

Conservation Strategy based on Regional Reef Connectivity and Environmental Load Assessment
in SEA-WP Region

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[Abstract]

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The core part of the South East Asia and West Pacific (SEA-WP) regions is a significant reservoir of the world's richest marine biodiversity, but is deteriorating in its coastal ecosystems due to various environmental threats. For providing a proper conservation strategy, this study aims at clarifying reef connectivity due to larval dispersal in various scales in SEA-WP region and thereby identifying important candidate areas to be properly managed as Marine Protected Areas (MPAs), based on two approaches; 1) numerical simulations on larval dispersal, and 2) molecular biological analysis on meta-population dynamics. In the first approach, we have developed an integrated model system consisting of multi-scale ocean models, marine ecosystem model, terrestrial environmental discharge model and regional atmospheric model. The multi-scale models cover areas at regional and semi-regional scale, island scale, bay and strait scale and reef scale. As one of outstanding computational results demonstrating high capability of the developed ocean model, we could find out characteristic eddying motion in Indonesian sea, which we named "Lombok Eddy". The existence of this unique eddy structure was verified by satellite-tracking drifter experiments. By properly coupling these models, we succeeded in dispersal simulations in various scale target areas; i.e., the middle of the Indonesian sea, the Verde Island Passage, Lingayen Gulf and Guimaras Strait areas in the Philippines, and the Yaeyama area in the Okinawa Islands, Japan. Then we found characteristic dispersal patterns in these areas and associated reef connectivity structures based on matrix connectivity analysis and others. In the second approach, we examined gene flow due to larval dispersal among populations in the SEA-WP region for the targeted marine invertebrate species (4 sea star, 9 sea cucumbers and 1 reef-building coral) either by mitochondrial loci (16s-rDNA, CO1 and Dloop) or by nuclear microsatellite loci. On the whole, the species with longer larval duration were found to have stronger connectivity among sites than those with shorter larval duration. In addition, some cryptic species were uncovered using newly developed markers that are crucial for

corroborating evolutionary interpretations and support applications such as biodiversity estimates. For long dispersal species, the upper stream areas of Kuroshio such as northern part of the Philippines are especially important for sustaining their populations downstream. For species with shorter larval duration, considering local connectivity in the areas such as east coast of Ishigaki Isl. for blue corals and highlighting some areas with high genetic diversity like Kume Isl. for Black Knobby are essential for conservation.