**METAGENOMICS SHEDS LIGHT ON THE EVOLUTION OF ‘SUNSCREEN’ PIGMENT METABOLISM IN THE TELOSCHISTALES (LICHEN-FORMING ASCOMYCOTA)**

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The Teloschistales (Ascomycota) is a cosmopolitan order with >1000 described lichen species. Its largest family, Teloschistaceae, has centres of diversity in mostly exposed, arid regions making it a key element of the biodiversity of deserts and high-altitude ecosystems. Part of the success of many Teloschistaceae within these hostile ecosystems is due to the production of anthraquinone secondary metabolites that allow the lichens to withstand intense UV radiation, temperature fluctuations and desiccation. It has been shown that anthraquinones may have evolved in these lichens in conjunction with ecological factors, allowing them to colonize unexploited habitats worldwide and facilitating an adaptive radiation. Though much has been done to describe the chemical diversity of lichen anthraquinones, we still know very little about the underlying genetic mechanisms leading to their biosynthesis. Here we introduce new research that implements a metagenomics approach to assemble and analyse over 30 new high-quality Teloschistales genomes. Using comparative genomics, we investigate the diversity and evolution of secondary metabolite gene clusters in Lecanoromycete lichens and putatively identify gene clusters involved in anthraquinone biosynthesis. We find that although secondary metabolite gene clusters in lichens are largely species-specific, the core biosynthetic genes are shared across the Lecanoromycetes. Our findings suggest that secondary metabolism diversification in lichens can occur through duplication and neofunctionalization of pre-existing biosynthetic genes combined with changes to surrounding accessory genes. This implies that the same core ancestral genes have evolved to produce very different compounds in different Lecanoromycete clades. Finally, we discuss how these genomes are the first of a larger project aiming to reconstruct a robust, comprehensively sampled phylogenomic tree for the Teloschistales. This research is funded by the UK Natural Environment Research Council (NERC) studentship NE/S007415/1 to T.L and the Evolution and Education Trust and Welcome Trust to E.G.