13th International Conference

AAGB-2025

ADVANCES IN ARACHIS THROUGH GENOMICS AND BIOTECHNOLOGY

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

ABSTRACT BOOK

AAGB GOA

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

ICRISAT
INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

THE PEANUT RESEARCH FOUNDATION

AAGB/FT-09: Candidate Gene Discovery and Marker Development for Fresh Seed Dormancy in Groundnut

Khaja Mohinuddin D.[1,2], Sunil S. Gangurde[1], Deekshitha Bomireddy[1], Priya Shah[1], Vinay Sharma[1], U. Nikhil Sagar[1], Namita Dube[1], Hasan Khan[2], B.V. Tembhurne[2], V. Hanumanth Nayak[2], Amaregouda A[2], Kisan Babu[2], Ramachandran Senthil[1], Baozhu Guo[3], Sandip K. Bera[4], Kuldeep Singh[1], Sean Mayes[1], and Manish K. Pandey[1*]

[1]Center of Excellence in Genomics & Systems Biology (CEGSB) and Center for Pre-Breeding Research (CPBR), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru-502324, Hyderabad, India
[2]Department of Genetics and Plant Breeding, University of Agricultural Sciences, Raichur, Karnataka-584104, India
[3]USDA-ARS Crop Protection and Management Research Unit, Tifton-31794 Georgia, USA
[4]ICAR – Indian Institute of Groundnut Research, Junagadh-362001, India
*Correspondence: manish.pandey@icrisat.org

Groundnut (*Arachis hypogaea* L.) suffers significant yield and seed quality losses due to pre-harvest sprouting. In order to identify associated genes and markers we used whole genome resequencing (WGRS) and generated two season of replicated phenotyping data on fresh seed dormancy (FSD) in minicore collection of ICRISAT (184 genotypes). The analysis revealed considerable phenotypic variability in dormancy durations, with days to 50% germination (DFG) ranging from 1 to 30 days. Statistical evaluations indicated highly significant differences in FSD among the accessions, with heritability estimates around 90%, suggesting strong genetic control over this trait. Using genome-wide association studies (GWAS), we have identified 27 MTAs for individual seasons and 12 MTAs for pooled seasonal data. Candidate genes linked to these associations encoded proteins from the *Cytochrome P450 superfamily*, *protein kinase superfamily*, *WRKY family transcription factors*, and *MYB transcription factors* involved in the abscisic acid (ABA) pathway. Additionally, *F-box interaction domain proteins*, *ATP-binding ABC transporters*, and *GATA-type zinc finger transcription factors* associated with the gibberellic acid (GA) pathway were also identified. The findings underscored the importance of the ABA-GA balance in regulating seed dormancy. We have developed and validated eight markers for tracking FSD in breeding programme. These results suggest that integrating favourable dormant alleles into breeding programs could lead to the development of high-yielding cultivars with a dormancy period of 2-3 weeks. This strategy could help reduce yield losses caused by pre-harvest sprouting due to early rainfall and advance breeding efforts aimed at enhancing seed dormancy traits in groundnut.

Keywords: Groundnut; Seed dormancy; Genome wide association study; Candidate genes; ABA and GA pathway.