

TITLE: DECIPHERING THE BIOLOGY OF *Austropuccinia psidii* FROM "OMICS" APPROACHES

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ABSTRACT:

Currently, the high-throughput sequencing approaches as genomics, transcriptomics and proteomics have contributed with a better understood of plant pathogens with significant economic importance and with incipient molecular information as the biotrophic fungus *Austropuccinia psidii*, causal agent of myrtle rust. Based on the system biology, we obtained a preliminary data of the genome, transcriptome and proteome of *A. psidii* under *Eucalyptus* spp. infection process. *A. psidii* MF-01, a monopustular isolate, had its DNA sequenced using the platforms: 454, Illumina and PacBio. The transcriptome analysis was performed during the infection process of *E. grandis*. It also performed the proteome analysis of uredospores from two *A. psidii* contrasting population from guava and eucalyptus. Using the qPCR technique the genome of *A. psidii* was calculated in 630Mb, one of the largest in the fungi kingdom. The genome *draft* annotation presented several genes related to plant-pathogen interaction as lytic enzymes, effectors and a high amount of retrotransposons. The mitochondrial genome (mtDNA) is bigger comparing with from rust pathogens. Just 144 hours after infection were identified significantly *A. psidii* transcripts. Among the differential expressed genes, we found transcripts related catabolic process, growth and reproduction. A significant amount of unique proteins were found for each sample, from guava populations many proteins correlated with fungal virulence were up-represented, supporting the physiological variability of the fungal populations according to their protein reservoirs and specific host interaction strategies. The obtained data have collaborated with a better understanding of the fungal biology and its pathogenesis process.

Keywords: myrtle rust, NGS, genome, transcriptome, proteome

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