Identification and variability analysis of monooxygenase gene family from *Chrysoporthe cubensis*

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The increasing interest in renewable sources of energy and materials has motivated studies in biochemical conversion of lignocellulosic materials to valuable products. The enzymatic saccharification is one of the critical steps of converting lignocellulosic material, characterized by applying enzymes to break down the polymers in their basic constituents. Some limiting factors of the enzymatic hydrolysis include high cost of the enzymes and the recalcitrance of lignocellulose Thus, the improvement of enzyme cocktails are continually sought. In this context, the auxiliary active enzymes has emerged as enhancers of efficiency of saccharification and the enzymes belonging to AA9 family, namely Lytic Polysaccharide Monooxygenases (LPMO), is one of the most promising family. Our research group has been working with the phytopathogenic fungus *Chrysoporthe cubensis*, which has been showing more efficient than some commercial enzyme cocktails for saccharification. This has motivated to search for possible factors that explain this high saccharification efficiency and of them, is possibly the secretion of AA9 enzymes. In order to evaluate this hypothesis, protein sequences belonging to AA9 family from eukaryots obtained from CAZy were aligned using tblastn algorithm with the complete draft genome of *C. cubensis* and only the alignments with more than 70% of coverage and 40% identity was selected as candidates of AA9 coding genes. It was observed 169 homologous regions and these regions were subject to a manual curation step for eliminating redundancies, resulting in 12 specific sequences. In order to obtain the complete CDS, the region coordinates were subjected to *ab initio* gene prediction using the program Augustus set to *Neurospora crassa* as model organism. Taking together, these results provide a strong indicative of AA9 production and secretion by *C. cubensis* and accounts for high potential of this fungus in biotechnological process. Moreover, these results opens the possibility of heterologous expression of these enzymes, enabling improvements in saccharification yields as well as biochemical and molecular studies of LPMOs. Acknowledgements: CAPES, CNPq and FAPEMIG.