# Coastal fish diversity in the South China Sea

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▶ Keywords: Coastal fish fauna, species diversity, genetic diversity, population structure, DNA barcoding

The coast of South China Sea is home to a tremendous biodiversity. More than 3,500 marine fish species are recognized, providing an important basis for livelihoods of local people in various ways. Accurate identification of fish species, each species having unique biological characteristics, is crucial for their sustainable utilization. In addition, understanding the processes by which such high marine fish diversity in the area has been generated and maintained is also necessary. The latter provides us with insights as to how the biodiversity will respond to the future impacts of global environmental changes and human activities, and thereby allows us to design appropriate management strategy. Notwithstanding, these issues have still largely not been addressed for marine fishes in this area, undermining appropriate resource management.

We have been conducting a research activity that is specifically designed to overcome the current situation in the South China Sea as mentioned above. The research activity is divided into two major components, focusing on different levels of marine fish diversity in the area: 1) Discovering the species diversity of marine fishes in the South China Sea, with providing practical identification methods of the species, and 2) clarifying spatial distribution of genetic diversity within species (= genetic population structure) of selected marine fishes, with particular focus on commercially important species in the Southeast Asian Countries. Outlines and progresses of these two activities are provided below.

1) In order to clarify the marine fish species diversity in the South China Sea, we aimed to make pictorial field guides to fishes of Northern Gulf of Thailand (Thailand), and Panay Island (Philippines) (as separate volumes). A color photograph of each species is provided in the field guides accompanied by information on ecology and distribution as well as morphological description. In addition, DNA barcodes will also be shown for some taxa for which DNA sequence data are available, providing a direct connection between the online DNA barcode database and the field guide for fishes of Panay Island (see below). Fish specimens used in the field guide for Panay Island are collected from several fish markets, so as to encompass all species found in those markets. We have already published the guide to the fishes of Northern Gulf of Thailand, which provides photographs and morphological descriptions of 372 species. For the guide to the fishes of Panay Island, more than 2,000 specimens including at least 500 species have been collected so far. The final number of species is expected to be around 600, making it the most extensive field guide

published to date for a single locality in Southeast Asia. Each specimen is given a unique voucher number and deposited in the University of the Philippines Visayas Museum of Natural Sciences. The specimens will be stored permanently and thereby shape a concrete basis for further fish diversity studies in the future. During the course of the study, we have discovered some specimens possibly representing new species. We have also published a fish collection building and procedures manual as a mean of capacity building for researchers interested in the fish diversity studies. Finally, we are now expanding the scope of our activity to cover the fish fauna in Batan Bay, located in the northern Panay Island. Researchers from UPV are taking an initiative of the survey in Batan Bay supported by Japanese collaborating members.

DNA barcoding is a species identification system based on sequence diversity in Cytochrome Oxidase subunit 1 gene (COI) of mitochondrial DNA (mtDNA). Development of a DNA barcode is highly dependent on the accurate initial (morphological) identification of the species: on the premise that the initial identification of the reference specimen on which reference barcode is developed is correct, the technique allows us to identify specimens for which morphological characters are not available. Such specimens include fishes in their early life history stages (eggs, larvae, or juveniles), processed foods, stomach contents of organisms etc. We combined the DNA barcoding technique with the field guide so that the species presented in the guide can be identified not only based on morphology, but also using the DNA barcoding technique. One or a few specimens from each species are subjected to mtDNA sequencing analysis to produce a reference DNA barcode of the species. These barcodes are made publicly available through online database that is specifically intended to serve as a DNA barcoding platform (BOLD system). On the other hand, direct links to the barcodes of each species deposited in the database are provided in the field guide.

2) Understanding the spatial distribution of genetic diversity within species (= genetic population structure) is fundamental to biodiversity studies. Each of the spatially distributed populations is considered as a single evolutionary unit, each of which undergoes genetic changes through time more or less independent from each other. It also has considerable significance for fisheries management, because each of those populations is considered as a single "stock", being demographically independently from each other. We have been studying genetic population structures of selected marine fish species that are commercially important in the Southeast Asian countries. The target species include *Atule mate*, *Megalaspis cordyla*, *Selar crumenophthalmus*, *Decapterus macrosoma*, *D. macarellus* (Carangidae), *Rastrelliger kanagurta*, *R. brachysoma*, *R. faughni* (Scombridae), *Scolopsis taenioptera* (Nemipteridae), and *Sillago sihama* (Sillaginidae). For each species, specimens are collected from 2–4 localities on the coast of South China Sea, including Panay Island (Philippines), Kuala Terengganu (Malaysia), Rayong (Thailand), and Ha-long Bay (Vietnam.) Partial sequences of mtDNA were obtained from each specimen, being subjected to a variety of population genetic analyses.

Marine fishes are generally thought to be genetically homogeneous across a wide geographic range owing to their high mobility. Our results showed a unique population structuring pattern for each species, with some species exhibiting significant spatial heterogeneity within the South China Sea. For example, specimens of *R. brachysoma* were clearly divided into two highly differentiated populations between Rayong and Panay Island. We propose that each of these two populations is representing a separate and independent stock, and therefore should be managed separately. On the other hand, most of the rest of the species are apparently geographically homogeneous within the South China Sea. Nevertheless, some of them exhibited significant genetic variation that are *not* associated with locality, and this calls for further investigation. We suggest that such a pattern can be explained by historical geographic events involving repeated sea level changes driven by the glacial-interglacial cycle in the Pleistocene.