

A first insight on the *Hemileia vastatrix* urediniospores proteome

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RATIONALE

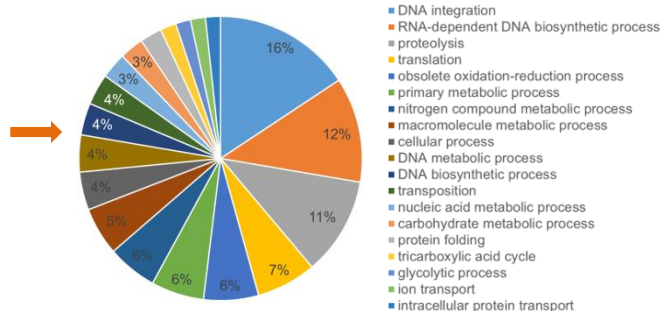
Coffee leaf rust (CLR) is caused by *Hemileia vastatrix*, an obligate biotrophic basidiomycota. The high pathogenic variability in CLR has been recognized for long as it is associated with the breakdown of coffee resistance [1]. Distinct *H. vastatrix* races have been identified through the differentiation of isolates on a set of 27 coffee plants (differentials), but their molecular characterization has been limited. In order to shed light on *H. vastatrix* diversity, a high-throughput analysis of the proteins from the urediniospores of three rust races were used: 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. Protein identification was achieved by nanoLC-MS/MS and searching in the NCBIprot Hv33_RustFungi_annot database [2].



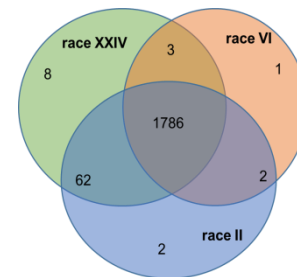
CLR disease symptoms

RESULTS

This approach allowed us to identify 1874 proteins and obtain functional annotation [3,4] for about 70% of them.



The three rust races share a 95% of the proteome as 1786 of the 1874 protein sequences were commonly detected in all 3 rust races.



CONCLUSION AND PERSPECTIVES

Our work provides the first tentative approach to establish the proteome of *H. vastatrix* urediniospores. In addition, a comparative analysis of the proteomes of the urediniospores of three *H. vastatrix* races is being undertaken in order to identify protein factors that clearly differentiate the three rust races contributing to pathogenicity.

Acknowledgements

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