

Glanville fritillary genome sequenced

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A Granville fritillary (*Melitaea cinxia*). Credit: Tari Haahtela

The Granville fritillary has long been an internationally known model species for ecology and evolutionary biology, whose population biology has been studied on the Åland Islands for more than twenty years. Now the species has become even more significant. Led by Research Professor Ilkka Hanski, the Metapopulation Research Group (MRG) at the University of Helsinki has sequenced the full genome of the Granville fritillary together with three groups from the Institute of Biotechnology at the same university.

Before the sequencing of the Glanville fritillary [genome](#), which is approximately 390 million base pairs long, the only genomes sequenced in Finland were those of viruses and bacteria. After the silk moth and longwing, the Glanville fritillary is now the third [species](#) of butterfly for which both the sequence of its full genome and a high-resolution genetic map is available. The map displays the location of approximately 16,000 genes in the species' 31 chromosomes.

The study also confirms the hypothesis that the ancestral lepidopteran species had 31 chromosomes, as originally proposed by Esko Suomalainen, professor of genetics at the University of Helsinki in the 1960s.

"The most astonishing thing is that it seems like the genes have stayed in the same chromosomes practically throughout the evolutionary history of butterflies –at least for 140 million years. Such stability is nearly unique among all organisms. What is even more surprising is that even though some chromosomes have fused during the lepidopteran evolution, the genes remain on their own side of the chromosome even after chromosomal fusions," explains group leader Mikko Frilander of the Institute of Biotechnology, who participated in the study.

Originally consisting of ecologists, MRG focused heavily on [genome sequencing](#), as its objective is to combine genetic and genomic research with its strong ecological and evolutionary biological research.

"We want the Glanville fritillary to become a new model species for integrative biology. The next challenge is to get more biologists interested in the species," states Research Professor Ilkka Hanski.

The sequencing of the Glanville fritillary genome was a four-year project, funded by the European Research Council and the Academy of Finland.

Most of the sequencing was conducted on the Viikki Campus, at the Institute of Biotechnology of the University of Helsinki, under the supervision of Petri Auvinen. Genome assembly was the responsibility of Panu Somervuo of MRG and Leena Salmela from the Department of Computer Science. Gene annotation and predicting their function was conducted by Virpi Ahola from MRG together with Liisa Holm, professor in bioinformatics, and Patrik Koskinen.

The high-resolution genetic map for the Glanville fritillary was constructed using a tool developed by Pasi Rastas, from MRG.

Provided by University of Helsinki

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