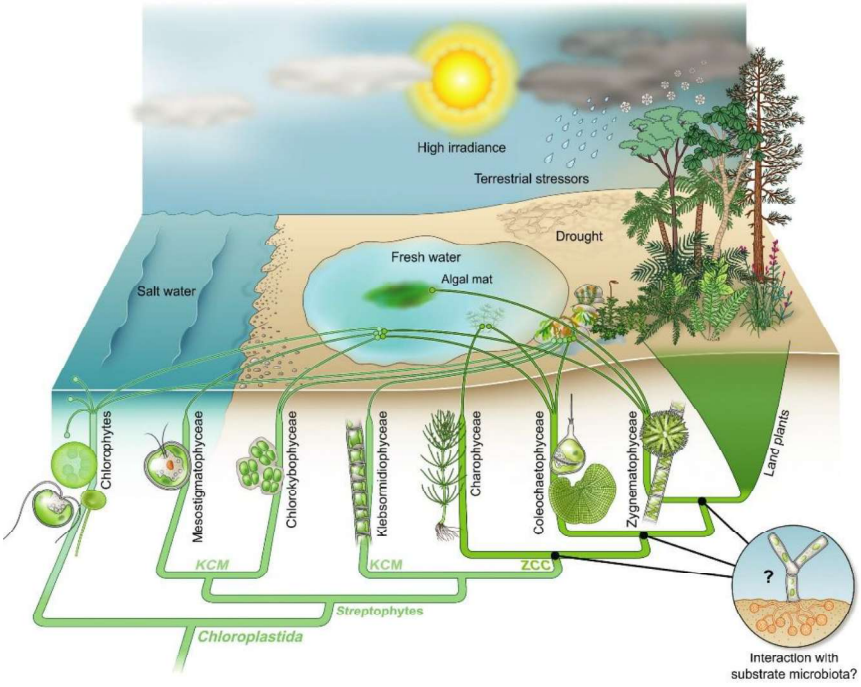
Evolutionary assembly of land plants: genomes, development and phenotype

Project ID: 3509

Supervisory team

Main supervisor: Prof Philip Donoghue (University of Bristol)
Second supervisor: Dr James Clark (University of Bath)
Other supervisors: Prof Davide Pisani (University of Bristol) & Prof Tom Williams (University of Bristol)

Host institution: University of Bristol



Project description: The origin of land plants represents one of the most profound episodes in evolutionary history, transforming the energy budget, albedo, and biogeochemical cycles of our planet. While the fossil record provides a good account of the emergence of living land plants lineages, it is essentially uninformative of the steps in which the land plant bodyplan was first assembled. Consequently, competing hypotheses on the assembly of the land plant bodplan are largely speculative, based in arguments of plausibility. However, recent sequencing efforts have generated a wealth of genome data for the living streptophyte relatives of land plants, providing crucial data for elucidating this key episode in Earth history. It has already demonstrated that the land plant genome was assembled over a protracted period of geologic time and characterised by widespread gene duplication and gene acquisition through transfer from symbionts. This project will exploit these data to go much further, establishing a new highly-resolved and integrative understanding of the evolutionary assembly of land plants by exploiting three methodological advances: (a) using Artificial Intelligence (AI) approaches to inferring the relationship between gene and phenotypic evolution based on their patterns of coevolution within phylogeny; (b) using Bayesian relaxed molecular clock methodology to establish the absolute timing of the gene duplications that characterise the ancestry of land plants, informing on the sequence in which land plant innovations were established; (c) using hierarchical models of trait evolution that are informed by development to establish the nature of the ancestral land plant and its forebears.The project will be largely computational and will involve applying phylogenetic, comparative genomic and AI-based methods to datasets of land plant and streptophyte algal genomes that are already available for study. You will use these methods to characterise the sequence in which genomic and phenotypic traits were acquired within the context of an absolute timescale. This will allow you to identify contributions to the genome from bacteria and eukaryotes like fungi, informing on the timing and sequence in which symbioses were established. The evolutionary and comparative genomic skills

developed as part of the project can also be used to address other cutting-edge questions in phylogenetics, developmental biology, comparative genomics and evolution. The rotation projects in the first year will help you to develop those skills and apply them to several interesting related questions.

Our aim as the SWBio DTP is to support students from a range of backgrounds and circumstances. Where needed, we will work with you to take into consideration reasonable project adaptations (for example to support caring responsibilities, disabilities, other significant personal circumstances) as well as flexible working and part-time study requests, to enable greater access to a PhD. All our supervisors support us with this aim, so please feel comfortable in discussing further with the listed PhD project supervisor to see what is feasible.