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Inheritance of Resistance to *Aspergillus flavus* in Groundnut

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Abstract

The fungus *Aspergillus flavus* strain commonly infects groundnuts (*Arachis hypogaea*) and produces a potent class of hepatocarcinogenic known as aflatoxins. Host-plant resistance to *A. flavus* infection is considered the most effective method for reducing aflatoxins, but the resistant germplasms are limited. This study was conducted to evaluate the types of gene action governing the inheritance of resistance to *A. flavus* infection at pre-harvest, by estimating combining ability in groundnut populations obtained from half-diallel crossing among 5 parental lines involving three resistant (J11, ICGX990093 and ICGX990094) and two susceptible (Khon Kaen4 and ICGV91066) groundnut genotypes. The 10 F1 hybrids and the 5 parental lines were evaluated for the quantitative character: percent-infected peg and the qualitative character: percent-infected peg area fluorescence. The results show that the general combining ability (GCA) mean squares were significant for all traits, demonstrating the variability of GCA of the parents. The specific combining ability (SCA) mean squares were only significant for percent-infected peg area fluorescence. This indicated that the importance of additive gene effects was the main cause of the observed genetic variation for percent-infected peg. However, the highly significant of GCA as well as SCA in percent-infected peg area fluorescence indicates the importance of both the additive and the non-additive gene effects. Thus, hybrid combinations with low percent-infected area fluorescence, with the favourable SCA estimates and involving at least one of the parents with high negative GCA in both quantitative and qualitative characters, would tend to increase concentration of favourable alleles, a situation of great interest to breeding for resistance to *A. flavus* infection.

Keywords: *Aspergillus flavus*, combining ability, groundnut, (*Arachis hypogaea*)