**Exploring the phylogenetic evolution and geographic transmission patterns of the rice blast *Magnaporthe oryzae***

Rice blast disease is caused by a fungal pathogen, *Magnaporthe oryzae.* Its outbreaks keep reoccurring in areas where rice is grown resulting in major losses to rice production globally and in turn threatening global food security. Having a better understanding of the pathogen’s evolutionary history will help in informing measures taken in future towards combating its spread and in managing the disease.

In previous studies, the pathogen has been widely studied and especially in Asia. Most of these studies place isolates from South East Asia in the basal position in the phylogeny. Only a few isolates from some African countries have been included in these population genetic studies involving whole genome sequencing and global phylogenetic studies. As a result, this has provided insufficient clues about patterns of introduction and migration routes of the pathogen in the continent.

This study will focus on whole genome data of 50 isolates from various African countries. We will identify and characterize these strains based on the variable sites in the genomes by focusing on SNPs. We will also look at the evolution of genes that are known to be important in virulence, pathogenicity and fitness in relation to the diversity of the germplasm currently present in East Africa. We will also examine signatures of adaptation in these African strains to dissect potential selection and demographic processes that may probably provide clues for the future management of this disease.