Brief CV

Current position: Maître de Conférence, MNHN
Qualification: HdR, MNHN (‘Impact of the taxonomic hypotheses in evolutionary biology’)
Professional background:

- Post-doc, CNRS/MNHN (2012). Impact of the taxonomy on conservation programs.
- Post-doc, Atheris Laboratories (2011). DNA markers for deep phylogeny analyses in Conoidea.
- Post-doc, CNRS/MNHN (2010-2011). Managment of the MarBOL (Marine Barcode of Life) project.
- Post-doc, University of Utah (2008-2009). Species diversity within Conus and conotoxin evolution.

Scientific responsabilities:

- Collection manager of the Molluscs
- Participant and organizer of Marine expeditions
- Co-organizer of courses in the Master 2 SEP and the Doctoral School of the MNHN
- Member of the “Conseil d’Unité” of the ISYEB
- Associate editor : Journal of Molluscan Studies

Research Interest

Phylogeny, species delimitation, and character evolution

My main reasearch interest is on developing integrative taxonomic approaches to analyze the species diversity, the phylogenetic relationships between species, and their interactions with the environment. Although specialized in the analysis of DNA variability and molecular systematic, my concern is also in developing complementary approaches to propose robust hypotheses based on several characters and criteria.
I am currently working on marine molluscs of the superfamily Conoidea (CONOTAX project).

- https://sites.google.com/site/conotax/

This hyperdiverse group is a real challenge for taxonomists and molecular approaches have proved useful in proposing robust hypotheses on both species delimitation and phylogenetic relationships. These hypotheses are placed in an integrative framework, as others characters (morphology, anatomy or ecology) are analyzed. The strength of the results also relies on the collaborative aspect : anatomists, morphologists, biochimists, phylogeneticians,etc are all involved in the project. Actually, the interest of the Conoideans, illustrated by the results obtained with the genus Conus, does not only concern their hyperdiversity and their utility as a model to study speciation and diversification pattern in a marine environment, but also on the evolution of the toxins they use to capture their prey. As a result to the adaptation to their environment (and especially to new prey), these toxins (named "conotoxins" for the genus Conus) are particularly diverse, and their evolution is driven by several biochemical and molecular mechanisms. These toxins are moreover of particular interest in medecine, as some have already revealed their potential as therapeuthic drugs. Combining molecular, morphological, anatomical and toxinology approaches also provides a robust framework to analyse the evolution of the group, and in particular the factors that drove their exceptional diversification.

Defining species and their relationships are thus not only interesting for taxonomists, but also for setting up subsequent analysis both for theorical consideration (definition of species, speciation) and concrete applications (conservation biology, interaction with the environment, character evolution, discovery of new drugs,etc).