

Genome sequencing and comparative genomics reveal insights into pathogenicity and evolution of *Fusarium zanthoxyli*, the causal agent of stem canker in prickly ash

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Abstract: *Fusarium zanthoxyli* is a destructive pathogen causing stem canker in prickly ash, an ecologically and economically important forest tree. However, the genome lack of *F. zanthoxyli* has hindered research on its interaction with prickly ash and the development of precise control strategies for stem canker. In this study, we sequence, assemble, and annotate a relatively high-quality genome of *F. zanthoxyli* with a size of 43.39 Mb, containing 55 contigs and encoding 11,316 putative genes. Furthermore, 279 tRNAs, 64 5s rRNAs, 5 18s rRNAs, 7 28s rRNAs, 2 sRNAs, 21 snRNAs and 2,491 repetitive elements known as direct repeats (DRs) were predicted in the genome of *F. zanthoxyli*. Pathogenicity-related factors are predicted, comprising 495 CAZymes, 217 effectors, 156 CYP450s, and 202 enzymes associated with secondary metabolism. Besides, a comparative genomics analysis along with 25 other fungal species from eight classes of Ascomycota and Basidiomycota revealed *Fusarium* and *Colletotrichum* diverged from a shared ancestor approximately 141.1~88.4 million years ago (MYA). Additionally, a phylogenomic investigation of 12 different phytopathogens within *Fusarium* indicated that *F. zanthoxyli* originated approximately 34.6~26.9 MYA, and events of gene expansion and contraction within them were also unveiled. Among the investigated fungal genomes, 3,929 ortholog families were found to be present in all 12 *Fusarium* species. Interestingly, with a mere 24 gene families, encompassing 59 genes, were identified as exclusive to *F. zanthoxyli*, representing a modest 0.24% of its gene families. The contracted gene families in *F. zanthoxyli* was the most across all the 12 species with the number of 4,002, while a comparatively fewer gene families underwent expansion with the number of 278. Finally, utilizing conserved domain prediction, the results revealed that among the 59 unique genes of *F. zanthoxyli*, the most enriched domains were PnbA, Czco and ULP1. Among the 783 expanded genes, the most enriched domains were PKc_like kinases and those belonging to the APH_ChoK_Like family. This study sheds light on the genetic basis of *F. zanthoxyli*'s pathogenicity and evolution which provides valuable information for future research on its molecular interactions with prickly ash and the development of effective strategies to combat stem canker.