

The Darwin Tree of Life



Reading the genomes of all life: a new platform for understanding our biodiversity

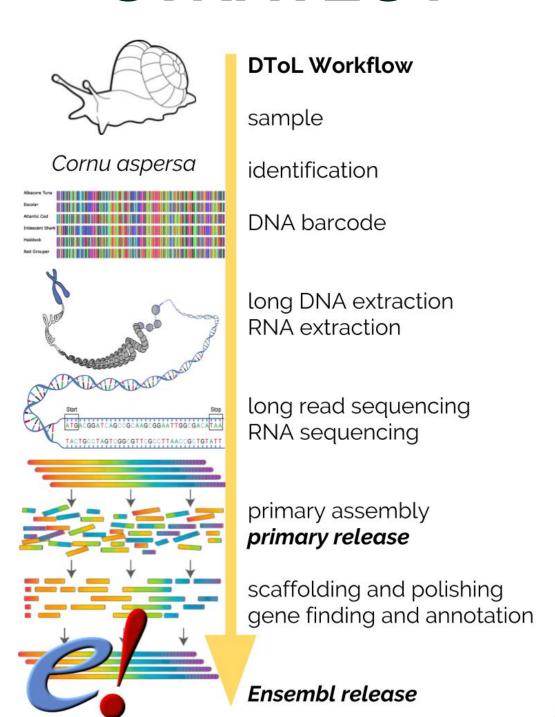
The Darwin Tree of Life project aims to sequence the genomes of all 60,000 species of eukaryotic organisms of the British Isles.

The Darwin Tree of Life Project will transform our understanding of the British fauna and flora, providing new insights from the level of the gene to the entire ecosystem.

We will use genomic data to understand the evolution of the diversity of life, to explore the biology of organisms and ecosystems, to aid conservation efforts and to provide new tools for medicine and biotechnology.

The project is one of several initiatives across the globe working towards the ultimate goal of sequencing all complex life on Earth, in a venture known as the Earth BioGenome Project

STRATEGY



The Darwin Tree of Life project will collect representatives of each species, use advanced DNA sequencing technologies to generate high quality genome sequences, and cutting edge computational tools to understand how the DNA sequence translates into the diversity of life.

Aims of Phase 1 - the first two years

Review of the species lists of the British Isles by experts at Natural History Museum London, RBG Kew, RBG Edinburgh and domain specialists. The species lists will form the basis for taxon acquisition and sequencing campaigns.

Collect ~ 8000 species We will establish a network of Genome Acquisition Labs (GALs) who will be responsible for sampling, identifying, vouchering, DNA barcoding, and preserving multiple specimens of each targeted species, ready for DNA and RNA extraction, in a series of collection campaigns.

Sequence the genomes of 2,000 species, including family level representation We will develop robust methods for long DNA extraction at scale across the diversity of Eukaryota.

Assembly and annotation of 2,000 species. We will deploy state of the art algorithms and approaches to generate fully annotated genome data. Specimen and genome metadata will be available to all.

We will analyse the genomes individually and collectively. Analyses will range from whole dataset - building the tree of life, to single species or families, using the genome to understand specific biological features.

The Darwin Tree of Life Consortium

The DToL consortium brings together a network of world-leading centres with complementary strengths in genomics, informatics, ecology, and taxonomy.























The Royal Botanic Garden Edinburgh (RBGE) is one of six Genome Acquisition Labs, tasked with the collection, identification and curation of samples for the project.



We will draw on our taxonomic expertise, existing research, and collections to collect and catalogue plants and fungi with a primary focus on Cryptogams.



We will engage with interest groups and learned societies to facilitate sampling.



We aim to have collected approx. 1/3 of the listed species by the end of 2021, including representatives from each family.



We will work with recording groups and specialist societies to explore Scotland's biodiversity and the value of biodiversity genomics in understanding and learning about nature.