

BREEDING STUDIES ON MAIZE  
I-LATE WILT DISEASE RESISTANCE

BY

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ABSTRACT

The differences between the two parental strains in each cross as well as the  $F_2$  genetic variability estimates for late wilt were found to reach the significant level only for two resistant X susceptible crosses, namely, K6 x G4 and Rg11 x G 303 A.

Highly significant negative heterotic effect and inbreeding depression were detected for the two crosses. Resistance to late wilt disease was found to be partially dominant over susceptibility in the two crosses. Epistatic deviation of  $F_2$  ( $E_1$ ) and back crosses ( $E_2$ ) were significant in the two crosses. Both additive and dominant types of gene action were important in the inheritance of resistance to late wilt disease. Furthermore, (ad) type of gene action was more important than (aa) and (dd) types. High estimates of heritability in both broad and narrow sense were found in both crosses. Also, high predicted genetic gain estimates were obtained in both crosses.

INTRODUCTION

Maize like other crops is attacked by several diseases and pests. One of the most destructive diseases is late wilt caused by cephalosporium maydis. This disease was found in all maize growing areas in both Lower and Upper Egypt. The degree of infection varies from zero to 80% in fields. Late wilt disease is wide spread and serious. So, it is imperative to breed varieties having a high degree of resistance to such disease. Therefore, the objective of the present investigation is study the inheritance of resistance to late wilt disease.

MATERIALS AND METHODS

The present investigation was carried at the Research and Experimental center of the Faculty of Agriculture, Moshtohor, Kalubia Governorate, during the three successive