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Comparative genomics of two races of the coffee leaf rust pathogen *Hemileia vastatrix*

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Introduction

Coffee leaf rust, caused by the biotrophic fungus *Hemileia vastatrix*, is the most important disease affecting this crop, leading to significant financial losses for producers and impacting global coffee production [1,2]. Despite its significance, genomic information *on H. vastatrix* remains scarce, limiting the understanding of the mechanisms underlying resistance breakdown. In this work, the genomes of two *H. vastatrix* races, race II and race XIII, were sequenced and annotated. Comparative genomics analyses were conducted to identify shared and specific gene clusters.

Materials/Methods

Genomic DNA was extracted from urediniospores of each isolate and sequenced using Illumina MiniSeq System. Adapter sequences were trimmed using Trimmomatic, and the quality of the filtered data was assessed with FastQC. A draft genome assembly was generated using SPAdes v3.15.5. Scaffolds were obtained with RagTag v2.1.0. Assembly statistics and genome completeness were evaluated using QUAST and BUSCO v5.0.0, respectively. Structural gene prediction was performed using AUGUSTUS via the BRAKER2 pipeline. To assess gene conservation, orthologous groups were identified by analyzing the predicted proteomes using OrthoFinder and OrthoVenn3.

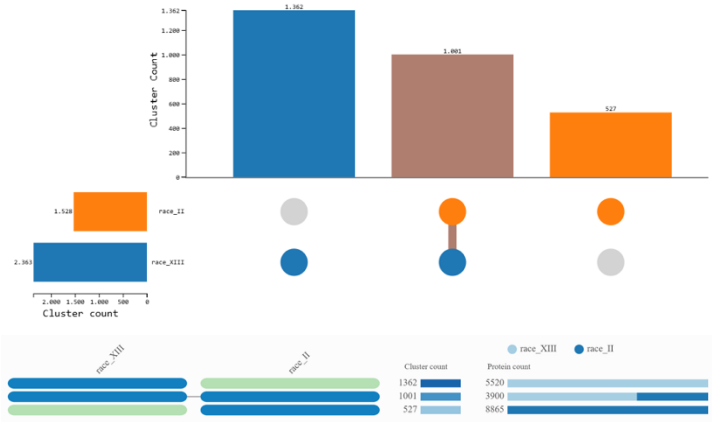

Figure 1: Distribution of orthologous clusters between race II and race XIII. The vertical bars represent the number of clusters that are either shared or unique to each genome and distribution of orthologous clusters and their associated proteins among the compared genomes.

Results/Discussion

The draft genome assemblies exhibited high contiguity, with N50 values of 5.4 Mb for race II and 7.3 Mb for race XIII, and maximum contig sizes of 13.7 Mb and 18.3 Mb respectively. Both genomes showed GC contents around 34%. Orthogroup analysis identified about 2,890 orthologous groups shared between the two races, suggesting a high level of genome conservation. Approximately 27,3% of the genes were classified as singletons. Functional annotation of these genes revealed a predominance of those encoding enzymatic activities, particularly hydrolases, transporters, and peptidases. These functions suggest potential roles in nutrient acquisition, host interaction, and race-specific adaptive processes.

Conclusion/Perspectives

The results of this work contribute to expanding the genomic knowledge of *H. vastatrix*. These assembled genomes provide a valuable resource for the identification and characterization of genes and effectors associated with virulence, which are critical for developing molecular tools to monitor pathogen populations and to support breeding programs focused on developing coffee cultivars with durable resistance to coffee leaf rust.

References:

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