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

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Introduction

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 (CGs) under positive selection that could provide insights on the pathogen virulence evolution.
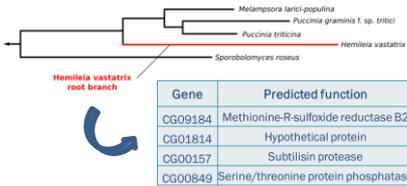
Fig. 1. Coffee Leaf Rust: a) Pustules of uredosporic sori on the abaxial side of a coffee leaf; b) Severe defoliation of coffee plants due to the disease.
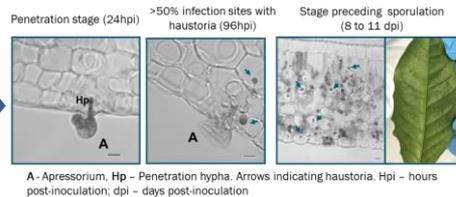
Material & Methods

■ **SELECTION OF CANDIDATE GENES**

From a genome-wide scan (Silva et al.,2015), candidate genes with a signal of positive selection captured at the phylogenetic branch leading specifically to *H. vastatrix*, were selected for analysis:

Melampsora larici-populina
Puccinia graminis f. sp. tritici
Puccinia triticina
Hemileia vastatrix
Sporobolomyces roseus

Hemileia vastatrix root branch

Gene	Predicted function
CG09184	Methionine-R-sulfoxide reductase B2
CG01814	Hypothetical protein
CG00157	Subtilisin protease
CG00849	Serine/threonine protein phosphatase

■ **SAMPLING & ANALYSIS**

Analysis of potential association of 4 CGs with Hv virulence profiles (pathotypes) using 3 coffee-*Hv* compatible interactions and at 3 crucial time-points of the infection process

Coffee host	CIFC isolates Hv pathotype/virulence
Caturra (S_H5)	Hv1427 (race II, v5) / ↓
C. arabica 32/1 ($S_H2,5$)	Hv741 (race I, v2,5) / ↑
C. arabica 128/2 (S_H1)	Hv995 (race III, v1,5) / ↑

Penetration stage (24hpi) — >50% infection sites with haustoria (96hpi) — Stage preceding sporulation (8 to 11 dpi)

A - Apressorium, Hp – Penetration hypha. Arrows indicating haustoria. Hpi – hours post-inoculation; dpi – days post-inoculation

Results

Significant differential expression for Hv 1427 (lowest virulent pathotype) at the two first key stages of infection:

✓ CG00849 is comparatively less activated at 24hpi
✓ CG09184 and CG00157 is comparatively more activated at 96hpi

A

CG00849

CG01814

CG00157

CG09184

Hemileia vastatrix isolates

B

CG00849

CG01814

CG00157

CG09184

Infection stages

Penetration (24hpi); >50% infection sites with haustoria (96hpi); Preceding sporulation (8-11dpi)

Significant differential expression between infection stages:

✓ All CGs are more activated at the fungal penetration stage (24h), except CG00849 for Hv1427,although following a similar descending expression profile
✓ For CG00157 and CG09184, expression differences between all infection stages are observed for Hv1427 and Hv741
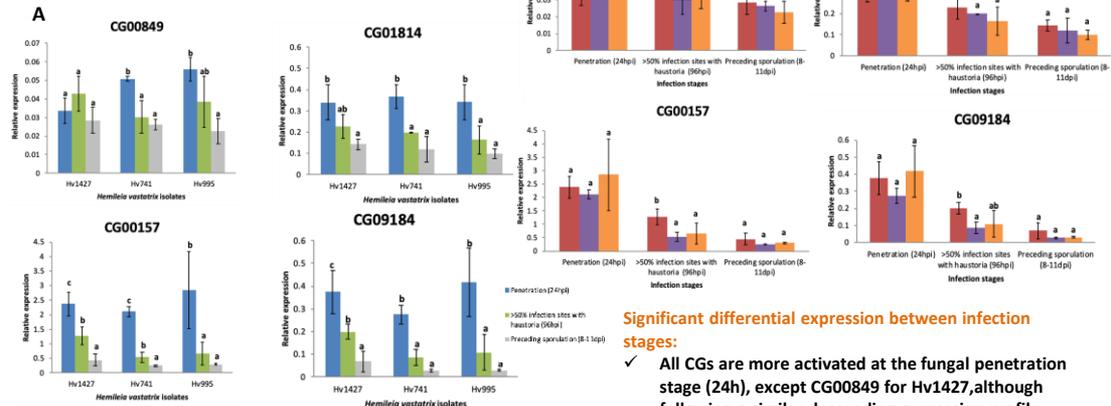
Fig. 2. Comparison of relative expression between (A) Hv isolates at different time-points of the infection process and (B) different infection stages among Hv isolates for the CG09184, CG01814, CG00157 and CG00849 genes. For each time-point, bars sharing the same letter do not differ significantly at p≤0.05 based on Fisher's Least Significance Difference test .

Conclusions/Perspectives

Our study revealed differential expression of CGs under positive selection associated to the infection process in coffee rust pathotypes. Largest differences of expression were detected at different infection stages for each isolate, rather than among isolates at each time point. Further studies are needed to better understand these patterns of expression and the underlying CGs role on virulence

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