ABSTRACT

Sorghum (*Sorghum bicolor* [L.] Moench) is a multi-purpose crop ranked fifth as the World's major cereal after Maize, Wheat, Rice and Barley in terms of worldwide production and acreage. In Uganda, it is the third most important staple cereal food crop after maize and millet occupying over 400,000 ha of the total arable land with a production of 580,000 metric tonnes. Despite the economic importance of Sorghum, its production is severely constrained by a downy mildew disease. Sorghum downy mildew (SDM) is caused by a seed-borne obligate fungi *Peronosclerospora sorghi*, which limits the production and productivity of the crop. It affects sorghum plants from seedling till harvesting stage, exhibiting both localized and systemic infections with recurrent epidemics. Economic losses reaching 100 % have been reported depending on the cultivar type, source of planting material (seeds), environment, and developmental stage of the host plant. There is currently no SDM resistant cultivar released in Uganda though the disease is endemic. Host plant resistance in disease management is sustainable and environmentally safe method for limiting inoculum build-up, spread and development of disease. The objectives of this study were to: (i) map the prevalence and distribution of sorghum downy mildew (SDM) disease and sample collection of *P. sorghi* biotypes; (ii) characterize the biotypes of *Peronosclerospora sorghi* in sorghum (iii) identify sources of resistance to downy mildew disease and (iv) determine the genetics of sorghum resistance to downy mildew disease. Field surveys were carried out between March-June, 2016 and September-December 2016 growing seasons in 13 major sorghum-growing districts across 10 agro-ecological zones. During the survey, disease leaf samples were collected from farmers' fields. Significant ($P < 0.001$) differences were recorded for disease incidence and severity across the different agro-ecologies. The mean downy mildew disease incidence varied significantly ($P< 0.001$) from 49.4 % for Pader to 78.9 % for Namutumba. Disease severity varied significantly ($P <0.001$) from 2.3 for Pader to 3.5 for Pallisa. Arua, Namutumba and Pallisa were identified as SDM disease hot spots. Following the field survey, morphological (based on the shape and size of conidia and oospore and the presence of sporangia) and molecular (based on random amplified microsatellites-*RAMS and inter-simple sequence repeat –ISSR markers)* techniques were used to determine variations within *P. sorghi* isolates in Uganda. A total of 195 *P. sorghi* isolates sourced from leaf samples were identified and used for this particular study. Cluster analysis of 195 *P. sorghi* isolates based on their morphological structures showed three significantly distinct morphological groups. A significant pathogenicity reaction ($P < 0.05$) with values ranging between 10.0 % - 93.3 %

was observed. Genetic variation among the studied regions (2.7 %, PhiRT = 0.022) was not significant. Seven distinct cluster molecular groups were formed from the 195 *P. sorghi* isolates based on their genetic similarity. Mantel test revealed no association between genetic differentiation and geographical distance and therefore implied that breeding different resistant sorghum cultivars for the different agro-ecologies in Uganda is not expedient. 100 sorghum genotypes, including five introductions from USDA-USA were screened at Makerere University Agricultural Research Institute Kabanyolo (MUARIK) and Abi-Zonal Agricultural Research and Development Institute (Abi-ZARDI) research station at Arua, between August –November, 2016. A 10 x 10 alpha lattice experimental design was used and six lines, comprised of two SDM resistant (P1 656061 and P1 533831) and four moderately resistant (E 40, MAKSO 8, P1 655990 and Epuripur) lines were identified across the two locations that could serve as parental lines. Six male lines (2 SDM resistant and 4 moderately resistant) were crossed with three female (all SDM susceptible) lines using North Carolina II mating design to generate 18 hybrids and advanced to F_2 seeds. The F_2 hybrids together with the 9 parental lines were evaluated at two different locations (Arua and Kabanyolo) to study the heritability and gene action controlling resistance to *P. sorghi*. General combining ability (GCA) and specific combining ability (SCA) across the two locations showed significant differences ($P < 0.001$ - $P < 0.05$) for four traits viz., Area under disease progress curve (AUDPC), plant height, 1000 seed weight and grain yield. Parents P1 656061 and P1 533831were the two best combiners for improvement in SDM severity, early maturity, 1000 seed weight and grain yield. The crosses SESO 1 x Epuripur and SESO 1 x P1 656061 significantly improved resistance to SDM disease and grain yield, respectively. Both additive and non-additive gene action effects were involved in traits for AUDPC, plant height, 1000 seed weight and grain yield but additive gene action was predominant over non-additive for the transfer of these traits.