cE3c
centre for ecology, evolution and environmental changes

6th Annual Meeting 2020

Frontiers in E3

1-2 October

Online

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Book of ABSTRACTS

1 October 2020 Thursday

TL 2 - Evolutionary processes that shape biodiversity and adaptation to environmental changes

Flash Talk

High-throughput transcriptome profiling of contrasting pathotypes of the coffee rust *Hemileia vastatrix*

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In the last decade, there has been a resurgence of fungal epidemics, causing devastations worldwide in agricultural plantations. With the goal of achieving sustainable disease control, the scientific community has been lately focused on supervising and investigating the expansion of virulent pathogens, such as *Hemileia vastatrix* (Hv), responsible for the Coffee Leaf Rust disease (CLR). Since 1869, Hv has been spreading across the globe and causing devastating social and economic consequences, becoming one of the most impacting diseases within agricultural production. The Hv virulent mechanisms haven't been entirely understood, and it is crucial to unveil its evolutionary adaptation. In this work, we generated and analyzed RNA-seq data from five Hv pathotypes during compatible interactions, at three key steps of the infection to identify candidate genes for virulence, either harbouring differential expression patterns and/or polymorphism, related to rust pathotypes. Sequencing through Illumina NovaSeq platform provided a mean of 45 million paired-end of 101bp reads per sample. Reads were cleaned and filtered using several software-tools, and a de novo assembly was performed using Trinity, enabling the identification of 27.679 unigenes and a total of 50.380 isoforms. For the differential expression analysis, we estimated and normalized the transcript expression quantitation, and distinguished a total of 3.095 differentially expressed genes (DEGs) in all sample comparisons between Hv pathotypes and time-points. Our results show clear distinct gene expression profiles between rust pathotypes and/or infection stages, and pathotype-specific differential expression. We are currently annotating the Hv de novo assembled transcriptome and selecting genes of interest within each pathotype/stage of infection, specifically targeting candidate genes for rust virulence, in particular potential effector proteins. The expected results could lead to future selection of candidate virulence markers of pathotype-specific *H. vastatrix*, expecting to contribute for future control measures of this epidemic.