

Press Release

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Fire ant: The biggest genome ever sequenced in Switzerland

The genome of the fire ant *Solenopsis invicta* was recently sequenced by the team of Prof. Laurent Keller at the Lausanne University, and by the SIB Swiss Institute of Bioinformatics. The Swiss teams applied sophisticated research methods previously restricted to biomedical research to sequence and assemble the whole genome of this particularly destructive species. The results of the study led by Dr Yannick Wurm, [The Genome of the fire ant *Solenopsis invicta*](#), are published this week in the prestigious journal PNAS.

The red fire ant owes its name to its color and to the painful burns induced by the toxic venom it injects when it stings. This ant was inadvertently introduced to the southern United States from South America in the 1930s. It is found today in many additional countries including Australia and China. Fire ants are aggressive predators that live in colonies of up to hundreds of thousands of individuals. The species is responsible for damages valued at 5 billion USD yearly across the United States. Because existing methods of fire ant control have failed to halt its spread, alternative control methods are urgently needed.

Sequencing, assembling and annotating: challenging tasks

Sequencing the genome of *Solenopsis invicta* offers new opportunities to control the fire ant. But getting this far required innovative techniques. Sequencing a genome means determining the order in which the four components of DNA, Adenine (A), Thymine (T), Guanine (G) and Cytosine (C) are arranged. Sequencing machines first generated hundreds of millions of fragments of approximately 100 'A's, 'C's, 'G's and 'T's. Combining these puzzle pieces into sequences up to 10,000 times longer required detailed comparisons. This task was entrusted to the powerful computers and creative team of SIB group Vital-IT under the leadership of Prof Ioannis Xenarios. Oksana Riba-Grognuz, Laurent Falquet and Yannick Wurm meticulously arranged and assembled the pieces based on partial sequence overlaps. The assembled sequences were then handed over to SIB group Swiss-Prot, also headed by Ioannis Xenarios. To identify and characterize the genes present in these long DNA sequences, Dr Nicolas Hulo and Dr Lorenzo Cerutti combined several approaches including the comparison of the ant sequences with all the data contained in the Swiss-Prot database. Approximately 15,000 genes were thus identified.

The ant, an insect with a sophisticated sense of smell

By comparing the ant genes with those of other insects, Yannick Wurm and his collaborators discovered unique aspects of the fire ant genome which are likely linked to unique aspects of the complex social behavior of this species. For example, the fire ant seems to have an

extremely developed ability to perceive odors, Indeed, the *Solenopsis invicta* genome harbors more than 400 odor receptors (compared to 10 for the body louse *Pediculus humanus* and to 60 for the fruit fly *Drosophila melanogaster*). Ants recognise their queen, their nestmates and their foes based on odors. Future pesticides that reverse-engineer and specifically manipulate odor perception of ants could be used to fool workers into executing their own queen. This would allow eradication of fire ant colonies without affecting other species or the environment.

About SIB

SIB Swiss Institute of Bioinformatics is an academic not-for-profit foundation recognised of public utility and federating bioinformatics activities throughout Switzerland. Its two-fold mission is to provide world-class core bioinformatics resources to the national and international life science research community in key fields such as genomics, proteomics and systems biology; as well as to lead and coordinate the field of bioinformatics in Switzerland. It has a long-standing tradition of producing state-of-the-art software for the life science research community, as well as carefully annotated databases. SIB includes 29 world-class research and service groups, which gather more than 400 researchers, in the fields of proteomics, transcriptomics, genomics, systems biology, structural bioinformatics, evolutionary bioinformatics, modelling, imaging, biophysics, and population genetics in Basel, Bern, Geneva, Lausanne, and Zurich. SIB expertise is widely appreciated and its services are used by life science researchers worldwide.

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