

Speciation and diversification in venomous organisms are often associated with prey and toxin diversification. In the conoideans, a group of marine gastropods predators of worms, molluscs and fish, studied since 40 years for the potential therapeutic applications of the toxins they produce, it is generally accepted that the apparition of the venom apparatus explain the high species diversity in this group. However, the number of species and the distribution area varies among lineages, and the apparition of the venom apparatus in itself cannot explain these differences. Recent studies showed that the structure of the venom apparatus, including the morphology of the radula and the presence of accessory anatomical structures, together with the toxin composition of the venom, can also vary among lineages. The goal of the project is thus to (i) estimate the rates of diversification in the Conoidea to eventually detect variations in time and among lineages, and (ii) correlate these variations with various characters linked to the venom apparatus (morpho-anatomy, toxin composition). This project is part of the ANR program CONOTAX (ANR-13-JSV7-0013-01) whose objective is to understand the process of diversification in the Conoidea, both at the phylogenetic and species level, combining the analysis of the species diversity, the prey diversity and the toxin diversity. More info can be found on the CONOTAX website (<https://sites.google.com/site/conotax/>). The post-doc will be in charge of the constitution of the dataset and the analyses: phylogenetic reconstruction, datation and estimation of diversification rates and correlation with character evolution. The first step of the work will thus be to complete the available molecular phylogeny of the groups. All the known families are represented in the collections of the MNHN (National Museum of Natural History), but expeditions on the field are already planned for 2015, at which the post-doc could participate. The methodology used until now (Sanger sequencing of traditional genes for gastropods COI, 12S, 16S, 28S, H3, 18S) does not resolve the deeper nodes, and the postdoc will thus have to set up a new methodology for the group using Next-Generation Sequencing (NGS). Three approaches will be explored: sequencing of complete mitochondrial genomes, sequencing of transcriptomes, and exon-capture. Available fossils for the group will then be used to date the tree and rates of diversification will be estimated. The successful candidate will be funded by the CONOTAX program (Net salary: 2,200 per month) and hosted in the Service de Systématique Mollusculaire and the UMR7205 / ISYEB, in the MNHN of Paris. It is a one-year position that can be extended for another year, and it will start on January 1st, 2015. Applicants should have: - a PhD degree in a relevant field - experience with molecular laboratory techniques, and in particular NGS - a good knowledge in molecular phylogeny and in phylogenetic approaches for studying diversification - a good scientific publication record - a good capacity to handle a scientific project, interact with other members of the lab and a willingness to train students. How to apply: send a full CV (including a list of your skills relevant for the position and a list of publications) and a 2-3 pages document to explain how you would handle the project, and in particular what strategy you would apply to resolve the phylogeny of the Conoidea. Provide also the name and coordinates of 2 referees. Send you application

before

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. Contact (questions, applications): Dr. Nicolas Puillandre, puillandre@mnhn.fr