

ABSTRACT

Groundnut rosette disease (GRD) is a viral disease endemic to sub-Saharan Africa (SSA), which severely devastates groundnut leading to pod yield losses of up to 100% in susceptible varieties. Deploying resistant groundnut varieties is the most sustainable approach to managing the disease. Over the years, several breeding programmes have done a great job in developing, testing, and releasing resistant varieties for the farmer using phenotypic data. However, the genetic diversity of these lines was not known. Moreover, the genetics of resistance to GRD were still vaguely understood. This work aimed to evaluate a genetically diverse Groundnut Improvement Network for Africa (GINA) core collection for GRD resistance, high yield and elucidate the genomics of resistance to GRD through genome-wide association studies (GWAS), haplotype analysis and linkage mapping. 229 lines from the GINA core collection were screened across two GRD hotspot locations in Uganda, namely Nakabango and Serere, over the course of three seasons (2020A, 2020B and 2021B). A maximum of 200 genotypes were planted per season in a lattice design. Data for GRD percentage disease incidence (PDI), severity and yield were collected. GWAS were done to identify marker-trait associations using the Enriched Compressed Mixed Linear Model (ECMLM). GWAS analysis used area under disease progress curve (AUDPC) for percentage disease incidence (PDI) in conjunction with 7523 stringently filtered high-quality single nucleotide polymorphisms (SNPs) to identify associations between markers and traits. Haplotype analysis was done by determining haplotype blocks using stable markers in the significant genomic regions identified by GWAS. Associations were tested between the haplotype blocks and AUDPC Best linear unbiased prediction (BLUP) values. Linkage analysis combined phenotypic and genotypic data from an F₂ bi-parental mapping population from parents Serenut 1R (susceptible parent) and ICGV-SM 91707 (resistant parent). Screening results revealed phenotypic variability for GRD resistance and yield in the GINA core collection; six (6) genotypes were identified with GRD resistance and high yields. GWAS successfully identified a total of thirty-two (32) significant marker-trait associations (MTAs) at the Nakabango location: twenty-one (21) were found on chromosome A04, ten (10) on chromosome B04 and one (1) on chromosome B08. Several genes were identified in this region, including a TIR-NBS-LRR disease resistance gene and an Argonaute protein associated with RNA silencing in viruses. Haplotype analysis identified five haplotypes that were highly significant with GRD resistance on the A04 and B08 genomic regions but not B04. Two genotypes, both from Uganda possessed all the five haplotypes. Linkage QTL mapping identified four QTLs, with the largest explaining up to 5.28% PVE. High-yielding and resistant genotypes with favourable haplotypes can be utilized as parents for breeding or widely tested for their adaptability and released to farmers. Molecular markers identified in the GINA core collection can be converted into easy-to-use molecular marker assays for GRD resistance breeding across Africa.