



Phylogeography of leafy and common seadragons based on over 1000 genetic markers

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The southern coastline of Australia is home to a unique biota that has been exposed to complex changes throughout the glacial cycles. Glacial impacts on marine organisms of the region are less understood than in the northern hemisphere and detailed reconstructions of population histories were often hampered by the limited availability of genetic markers. Here, we investigate patterns of genetic structuring of two seadragon species that are sympatric in parts of Australia's temperate coast. Both leafy seadragons (*Phycodurus eques*) and common seadragons (*Phyllopteryx taeniolatus*) are known for their remarkable camouflage mimicking seagrass and kelp. We used range-wide sampling of both species and sequenced ~1000 Ultraconserved Elements (UCEs) for >300 individuals. The genetic data is integrated with information on life history and geology to elucidate the phylogeographic structure and demographic history of each species and compare patterns between them. Both seadragons showed strong geographic structuring, consistent with their low dispersal potential. Considerable differences in genetic diversity existed regionally, some of which bearing signatures of recent changes in population size. A genetic break between populations of common seadragons in the southeastern part of the range coincides with the historical location of a land bridge connecting Tasmania to mainland Australia. Reopening of the seaway ~14,000 years ago resulted in opportunities for secondary contact and we found low levels of gene flow across the phylogeographic barrier. Overall, the high-throughput data provide a detailed picture of histories of both species and point towards complex factors influencing marine organisms in southern Australia.

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