**Genomics reveals the chemical potential of the lichenic fungi, *Endocarpon pusillum* and *Heterodea muelleri***

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Lichens produce a varied array of novel molecules with over 1,000 secondary metabolites identified to date. These molecules are often valuable to pharmaceutical and healthcare industries making the chemical potential of lichens an important natural resource. However, the discovery and production of lichen metabolites have been limited by the need to extract compounds from these extremely slow-growing organisms. A recent and increasing flourish of lichen mycobiont genomes has been reported that may circumvent this challenge. The chemical potential of a lichen species can be predicted in silico by identifying biosynthetic gene clusters in the mycobiont genome. These gene clusters, traditionally, have been manipulated in the native host or heterologously expressed to overproduce the compound of interest. This allows the compound to be identified or produced industrially. Unfortunately, traditional expression methods have, thus far, not proven successful in lichenic fungi. We report the chemical potential of two Australian lichens - Endocarpon pusillum and Heterodea muelleri. E. pusillum was previously considered chemically silent with no detected compounds with TLC or HPLC. Whole-genome sequencing of the Australian isolates E. pusillum CBR01 and H. muelleri BMT01 identified a suite of biosynthetic gene clusters, most with no homology to described clusters. To characterize these clusters, we are developing a novel heterologous expression system not phylogenetically too distantly related to the native host species. Simultaneously, we are developing transformation methods to employ traditional and non-traditional genetic manipulation of the native hosts. These methods will accelerate the identification of novel compounds and link them to their biosynthetic gene clusters.