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Studies on Combining Ability and Heterosis in Maize (Zea may, L)

1. Growth Attributes

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A complete diallel cross analysis among eight inbred lines and Pioneer 514 were evaluated in two planting dates (early and late) for tasseling date, Silking date plant height, ear height and leaf area. Data were ganetically analysed by the procedures developed by Griffing (1956). Planting date mean squares were highly significant for all attributes. Genotypes mean squares reached the significance level of probality for all traits. Appreciable genotype by planting date interactions were detected for all traits except eat area. Significantly positive correlation coetficinnt values between mid-poritenf values and F_1 mean values obtained for, tasseling date, plant height, ear height and leaf area.

The mean squares associated with general GCA and specific SCA combining abilities were highly significant in all traits. High rations which largely exceed the unity were obtained in all traits except plant height, indicating that the largest part of the total genetic variability associated with those traits was result of additive and additive by additive gene action. Significant reciprocal SCA mean squares were obtained for, tasseling date, ear and plant height. Significant GCA and SCA by planting dates mean squares were obtained in all traits.

Both inbred lines R_{g10} and K_{64} expressed the best combiners for Silking and tasseling dates, and plant and ear heights. While. both inbred lines G. 444 and G. 227 B seemed to be the best combiners for leaf area. The crosses (1 × 8) and (3 × 8) had the lowest values of SCA effects for earliness. Insignificant SCA effect was detected in seven crosses for plant height. Leaf area, six crosses had significantly positive SCA effect.

EARLINESS, if found in corn, is favourable for escaping destructive injuries caused by **Sesamia cretica** Led, **Chilo simplex** and **Pyrausta nubilalis** Hb. Much efforts are devoted nowadays to increase its productivity through genetiacal improvement. To carry out a successful breeding programme, the breeder should have enough knowledge about the type and relative amount of genetic variance components and their interactions by environments for the attribute in question.