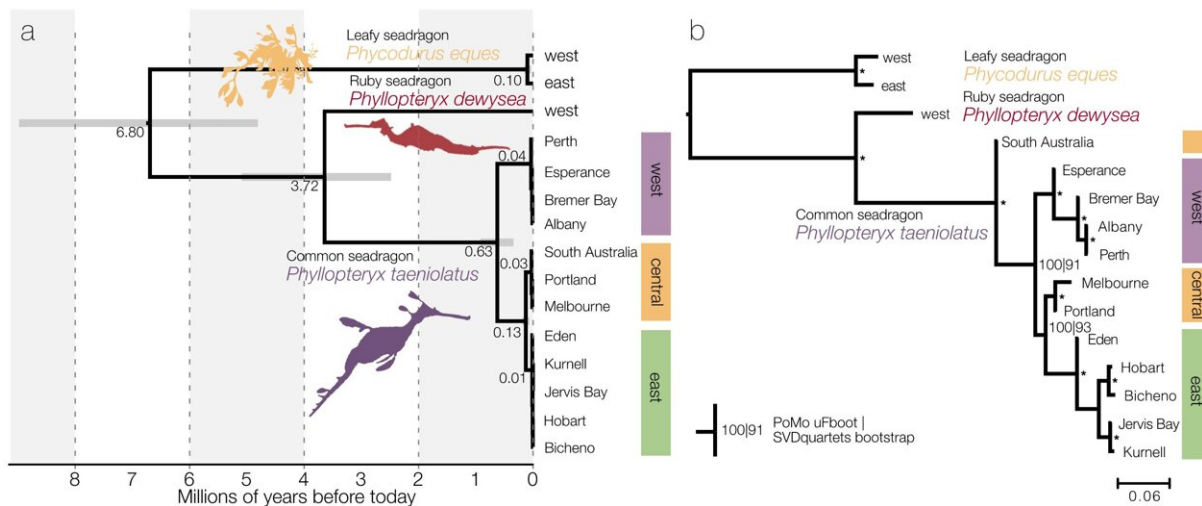


Study finds weedy seadragons genetically connected across the Great Southern Reef

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Relationships between seadragon species and within common seadragons. a Multi-individual species tree with dated divergences based on mitochondrial protein-coding genes using STARBEAST2 (155 individuals total, 14,075 base pairs). The ages of divergence among the lineages of common seadragons are very recent compared to the divergences among the seadragon species. b Multi-individual species tree of leafy, ruby, and common seadragons based on nuclear SNPs using PoMo (268 individuals, 13,748 SNPs). The topology from SVDquartets was identical (Additional File 1: Fig. S1); bootstrap support values from both analyses are annotated, with asterisks indicating full support in both analyses. Credit: *BMC Biology* (2023). DOI: 10.1186/s12915-023-01628-9

Common, or weedy, seadragons (*Phyllopteryx taeniolatus*) are iconic

fish in their native waters of the Great Southern Reef, the southern coastline of Australia.

They are beloved by SCUBA divers and aquarium visitors around the world, endlessly fascinating because of their charming behavior, unique camouflage and fantastic coloration. Now, a team of researchers have used modern genetic sequencing to assess the genetic makeup of common seadragons across their entire range, spanning over 5,000 kilometers of often remote Australian coast.

Gathering the samples for this [dataset](#) took long hours in the water and keen eyes because seadragons are difficult to find in their underwater habitats. The researchers only took small tissue clips of their leaf-like adornments that are not used for swimming, and were possible used existing samples from [museum collections](#) and aquaria to generate extensive genomic data.

"The dataset gives us a more complete picture of the biology of common seadragons because it characterizes the genetic makeup of individuals from every corner of their range," said author Dr. Josefin Stiller, Department of Biology, University of Copenhagen.

Using this genomic data, the team investigated how the genetic diversity of populations was distributed around the coastline. They found that although populations are geographically structured, there is [gene flow](#) that connects populations as a [single species](#).

This proved important to address a previous hypothesis that the east coast of Australia may hold a separate subspecies of seadragon, for which the new study found no evidence. Instead, with the [large dataset](#) and comprehensive sampling in this study, it is clear that common seadragons are connected as a species across the entire Great Southern Reef.

The study also found low genetic diversity in some areas, particularly on the west and the east edges of their distribution, which is concerning because these are also areas that are predicted to be strongly impacted by [climate change](#).

"This study establishes a sound baseline of genetic data for common seadragons that will be valuable for future comparisons. It also allowed for nuanced insights into the past history of the species given sea level changes owing to recent ice ages," said Dr. Greg Rouse, one of the authors of the study. This is important information for the management of these species, and tracking any range reductions is critical as animals are predicted to keep moving to cooler waters.

Importantly, the team used this dataset to identify the likely origin of two individuals that had been illegally captured and exported in the aquarium trade. They were able to use the genetic data of samples of known origin to extrapolate the probable source of the individuals to be west of Albany, in southwest Western Australia.

Author Dr. Nerida Wilson from the Western Australian Museum said "Applying genomic tools to issues in marine wildlife forensics has huge potential, and will assist with better management of our precious marine animals." This new study contributes important information on the biology of this charismatic species and will be an important step towards conservation of these iconic fish.

Institutions involved in this work include The University of Copenhagen, Western Australian Museum and the University of California San Diego.

The findings are published in the journal *BMC Biology*.

More information: Josefin Stiller et al, Range-wide population genomics of common seadragons shows secondary contact over a former

barrier and insights on illegal capture, *BMC Biology* (2023). [DOI: 10.1186/s12915-023-01628-9](https://doi.org/10.1186/s12915-023-01628-9)

Provided by University of Copenhagen

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