

Relationship Among Field and Post-Harvest Evaluations of Spotted Wilt in *Arachis* Germplasm

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Spotted wilt resistance evaluation in peanut is challenging due to its quantitative/horizontal nature, including a highly variable number of symptomatic plants with different severities in field plots. Under severe epidemic conditions in the 2018 season, we evaluated the wild ancestors of peanut (*A. ipaënsis* and *A. duranensis*), a synthetic polyploid (IpaDur1) and seven breeding lines related to the wild ancestors. TifNV-High O/L and SunOleic 97R were the resistant and the susceptible checks. Resistance evaluations in the field were recorded as disease intensity rating (DIR1), disease index at the beginning (ISEV1) and at the end of the growing season (ISEV4) and area under disease progress curve for the disease index (AUDPC ISEV). Evaluations of the seeds (testa) were recorded as number of symptomatic (NSymp) and normal (NNormal) seeds, and disease intensity rate (DIR seeds). *Tomato spotted wilt orthotospovirus* was detected from both leaf samples (Immunostrip-ELISA) and seed (testa) samples (RT-PCR) against Nucleo capsid protein.

A wide range of variation among the wild species and breeding lines was observed. *A. ipaënsis* and two breeding lines ranked close to TifNV-High O/L. Accuracy was high for all the variables evaluated. Both ISEV4 and AUDPC ISEV were positively correlated to DIR seeds. ISEV4 and AUDPC ISEV were negatively correlated to NNormal.