60	32.40	06.00	26.80
V 13 × V 17	55.15	48.28	54.49	4.00	13.40	08.12	02.20	73.10	32.90
V 128 × V 17	70.23	44.71	61.02	26.46	07.10	18.40	19.79	02.60	06.80

variance present in the parents. High heritability was also reported in the study conducted by Welz and Geiger (2000) for resistance to turcicum leaf blight. The genetic advance ranged from 2.20 to 32.40% in E_1, 1.02 to 73.10% in E_2 and 0.79 to 32.90% in pooled analysis. The genetic advance was relatively higher in E_1 in 11 out of 15 crosses. The broad and narrow sense heritability estimates were higher in more number of crosses in E_1 than in E_2 for reaction to turcicum leaf blight. The higher estimates of additive component of variance, heritability and genetic advance in E_1 environment indicated that selection for turcicum leaf blight is likely to be more effective in E_1 than in E_2 environment.

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