

SUMMARY – Marinda Visser

Fusarium oxysporum f. sp. *cubense* (*Foc*) is a fungal pathogen that is highly successful in its ability to cause Fusarium wilt of banana. Apart from its specificity to the banana plant (*Musa* spp.), genotypic variants of the pathogen have proven to evolve sufficiently to target specific banana cultivars under different environmental conditions. This variability in the fungus has been illustrated in numerous studies in the past, and involved phenotypic markers such as vegetative compatibility groups (VCGs) and genotypic markers such as DNA amplified fingerprints (DAFs), random amplified polymorphic DNAs (RAPDs) and sequencing. This thesis has made an attempt to investigate the underlying reasons for diversity and diversification of a worldwide population of *Foc*, with emphasis on a South African population. The application and development of molecular biological tools for phylogenetic and host-specificity studies which included techniques such as vegetative compatibility studies, analysis of sequence data of a nuclear and mitochondrial gene region, searching for mating type genes, transformation of *Foc* and the development and testing of microsatellite markers.

Many studies on *Foc* have been useful in demonstrating the diverse nature of the banana pathogen. Few of these, however, have made any attempts to investigate the nature of its diversification. In an examination of the reproductive potential of a worldwide population of *Foc*, it has been proven that the fungus is clonal with an apparent absence of sexual recombination. It may be that *Foc* has become such a genetically isolated population and such an evolutionary advanced pathogen that no sexual stage will ever be found. Mutations therefore, are expected to be the primary mechanism responsible for genetic variation in *Foc*.

Sequence data of nuclear and mitochondrial gene regions with different evolutionary rates proved that *Foc* consists of several clonal lineages that maybe genetically distinct. These clonal lineages group into separate groups. The first of these groupings included the South African population while the second included isolates from the Australasian region. It is suggested that clonal lineages could be linked with distinct pathotypes of the fungus. All isolates of *Foc*, however, maintain one common link, their ability to cause disease on the banana host.

The relationship between *Foc* and the banana plant has been studied extensively many years ago on the Gros Michel cultivar. The successful transformation of *Foc* with the green fluorescent protein, however, now makes it possible to better understand the interactions between different fungal pathotypes and host genotypes. It will also substantially assist in

understanding the process of fungal infection and host defence responses. Details of the interactions, especially between Cavendish varieties and the pathogen, need to be investigated further in future.

A study of the population structure of *Foc*, using VCGs and microsatellite markers, provided valuable insights into the diversity of the South African population in relation to a worldwide collection of the fungus. Both markers showed that the South African population of *Foc* was remarkably homogeneous, strongly reminiscent of an introduced population. This was in clear contrast to the large genetic diversity apparent in populations from Southeast Asia, the reported centre of origin of the pathogen. VCGs are believed to represent clonal lineages within a species. They are useful but not ideal markers for defining diversity in a pathogen like *Foc* that has no defined genetic basis for race assignment. While VCGs are believed to represent clonal lineages within a species, the assumption that isolates in the same VCG are genetically very similar can be misleading.

The development of microsatellite markers for *Foc* has provided an opportunity to study evolutionary relationships among populations and subpopulations of the Fusarium wilt pathogen. Differentiation between subpopulations was found to be high due to restricted gene flow and random drift. The high gene diversity revealed within the native *Foc* population is a clear indication that management of Fusarium wilt should involve the development of resistance cultivars.