CORVETTE - CORal VEnom Toxin evoluTion, Ecology and biotechnological applications

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Abstract

Venoms are complex cocktails containing mostly peptide toxins that have evolved independently in multiple animal lineages, often through the convergent recruitment of orthologous peptides. The phylum Cnidaria is entirely composed of venomous species, but venom composition has been investigated only in a few jellyfishes and sea anemones, revealing a remarkable molecular diversity. Specifically, sea anemones venoms are rich in neurotoxic peptides, some of which have been developed in drug leads. However, the role of eco-evolutionary factors in shaping toxin diversity, as well as their biotechnological potential, remain to be fully characterized in most lineages.
To fill this gap, CORVETTE will focus on two abundant gorgonian species that play an important role as ecosystem engineers in the Western Mediterranean, *Paramuricea clavata* and *Leptogorgia sarmentosa.* Recent work has highlighted the richness and novelty of gorgonians' venom toxins. The two target species of CORVETTE can tolerate anthropogenic stressors, are characterized by divergent trophic strategies, and have not been characterized yet in terms of venom composition, representing an ideal model to investigate toxin diversity patterns and the underlying eco-evolutionary mechanisms.
Using a multidisciplinary approach, this study will tackle three key scientific objectives: 1) assess the impact of trophic strategy, environmental variables and anthropogenic stressors on venom composition at the intra- and inter-specific level; 2) reconstruct the evolutionary patterns of main venom protein families across the entire Octocorallia radiation, leveraging existing genomic resources; 3) investigate the functional role and pharmacological potential of novel toxin families using cutting-edge *in silico* approaches.
The interest of this project lies in its interdisciplinary approach merging proteotranscriptomics, MALDI-MSI, molecular phylogeny, comparative genomics, and *in silico* molecular modelling; in its focus on a neglected yet promising lineage in terms of toxin diversity; and in its potential for the discovery of a repertoire of previously unidentified toxins, some of which might convey a relevant translational potential in a drug discovery context.
The integration of this project with the EU-funded Biodiversa+ project "B2D - Biodiversity2Drugs" (https://www.gruber-lab.com/b2d), involving the entire supervision team, will offer high-level training, international collaborations and invaluable career opportunities to the Ph.D. fellow.