

Estimating an efficient spatial arrangement for the future network of Marine Protected Areas (MPA) of Madagascar, based on the connectivity of marine population

Ratsimbazafy Hajaniaina A.^{1,2}, Thierry Lavitra², and Marc Kochzius¹

¹ Marine Biology, Vrije Universiteit Brussel (VUB), Pleinlaan 2, B-1050 Brussels, Belgium
E-mail: h.ratsimbazafy@ihsm.mg

² Institut Halieutique et des Sciences Marines (IH.SM), Université de Toliara, BP 141 – Route du Port, Avenue de France, Tuléar 601, Madagascar

Madagascar is ranked as the 9th poorest country in the world and 80% of the population are entirely dependent on natural resources (IMF 2014, MEEF 2012). However, Madagascar is also well known as a biodiversity hotspot (Myers *et al.*, 2000). This high importance of natural resources has led to the engagement during the IUCN World Parks Congress of 2003 in Durban to triple the total area of protected areas in Madagascar, which will occupy about 10% of the total area of the country. Only 79% of that goal was achieved in 2012 and it was observed that only 0.1% was assigned for Marine Protected Area (MPA) (MEEF 2012). This year (November 2014), during the latest World Parks Congress in Sydney, Madagascar took again the engagement to triple the extent of its MPAs by 2020. Thus, there is an urgent need of information in order to identify the most efficient spatial arrangement for a network of MPA around the Island. It is proposed that the spatial distribution of MPAs should match the dispersal capabilities of the species to be protected. The present study uses 3 key species (*Linckia laevigata*, *Penaeus monodon* and *Octopus cyanea*) in order to investigate the genetic population structure and connectivity for 25 potential conservation sites (identified by stakeholders and personal perception) along the Malagasy coast using the mitochondrial CO1 and microsatellites genetic markers. In addition to this, biodiversity indexes will be collected from each site using quadrates and transects techniques. The results are expected to reveal the genetic diversity of the key species which can be used as proxy for other species that have similar biological feature, the level of connectivity as well as the status and comparison between the biodiversity profile between these potential sites. Such information will help the stakeholders and influence on their process of decision-making.

References

- International Monetary Fund (IMF). 2014. www.imf.org/
- Ministère de l'Environnement, de l'Ecologie et des Forêts Malgache (MEEF). 2012. Quatrième rapport national de la convention sur la diversité biologique. <http://www.ecologie.gov.mg/download/>
- Myers N., R.A. Mittermeier, C.G. Mittermeier, G.A.B. Da Fonseca, and J. Kent. 2000. Biodiversity hotspots for conservation priorities. *Nature* 403:853–858.