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Transcriptional study of cerato-platanin encoding genes in homokaryotic and heterokaryotic isolates of the forest pathogen *Heterobasidion irregulare*

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**TRANSCRIPTIONAL STUDY OF CERATO-PLATANIN
ENCODING GENES IN HOMOKARYOTIC AND HETEROKARYOTIC
ISOLATES OF THE FOREST PATHOGEN**

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The forest pathogen *Heterobasidion irregulare* (Basidiomycota) was recently sequenced and three cerato-platanin encoding genes were found in its genome (*HiCPs*). Cerato-Platanin Proteins (CPPs) are a family of proteins well known for their resistance-inducing ability when applied on plants. What is still poorly understood is their role in fungal life. These proteins seem to play both a role in the fungal cell wall and a role in the fungus-plant interaction, but most data available to date on CPPs derive from studies performed on Ascomycetes. In the present study, we investigated the expression of *HiCPs* in three homokaryotic isolates and two heterokaryotic isolates of the plant pathogen *H. irregulare*. Homokaryotic and heterokaryotic mycelia not only play different roles in the infectious process but also differ in their biology: clamp connections are formed in the heterokaryotic mycelia. Transcription of *HiCPs* was analysed both at the edge and at the centre of the fungal colony and compared between homokaryon and heterokaryon. Results showed *HiCP1* to be the gene with the highest transcript abundance among *HiCPs*. *HiCP1* did not show any preferential expression in different sections of the fungal colony, while *HiCP2* was significantly more expressed at the colony centre, thus suggesting a link with the production of conidia. The level of expression of *HiCPs* in heterokaryons was generally comparable to that of one or both the parental homokaryons, irrespective of the colony section, thus demonstrating that *HiCPs* are not transcriptionally influenced by the heterokaryotic stage.