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LAUNCH OF GLOBAL EFFORT TO READ GENETIC CODE OF ALL COMPLEX LIFE ON EARTH

The Earth BioGenome Project (EBP), a global effort to sequence the genetic code, or genomes, of all 1.5 million known animal, plant, protozoan and fungal species on Earth, officially launches today (1 November) as key scientific partners and funders from around the globe gather in London, UK to discuss progress in organising and funding the project.

The EBP will ultimately create a new foundation for biology to drive solutions for preserving biodiversity and sustaining human societies.

The EBP aims to sequence, catalogue and categorise the genomes of all of Earth's eukaryotic* biodiversity over a period of ten years. The estimated cost of the EBP is \$4.7 billion. Accounting for inflation, the Human Genome Project today would cost \$5 billion.

The EBP is made possible by recent and future advances in sequencing and information technology that will enable the reading and interpretation of tens of thousands of species' genomes each year by partner institutions across the globe.

A greater understanding of Earth's biodiversity and the responsible stewarding of its resources are among the most crucial scientific and social challenges of the new millennium. The overcoming of these challenges requires new scientific knowledge of evolution and interactions among millions of the planet's organisms.

Currently, fewer than 3,500, or about 0.2 per cent of all known eukaryotic species have had their genome sequenced, with fewer than 100 at reference quality. Sequencing all known eukaryotic genomes, thousands at reference quality, will revolutionise our understanding of biology and evolution, bolster efforts to conserve, help protect and restore biodiversity, and in return create new benefits for society and human welfare.

Professor Harris Lewin, University of California, Davis, United States and Chair of the EBP Working Group, said: "The Earth BioGenome Project can be viewed as infrastructure for the new biology. Having the roadmap, the blueprints for all living species of eukaryotes will be a tremendous resource for new discoveries, understanding the rules of life, how evolution works, new approaches for the conservation of rare and endangered species, and provide new resources for researchers in agricultural and medical fields."

The EBP has made extraordinary progress in the last year leading up to the official launch. The initial stages of the EBP has served as an organizing glue for existing large-scale genome projects and their partnering institutions on eukaryotic species around the globe. Toward this end, 17 institutions from across the globe, including the USA, United Kingdom, China, Germany, Denmark, Australia and Brazil, have signed a Memorandum of Understanding** that commits each institution to work together towards the common goals of the project. It is expected that additional partner institutions, organisations and communities will join as the project progresses.

The amount of biological data that will be collected and produced from this project is expected to be on the exascale; more than the data accumulated by Twitter, YouTube or astronomy. The project's participants have agreed in the EBP Memorandum of Understanding that data will be stored in public domain databases and access will be open to all for research purposes.

This project will build on recent achievements of sequencing sets of species' genomes for the first time. For example, the Vertebrate Genomes Project, Chaired by Erich Jarvis of Rockefeller University, aims to sequence the genetic code of all 66,000 extant vertebrates, released the genomes of 14 species, including bat and fish species, the Canadian Lynx and Kakapo***.

The BGI (Shenzhen, China) is also playing a major role in the project by leading the effort to sequencing 10,000 plant genomes and the Global Ant Genomes Alliance, which aims to sequence around 200 ant genomes. Similarly, the USDA is launching an effort to sequence 100 genomes of agriculturally important insects and mites. In total, there are now 15 scientific communities and national and regional projects that are affiliated with the EBP.

To mark the 25th anniversary of the Wellcome Sanger Institute, the Institute and its collaborators sequenced the genomes of 25 species found in the United Kingdom (UK) for the first time****, including red and grey squirrels, the European robin, Fen raft spider and blackberry. The completed genome sequences will lead to future studies to understand the biodiversity of the UK and aid the conservation and understanding of UK species.

The Sanger Institute will lead the UK contribution to the EBP by sequencing all 66,000 eukaryotic species across the British Isles, in a new project known as the Darwin Tree of Life Project. Sanger has committed to creating a new programme of research, called the Tree of Life programme, to fulfil this mission and will work alongside partners at the Natural History Museum in London, Royal Botanic Gardens, Kew, Earlham Institute, EMBL-EBI and Edinburgh Genomics at the University of Edinburgh. The EBP will help coordinate this effort with other affiliated projects to help reduce redundancy and maximize resources.

Professor Sir Mike Stratton, Director of the Wellcome Sanger Institute, said: “Globally, more than half of the vertebrate population has been lost in the past 40 years, and 23,000 species face the threat of extinction in the near future. Using the biological insights we will get from the genomes of all eukaryotic species, we can look to our responsibilities as custodians of life on this planet, tending life on Earth in a more informed manner using those genomes, at a time when nature is under considerable pressure, not least from us.”

Sir Jim Smith, Director of Science at Wellcome, said: “When the Human Genome Project began 25 years ago, we could not imagine how the DNA sequence produced back then would transform research into human health and disease today. Embarking on a mission to sequence all life on Earth is no different. From nature we shall gain insights into how to develop new treatments for infectious diseases, identify drugs to slow ageing, generate new approaches to feeding the world or create new bio materials.”

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Notes to Editors:

*Eukaryotic species (animal, plant, protozoa and fungi) are defined as organisms whose cells have a nucleus enclosed within membranes, unlike prokaryotes, which are unicellular organisms that lack a membrane-bound nucleus, mitochondria or any other membrane-bound organelles (Bacteria and Archaea).

***For more information on the Vertebrates Genome Project, visit:
<https://vertebrategenomesproject.org/>

****For more information on the Sanger 25 Genomes Anniversary Project news story, visit:
<https://www.sanger.ac.uk/news/view/25-uk-species-genomes-sequenced-first-time>

Funding:

Activities of the EBP are currently being funded by the participating organisations as well as

private foundations, governmental organisations and crowd-funding sources. Participating institutions are committed to raising funds to complete the project in 10 years. Significant funds have already been raised by taxon-based communities, national and regional projects to meet the \$600 million goal necessary to complete Phase 1 of the project, which aims to produce approximately 9000 reference quality genomes across all taxonomic families.

Appendix of panel member quotes:

Professor Jenny Graves, from La Trobe University, Melbourne Victoria Australia, said: “There is great power in comparing genomes of closely related species to reveal recent changes and probe the genetic health of species. And there is great power in comparing distantly related species, allowing us to go back far in evolutionary time to discover how the most fundamental life processes work and how they evolved. You never know where the next big breakthrough is going to come from, so it makes sense to sequence everything.”

Dr W. John Kress, from the Smithsonian Institution, United States, said: “Natural history museums have been collecting and storing information on the Natural World for centuries. The Earth BioGenome Project will enable us to more completely analyze, synthesize, and share that information, in part through the billions of biodiversity specimens housed within our walls, currently and in the future.”

Professor Katherine Belov, from the University of Sydney, said: “Off the back of the koala genome, which was sequenced earlier this year, Australian researchers plan to sequence 50 of Australia’s most endangered animals over the next five years. This genomic data will provide the foundation for strategic genetic management of small, isolated populations of iconic and unique marsupials, amphibians and birds. The Earth Biogenome Project allows us to join a global network of experts, to tap into their expertise and computational pipelines and to achieve our goals much more quickly than we could if working alone.”

Professor Federica Di Palma, Director of Science at the Earlham Institute, said: “Our GCRF work in Colombia is demonstrating how equally important biodiversity is to the climate change context in both developing and developed countries, like the UK. As these countries adapt to new policy landscapes and evolving political challenges, there has never been a greater need for academics, NGOs, businesses and decisions-makers to join forces to collectively characterise, conserve and manage such biodiversity for sustainable economic growth and social wellbeing. The Global impact BRIDGE Colombia network is a great example of how to facilitate crucial dialogue and collaborative partnerships around these important biodiversity issues.”

Dr Xin Liu, from BGI Shenzhen, China, said: “The 10,000 plants project (10KP) aims to sequence over 10,000 genomes representing every major clade of plants and eukaryotic microbes on Earth. This project will generate large-scale plant genome data within the next four years, addressing fundamental questions about plant evolution. The Earth BioGenome Project provides a framework in which global collaboration can be effectively carried out, making it possible for execution of our project.”

****Partners and participating communities** (Please note, the joining of project participants is ongoing)

Institutions (Memorandum of Understanding executed):

- Australian Museum
- Baylor College of Medicine
- BioPlatforms Australia
- Beijing Genomics Institute at Shenzhen, China
- George Washington University
- Natural History Museum of Denmark
- Max-Planck Society

- Novim Group, USA
- Royal Botanic Gardens at Kew, UK
- SpaceTime Ventures, Brazil
- University of California, Davis, USA
- University of California, Santa Cruz
- University of Santiago, Chile
- University of Florida, USA
- University of Illinois at Urbana-Champaign, USA
- University of Sydney, Australia
- Wellcome Sanger Institute, UK

Affiliated communities, regional and national projects:

- 1000 Fungal Genomes Project (1KFG)
- Global Invertebrates Genome Alliance (GIGA)
- 5000 Insect Genomes (i5K)
- Ag100 Pests (USDA)
- 10,000 Plants Project (10KP)
- 10,000 bird genomes (B10K)
- Genome 10K
- Oz Mammals Genome Project (OMG)
- Darwin Tree of Life (UK)
- LOEWE Centre for Translational Biodiversity Genomics
- University of California Consortium for the Earth BioGenome Project (CalEBP)
- 1000 Chilean Genomes
- Taiwan BioGenome Project
- Global Genome Initiative (Smithsonian)/Global Genome Biodiversity Network

The EBP will coordinate currently independent biodiversity genome sequencing projects and organizations involved in specimen collection, including in Australia, Brazil, Chile, Columbia, Denmark, Germany, Norway, the United Kingdom, and the United States. Coordination functions will include planning, strategy, communications and funding. The EBP aims to achieve common standards across all taxonomic groups of eukaryotes for sample collection, DNA sequencing, annotation and genome analysis.

Selected websites:

Earth BioGenome Project

www.earthbiogenome.org

Carl R. Woese Institute for Genomic Biology

<https://www.igb.illinois.edu/>

BGI Shenzhen

www.genomics.cn

University of California, Davis Genome Center

The UC Davis Genome Center serves the Omics needs of a large community of scientists, government and industry partners. State-of-the-art facilities for genome sequencing, gene expression analysis, an NIH-funded metabolomics core, proteomics and bioinformatics support research activities of more than full-time 40 faculty members involved in fundamental and translational research on agriculture, the environment and human health. The Genome Center is the current administrative home of the Earth BioGenome Project.

<http://genomecenter.ucdavis.edu/>

The Earlham Institute

The Earlham Institute (EI) is a world-leading research Institute focusing on the development of genomics and computational biology. EI is based within the Norwich Research Park and is one of eight institutes that receive strategic funding from Biotechnology and Biological Science Research Council (BBSRC) - £5.43m in 2017/18 - as well as support from other research funders. EI operates a National Capability to promote the application of genomics and bioinformatics to advance bioscience research and innovation.

EI offers a state of the art DNA sequencing facility, unique by its operation of multiple complementary technologies for data generation. The Institute is a UK hub for innovative bioinformatics through research, analysis and interpretation of multiple, complex data sets. It hosts one of the largest computing hardware facilities dedicated to life science research in Europe. It is also actively involved in developing novel platforms to provide access to computational tools and processing capacity for multiple academic and industrial users and promoting applications of computational Bioscience. Additionally, the Institute offers a training programme through courses and workshops, and an outreach programme targeting key stakeholders, and wider public audiences through dialogue and science communication activities. www.earlham.ac.uk

BRIDGE Colombia

www.bridgecolombia.org or follow @bridgecol

The Wellcome Sanger Institute

The Wellcome Sanger Institute is one of the world's leading genome centres. Through its ability to conduct research at scale, it is able to engage in bold and long-term exploratory projects that are designed to influence and empower medical science globally. Institute research findings, generated through its own research programmes and through its leading role in international consortia, are being used to develop new diagnostics and treatments for human disease. To celebrate its 25th year in 2018, the Institute is sequencing 25 new genomes of species in the UK. Find out more at www.sanger.ac.uk or follow @sangerinstitute

Wellcome

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