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Text

Blast disease epidemics caused by the fungus *Magnaporthe* (syn. *Pyricularia*) *oryzae* are often dominated by clonal pathogen lineages. In absence of sexual recombination, a major driver of genomic diversity and purging of deleterious mutations, these lineages manage to continuously adapt to their host plants. Contrary to their very low genetic diversity in core genomic regions, we observed vast chromosome diversity in clonal blast fungus populations. We found that variable mini-chromosomes (mChr) contribute to megabase-scale genome rearrangements, chromosome duplications, and horizontal transfer of mChr between diverse host-specialized lineages. These transfer events include mChr-encoded virulence effector candidates. We hypothesize that mChr rearrangements and inter-lineage transfer contribute to blast fungus genome diversity and to the adaptive potential of the blast fungus.

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NOVEL PIPELINES FOR ASSEMBLING AND ANNOTATION OF GENOMES FOR PLANT PATHOGENIC FUNGI. APPLICATION ON TWO MAJOR BANANA PATHOGENS.

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Text

An understanding of the evolutionary dynamics that allow plant pathogens to break down host resistance and develop fungicide resistance, is needed to develop durable and efficient control methods. To address the plasticity of fungal genomes, long-read genome sequences and adequate bioinformatic support is required to generate high-quality chromosome-level assemblies. In this study, the variability in the structural genomes of two important banana pathogens, *Pseudocercospora fijiensis* (causing the black Streak) and *Fusarium oxysporum* f.sp. *ubense* TR4 (causing the Fusarium wilt), were investigated. We first developed the workflow « Podium ASM » to assess the quality of long-read genome assemblies, based on contig numbers, genome completeness, and the presence of telomeric sequences. A second workflow, named « EffiCAZ », was then used to improve functional annotation of pathogenicity-related effectors and CAZymes. Chromosome-level genome assemblies were obtained from four Nanopore sequences of each species, and compartmentalised into a core and an accessory part, with contrasting gene densities and effector distribution. A much higher proportion of transposable elements was observed in *P. fijiensis* than in *F. oxysporum* f.sp. *ubense* TR4. These new pipelines pave the way for the comprehensive characterization of the pangenomes of the two banana pathogens.

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