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.