











33907\_Dênia Almeida.pdf









# Draft genome of the Híbrido de Timor coffee reveals resistance genes against Hemileia vastatrix

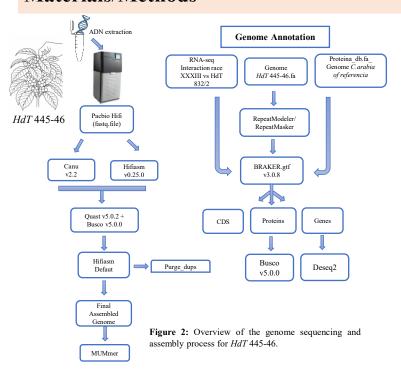
Dênia Pires de Almeida <sup>1</sup> (denia.almeida@ufv.br), Edson Mario de Andrade Silva<sup>2</sup>, Deisy Guimarães Carneiro<sup>1</sup>, Juliana Costa Rezende Abrahão<sup>3</sup>, Deila Magna dos Santos Botelho<sup>3</sup>, Antônio Carlos Baião de Oliveira<sup>3,4</sup>, Eveline Teixeira Caixeta<sup>1,4</sup>

<sup>1</sup>Universidade Federal de Viçosa - UFV, Instituto de Biotecnologia Aplicada à Agricultura; <sup>2</sup>University of Florida; <sup>3</sup> Empresa de Pesquisa Agropecuária de Minas Gerais—EPAMIG; <sup>4</sup>Empresa Brasileira de Pesquisa Agropecuária—Embrapa-Café

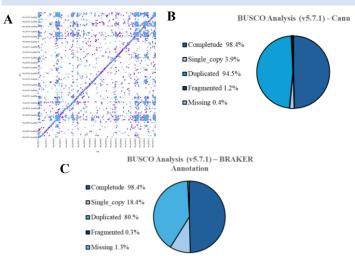
### Introduction

The Híbrido de Timor (HdT) is a natural interspecific hybrid between Coffea arabica and Coffea canephora. HdT is an important source of durable resistance to coffee leaf rust (Hemileia vastatrix) and is widely used in breeding programs worldwide [1]. Despite the high variability of the pathogen, most HdT coffees maintain resistance, probably due to unique combinations of major  $S_H$  resistance genes and genes with minor effects [2]. Given its importance in breeding programs, the lack of an available genome for HdT highlights the need for its sequencing and annotation to better understand the molecular basis of resistance and accelerate the development of resistant cultivars.

### Materials/Methods



#### **Results/Discussion**



**Figure 1:** MUMmer-based genomic collinearity plots comparing *HdT* 445-46 assemblies obtained with (A) Canu, (B) BUSCO analysis for the Canu assembly, and (C) BUSCO analysis after BRAKER annotation using the eudicots\_odb10 (2326).

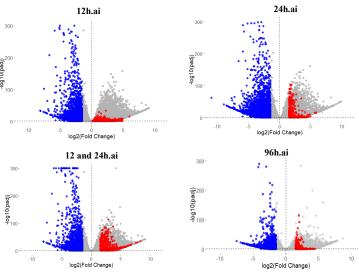


Figure 3: Volcano plot of differential gene expression (DESeq2) at 12, 24 (12 and 24), and 96 hours after inoculation (h.a.i). Up-regulated genes exclusively in the resistant genotype are shown in red, down-regulated genes across both compatible and incompatible interactions in blue, and all other genes in gray.

## **Conclusion/Perspectives**

We report the first draft genome of *HdT* (UFV 445-46), providing for the first time a crucial reference for understanding the genomic basis of durable resistance in *C. arabica*. The gene expression and annotation data allowed us to reveal genes involved in defense responses to *H. vastatrix*. These data are being exploited in comparative genomics analyses to identify conserved resistance mechanisms and defense pathways, with the aim of advancing genetic improvement strategies for rust resistance.

#### **References:**

1-Zambolim, L.; Caixeta, E. T. 2021. An overview of physiological specialization of coffee leaf rust: new designation of pathotypes. International Journal of Current Research, 13: 15479–15490.

2-Alves, D. R. et al. 2024. Unravelling the role of key genes involved coffee leaf rust resistance. Current Plant Biology, 38: 100347.