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Small-RNA characterization of Coffee Leaf Rust races having different virulence profiles

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INTRODUCTION

The obligate biotrophic rust fungus *Hemileia vastatrix* (causal agent of Coffee Leaf Rust), which is the most widespread pathogen of Arabica coffee, causes severe yield losses. More than 50 rust physiological races have been detected resorting to 27 coffee differentials, since their molecular identification has not yet been possible [1]. In the present study we have identified small-RNAs from urediniospores of three rust races with different spectra for virulence: race VI (v?-unknown) non-pathogenic to all known *C. arabica* genotypes and races II (v5) and XXIV (v2,4,5) pathogenic to the majority of *C. arabica* genotypes. Urediniospores of the three races were frozen in liquid nitrogen, and total RNA was isolated using the NOGEN KIT Plant/Fungi Total RNA Purification Kit and then sent to small-RNA-sequencing. The genome of *H. vastarix* race XXXIII [2] and miRBase v22.0 were used to analyze the small-RNA-seq data by using the miRPursuit pipeline [3].

RESULTS

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Read counts throughout the analysis

	Hv races	Fasta	Filter	Genome	Conserved	Novel	TaSi
Total road	VI	8415524	2714494	1955284	1295	15029	11865
counts	П	9845643	3044992	2222770	1981	15850	13531
counts	XXIV	9095881	1280402	1127374	425	4377	1620
Distingt your	VI	2025882	127449	69281	28	189	583
Distinct read	П	2474009	152379	92711	51	292	722
counts	XXIV	3901813	43066	30272	17	61	111

The majority of the miRNAs present in *H. vastatrix* was not yet reported in miRBase and so the number of sequences annotated as conserved miRNAs is low, with only about 10 conserved miRNAs being found.

CONCLUSION AND PERSPECTIVES

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H. vastatrix small-RNA profile revealed a higher abundance of species with 22 and 29 nt. With this approach we have identified differences between the three races that will potentially contribute to unveil the virulence divergence observed among H. vastatrix races.

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