GENOME WIDE ASSOCIATION STUDY TO ESTABLISH THE GENETIC BASIS FOR BLAST INFECTION TOLERANCE IN FINGER MILLET AND ITS BLAST PATHOGEN IN EASTERN AFRICA

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Finger millet is one among the small grain millets which is an important food and income source for most of the people in the rural and semi-arid areas in eastern Africa. Most of the farmers use unimproved varieties which are vulnerable to biotic and abiotic stresses. Finger millet blast disease, caused by the filamentous oomycete fungus *Magnaporthe oryzae*, accounts for up to 90% of yield losses experienced in combination with other abiotic stresses. Efforts to characterize the population diversity of this fungus in eastern Africa have been done recently. The development of blast-resistant finger millet varieties is widely accepted as the preferred approach towards blast management, compared to the alternative use of pesticide, which is expensive. For this to be achieved, knowledge of the genetic basis of resistant traits in finger millet is essential. To date, no literature identifies the genomic regions in finger millet and *M. oryzae* which are associated with the blast resistance trait and virulence of the pathogen. The proposed study, therefore, aims to perform genome-wide association analysis for blast resistance to identify genomic regions both in finger millet and *M. oryzae* and determine their contribution towards the finger millet blast resistance trait. To achieve this, 182 finger millet accessions genotyped by genotyping by sequencing (GBS) and a panel of 226 blast isolates for which Illumina whole-genome sequencing was completed and single nucleotide polymorphisms (SNPs) identified, will be used. Two genome-wide association approaches will be followed. First, finger millet genomic regions associated with blast resistance will be determined using a classic genome-wide association study (GWAS) followed by a similar, but inverse approach that we refer to as "reverse-GWAS" (rGWAS), which will identify fungal genomic regions enabling virulence on the finger millet host. Visual blast rating score (ranging from 0 - 4) data was previously collected from infection assays with (1) four diverse and virulent blast isolates on the panel of 182 finger millet accessions and (2) all 226 blast isolates on four diverse finger millet varieties. These scores will be used as phenotype data for GWAS and rGWAS, respectively. Quality control and data manipulation will be done in TASSEL v.5.2.67 and R v.4.03, respectively. Both population structure, linkage disequilibrium analysis and marker-trait association, using the linear mixed model, will be done using the GAPIT R package. The findings of this work can be used in genomic selection to develop blast resistance in agronomically important finger millet varieties that are preferred by farmers and well adapted for specific agro-ecologies, in order to design biological control strategies against the blast pathogen as well as in future research focusing on isolating blast-resistance gene(s) in finger millet.

Biography

Hesborn has completed his Masters in Bioinformatics at the age of 25 years from Pwani University and has a degree in Biomedical sciences and Technology from Egerton University. He is currently a research fellow at Pwani university biosciences research lab

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