

A **PhD position** is available in the Conservation and Evolutionary Genetics Group at Estación Biológica de Doñana, Seville (Spain) on Amphibian Evolutionary Genomics. The PhD position is part of the project: A stroll with amphibians along the path of speciation: from micro to macro evolutionary processes funded by the Spanish Government ("Procesos micro y macro evolutivos en la diversificación de anfibios", CGL2013-47547-P). Recent years have seen an increase in the knowledge of the amphibian diversity in the Neotropics. Many new species are being described every year at the same time that many others become part of the lists of endangered species. However, little is known about the patterns and processes that explain this diversity. In this proposal we join the efforts of research groups in four countries (Spain, Sweden, Mexico, USA and Brazil) to study the origin of the diversity of amphibians at very different spatial and temporal scales and using diverse analytical approaches. We will assemble one transcriptome and use genomic approaches to study the demographic and evolutionary history of a genus of Neotropical frogs in the absence of a genome sequence of a closely related species that could be used as a reference. This genus includes species adapted to highland and lowland environments. We will investigate the phylogenetic relationships between species, we will track demographic changes through time and their correspondence with habitat changes, and we will identify portions of the genome that are differentiated between populations with different degrees of isolation and that could indicate incipient speciation. Methods: -Transcriptome assembly, mapping sequences obtained with Next Generation Sequencing approaches, demographic inference. -Analysis of population structure using genotyping-by-sequencing approaches. Candidates: -The candidate should have a masters degree or equivalent degree in Biology, Evolutionary Biology, Biotechnology or Bioinformatics -Previous experience working with next-generation-sequencing data and bioinformatic analyses is highly desirable -Analytically inclined, familiarity with work in a Linux/Unix environment is highly desirable. The project will require programming in Perl or Python and the analysis of large genomic databases -Proficient in both written and spoken English -Willing to work abroad (we expect that part of the work will be carried out in close collaboration with our Swedish colleagues) -Dynamic, eager to learn and willing to participate in all the activities run by the research group (weekly meetings, seminars, discussions) The project does not include field work. Samples are already available in scientific collections. For more information about the research group lines of work, please check:

<http://www.consevol.org/>

Evaluation of applicants will be initially carried out by government agencies. All applications should be submitted via (instructions in Spanish): webpage
<Evaluation%20of%20applicants%20will%20be%20initially%20carried%20out%20by%20government%20agencies.,All%20applications%20should%20be%20submitted%20via%20%28instructions%20in%20Spanish%29:%20,

<http://www.idi.mineco.gob.es/portal/site/MICINN/menuitem.dbc68b34d11ccbd5d52ffeb801432ea0/?vgnnextoid=186f39d05c7d6410VgnVCM1000001d04140aRCRD&vgnnextchannel=11f35656ecfee310VgnVCM1000001d04140aRCRD, Candidates+must+also+send+documentation+to+Carles+Vil%C3%A0>

.> Candidates must also send documentation to Carles Vilà (before September

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carles.vila@ebd.csic.es

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