Transcriptome profiling of *Heterobasidion annosum* in saprotrophic and abiotic stress conditions

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The basidiomycete *Heterobasidion annosum* is a filamentous fungus which is considered to be one of the most destructive conifer pathogen in temperate forests of the northern hemisphere. The aim of this study was to characterize the changes in the transcript profiles when the fungus is exposed to general abiotic stress compared to the growth in natural pine wood material. *H. annosum* was cultivated under different abiotic stresses (0.5 M NaCl and 0.5 M CaCl$_2$ for 60 min, 8°C and 27°C for 3 weeks, 5 mM H$_2$O$_2$ for 60 min, and nutrient starvation for 3 days) and saprotrophic conditions (pine bark, heartwood, and sapwood for 3 months).

NimbleGen microarray experiments were performed using the *H. annosum* cDNA from the different conditions and the gene models from the *Heterobasidion* JGI gene catalogue to be synthesized on the array. Preliminary data analysis based on hierarchical clustering of the transcript levels revealed that the transcriptome profile of the fungal culture in saprotrophic conditions (wood material) differs clearly from the profile of cultures exposed to abiotic stresses (salts, oxidative, temperature, and nutrient starvation) indicating the activation of genes which are specifically involved in saprotrophic growth. On the other hand, activation of basic intracellular pathways and up-regulation of protein kinases suggest a fast adaptation response of *H. annosum* during change in environmental conditions (simulated by the abiotic stresses). Interestingly, different enzymes involved in wood degradation (laccases, glycosyl hydrolases, and cytochrome P450) are selectively up-regulated in different wood material suggesting specific adaptation of *H. annosum* to diverse substrates.

Based on the data analyzed so far, we concluded that fast changes in the environmental conditions (abiotic stress) activates signaling proteins (i.e. Kinases) while prolonged growth in different wood materials requires specialized battery of enzymes to be able to degrade and penetrate the specific substrate.