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Retrotransposons as putative key elements on the genetic variability and regulation of virulence in *Hemileia vastatrix*

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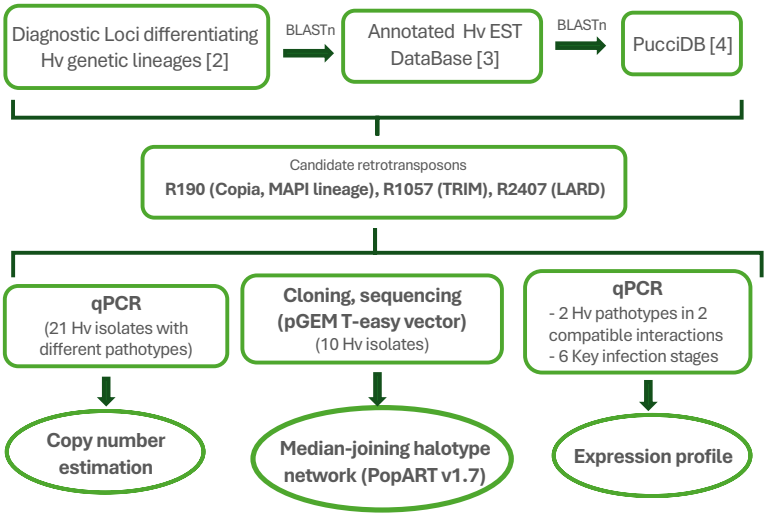
1. Introduction

Hemileia vastatrix (Hv) is the causal agent of Coffee Leaf Rust, the major constraint to Arabica coffee production. The dynamic co-evolution of the Hv-coffee pathosystem promotes the emerging of new pathotypes with increased virulence profiles, capable of overcoming the resistance mechanisms of the host. The continuous resistance breakdown observed in the field has been providing evidence of the high pathogenic variability in *H. vastatrix*. Unveiling the mechanisms that promotes genetic variability and virulence in this pathogen is important to improve disease control. Retrotransposons have been implicated in genome shaping and expansion events, as well as in virulence increase [1].

To assess the putative involvement of retrotransposons in diversity and virulence profiling of Hv, this study aims to understand the genetic variability (nucleotide sequence and copy number) and relative expression profiles along the course of the infection process of three retrotransposons among Hv contrasting pathotypes.

2. Material and methods



3. Results

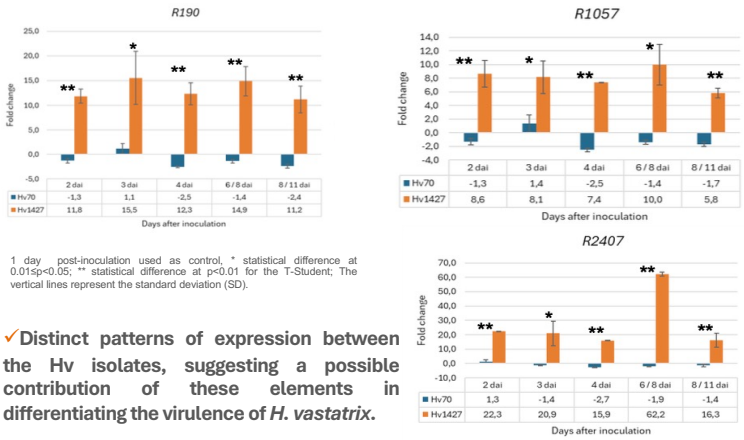
Copy number

Hv isolates	Genome size (Mbp)	No copies per genome		
		RHv00190	RHv01057	RHv02407
Hv999	719	800	1	1216
Hv1321	721	1781	3	3377
Hv1427	751	1108	3	578
Hv741	758	873	4	1949
Hv999a	771	623	4	304
Hv178a	772	934	4	1008
Hv178	774	663	2	1109
Hv166	777	932	2	889
Hv1065	782	1650	103	1515
Hv995	783	725	3	1144

Hv isolates	Genome size (Mbp)	No copies per genome		
		RHv00190	RHv01057	RHv02407
Hv264	788	1079	41	758
Hv3302	789	1435	6	649
Hv3305	792	3486	4	4457
Hv92	794	495	10	923
Hv71	824	1008	24	408
Hv264a	824	1771	39	728
Hv535	827	1934	2	1067
Hv22	834	725	NA	1322
Hv2191	842	1447	28	3460
Hv70	879	1848	2	1486

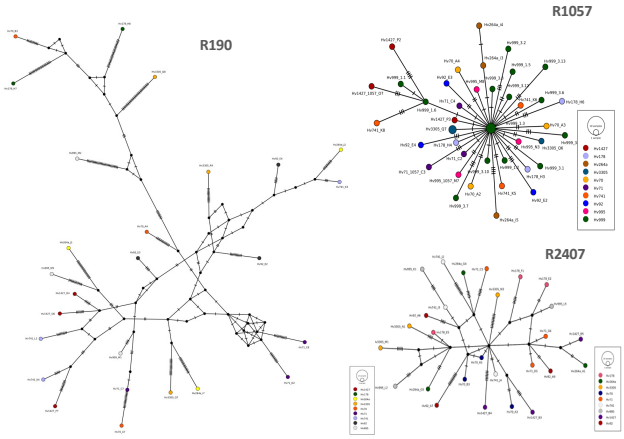
Copia/MAPI lineage and LARD are the most proliferative elements, reaching over 3000 copies per genome

Expression profile



1 day post-inoculation used as control, * statistical difference at 0.01≤p<0.05; ** statistical difference at p<0.01 for the T-Student; The vertical lines represent the standard deviation (SD).

✓**Distinct patterns of expression between the Hv isolates, suggesting a possible contribution of these elements in differentiating the virulence of *H. vastatrix*.**



✓**Hight level of genetic variation with very divergent haplotypes/copies (>30 SNPs, up to 84 bp Indels), both between isolates and within the same isolate**

✓**Analysis of haplotype network topologies: Complex diversification and proliferation patterns without apparent correlation with isolate or pathotype group**

✓**The most proliferative retrotransposon seems to have more complex diversification patterns**

✓**All retrotransposons were upregulated in all time-points for the Hv1427 compatible interaction, and mostly downregulated in the Hv70 compatible interaction**

✓**RHv2407 shows a much higher level of expression for at all time-points, in relation to RHv190 and RHv1057 (for Hv1427 compatible interaction)**

4. Conclusions / Perspectives

This study reveals new insights about the *Hemileia vastatrix* adaptative evolution, by suggesting that retrotransposons might contribute to the generation of genetic diversity and virulence of this rust fungus

References:
[1] Lorrain et al. (2021). DOI:10.1016/B978-0-12-819990-9.00042-1.
[2] Silva et al. (2018). DOI : 10.1111/mpp.12657.
[3] Talhinhas et al. (2014). DOI: 10.3389/fpls.2014.00088.
[4] Orozco-Arias, S et al.,(2022). DOI: 10.3390/agronomy12071665

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