

Mitochondrial genomes of selected *Fusarium* species

Prepared by Dr Mesfin Bogale (Post-doctoral fellow working on the sequencing of Fusarium mitochondrial genomes)

The fungal genus *Fusarium* consists of many species that cause different types of diseases in a wide range of plant species. For example, *F. circinatum* causes pitch canker disease in pine trees. *F. mangiferae* causes mango malformation, where infected flowers bear no fruit. *F. subglutinans* is commonly associated with stalk and cob rot of maize, but it also affects several other crops including cowpea, millet, soybean, teosinte and wild rice. Such diseases caused by these and other species of *Fusarium* present major limiting factors in forestry and crop production.

Members of the genus *Fusarium* are commonly classified into species and subspecies groups based on the appearance of their reproductive structures. This morphology-based classification, however, has a number of limitations that mostly arise from lack of sufficient variation among the constituting species. DNA-based studies have also shown that a single morphological species may consist of a number of physiologically and genetically different groups. For example, *F. circinatum*, *F. mangiferae* and *F. subglutinans* are difficult to differentiate based on morphology. Consequently, *F. circinatum* was treated as a form species of *F. subglutinans*, whereas *F. mangiferae* was described from isolates that were previously regarded as *F. subglutinans*. DNA-based tools and mating type tests are used to differentiate among these species, with the former generally preferred for its accuracy, ease and speed. This indicates that novel tools that allow a more refined grouping of species in this important genus are needed.

Cells of most eukaryotic organisms consist of mitochondria. These organelles serve as the powerhouse of such cells as most of the cells' energy is produced in these organelles in the form of an energy molecule called adenosine tri-phosphate (ATP). Mitochondria are found in each cell in large numbers, and contain DNA that is capable of replicating independently of the DNA found in the nucleus of the cells. Mitochondrial DNA (mtDNA) is much smaller in size, and is known to evolve at a faster rate than nuclear DNA. This high rate of evolution coupled with its predominantly maternal line of inheritance, makes mtDNA a good source of phylogenetic information for the study of closely related groups/individuals. Information from mtDNA has been efficiently used in phylogenetic studies involving a large number of animals and plants. Such information, however, is generally lacking in fungi including *Fusarium*.

This study has two objectives: i) to sequence mitochondrial genomes of *F. circinatum*, *F. mangiferae* and *F. subglutinans*, and compare this sequence information with that of other *Fusarium* spp for which such information is available in the public database; and ii) to determine regions of mtDNA that can be used in phylogenetic studies of *Fusarium* spp. and design appropriate primers for this purpose. So far, sequencing of the mtDNA of a *F. circinatum* isolates has been nearly completed. Fifteen sets of primers, each of which amplifies ~1.2 kb segment of mtDNA have been designed and used successfully. These sets of primers provide access to more than half (~20 kb) of the mitochondrial genome of *F. circinatum*.