

*Molecular and bioinformatic analysis of signal transduction genes important for adaptation of *Heterobasidion annosum* to stress*

Tommaso Raffaello, Susanna Keriö and Fred O. Asiegbu

Department of Forest Sciences, University of Helsinki, Finland

The basidiomycete *Heterobasidion annosum* (Fr.) Bref. is a filamentous white rot fungus, considered to be the most economical important pathogen of conifer trees. A bioinformatic analysis has been performed to identify all putative MAP kinases (MAPKs) pathway and cyclic-AMP (cAMP) pathway related genes which are present in the *H. annosum* genome. The role of the specific stress related *HOG1* MAP kinase which is thought to be involved in the fungal osmotic tolerance was studied under different osmotic stress conditions. The comparative genome analysis reveals a high degree of conservation of MAPKs and cAMP genes among all the selected fungi. To assay for functional relevance of the gene during osmotic stress, the expression level of the *HOG1* transcript was quantified by qPCR in different conditions. The result showed that the fungus displayed a decreased growth when exposed to increased salt osmolarity conditions. Increased levels of the MAPK *HOG1* gene transcript was observed in high stress conditions. Taken together these results show the possible involvement of the *HOG1* gene in the capacity of *H. annosum* to overcome osmolarity stress conditions.