

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

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Abstract

Rice blast disease is caused by a fungal pathogen, *Magnaporthe oryzae*. Outbreaks of the disease reoccur in rice growing areas resulting in major losses to rice production, consequently threatening global food security. Previous studies have determined the origin and lines of descent, population structure and virulence dynamics of the pathogen. Some studies place isolates from South East Asia in the basal position in the phylogeny. This supports the idea that *M. oryzae* originated from Asia, from where it dispersed to the rest of the world.

In Africa, molecular analysis based on non-sequence based markers and a few conserved genes have shown minor differences between strains from major rice growing areas. However, only a few isolates from limited African countries have been included in 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 Africa.

This study will focus on whole genome data obtained by illumina sequencing. 50 isolates of *M. oryzae* from various African countries will be primarily characterized based on the occurrence of SNPs throughout the genome. We will then look at the evolution of particular genes such as *Pi9*, *Pita2*, *Pil2* known to be important in virulence and pathogenicity according to previous studies. Signatures of adaptation to different environmental conditions in these strains will be studied. Having a better understanding of the pathogen's phylogeography will help in informing future measures taken towards combating its spread and in managing the disease.

My motivation...

Food is a basic human need. It is the sole source of energy for the human body. The size of the human population is projected to increase in the coming years. Consequently, food production will be expected to increase in order to feed the growing population. Increased food production will only be possible if the plants in the fields are healthy. Suffice to say that productivity is directly proportional to improved health. Rice is among the most common staple foods in many households around the world. It is very versatile with regards to how it can be prepared and served. However, this favourite dish is in trouble!

Rice blast disease is a “cereal killer” and therefore a threat to rice production everywhere. There are many people who rely on rice as a source of livelihood. With the expected increase in cultivation of rice, the disease will inevitably continue to spread and cause havoc in all the rice growing fields. The consequences are significant reductions in rice production as well as a strain on economies. The global food security is also being threatened. If the pathogen is not contained, rice will continue to die in the fields and fail to make it to our dinner tables and rob us the pleasure of savouring it.

This project will contribute to the many discoveries being made in a bid to understand this “cereal killer”. It seeks to fill in the knowledge gap regarding the genetic diversity of the pathogen within Africa. It is a chance to make a difference albeit small. Hopefully, it will feed into the efforts being put in towards management and combating the spread of the disease. I would like to get a chance to attend this conference. It will provide a platform for me to showcase my work as I network with other bioinformaticians and possibly attract future collaborators. I believe seeing what other people are doing will broaden my perspective.