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BOOK OF ABSTRACTS

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## A chromosome-level genome resource for studying virulence mechanisms and evolution of the coffee rust pathogen *Hemileia vastatrix*

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Recurrent epidemics of coffee leaf rust, caused by the fungal pathogen *Hemileia vastatrix*, have constrained the sustainable production of Arabica coffee for over 150 years. The ability of *H. vastatrix* to overcome resistance in coffee cultivars and evolve new races is inexplicable for a pathogen that supposedly only utilizes clonal reproduction. Understanding the evolutionary complexity between *H. vastatrix* and its only known host, including determining how the pathogen evolves virulence so rapidly is crucial for disease management. Achieving such goals relies on the availability of a comprehensive and high-quality genome reference assembly. To date, two reference genomes have been assembled and published for *H. vastatrix* that, while useful, remain fragmented and do not represent chromosomal scaffolds. Here, we present a complete scaffolded pseudochromosome-level genome resource for *H. vastatrix* strain 178a (Hv178a). Our initial assembly revealed an unusually high degree of gene duplication (over 50% BUSCO basidiomycota\_odb10 genes). Upon inspection, this was predominantly due to a single scaffold that itself showed 91.9% BUSCO Completeness. Taxonomic analysis of predicted BUSCO genes placed this scaffold in Exobasidiomycetes and suggests it is a distinct genome, which we have named Hv178a associated fungal genome (Hv178a AFG). The high depth of coverage and close association with Hv178a raises the prospect of symbiosis, although we cannot completely rule out contamination at this time. Our research is ongoing to address phasing of the haploid genomes and further characterising the unusual Hv178a AFG. The highly contiguous Hv178a genome (546 Mbp) is localised to 11 pseudochromosomes (51.5 Mb N50), and provides the foundation for advanced studies into the evolution, pathology and genome structure of this important pathogen of coffee.