

# **Genomics of the diversification of the clownfish skunk complex**

## **(*Amphiprion akallopisos*, *A. sandaracinos* and *A. perideraion*)**

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Clownfish are an iconic group of coral reef fish that evolved a mutualistic interaction with sea anemones, which triggered the adaptive radiation of the group. Within clownfishes, the skunk complex is particularly interesting as, besides ecological speciation, hybridization events were suggested to shape the divergence of the group. Thus, we investigated here the mechanisms underlying the diversification of this complex. By taking advantage of their disjunct geographical distribution, we obtained whole-genome data of sympatric and allopatric populations of the three main species of the complex. We examined population structure, genomic divergence patterns, and introgression signals, and we performed demographic modelling to identify the most realistic diversification scenario. We excluded scenarios of strict isolation and of hybrid origin of *A. sandaracinos*, and we ruled out the presence of extensive gene flow in sympatry. However, we discovered moderate gene flow from *A. perideraion* and the ancestor of *A. akallopisos* + *A. sandaracinos* and weak gene flow between the species in the Indo-Australian Archipelago throughout the diversification of the group. We identified introgressed regions in *A. sandaracinos*, and we detected two large regions of high divergence in *A. perideraion*, likely maintained by the disruption of recombination. Altogether, these results show that hybridization events in the skunk complex are less pervasive than initially thought and suggest a role of host repartition in maintaining the genetic identity of the species in sympatry.