

SELECTION IN SESAME UNDER GREENHOUSE AND FIELD  
CONDITIONS FOR IMPROVING YIELD AND  
FUSARIUM WILT RESISTANCE  
BY

Ghallaab, K.H\* and Bakeer, A.T.\*\*

\* Agron. and \*\*Agric.Botany Dept., Fac. Agric. at Fayoum, Cairo Univ.

ABSTRACT

Selection for yield and wilt tolerance was practiced in early generations of some sesame crosses, at the experimental Farm, Fac. Agric. at Fayoum, Cairo Univ., during 1998, 1999 and 2000 summer seasons. From  $F_2$  populations grown in a naturally infested field in 1998 season, 46 genotypes were selected. Wilt pathogen was isolated and identified as *Fusarium oxysporum f. sp. sesame* (Schlecht). In 1999 season among five isolates, the highly virulent one (IV) was propagated, and used for artificially infection to the 46  $F_3$  progenies and the check cv. "G.32" in greenhouse. During the same season, all progenies were grown in the naturally infested field and subjected to selection. In 2000 season, 14 selected  $F_4$  lines were evaluated.

Analysis of variance showed highly significant differences among the tested genotypes in yield, yield components and disease characters in  $F_3$  and  $F_4$  generations. Genotypic differences were also detected for total phenol contents as well as the activity of polyphenoloxidase and peroxidase enzymes estimated either in healthy or diseased plants of either the highest or the lowest susceptible genotypes; indicating their importance of the biochemical changes for wilt tolerance. Depending upon the  $F_3$  performance, and correlations among yield and its components and disease characters, 14 high yielding and tolerant lines were selected and evaluated in  $F_4$  generation. Dissimilar performance was observed between the base populations ( $F_3$ ) and selected ones ( $F_4$ ) due to the effect of selection as well as changes in homozygosity, gene actions and environmental influences. Nevertheless, some of these selected  $F_4$  lines showed consistency for some characters over generations.

The  $F_4$  selected lines showed visible improvement in most of the studied characters. Among them 12 wilt tolerant lines out-yielded the check cv. G.32. Further improvement for yield and tolerance by selection procedures was proposed.

Key words: Selection, Genotypes, wilt disease, chemical composition and character association