Association mapping and genomic selection for resistance to leaf spot diseases and agronomic traits in groundnut (*Arachis hypogaea* L.)

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Abstract

Groundnut (*Arachis hypogaea* L.) is one of the most important climate-resilient oil crops in sub-Saharan Africa (SSA). There is a significant yield gap for groundnut in Africa because of poor soil fertility, low agricultural inputs, biotic and abiotic stresses. Cross-country evaluations of promising breeding lines can facilitate the varietal development process. The objectives of the study were to: (1) determine the performance of advanced groundnut genotypes for yield traits and reaction to leaf spot diseases across different environments, (2) identify genomic regions associated with resistance to leaf spot diseases and yield traits, and (3) determine the potential of genomic prediction for resistance to leaf spot diseases and yield traits. Phenotypic data was generated for 192 breeding lines for yield-related traits, while genotypic data was generated using skim sequencing. A significant variation ($P<0.001$; $P<0.01$; $P<0.05$) across genotypes for all yield-related traits; days to flowering (DTF), pod yield (PY), shelling % (SH%), hundred seed weight (HSW) and grain yield (GY) within and across locations was observed. Nakabango, Chitedze and Serere were clustered as one mega environment with the top 5 most stable genotypes being ICGV-SM 01709, ICGV-SM 15575, ICGV-SM 90704, ICGV-SM 15576 and ICGV-SM 03710, all Virginia types. Population structure analysis clustered the genotypes in three distinct groups based on market classes. Eight and four marker-trait associations (MTAs) were recorded for DTF and PY, respectively. One of the MTAs for DTF was co-localized within an uncharacterized protein on chromosome 13, while another one (TRv2Chr.11_3476885) was consistent across the 2 countries. Days to flowering gave the highest predictive ability across all models. Prediction accuracies (PA) for shelling percentage and pod yield were country-specific, unlike other traits. Fitting associated SNPs as fixed effects consistently improved PA of all traits. The results of this study provide insights into the nature of genetic variations governing leaf spot diseases and yield traits in groundnut.