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BOOK OF ABSTRACTS

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## First report of a genome sequence resource of *Colletotrichum kahawae*, the causal agent of coffee berry disease

Cabral Ana<sup>1,2</sup> (anacgpcabral@edu.ulisboa.pt), Carvalho Jessica<sup>1</sup>, Talhinhas Pedro<sup>1,2</sup>, Baroncelli Riccardo<sup>3,4</sup>, Shittu Taiwo<sup>5</sup>, Loureiro Andreia<sup>2,6</sup>, Várzea Vitor<sup>2,6</sup>, Diniz Inês<sup>2,6</sup>, Batista Dora<sup>2,6</sup>, Sreenivasaprasad S.<sup>5</sup>, Silva Maria do Céu<sup>2,6</sup>, Azinheira Helena<sup>2,6</sup>

<sup>1</sup> Instituto Superior de Agronomia (ISA), Universidade de Lisboa, Lisbon, Portugal; <sup>2</sup> LEAF - Linking Landscape, Environment, Agriculture and Food Reseenter, Lisbon Associate Laboratory Terra, ISA, Universidade de Lisboa e Salamanca, Institute for Agrobiotechnology Research (CIALE), Universidad de Salamanca, Salamanca di Bologna, Dipartimento di Scienze e Tecnologie Agro-Alimentari, Università di Bologna, Bologna, Italy; <sup>5</sup> Division of Science, Faculty Creative Arts, Techn. Sci. University Bedfordshire, Institute of Research in Applied Natural Sciences, Bedfordshire, United Kingdom; <sup>6</sup> CIFC-Centro de Investigação das Ferrugens do Cde Agronomia, Universidade de Lisboa, Oeiras, Portugal

### Rationale:

Coffee Berry disease is one of the most important diseases of Arabica coffee plants in Africa, which is caused by *Colletotrichum kahawae* a fungus from the Sordariomycetes class. *C. kahawae* is a specialized hemibiotrophic pathogen of green coffee berries, whose impact is especially important at high altitudes, where it causes yield losses of up to 80% if control measures are not undertaken. In the present work, the *C. kahawae* type strain CIFC\_Que2 from Kenya was used for whole genome sequencing based on the Illumina sequencing platform aiming to generate a genome resource for understanding the pathogenicity mechanisms underlying the ability to infect green coffee berries and disclosing the underlying evolutionary events.

### Methods:

Genomic DNA of the *C. kahawae* isolate CIFC\_Que2 was obtained from mycethroughusing the DNeasy Plant DNA kit (Qiagen), and used for Illumina sequencing. The reads were assembled into scaffolds. Gene predictions were performed, making use of the transcriptome information previously obtained. A batch of software tools was used to predict gene functions such as protein domains, putative secondary metabolite genes, candidate transcription factors, and secretome prediction.

### Results:

The nuclear genome of *C. kahawae* was assembled into 886 contigs with 59,142,311 bp with a 98.9 % of completeness according to BUSCO. A total of 19181 protein-coding genes were predicted. The proteome was annotated using multiple public databases. Among the annotated protein-coding genes, 1774 were predicted as secreted proteins, of which 1549 were in the secretome and 358 were predicted as putative effectors. *In silico* analysis of the *C. kahawae* proteome allowed the identification of 869 proteases, a total of 967 carbohydrate active enzyme families, and the existence of 58 clusters of genes associated with secondary metabolites and 67 backbone enzymes. Further, transcriptomic studies showed that cutinases are essentially involved at the beginning of the infection, probably resulting in the penetration of the host tissues. Pectate lyases and lysine domain proteins probably play an important role during the switch to necrotrophy and the colonization of host tissues during the necrotrophic phase.

### Cusions & Perspectives:

The *C. kahawae* genome described in this study can serve as a resource for better understanding the pathogen population evolution as well as the pathogenic mechanism that allows *C. kahawae* to infect green coffee berries.