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ALLELIC VARIATION OF A CANDIDATE AVIRULENCE GENE FROM *Hemilea vastatrix* / Variação alélica de um candidato a gene de avirulência em *Hemileia vastatrix*.

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In previous studies we have identified a candidate avirulence gene (*HvEC-016*) in *Hemileia vastatrix*. Different strategies are being used to prove that *HvEC-016* indeed is an *Avr* gene. Among them, we are searching different natural allelic variants of this gene. Isolates carrying these allelic variants will be test to their ability to cause disease in coffee genotypes carrying the $S_{H}1$ rust resistance gene. Seven single-pustule isolates derived from the second generation of urediniospores was used for genomic DNA purification in order to clone the sequences encoding the mature protein HvEC-016. The corresponding sequences were amplified by PCR, cloned and sequence characterized. Six different alleles were identified in the seven isolates investigated (Hd = 0.952). Twelve point mutations were pinpointed in the sequences that code for the mature HvEC-016, 75% of them were associated with nonsynonymous modifications (amino-acid substitutions). A mutation (g.368A>T) leading to a premature stop codon was found in the isolate from Rio Paranaíba-MG. The ability of these allelic variant sequences that code altered forms to trigger defense responses in coffee plants carrying the $S_{H}1$ rust resistance gene will be tested. In addition, sequencing a greater number of cloned PCR product/isolates of the fungus is been done to obtain information on heterozygosity at *HvEC-016* locus in *H. vastatrix* natural populations.

Key words: Avirulence gene, Effector protein, Coffee rust