

# Experts sequence the genome of an endemic spider from the Canary Islands

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This species, which lives in the insular laurel forests in the Canary Islands (Spain), is a big generalist predator that does not use a web to hunt its prey.  
Credit: Miquel Arnedo (UB-IRBio)

A research team of the Faculty of Biology and the Biodiversity Research Institute (IRBio) of the University of Barcelona has sequenced the

genome of the spider *Dysdera silvatica* Schmidt 1981, an endemic species living in the laurel forests in the islands La Gomera, La Palma, and El Hierro in the Canary Islands (Spain). The new study reveals the first genome sequencing of an arthropod in the Canary Islands, an archipelago with a rich biodiversity regarding endemic species that are distributed around the insular area.

Participants in the new study, published in the journal *GigaScience*, are the experts Julio Rozas, Miquel Arnedo, José Francisco Sánchez-Herrero, Cristina Frías-López, Paula Escuer, Silvia Hinojosa-Alvarez and Alejandro Sánchez-Gracia (UB-IRBio).

## **Dysdera silvatica: a ravening predator in the Canary laurel forests**

The *Dysdera* genus, which belongs to the [species](#) *Dysdera silvatica*, includes more than 250 [spider species](#) mainly distributed around the Mediterranean area. The Macaronesian archipelagos represent the western limits of the distribution of this taxon, which reached a significant diversification in the Canary Islands, where there are about 50 endemic species currently.

"One of these species is *Dysdera silvatica*, integrated in an evolutionary lineage that became one of the main predators, both in abundance and diversity, in the insular terrestrial invertebrate trophic networks," notes Professor Miquel Arnedo from the Department of Evolutionary Biology, Ecology and Environmental Sciences of the Faculty of Biology and the Biodiversity Research Institute (IRBio) of the UB.

"The species *D. silvatica* is a generalist predator. Unlike other spider groups, the *Dysdera* includes experts on hunting and consumption of terrestrial isopods. All these species live in the Canary Islands, where the

crustacean trophic specialization seems to have evolved independently several times," adds the researcher, head of the research group on Arthropod Systematics and Animal Evolution of the UB.

## **The first genome sequencing in the Dysderoidea superfamily**

This is the first sequencing of the nuclear and mitochondrial genome for a species of the Dysderoidea superfamily, and the second one known in the Synspermiata group, one of the main spider lineages. Regarding this group, the first species with the available genomic data was the brown recluse spider (*Loxocles reclusa* Gertsch & Mulaik, 1940), a species distributed around the American continent and quite known for its necrotic venom.

According to the conclusions, the genome of the *D. silvatica* species is large (1.7 Gb) and shows a high complexity, with a high fraction of repetitive elements. According to Professor Julio Rozas (UB-IRBio), who co-led the study together with Alejandro Sánchez-García, "Within this study, we created a 1.4 Gb genomic sequencing assembly, 54 percent of which is built by repetitive elements."

"We identified and characterized a total of 36,000 protein-coding genes," notes Professor Julio Rozas (UB-IRBio), head of the research group on Evolutionary Genomics and Bioinformatics at the UB, part of the platform Bioinformatics Barcelona (BIB).

The *D. silvatica* species has a diploid chromosome set of six pairs of autosomes and two (females are XX) or one (males are X0) sex chromosomes (XX-X0), females have six non-sexual chromosome pairs (autosomes) and the XX sexual paired chromosomes. Males have six pairs of autosomes and only one X sexual chromosome.

## **Third generation sequencing techniques to treat a complex genome**

The study started about five years ago with the application of next-generation massive sequencing (NGS) such as Illumina. With this protocol, the researchers created 1 billion short sequences (100 paired bases) that were not enough to get a quality assembly for the complex genome of the species.

Therefore, the research team completed these data with PacBio and Nanopore single molecule sequencing (SMS) techniques, "more expensive, but more efficient methodologies to obtain larger genome sequencing, and provide a quality genomic assembly using the hybrid assembly strategy, combining data from the obtained sequencing through different technologies," notes José Francisco Sánchez-Herrero, member of the Department of Genetics, Microbiology and Statistics of IRBio and first author of the article.

## **Ecology, evolution and reproductive behavior**

From a global perspective, the study brings new views to know more about the genetic bases of the eco-phenotype change that takes place during the adaptive radiation phenomena over biological evolution. In particular, the models from the *Dysdera* genus in the Canary Islands, the genome sequencing of this first species can bring valuable information on the underlying genetic architecture in the phenotype and physiological changes related to the trophic specialization, as well as the underground environment adaptations, a natural environment where some species got used to live exclusively in the lava tubes.

Regarding their [reproductive behavior](#), the Dysderidae family includes species that show a cryptic female choice mechanism, that is, a

reproductive strategy that consists of the female's post-copulatory choice of a male's sperm to fertilize their ova. This choice is conducted through a complex system of diverticulum and glands associated with the female vulva. Knowing the features of the genome of a species from this family could contribute to determine the genetic bases of this behavior, through a comparative study of several regions of the [genome](#) under different selective constrictions between sexes, and among species with different sexual strategies.

Last, the study provides useful resources to treat studies on other evolutionary and essential issues, such as the origins and evolution of products with medical and commercial interests produced by spiders (venom, silk, etc.).

**More information:** Jose Francisco Sánchez-Herrero et al. The draft genome sequence of the spider *Dysdera silvatica* (Araneae, Dysderidae): A valuable resource for functional and evolutionary genomic studies in chelicerates, *GigaScience* (2019). [DOI: 10.1093/gigascience/giz099](https://doi.org/10.1093/gigascience/giz099)

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