

# *Fusarium oxysporum* mitochondria in the Next Generation Sequencing era

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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.