ERGA: COLLABORATING TO UNDERSTAND AND MANAGE EUROPEAN BIODIVERSITY

The European Reference Genome Atlas (ERGA) initiative is a pan-European consortium of multidisciplinary scientists dedicated to establishing a catalog of genomic information to further our understanding of biodiversity – what it is, how it functions, and current forces causing declines. Their efforts have centered on generating an atlas containing high-quality, complete reference genomes for each of Europe's ~200,000 eukaryotic species, many of which are already at risk of extinction.

ERGA began in 2020 with a focus on building a partnership capable of managing the unprecedented scope of their task. In only two years, it has grown from ~60 to over 750 members and counting, representing 234 research institutions. ERGA's leadership hierarchy includes a board of chairs, council members representing 37 European and associated countries, and 9 committees.

To demonstrate the feasibility of a collaboration of this scale, ERGA launched a pilot project – established, funded, and driven entirely by its members – to create a genomics infrastructure that could support the inclusion and equal participation of each country at each step. The pilot project asked representatives of each country to provide one species as a test of the distributed model of reference genome generation.

To ensure high-quality genomic results, the group implemented guidelines for species selection: easy collection, small genomes, and possession of national or international permits.
Today, there are more than 90 species in the pilot project that meet these criteria.

Furthering the collaborative nature of this project, several sequencing hubs and trans-border genome teams promoted a cooperative approach among members at each step, with some labs performing sample collection and nucleic acid extraction, followed by RNA sequencing and generation of high-throughput chromosome conformation capture (Hi-C) sequencing libraries at one of the three sequencing hubs. This framework provided resource availability for every country involved while creating a feeling of partnership. The project also committed to test compliance with Earth BioGenome Project standards (https://www.earthbiogenome.org/), aiming for reference genomes with almost chromosome-level quality.

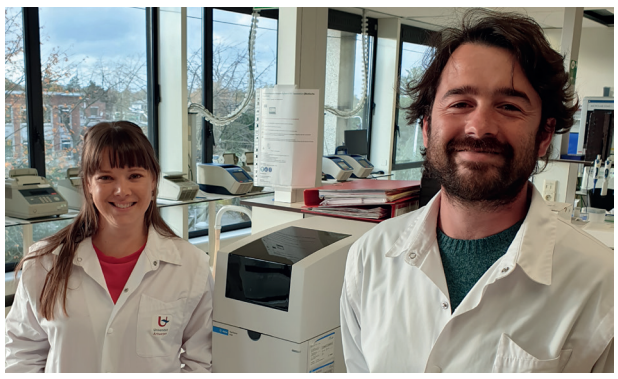
Producing high-quality libraries and optimal sequencing results requires a focus on sample preparation and extraction, no matter the sequencing method or genetic starting material. The nucleic acid samples were then sent to one of the three sequencing hubs, where RNA sequencing and high-throughput chromosome conformation capture (Hi-C) sequencing libraries are generated.

Dr. Genevieve Diedericks is a member of one of these highly specialized labs – the Svardal Lab at the University of Antwerp. Dr. Diedericks and her team discovered just how crucial quality control is, especially when faced with limited initial sample input and budget constraints. By focusing on intermittent sample quality control (QC) assessments, her team identified ideal samples for producing high-quality sequencing results.

The challenge of limited resource availability was also addressed through guidelines that simplify the workflow and mitigate potential library preparation failures. These included instructions for sample collection, storage, and shipment to limit sample degradation. The Svardal Lab, for example, relied on two main methods for RNA and DNA homogenization: a simple and inexpensive needle and syringe method, and a second, more specialized bead bashing method requiring ceramic beads and specialized equipment. Once samples were completely homogenized, the extractions were performed per kit-specific protocols for each species type. It was also essential to apply quality control prior to library preparation.

Dr. Diedericks and the Svardal Lab team chose to quantify RNA and DNA fluorimetrically and assess quality with an Agilent TapeStation system. "We are fortunate enough to have access to a 4150 TapeStation system, so we used the Agilent RNA ScreenTape assay to assess RNA degradation before continuing with library prep," she said. They noted the ease-of-use of the TapeStation system, including step-by-step loading instructions, run progress bar, and specific post-run software for sample analysis, as factors in their decision. "The software's color coordination of each sample's RNA integrity number equivalent (RINe) helped us interpret the results and determine which samples were most suitable to move onto library preparation."

The DNA in Hi-C samples was also assessed prior to library preparation, and again they chose the Agilent TapeStation system. "We used the TapeStation system with a high-sensitivity DNA ScreenTape assay to generate our quality profiles," said Dr. Diedericks. Using assay-specific reagents and protocols, the flexible TapeStation system met their needs for both RNA and DNA sample quality control.



Dr. Genevieve Diedericks and Henrique Leitão

ERGA acts as well as a network of similar initiatives happening at the national level. Members continue to pursue funding initiatives to promote the expansion of their efforts. The pilot project, which is now closed, will conclude when all the genomes for these species will be published either in a genome note or within a research article within the next year or two.

In addition to the pilot project, another venture of the ERGA consortium has been to establish a collaboration with the DNA barcoding community (BIOSCAN) to lead the Biodiversity Genomics Europe (BGE) Project – an initiative funded by Horizon Europe until 2026 with an ambitious goal of adding 350 to 500 reference genomes to the atlas within the next three years. Their mission is to link reference genome initiatives happening across Europe under the ERGA umbrella, connecting the infrastructure and expertise available within the consortium.

"The use of reference genomes will become a new standard in the years to come for the study of biodiversity genomics. This pilot project showed how the partnership, the collaboration and the knowledge transfer between countries, institutions and researchers is fundamental to achieve such goals."
Summarized Dr Alice Mouton, co-leader of the pilot project with Ann Mc Cartney and Giulio Formenti.

Read more about the ERGA initiative at: www.erga-biodiversity.eu/ and about the Biodiversity Genomics Europe (BGE) project at: https://biodiversitygenomics.eu/

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