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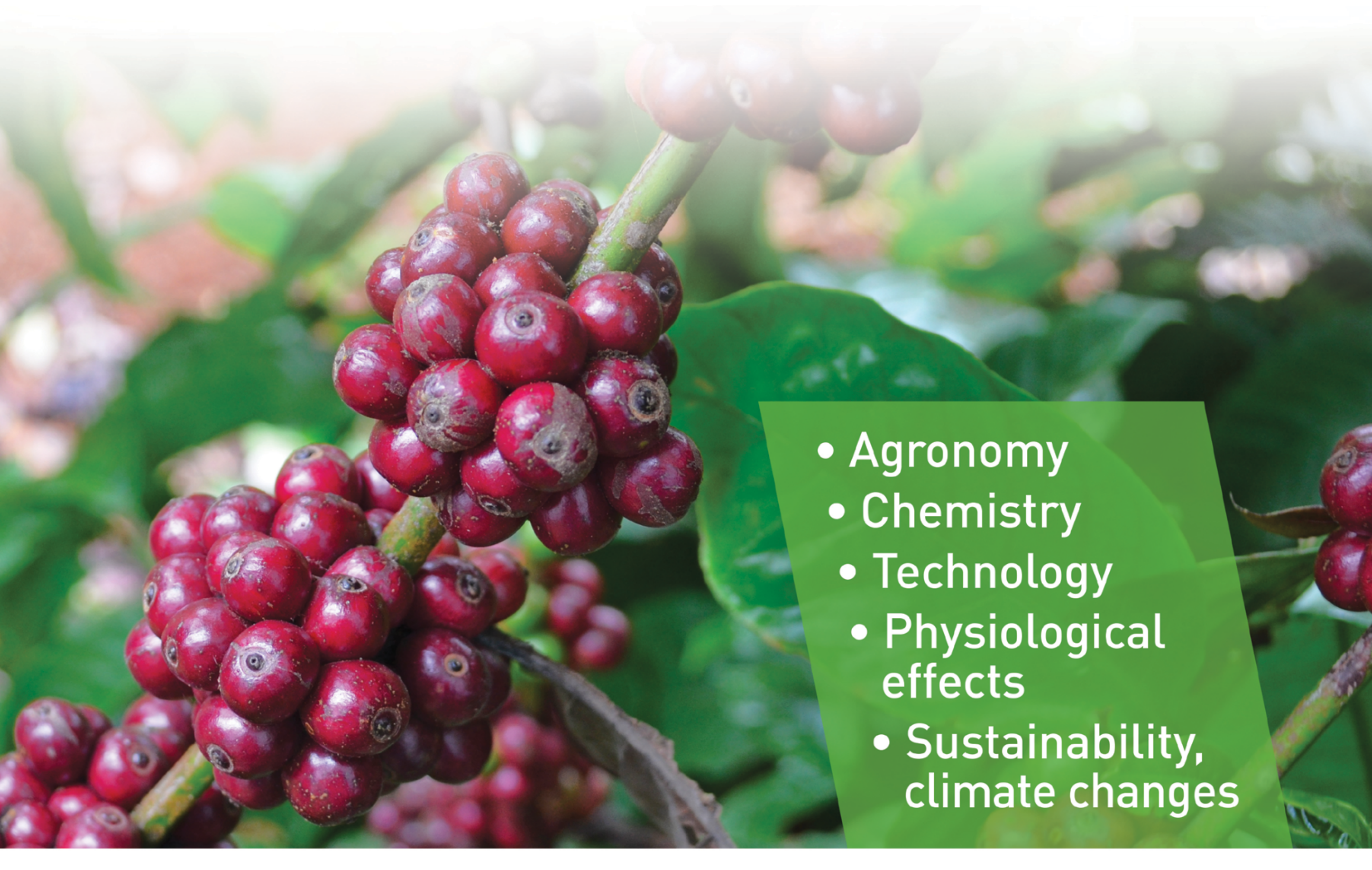
BOOK OF ABSTRACTS



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Identification of distinctive transcriptomic profiles among *Hemileia vastatrix* pathotypes throughout key stages of the infection process

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RATIONALE

Hemileia vastatrix (Hv), the pathogen responsible for Coffee Leaf Rust, has been spreading across the globe and causing devastating socio-economic consequences within coffee production. Nowadays, more than 50 races of Hv have been identified, but its virulence mechanisms are still poorly understood. To achieve a sustainable disease control, it is crucial to unveil the evolutionary adaptation behind this host-pathogen interaction. In this study, we applied a transcriptomic approach to identify candidate virulence genes harbouring differential expression patterns, related to rust pathotypes during its compatible interaction.

METHODS

RNA-seq data was obtained from five pathotypes during compatible interactions, at three key steps of the infection process. A *de novo* assembly of the fungus transcriptome was performed with Trinity and the transcript expression quantification was assessed by Salmon. Differentially expressed genes (DEGs) were identified using EdgeR. Functional annotation was done using Blastx and Blastp searches against the Uniprot database and a HMMER search against the Pfam database. Secreted proteins were searched using SignalP and TMHMM.

RESULTS

Data analysis enabled the identification of 27.679 unigenes and a total of 50.380 isoforms. Within these, 1596 transcripts were exclusively expressed in one of the five pathotypes across all infection time-points. We identified 3.095 DEGs in all sample comparisons between Hv pathotypes and infection time-points. Three distinct clusters of gene expression profiles were recognized in all pathotypes, while five expression profiles were specifically associated to pathotype groups, providing the information to distinguish pathotype-specific expression patterns. Functional annotation assigned protein functions to 9174 unigenes, with a predominance of catalytic activity and binding categories. In addition, 2347 potential secreted proteins with signal peptides were identified that may represent putative effectors. Our results show clear distinct gene expression profiles between rust pathotypes and/or infection stages, and pathotype-specific differential expression.

CONCLUSIONS & PERSPECTIVES

Our study provides a deeper insight on the virulence mechanisms of Hv, unveiling vital information about candidate genes and differential expression patterns linked to rust pathotypes, which will allow future functional studies and to exploit diagnostic markers for Hv pathotypes.

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