MASON HALE AWARD TO THEO LLEWELLYN

I am very pleased that Theo Llewellyn has received the Mason Hale Award for best PhD Dissertation.

I was his MSc mentor and PhD supervisor and it was a pleasure to supervise Theo all these years. He is an extremely talented scientist.

Theo Llewellyn collecting lichens, Portland Island, UK (*Photo: Ester Gaya*)

In his thesis, Theo focused on photoprotective anthraquinone pigments in the diverse order *Teloschistales* (Ascomycota) as a case study exploring how adaptive metabolic traits arise and diversify in lichen-forming fungi. He generated a genome-scale phylogeny for the *Teloschistales*, developing and implementing a lichen-specific metagenomics pipeline to sequence, assemble and annotate lichen-forming fungal genomes. Through comparative genomics, Theo identified putative anthraquinone biosynthetic gene clusters (BGCs) in *Teloschistales* genomes and demonstrated that BGC diversification occurred via re-shuffling existing enzyme-coding genes with novel accessory genes. To understand anthraquinone evolution across the whole clade, he then combined his genomic dataset with densely sampled multilocus data to produce a robust genome-scale time tree. Phylogenomic analysis showed around half of current *Teloschistaceae* genera to be unsupported, and he proposed a set of stable, evolutionarily relevant higher taxa instead. To understand how genomic variation affects the metabolite phenotype, he jointly analysed the genomes with new, untargeted metabolome data. This revealed a complex interplay between genomic and metabolic variation and suggested that, for anthraquinones, BGC variation affects compound regulation and transport more than structural diversity. Finally, as anthraquinones are broadly cytotoxic, he hypothesized that anthraquinone-producing *Teloschistaceae* lichens evolved resistance mechanisms to avoid self-toxicity. Enzyme assays, axenic culture experiments, selection analysis and *in silico* protein modelling in combination indicated that *Teloschistaceae* lichens achieved self-

resistance through the evolution of efflux pumps, toxin methylation, and resistant target enzymes. Together, the results of Theo's dissertation demonstrate the power of multiomic approaches in investigation of the evolutionary processes that shape metabolite diversification in lichens.

Theo Llewellyn collecting lichens, Namibia (*Photo: Ester Gaya*)

Interestingly, Theo's dissertation shows how generally accepted patterns in non-lichenised fungi apply equally to lichens. It fills in a major gap in the *Lecanoromycetes* tree of life. It is the first study to directly explore self-resistance mechanisms in lichens and investigates processes in BGCs that not even research in model fungi such as *Aspergillus* has dealt with.

I believe this thesis has made major advances in our understanding of lichen biology and the evolution of secondary metabolites. This is the first fungal study to use whole genome sequences with a Bayesian time-calibration approach. This is also the first study to identify anthraquinone BGCs in the *Teloschistales*, and the largest lichen phylogenomics study in terms of number of loci and genomes. Again, it is the first to jointly analyse genomes and metabolomes of lichen-forming fungi using a comparative and evolutionary-based approach that directly tests joint trait evolution, and challenges previous assumptions of metabolite evolution in lichens. It also presents for the first time an assessment of genome size in lichens using cytometric data. Last but not least, it tackles the ongoing debate on the classification of higher taxa in *Teloschistaceae*.

Theo's viva panel (defense panel in Britain), composed by Prof. Paul Dyer and Prof Matthew Fisher, praised his performance enthusiastically. A quote from their report: '*Excellent high-level viva, impressive range of responses, creative and engaged constructively with all the criticisms. The work was clearly that of the candidate*.'

Well done Theo!!! *Ester Gay*