Fusarium oxysporum mitochondria in the Next Generation Sequencing era

In recent years more and more WGS (whole genome sequencing) projects are becoming publicly available. Despite this fact, the number of published mitochondrial genomes is lagging behind. There are only six mitochondrial genomes ready for Fusarium spp., but there are more than twenty WGS projects available.

Our group has developed a program, GRABB (Genomic Region Assembly by Baiting), which can selectively assemble regions of the genome from next generation sequencing reads. Using this program and the publicly available WGS reads we have assembled and annotated twenty-seven mitochondrial genomes of Fusarium oxysporum strains. We also re-sequenced the first F. oxysporum strain (F11) that had its mitochondrion sequenced and a F. proliferatum strain to be used as an outgroup. Besides the mitochondrial genomes we also extracted seven nuclear marker sequences that have been used for phylogenetic study of the FOSC.

Previous studies have identified a highly variable region in the mitogenome of Fusarium spp, which is found between MT-RNR2 and MT-ND2 genes. This variable region encodes a large (~6kb) ORF. In our dataset we found that within the FOSC there are two more variants of this region. All three variants contain the same tRNA genes, except for one of the variants, which contains an additional tRNA gene. Only one of the variants contains the typical large ORF which was described in other Fusarium spp. The variants are not clade specific and the trees inferred from the variable regions are similar to the trees inferred using an eight-marker dataset. These findings make it likely that there is mitochondrial recombination going on within the species.

Relocation and co-regulated gene expression patterns in Fusarium graminearum

Genome comparisons between closely related species often show non-conserved regions across chromosomes. Some of them are located in specific regions of chromosomes and some are even confined to one or more entire chromosomes. The origin and biological relevance of these non-conserved regions are still largely unknown. The genome of Fusarium graminearum was studied to elucidate the significance of non-conserved regions. In the genome of F. graminearum harbours thirteen non-conserved regions dispersed over all of the four chromosomes. Using RNA-Seq data from the mycelium of F. graminearum, we found weakly expressed regions on all of the four chromosomes that exactly matched with non-conserved regions.

Comparison of gene expression between two different developmental stages (conidia and mycelium) showed that the expression of genes in conserved regions is stable, while gene expression in non-conserved regions is much more influenced by the developmental stage. In addition, genes involved in the production of secondary metabolites and secreted proteins are enriched in non-conserved regions, suggesting that these regions could also be important for adaptations to new environments, including adaptation to new hosts. Finally, we found evidence that non-conserved regions are generated by sequestration of genes from multiple locations. Gene relocations may lead to clustering of genes with similar expression patterns or similar biological functions, which was clearly exemplified by the PKS2 gene cluster. Our results showed that chromosomes can be functionally divided into conserved and non-conserved regions, and both could have specific and distinct roles in genome evolution and regulation of gene expression.

Reference:
Relocation of genes generates non-conserved chromosomal segments in Fusarium graminearum that show distinct and co-regulated gene expression patterns. C Zhao, C Waalwijk, PJGM de Wit, D Tang, T van der Lee. BMC genomics 15 (1), 191