

# New resource could provide clues on the past, present, and future of clownfish

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Researchers have published the genome of the false clownfish (*Amphiprion ocellaris*), a species found around Okinawa, Southeast Asia, the Philippines, and northwestern Australia. Credit: Kina Hayashi, OIST

Clownfish may have been made famous through the popular film *Finding Nemo*, but probably only a few people realize that these charismatic orange-and-white fish offer huge potential for scientific research. Scientists can use them to answer a myriad of biological questions, from how larvae disperse in the open ocean to how coral reef fish will react to climate change. To help achieve these answers, researchers from the Okinawa Institute of Science and Technology Graduate University (OIST) have pieced together a comprehensive genome of the false clownfish (*Amphiprion ocellaris*). The study was published in *G3 Genes|Genomes|Genetics*.

"This [genome](#), which is like the blueprint of the false [clownfish](#), will be a very useful resource for scientists across biological fields," explained Dr. Marcela Herrera Sarrias, one of the two first authors of the study and Postdoctoral Scholar in OIST's Marine Eco-Evo-Devo Unit.

"We can use the false clownfish as a model species for studying ecology, evolution, adaption, development biology, and more," added Prof. Vincent Laudet, Principal Investigator of the Marine Eco-Evo-Devo Unit.

The false clownfish is found in both tropical and subtropical areas and relies on sea anemones, and thus the coral reef, for survival. Like many coral reef fish, it is expected that their populations will decline as coral reefs decrease in size due to climate change. This species looks very similar to orange clownfish—the true Nemo—but the two live in different areas. The false clownfish is found around Okinawa, Southeast Asia, the Philippines, and northwestern Australia while the orange clownfish is around northeastern Australia and some of the Pacific Islands. A comprehensive genome of the orange clownfish was published a few years ago so it was only fitting that, for comparative research, publication of the false clownfish's genome followed suit.

Although previous research has resulted in the genome of the false clownfish, this study produced by far the most high-quality version. The researchers highlighted that this was due to their version being at the scale of chromosomes.

The genome of the false clownfish is like the comprehensive instruction manual located in every one of its cells. It contains all the information needed for the operation of the fish. This instruction manual is divided into chapters—the chromosomes—and these are, in turn, divided into pages—the genes. Previously published genomes on the false clownfish comprised of scattered genes or chunks of genes, with little understanding of how they were arranged on the chromosome. In this new study, the genome is more fully assembled.

For this research, false clownfish were collected from Onna-son in Okinawa. The researchers extracted their DNA and RNA and used a sequencing technology to assemble the genomes at a chromosome scale. Then they could start answering some of the biological questions.

The two species of clownfish fit into the subfamily of anemonefish, which is made up of 28 [fish species](#) in total. The researchers decided to compare the two genomes to find out what genes the two species shared that might be missing from the other 26 species.

"Evolutionary speaking, the two clownfish species are separated from the other 26 species in the subfamily," said Dr. Taewoo Ryu, who led the project and is a Group Leader in OIST's Marine Climate Change Unit. "We wanted to find out what makes them special."

They uncovered 70 genes that were conserved in the genomes of the two species of clownfish, but not in the other 26 species. The other species still had some of the genes, but they were a little bit different. Furthermore, the researcher found that a subset of these genes is related

to neurobiological function, so likely impacts the behavior and ecology of the two species of clownfish, in a way that makes them different from the rest of anemonefish.

"We've already started generating results using the published genome and there is a huge capacity for further [climate change](#) research on this species," concluded Prof. Tim Ravasi, senior author of the paper and Principal Investigator of the Marine Climate Change Unit. "This resource provides a new baseline to start other experiments."

**More information:** Taewoo Ryu et al, A chromosome-scale genome assembly of the false clownfish, *Amphiprion ocellaris*, *G3 Genes|Genomes|Genetics* (2022). [DOI: 10.1093/g3journal/jkac074](https://doi.org/10.1093/g3journal/jkac074)

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