Fusarium oxysporum mitochondria in the Next Generation Sequencing era

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Re-sequencing of a Fusarium oxysporum 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

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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* genome was studied to elucidate the significance of non-conserved regions. In the genome of *F. graminearum* harbours thirteen non-conserved regions. In the mitogenome of *Fusarium oxysporum* strains. We also re-sequenced the first *F. oxysporum* strain (F11) that had its mitochonrdion 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.

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