

Evolutionary modeling of the clownfish adaptive radiation

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The build up of biodiversity through time is through to be associated with several different evolutionary processes. Among them, adaptive radiations, where a single species diversifies into many descendant lineages adapted to a wide range of ecological conditions, is often proposed as a key process. There are now several well-known examples of adaptive radiations, but much remains to be understood about the genomic mechanism of adaptive radiations. In this project, we will use genomic data to better understand the mechanisms driving the adaptive radiation of clownfishes. We will first study in details the genomic architecture of the radiation to characterize the drivers that have been shaping the evolution of clownfishes since the acquisition of the mutualism with sea anemones. Although this first step has been critical to create the new ecological opportunities necessary for starting up the adaptive radiation, we still do not know what are the genetic mechanisms responsible for driving this processes. Using a combination of genomic and evolutionary modeling, the goals of this project is to fully understand the current diversity of shape, color and specialization levels in clownfishes. Being able to identify the mechanisms behind this diverse group of fishes will also provide new insights into i) the role played by ecological speciation in the build up of biodiversity in a marine environment and ii) the characterization of the genomic architecture enabling the speciation process to occur despite little barrier to gene flow and the presence of hybridization. Finally, the analyses of such data reinforce the needs to develop novel models of evolution that can bridge between evolutionary scale and thus enable testing new hypotheses to advance our understanding of the origin of biodiversity.