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First insights on the differential expression of adaptive candidate genes among contrasting pathotypes of *Hemileia vastatrix*

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RATIONALE

Hemileia vastatrix (Hv) causing coffee leaf rust, remains the major threat to Arabica coffee production worldwide. Under the constant risk of new Hv pathotypes emerging under a strong selective pressure, a better understanding of the adaptive genetic variation of Hv populations is needed. Since genes involved in coffee-rust interaction are expected to evolve under strong selection, this study aimed at the analysis of expression differences in putative candidate genes under positive selection that could provide insights on the pathogen virulence evolution.

METHODS

In this study, we selected seven candidate genes (CGs) with a signature of positive selection identified in a previous genome-wide scan integrated into a phylogenomics framework (Silva et al., 2015). To assess their potential association with Hv virulence profiles, expression analysis of CGs was initiated by qPCR for five isolates with contrasting pathotypes during compatible interactions at three key stages of the infection process [penetration stage (24hpi), >50% infection sites with haustoria (96hpi) and a stage preceding sporulation (8-11dpi)].

RESULTS

qPCR data analysis showed that most of the CGs studied were mainly activated during the penetration phase, suggesting their involvement in the early stages of the infection. Comparison between Hv isolates revealed significant differential expression of CGs involved in signaling for Hv1427 (lowest virulent pathotype) at the two first key stages of infection. However, in general, largest differences of expression were detected at different infection stages for each isolate, rather than among isolates at each time point.

CONCLUSIONS & PERSPECTIVES

First results revealed differences in expression among isolates, either regarding up or down-regulation at different infection stages, or the level of expression at each time point studied, suggesting that these candidate genes may be involved in Hv virulence. Putative causal relations and possible adaptive significance is being assessed. This study provides a first insight on the molecular variation underlying virulence divergence in coffee rust.

References:
- Silva et al. PLoS ONE, 2015, 10(12):e0143959, DOI:10.1371/journal.pone.0143959