

Patterns in diversity of seagrasses in the tropical Indian Ocean

McMahon, Kathryn*¹, Udhi Hernawan^{1,2}, Kor-Jent van Dijk³, Gary Kendrick⁴, Michelle Waycott³ and Richard Evans⁵

¹ Centre for Marine Ecosystems Research, Edith Cowan University, 270 Joondalup Dr, Joondalup WA 6027

² Research Centre for Oceanography (P2O), Indonesian Institute of Sciences (LIPI), Ancol Timur, Jakarta 14430, Indonesia

³ School of Biological Sciences, University of Adelaide, North Terrace, Adelaide SA 5005

⁴ Oceans Institute, University of Western Australia, 35 Stirling Highway, Perth WA 6009

⁵ Department of Parks and Wildlife, 17 Dick Perry Avenue, Technology Park, Kensington WA 6151
k.mcmahon@ecu.edu.au

The Indo-Pacific is a biodiversity hotspot for seagrasses with meadows threatened by human activities and global change. Resilience of these meadows is dependent in part, on the genetic diversity of populations to resist pressures and the connectivity among populations to enable recovery following loss. We assessed the clonal richness and genetic diversity of three seagrass species with differing dispersal potential (*Thalassia hemprichii*, *Halodule uninervis*, *Halophila ovalis*), across a range of spatial scales (m's – 1000's km) from Indonesia to NW Australia using a combination of microsatellite markers and SNP's. There was a large variation in the genotypic diversity among populations, and also among species. For *T. hemprichii* the average clonal richness (R) was 0.67 (range 0.09-1.00), the average for *H. uninervis* 0.32 (range 0.00-0.79) and 0.44 for *H. ovalis* (range 0.05-0.96). Low genotypic diversity was more commonly observed in species with lower dispersal potential. No obvious spatial patterns in genotypic diversity were observed for *T. hemprichii* over the large spatial scale it was sampled (Indonesia – Australia). Allelic diversity also varied among populations within species, and the western Kimberley had the lowest diversity. For *T. hemprichii* average allelic diversity was 1.6 in the Kimberley compared to 3.0 in Indonesia and other areas of NW Australia, and *H. ovalis* was on average 3.0 in the Kimberley vs. 4.1 in other areas. A large-scale spatial pattern in allelic richness was evident in *T. hemprichii* with reductions away from the centre of diversity in the Coral Triangle towards the edge of the range, but the western Kimberley was an outlier due to its much lower allelic diversity. This lower diversity in the Kimberley is potentially driven by historical or oceanographic isolation. Based on this genetic information, we propose spatial management units at different spatial scales, across the Indo-Australian archipelago and at more local scales e.g. the western Kimberley. In addition, we propose an index of genetic resilience taking into account the potential to resist and recover from disturbance and adapt to pressures over generational times.



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