

Relative Importance of Variability Sources in Smut Resistance Assessment in Field Tests

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Genetic resistance seems the most promising tool for peanut smut management. Resistance sources for breeding use are sought without a clear idea of how important is each source of variation (season, genotype, blocks) in a smut resistance assessment test in each location. Data from tests looking for resistance among different genotypes were analyzed in order to quantify the relative importance of each variation source in the test.

Seven seasons of a smut resistance test carried out at a farm were analyzed. The test included 13 commercial cultivars with little degree of common ancestry, 4 breeding lines and 2 necrotrophe-resistant PIs. Two checks were planted all the 7 seasons while other 17 genotypes were tested in variable number of them.

An RCB design with four reps was mostly used except in one season, where that number was reduced to three. Two row plots (12 ft long) were always used with a plant density of 3.3 seeds/ft. Tests were planted in fields of the same farm, downwind from a processing peanut plant which assured high smut inoculum in the soil (5500 spores/g). Smut incidence (SI) in a plot was calculated as $SI = (\text{number of infected pods} / \text{total number of pods}) * 100$. A factorial structure ANOVA (season & genotype) was performed on SI assuming both factors (season & genotype) as random. The relative size of the covariance parameters was estimated.

Season was the most important variability source with 298 ± 176 (variance component \pm standard error), while the genotype was much smaller but still reasonably important (67 ± 27) as compared with a residual of 74 ± 8 . The main factors' interaction was relatively small (19 ± 9) while block had very small estimate (5 ± 3). These results highlight the importance of multiple years for a correct characterization of resistance as disease can go from mild to severe depending on the season and that in years of low incidence can cause difficulties in separating levels of resistance. GxE I seems to pose a small danger of mischaracterizing genotypes' resistance.