Master project 2024-2025

Personal Information

Supervisor	Jesus Lozano-Fernandez
Email	jesus.lozano@ub.edu
Institution	Department of Genetics, University of Barcelona
Website	http://jesuslozanofernandez.weebly.com
Group	Deep Evolution Lab

Project

Computational genomics

Project Title:

Establishing ancestral whole genome duplications in arachnids

Keywords:

Genome assembly, phylogenomics, arachnids, whole genome duplication, synteny

Summary:

In this project, the student will have access to a set of newly generated arachnid chromosome-scale genome assemblies made by the host lab. Their role will be to establish whether some of the groups share or not ancestral whole genome duplication events, which have been previously used as a phylogenetic character. To do so, she/he will study the patterns of micro- & macrosynteny, employ phylogenomic techniques and study the evolution of gene families within the group, with the aim of establishing a solid species tree for the group.

References:

-LOZANO-FERNANDEZ, Jesus, et al. Increasing species sampling in chelicerate genomic-scale datasets provides support for monophyly of Acari and Arachnida. Nature communications, 2019, vol. 10, no 1, p. 2295. -LEITE, Daniel J., et al. Homeobox gene duplication and divergence in arachnids. Molecular biology and evolution, 2018, vol. 35, no 9, p. 2240-2253. -LOZANO-FERNANDEZ, Jesus. A practical guide to design and assess a phylogenomic study. Genome Biology and Evolution, 2022, vol. 14, no 9, p. evac129.

Expected skills:

Interest in evolutionary biology. Experience in handling large datasets. Ideally, some experience in genomic assembly

Possibility of funding:

To be discussed

Possible continuity with PhD:

Yes

Comments:

The lab is located in the Faculty of Biology of the University of Barcelona. We are a young research group with a group of international members. We are open to remote/hybrid work model. Currently, we have 2 active grants, so there are chances of continuing the research with a funded PhD.