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## **DIFFERENCES IN *F. MUSAE* GENOMES**

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### **Text**

*Fusarium musae* has recently been described as a cross-kingdom pathogen causing crown rot of banana, a post-harvest disease, keratitis and skin infections as well as systemic infections in immunocompromised patients. To better understand the diversity within strains of the species, the entire genome of 19 *Fusarium musae* strains was obtained through Illumina and Nanopore sequencing assembling short and long reads. The length of the assembled nuclear DNA ranged from 43.04 Mbp to 45.54 Mbp. A similar divergence is shown in mitochondrial DNA ranging from 56493 bp to 59256 bp. Comparative analysis revealed differences in number of secondary metabolites gene clusters (from 41 to 47). A special focus on Enniatin-Beauvericin cluster in *F. musae* identified evolutionary divergences of NPRS gene within the species. Our results are a fundamental step to better investigate phylogenetic relationship within *F. musae* strains with diverse origin and will provide essential knowledge for functional studies of genes involved in the environmental adaptation and in the infection process on humans and banana fruit.