



Newsletter

March 2021

Welcome to the first issue of the DToL project Newsletter.

In the newsletter we aim to share with everyone involved in the DToL project the current state of play in terms of collection and production, share news of developments across the partners, and highlight new staff, new initiatives and exciting findings.

The last year has been difficult for all, with the Sars-CoV pandemic shutting sites, preventing collection trips, and slowing our production. Despite this, and through creative innovation and dogged hard work, we have been able to collect, sequence and assemble: our first half-century of genomes are now making their way into the European Nucleotide Archive, and from there to the rest of the world. The next hundred, and more, will follow in quick succession.

The newsletter will come out every two months, and if you have something to communicate to your colleagues, please do send a short (very short - two sentences) report to Chloe Leech (cl22@sanger.ac.uk), perhaps with a picture.

Best wishes && stay safe

Mark Blaxter, Sanger Institute

DToL All Hands 2021 meeting | 8-11 March 2021 | Online

The annual DToL All Hands Meeting will be held from 2-5 pm on Monday 8th- Thursday 11th March, and will be an opportunity to catch up on everything that has happened in the project in the last year, and also to plan for the future. Attendance is free, but we do need to know numbers. Please register here by 9 am on Thursday 4th March: www.eventbrite.co.uk/e/dtol-all-hands-2021-tickets-136293540649

Updates from DToL Partners

NHM NHM has been working to establish a formal collaboration with Cryoarks, including shared fieldwork and shared species lists. Roving bioblitzes are being planned. DNA barcoding is established (with covid-induced delays) The Museum is forecast to be fully open (to the public) during May, and full science activities should restart similarly.

RBG Kew Kew have planted seeds from 56 priority species belonging to 33 families, all on the priority list. The first plates of fungal samples, from cultures and field collections, have been sent on to Sanger. Work is ongoing to optimize protocols for estimating genome sizes in fungi. Kew have appointed a project coordinator who will start 1st May.

RBGE & University of Edinburgh The first DNA extractions for the large genome work, from mistletoe, have been successful, and test sequencing is ongoing at Edinburgh Genomics. Field collection of bryophyte material to propagate at RBGE for R&D planned next week, and a plants sampling strategy meeting is planned for 25th & 26th Feb to develop fieldwork plans for the year.

MBA MBA have been sampling from the littoral and from marine sources as lockdown permitted, and are planning activities for spring and summer, with an early focus on macroalgae.

University of Oxford & Wytham Woods Some sampling is continuing, and the plan for targeted sampling through 2021 is being finalised. The species list for Wytham (all taxa) is being updated to remove gaps, synonyms and inaccuracies.

Earlham Institute and Oxford Protists COPO development has continued apace. Single cell pipeline development continues including testing of processing in 384 well plates. The cell sorter is operational in Oxford and sorting from environmental samples is starting, including 20L marine samples from MBA every fortnight from March. Our culture collections collaborators are growing the next batches of strains to be delivered to Sanger.

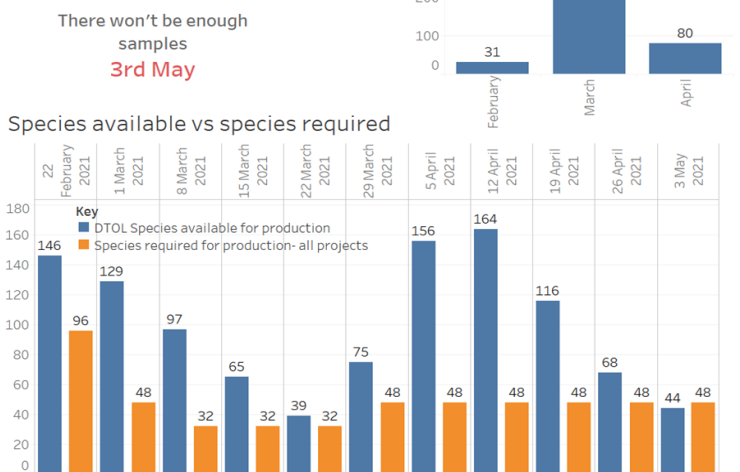
Sanger Institute Samples have continued to arrive at Sanger: 5313 samples form 1258 species from 510 families (see dashboards above) and the institute has installed new Sequel IIe sequencers to deal with the expected flood of sequencing requests. We have recruited a Genome Note editor to expedite the automation of Genome Note publication.

EBI Ensembl Rapid Release development is ongoing, and analyses of DTOL (and 25 genomes) species (including the Eurasian water vole) have been released. The annotation pipeline is being tested with the first insect assemblies. The DTOL Data Portal is live and work is ongoing to improve linkages and automate data flow, including DNA barcode data processing. Issues with timely processing of submitted assemblies are being solved through negotiation with NCBI colleagues.

University of Cambridge The Cambridge team continues to work on assembly, and on extending the analysis toolkit, in particular on whole genome alignment.

The Dashboards to the right are from the Sanger Production monitoring system, which uses the STS and COPO systems to track progress of sample acquisition, extraction, submission for sequencing, assembly and submission

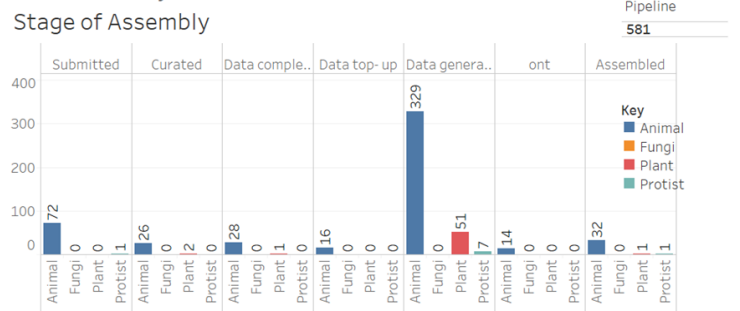
DTOL Pipeline Summary



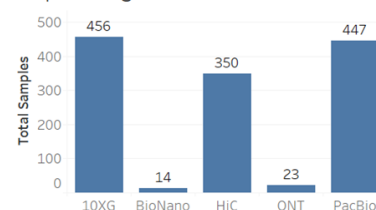
Production Summary



DTOL Assembly Dashboard



Sequencing methods used



Kingdoms sampled (%)

