

Study of Combinability and Gene Effects of Yield and its Components in Corn Hybrids

Abstracts

In plant breeding programs selection of parents should be done based on general and specific combinability to achieve the desirable results. In this study 20 S₆ inbred lines as female and three S₆ elite inbred lines (K19, K18 and K1264/5-1) as male parents were crossed in 3 isolated fields and then 60 test crosses were planted in RCBD with 3 replications. The measured traits were days to anthesis and silking, anthesis silking interval (ASI), plant height, ear height, stem diameter, leaves no. above ear, total leaves no., ear no./plant, kernel no. /row, rows no., kernel no./ear, ear diameter, ear length, kernel depth, physiological maturity time, 1000-seed weight, percentage and severity of smut disease and tassel disease percentage, no. disease plant, stalk and leaf infection, grain and forage yield. The results showed significant differences between test crosses for all of measured traits except for ear no./plant (in grain yield) and ASI, percentage and severity of smut disease and tassel disease percentage (for forage yield). The line × tester analysis showed significant lines and testers variances for plant height, ear height, days to anthesis and silking, leaves no./plant, ear no./plant (in forage yield), kernel no./row, rows no./ear, kernel no./ear, ear diameter, ear length, kernel depth, 1000-seed weight, grain and forage yield. Also variance of tester for stem diameter and physiological maturity was significant, while variance of lines was significant for ear no./plant (forage yield). The line × tester variance was significant for days to anthesis and silking, rows no., kernel no./ear, and physiological maturity. Estimation of GcA showed that lines no. 4, 9 and 25 (for forage yield) and lines no. 6 and 9 (for grain yield) had significant differences (p=0.05). The tester K1264/5-1 had the highest GcA for forage and grain yield. For smut disease tolerance, also, only the no. of infected plants and no. of stem and leaf disease traits was significant for crosses variance. Division of cross variance showed testers effects was significant for stem and leaf disease, while line effects was important for the no. of infected plants, which shows the additive effects role of genes in control of smut disease tolerance.

Key words: *Zea mays L.*, test cross, gene effects, GcA, ScA, inbred line, tester.



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