**ANALYSIS OF SECONDARY METABOLITE TRANSCRIPTS IN THE LICHEN-FORMING FUNGUS *Cladonia rangiferina***

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Secondary metabolites are produced by the fungal symbiont (mycobiont) of lichens in response to environmental changes. The cultured mycobiont is also capable of their production but little is known about their biosynthesis and their expression during early co-culturing stages of the lichen symbionts. The key enzymes in secondary metabolite production cycles include several synthases: Polyketide Synthases (PKS), Terpene Synthases (TPS) and Nonribosomal peptide synthetases (NRPS). Using a previously established method of resynthesis for *Cladonia rangiferina* as well as the sequenced and assembled genome of that species, we compared the *C. rangiferina* axenic culture, the fungus co-cultured with *Asterochloris glomerata*, and its wild type (fully lichenized, collected from its natural habitat), to reveal transcriptionally active genes in secondary metabolic gene clusters (as well some neighbouring genes) induced by the presence of the photobiont and events of lichenization. We identified several secondary metabolite synthases and supporting genes within predicted biosynthetic gene clusters affected by the events of lichenization. The difference between the expression profile of the co-culture and the wild type of *C. rangiferina* suggests an inhibitory effect of lichenization processes on secondary metabolite production. The inhibitory effect was observed for nine out of 30 predicted and differentially expressed synthases (PKS, NRPS, TPS) in the genome of *C. rangiferina*, as well as for five co-expressed proteins potentially involved in polyketide production. This study provides the basis of the research for further investigation of the potential biosynthesis of polyketides in an artificial host. This study was funded by the Natural Science and Engineering Research Council of Canada (NSERC) to MPN.