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ABSTRACT BOOK



AAGB/PP-02: Exploring Novel Sources of Resistance to Late Leaf Spot in Groundnut (*Arachis hypogaea* L.)

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Peanut (*Arachis hypogaea* L.), commonly known as groundnut, is a significant oilseed crop cultivated in over 100 countries worldwide. Late leaf spot (LLS) is a severe disease affecting groundnut, leading to yield losses of up to 50%. Development of resistant varieties is considered a preferred strategy to manage LLS due to its cost-effectiveness and reduced environmental damage compared to other control methods. To date, GPBD 4, derived from *Arachis cardenasii*, is the sole source of resistance against LLS globally, serving as a basis for developing disease-resistant or tolerant varieties. However, encouragingly, other wild species have been identified with high resistance. Introgression lines, developed from synthetic crosses with these wild species (*A. kempffmercadoi*, *A. hoehnei*, *A. duranensis*, *A. batizocoi* and *A. ipaensis*) have shown a disease score of 2, outperforming GPBD 4. SNP-based allele mining of these introgression lines, using markers from GPBD 4 for LLS resistance (Chr13_142435734 (C/T), Chr13_144038674 (T/C), Chr13_143296024 (AG/A)) which encode for the proteins receptor like protein 29 and Pentatricopeptide repeat-containing protein revealed the absence of those alleles, suggesting the presence of additional significant alleles for resistance from the wild species. Identifying the genes responsible for resistance present in these new sources is critical. A total of 705 introgression lines, developed through back-crossing (ICGV91114 × ISATGR 121250, ICGV87846 × ISATGR 265-5A, ICGV87846 × ISATGR-278-18, TMV2 × ISATGR 121250) and advanced to BC₂F₁₀ and BC₂F₇, were screened for resistance, and the best-performing lines, superior to GPBD 4, were selected during rainy 2024. These best performing ILs will again phenotype during rainy 2025 for trait confirmation, followed by making these available to global research community.

Keywords: Introgression lines, Wild species, Back-crossing, Allele mining