13th International Conference

AAGB-2025

ADVANCES IN ARACHIS THROUGH GENOMICS AND BIOTECHNOLOGY

23rd-25th MARCH 2025 | NOVOTEL, CANDOLIM, GOA, INDIA

ABSTRACT BOOK

AGB GOA

23rd-25th MARCH 2025,
NOVOTEL, CANDOLIM, GOA, INDIA

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AAGB-09: Uncovering Novel Sources of Stem Rot Resistance in Groundnut: Insights from Diverse Gene Pools and Genomic Regions

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Stem rot, caused by the soil-borne pathogen *Sclerotium rolfsii*, is a significant threat to groundnut cultivation, particularly in regions like the United States, India, and Australia, leading to yield losses of up to 80%. A multi-season phenotyping study was conducted on 184 minicore germplasm accessions under both sick field conditions and oxalic acid assays, revealing high heritability with a substantial environmental influence (36%). The oxalic acid assay demonstrated an 80% concordance with field screening, providing a reliable complement to field-based phenotyping. Genotypes ICG163, ICG875, and ICG111 exhibited consistent and stable resistance across seasons. Resistance was exclusive to Virginia-type groundnut, including both bunch and runner types. Genotyping with the 'Axiom_*Arachis*' array (58,000 SNPs) identified 13 stem rot resistance-associated genomic regions across 8 chromosomes through GWAS, with LOD scores between 4.5 and 12.4, and R^2 values ranging from 6.9% to 58%. A total of 145 candidate genes linked to resistance stages were identified, including those involved in pathogen perception, inhibition, toxin detoxification, stress tolerance, and transcription factors for protective compound synthesis. Pathway analysis highlighted immune response mechanisms during early stage of infection and triggered a hypersensitive response in severe infection conditions leading to apoptosis. All Marker-trait associations (MTAs) were validated using allele-specific markers, facilitating their direct application in breeding. Introgression lines developed from secondary gene pool species (*A. kempff mercadoi* × *A. hoehnei*) and tertiary gene pool (*A. glabrata*) identified higher resistance genotypes, with lines like ICGIL 17101 showing <10% mortality. Ongoing efforts involve crossing *A. glabrata* with cultivated groundnut using embryo rescue techniques, providing valuable resources for breeding programs.

Keywords: Resistance source, Secondary gene pool, Introgression lines, Stem rot disease