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**ABSTRACTS**

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### **A high genomic variability is found among *Hemileia vastatrix* pathotypes**

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Coffee leaf rust is a devastating disease caused by *Hemileia vastatrix* (Hv), leading to huge losses in coffee production. There are over 50 races/pathotypes of Hv, so it is of great importance to comprehend how the genetic variation is promoted, as well as the regulator mechanisms of the differentiated pathogen virulence profiles. Retrotransposons are associated with genome structural variations and gene expression regulation in plant pathogens. These features may be associated to their capacity to rapidly evolve virulence. In this study, the genome size and the variability of a Ty1/Copia-like retrotransposon, concerning nucleotide sequence and copy number, were investigated among Hv contrasting pathotypes to assess their putative association with virulence profiles. Estimation of the holoploid genome size (1C) by flow cytometry for 46 Hv pathotypes revealed a huge genomic variation, ranging from 713 to 879 Mbp, with a global average of 789 Mbp. This is in sharp contrast with the global average for the kingdom Fungi (60 Mbp) and still over 10× larger than that of the phylum Basidiomycota (74 Mbp). To start assessing a putative causal relation of genome size variation with retrotransposon expansion, we analyzed a Ty1/Copia-like retrotransposon previously selected from an annotated EST database of three *H. vastatrix* differentiation/ infection stages (Talhinhos *et al.* 2014). Upon cloning and sequencing, 16 different copies were identified with a high level of genetic variation in 7 Hv isolates. Absolute quantification of retrotransposon copy number by qPCR ranged from 2 to 8 copies per diploid nucleus. Further analyses are being carried out and will allow us to better understand the genetic variation pattern and putative causal relations with virulence profiles. This study provides a novel approach to address coffee rust adaptive evolution and offers a first insight on *H. vastatrix* virulence divergence as related to genome size fluctuations and retrotransposon copy number.