

# Host use drives convergent evolution in clownfish and disentangles the mystery of an iconic adaptive radiation

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December 6, 2022

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Clownfish (Amphiprioninae) are a fascinating example of a marine adaptive radiation. From a central Pacific ancestor, they quickly colonized the coral reefs of the Indo-Pacific and diversified independently on each side of the Wallace line. The association with the venomous sea anemone is often thought to be the key innovation that allowed the clownfish radiation. However, this intuition has little empirical or theoretical support given our current knowledge of the clade. Our synthetic work aims at filling this gap by testing the influence of anemone host-use on gene selection and on genetic and phenotypic divergence. We gathered multiple in-situ pictures of clownfish individuals in their host for each clownfish species, from which we estimated variation in coloration patterns, morphology and host use. We significantly updated known clownfish-host associations based on this new data. We also sequenced whole-genomes for each clownfish species and reconstructed the most up-to-date phylogenetic tree for the Amphiprioninae. In the light of this new data, we found robust evidence for convergent evolution of morphology and coloration driven by differential host-use. Clownfish colonized the same hosts in parallel in different regions and evolved the same phenotype in both replicates of similar events. We also identified several genes under positive selection during host shifts events. We provide empirical evidence of an adaptive radiation triggered by a key innovation and isolate genetic markers involved in this mechanism.