The evolution of organismal multicellularity: from phenotype to genotype

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Project descriptor: The evolution of multicellular organisms from their unicellular ancestors is widely recognised among the most formative events in evolutionary history although, unusually, it is an event that has happened tens of times, in eukaryotes and even prokaryotes. However, among these lineages, it seems only the plants, animals and fungi that were pregnant with the evolutionary potential to generate disparate organismal-grade bodyplans. Both clades have been interpreted to exhibit an explosion of bodyplans early in their evolution ('maximal initial disparity') and in both instances, the realisation of organismal disparity scales is correlated with the origin and evolution of a class of non-coding regulatory genes called microRNAs which have been identified independently as causal factors in the macroevolution of these Kingdoms. To determine whether these patterns and processes are general laws in the emergence of novelty, this project seeks to characterise the evolution of bodyplans within the third great kingdom of organismal multicellularity, the fungi – which have also independently evolved microRNAs.

The overarching goal of this research project is to establish the disparity of Kingdom Fungi in a parametric framework for understanding the pattern and tempo of multicellular evolution within Holomycota. This work will entail characterising the anatomy of fungal clades as a basis for establishing an empirical morphospace that will be interrogated to determine the pattern in which bodyplans of component and aggregate clades were established (i.e. early burst versus gradual increase in variance/disparity). Once established, you will test hypotheses of causality, discriminating whether that variance is the consequence of cumulative random variation, or whether other driven factors, such as the evolution of protein coding genes (using protein domains as a proxy), or gene regulation (using miRNAs – which you will characterise through de novo sequencing), are responsible for the emergence of fungal disparity

Ultimately, you will integrate the results of your study with empirical morphospaces already established for the animal and plant kingdoms, providing an holistic comparative framework in which to explore the role of contingency and convergence in the evolution of organismal mulitcellularity.

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Hughes, Martin, Sylvain Gerber, and Matthew Albion Wills. "Clades Reach Highest Morphological Disparity Early in Their Evolution." *Proceedings of the National Academy of Sciences of the United States of America* 110, no. 34 (2013): doi:10.1073/pnas.1302642110.