

## **Introgression of Wild *Arachis cardenasii* Alleles into Cultivated Peanut to Confer Resistance to Early and Late Leaf Spot**

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Cultivated peanut (*Arachis hypogaea* L.) has low to moderate level of resistance to both Early (ELS) and Late leaf spot (LLS). These diseases can cause tremendous yield loss when not properly managed. Effective fungicide spray programs are currently used to control these diseases but resistant cultivars are still the best way to mitigate them. Hence, this study aims to obtain lines with multiple resistances that combine wild-derived segments that confer long-term, high level of resistance to foliar diseases with resistance to root-knot nematode (also from *A. cardenasii*) and the high oleic property from cultivar 'TifNV H/O'. Crosses were also performed using cultivar 'Bailey', with resistance to various diseases including ELS and an advanced line (IAC 321) with resistance to LLS and rust. Both peanut genotypes have different segments derived from *A. cardenasii*. F<sub>1</sub> seeds were harvested and hybridity was confirmed using Kompetitive Allele Specific PCR (KASP) analysis. Two true hybrids (Bailey x IAC321\_F1) were germinated and used as male parents for backcrossing to Bailey and TifNV H/O. BC1F1 seeds were harvested and hybridity was confirmed. Then, BC1F1s with different segments were evaluated for ELS and LLS resistance using a detached leaf bioassay. Four different components of resistance were measured: incubation period (IP), lesion number per leaf area (LN/LA), number of sporulating lesions per leaf area (SL/LA), and percent diseased leaf area (DLA). ELS bioassay results revealed significant differences among hybrids and susceptible controls based on the LN/LA, SL/LA and DLA. On the other hand, results in the LLS bioassay showed significant differences among hybrids and susceptible controls based on the IP, LN/LA, and DLA. AUDPC values on both ELS and LLS bioassays also statistically varied between hybrids and susceptible controls. Overall results suggest that hybrids with segments from Bailey and IAC 321 exhibited higher level of resistance to both ELS and LLS than the parents. Development of advanced lines with different alleles conferring various disease resistance segments will provide long-term protection to these fungal diseases.