

25 UK species' genomes sequenced for first time

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The genomes of 25 UK species have been read for the first time by scientists at the Wellcome Sanger Institute and their collaborators. The 25 completed genome sequences, announced today (4 October) on the Sanger Institute's 25th anniversary, will lead to future studies to understand the biodiversity of the UK and aid the conservation and understanding of our species.

The newly-sequenced genomes will enable research into why some brown trout migrate to the open ocean, whilst others don't, or investigations into the magneto receptors in robins' eyes that allow them to 'see' the magnetic fields of the Earth. The genomes could also help to shed light on why red squirrels are vulnerable to the squirrel pox virus, yet grey squirrels can carry and spread the virus without becoming ill.

The Sanger Institute was founded in 1993 by Professor Sir John Sulston as part of the Human Genome Project. The Institute made the largest single contribution to the gold- standard sequence of the first human genome, which was published in 2003.

A genome is an organism's complete set of genetic instructions written in DNA. Each genome contains all of the information needed to build that organism and allow it to grow and develop.

Since the landmark completion of the human genome, the Sanger Institute has become a globally recognised leader in the field of genomics. Many more important reference genomes have already been

sequenced—from the mouse and zebrafish genomes to the pig, gorilla, mosquito and many others. Beyond animal [species](#), infectious diseases and bacteria also feature prominently on the list of reference genomes, from salmonella and MRSA to chlamydia and malaria. All of these have offered up important insights about these species in health and disease.

Now, the Sanger Institute and its partners have comprehensively sequenced 25 UK species for the first time. The first [human genome](#) took 13 years and billions of dollars to complete. With the great advances in technology and falling costs of sequencing, scientists have been able to newly sequence 25 species' genomes in less than one year and at a fraction of the cost.

Dr. Julia Wilson, associate director of the Sanger Institute, said: "We are thrilled to announce the completion of 25 genomes from UK species. Sequencing these species for the first time didn't come without challenges, but our scientists and staff repeatedly came up with innovative solutions to overcome them. We have learned much through this project already and this new knowledge is flowing into many areas of our large scale science. Now that the genomes have been read, the pieces of each species puzzle need to be put back together during genome assembly before they are made available."

Dan Mead, co-ordinator of Sanger's 25 Genomes Project, said: "We are already discovering the surprising secrets these species hold in their genomes. We've found that King scallops are more genetically diverse than we are, and the Roesel's bush cricket's genome is four times the size of the human [genome](#). Similar to when the Human Genome Project first began, we don't know where these findings could take us."

The 25 Genomes Project has been made possible by PacBio long-read sequencing technology, which generates high-quality genomes. The Institute partnered with PacBio and other leaders in the technology

sector, 10x Genomics and Illumina, to create the most comprehensive view of these genomes.

The high-quality genomes will be made freely available to scientists to use in their research. Researchers could discover how UK species are responding to environmental pressures, and what secrets they hold in their genetics that enables them to flourish, or flounder.

Dr. Tim Littlewood, Head of Life Sciences at the Natural History Museum, London and a partner of the 25 Genomes Project, said: "The 25 Genomes Project has uncovered the blueprints of a diversity UK life, which will effectively re-write what we know about these species. By comparing those blueprints within and between species we can understand the genetic diversity of fauna and flora from the UK and beyond. These newly-sequenced genomes are a starting point that will reveal aspects of evolution we've not even dreamt of."

This project is a small contribution to a much larger undertaking, where scientists from around the world are coming together to form a plan to sequence all life on Earth.

Professor Sir Mike Stratton, director of the Sanger Institute, said: "DNA sequencing technology has advanced over the last number of years to a point at which we can at least discuss the possibility of sequencing the genomes of all of life on Earth. From those DNA sequences we will obtain inestimable insights into how evolution has worked, and to how life has worked."

More information: The 25 species that have had their genomes sequenced are:

Flourishing species:

- Grey squirrel
- Ringlet butterfly
- Roesel's bush cricket
- Oxford ragwort

Floundering species:

- Red squirrel
- Water vole
- Turtle dove
- Northern February red stonefly

Dangerous species:

- Giant hogweed
- Indian balsam
- King scallop, also known as Great scallop, Coquilles Saint-Jacques
- New Zealand flatworm

Iconic species:

- Golden eagle
- Blackberry
- European robin
- Red Mason bee

Cryptic species:

- Brown trout
- Common pipistrelle bat
- Carrington's featherwort
- Summer truffle

Five species chosen by the public:

- Common starfish
- Fen Raft spider
- Lesser spotted catshark
- Asian hornet
- Eurasian otter

For more information on the 25 Genomes Project, visit

<http://www.sanger.ac.uk/science/collaboration/25-genomes-25-years>

Provided by Wellcome Trust Sanger Institute

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