

**Abstract:**

Microbial enzymes implicated in plant cell hydrolysis may have several potential applications such as biomass degradation biocatalysts or with biofuel production. Bark beetles establish symbiosis with several microbial strains which play different roles benefiting the beetle, as the production of hydrolytic enzymes to degrade the ingested wood, the protection against microbial antagonist or the detoxification of the environment. Fungal symbionts have been traditionally the best studied, but several recent research with bacterial symbionts of several bark beetle species show that bacterial also display important functions for the host. In this study, the bacterial communities of the bark beetle species *Cryphalus piceae* and *Pithophthorus pithophthorus*, collected in the Czech Republic from pine and fir trees, respectively, were isolated and 55 out of 89 samples were identified by 16S rRNA gene amplification and sequencing. Members of the genera *Erwinia*, *Pantoea*, *Curtobacterium*, *Yersinia*, *Pseudomonas* and *Staphylococcus* were detected. The isolates were object of study for their possible biotechnological potential in (ligno)cellulose materials degradation by screening several enzymes implicated in plant cell hydrolysis, as cellulases, xylanases, amylases, laccases, as well as their capability for colorant degradation, with potential applications in water cleaning processes. Cellulolytic and xylanolytic potential of selected isolates was further studied by quantification of the enzymatic activity under different growth conditions. Bacteria from the genus *Erwinia*, of the gammaproteobacterial family Enterobacteriaceae, presented the best biotechnological potential, considering the enzymatical activity in cellulose and xylan degradation. Their cellulases and xylanases had the highest activity, and in the best candidates those enzymes appeared mainly as binded to the cell membranes.

**Key words:** bark beetles, bacterial endosymbionts, biomass degradation, cellulases, xylanases, amylases, laccases, colorants degradation, 16S rRNA gene, biotechnological potential