Exploring the genome variability of *Fusarium musae*

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Fusarium musae is a recently described species which causes crown rot disease on banana fruits and infections in humans. Genomic tools can help decipher the mechanisms of adaptability and success of a pathogenic species in multiple environments. Previous data suggest that both strains isolated from humans and bananas share the ability to cause a similar level of disease on banana fruits and *Galleria mellonella* (used as a model for human infection). Genome size of 18 strains obtained from the two hosts shows variability of more than 2 Mbs with unique genes compared to the sister species *F. verticillioides*. Telomere-to-telomere complete genomes obtained by combining nanopore and Illumina sequencing of two strains collected from a banana and a human patient, reveal the existence of supplementary chromosomes, which partially explain genome diversity. Transposons are active in some strains, likely contributing to genome rearrangements. This variability might explain the cross-kingdom adaptation of the species.

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