

LTR retrotransposons in *Hemileia vastatrix* genome

Rafaela Leite Prado Rocha¹, Pedro Ricardo Rossi Marques Barreiros¹, Tiago Antônio de Oliveira Mendes², Laércio Zambolim^{1,3}, Ney Sussumu Sakiyama^{1,4}, Eveline Teixeira Caixeta^{1,5}

¹Laboratório de Biotecnologia do Cafeeiro, BIOAGRO UFV; ²Departamento de Bioquímica e Biologia Molecular, UFV; ³Departamento de Fitopatologia, UFV; ⁴Departamento de Fitotecnia, UFV; ⁵EMBRAPA Café

Rust is the most harmful disease that affects coffee trees, which may cause drastic drops in productivity if not controlled. The pathogen fungus *Hemileia vastatrix* displays high levels of genetic variability leading to appearance of new races and supplanting the resistance of varieties of coffee obtained in breeding programs. Since sexual reproduction was not previously related, the mechanism that causes such variability is yet not known. Thus, there is a chance that the DNA transposable elements are responsible for increasing genetic variability of the fungus. The goal of the first stage of this study was to identify the presence, frequency and location of LTR retrotransposons, a subclass of transposons present in the genome of *H. vastatrix*. For the analysis, we used an in house database of DNA sequences of *H. vastatrix* reference genome that is being developed in our group. This genome, which will be the first genome of this species, has been assembled and is available for analysis of the working group. The assembly of this genome contains 58,535 contigs with N50 and N90 of 11,385 and 3,762 bp, respectively. To search LTR retrotransposons we used LTR-Finder online software. A total of 1,117 LTR retrotransposons were found in different contigs with a density ranging from 1 to 12 LTR per contig. When we look at the density of those LTR in the genome it was found that a large number of LTR are present only in a few contigs and none or few can be found in many contigs. This indicates that there is not a pattern of insertion of those LTR retrotransposons throughout the genome. It is known that if a retrotransposon insert itself around genes that could change genes pattern of expression or function from multiple mechanisms. A mechanism example is the RIP (repeat-induced point mutation) that is a point mutations induced by repetition associated with mechanisms of defense against transposable elements. Studies suggest that such point mutations can extend beyond those repetitive regions and may lead to mutation on coding regions of the genome. Thus, the next step of this project will be to predict the proteins present in contigs where the retrotransposons were found and analyze the possible influence of those on coding regions. Take together the large number of retrotransposons present in *H. vastatrix* genome and those may be related to high genetic variability of this fungus that causes an important coffee disease.

Acknowledgements: CAPES, CNPq and FAPEMIG.