

Component 2 (Biodiversity): Thailand

Report on the activities of the Component 2 (Biodiversity team) in Thailand

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The coast of Southeast Asia is home to a tremendous biodiversity based on high primary production, which in turn provides an important basis to local livelihoods in various ways. The goal of the Component 2 (Biodiversity team) is to clarify the species-level and within-species-level diversity of coastal organisms in Southeast Asia, thereby offering key information for evaluating the ecosystem health in the area. For this purpose, we have been working on the following topics in Thailand.

Field guide. “Fishes of Northern Gulf of Thailand” was recently published as a product of a collaborative work among National Museum of Nature and Science of Japan, Kagoshima University and RIHN. Photographs, morphological descriptions and distributions of 372 commercial fishes belonging to 109 families are given based on the specimens collected during a period between 2009 and 2012.

Collection building. As of Sep. 2014, we have collected 790 fish specimens from off Rayong. These specimens were fixed in formalin at EMDEC, subsequently transferred to National Science Museum, Thailand. Under the curation of Dr. Veera Vilasri, these specimens have been given individual catalog numbers.

Genetic population structure. It is widely accepted that deciphering intraspecific genetic diversity and its geographical distribution pattern is the most important aspect of biodiversity study, because each population represents a fundamental conservation unit that needs to be managed separately for sustainable use. In addition, based on these information we can infer the historical processes by which the present diversity of the species has been shaped, which is central to evolutionary biology.

We selected ca. 20 commercially important coastal fish species to be subjected to genetic

analysis. Specimens are collected from four localities facing the South China Sea including Rayong, Thailand (Table 1). Several aspects of intraspecific genetic diversity, including genetic differentiation among localities, were examined using the sequences of mitochondrial DNA (mtDNA) Cytochrome Oxidase I (COI) and Cytochrome b (Cytb) genes for each species. In addition, for a subset of target species we have obtained a source data to be used to develop novel primers for microsatellite markers using Next Generation Sequencing. Below we show some of these results for selected species.

Atule mate. A neighbor joining tree was constructed on the basis of Cytb sequences of 80 specimens from Thailand, Philippines and Malaysia. The tree showed two distinct clades, one clade composed of only a single specimen from the Philippines and the other of all the remaining specimens. The latter clade was highly diverse, suggesting its large effective population size, but showed no notable structuring according to sampling localities. Genetic differentiation among three sampling localities was not statistically significant, possibly reflecting its highly migratory nature. On the other hand, we have developed 12 novel microsatellite makers for the species using Next Generation Sequencing, which will be used to clarify the genetic variation in the nuclear genome.

Megalaspis cordyla. A neighbor joining tree was constructed on the basis of Cytb sequences of 79 specimens from Thailand, Philippines and Malaysia. The tree showed two distinct clades just like in *Atule mate*. However, the branching pattern in relation to sampling locations were strikingly different between the two species. In *M. cordyla*, one of the two clades composed of all specimens from the Philippines, while the other clade composed of all specimens from Thailand and Malaysia. Both clades were extremely deficient of diversity, suggesting their small effective population sizes. Genetic differentiation between the Philippines and the other two localities were statistically significant, while that between the latter two was not. We have also developed 12 novel microsatellite makers for the species to be used for further analysis focusing on their nuclear genome.

Sillago sihama For this species, only specimens from Thailand have been analyzed, nevertheless showing remarkable result. Neighbor joining tree of COI sequences of *S. sihama* revealed three distinct clades. A Discriminant Analysis of Principal Component based on microsatellite markers separated the specimens into three distinct clusters, in such a way that the pattern was consistent with the branching pattern of the mtDNA tree. Because all specimens were collected from a single locality (Thailand), these three groups are regarded as separate species.

Expected final outcomes. The final outcome of our activity in Thailand include 1) a series of individual papers of genetic or taxonomic studies (see Appendix below), 2) a review paper on

the origin of coastal marine fish diversity in the South China Sea, synthesizing the results of individual papers.

Table 1 Number of specimens collected from four localities to be subjected to population genetic analysis.

Scientific name	Rayong (Thailand)	Panay (Philippines)	Terengganu (Malaysia)	Ha long (Vietnam)
<i>Selar crumenophthalmus</i>	24	49	30	0
<i>Atule mate</i>	35	32	34	0
<i>Gerres filamentosus</i>	22	45	0	0
<i>Lutjanus vitta</i>	27	26	16	0
<i>Priacanthus tayenus</i>	18	42	0	0
<i>Rastelliger kanagurta</i>	54	22	30	0
<i>Megalaspis cordyla</i>	33	22	30	0
<i>Terapon jarbua</i>	15	34	0	0
<i>Sillago aeolus</i>	37	20	0	0
<i>Sillago sihama</i>	40	26	0	0
<i>Rastelliger brachysoma</i>	44	55	0	0
<i>Decapterus macrosoma</i>	0	29	0	0
<i>Decapterus macarellus</i>	0	28	0	0
<i>Gerres oyena</i>	12	30	0	0
<i>Scolopsis monogramma</i>	10	0	0	0
<i>Scolopsis taenioptera</i>	28	19	16	0
<i>Priacanthus macracanthus</i>	0	26	0	0
<u><i>Sphyraena putnamae</i></u>	8	0	30	0
<i>Gerres erythrourus</i>	22	35	0	0
<i>Stolephorus indicus</i>	0		30	0
<i>Rastrelliger faughni</i>	0	27	0	0
<i>Upeneus guttatus</i>	0	29	0	0

Appendix : Expected papers from genetic, morphological or taxonomic studies.

- Population structure of *Atule mate*
- Population structure of *Megalaspis cordyla*
- Population structure of *Gerres filamentosus*
- Population structure of *Terapon jarbua*
- Population structure of *Selar crumenophthalmus*
- Population structure of *Gerres oyena*
- Population structure of *Lutjanus vitta*
- Population structure of *Scolopsis taenioptera*
- Population structure of *Decapterus macrosoma*
- Population structure of *Decapterus macarrelus*
- Population structure of *Scolopsis monogramma*
- Genetic and morphological differentiation within genus *Rastrelliger*
- Cryptic speciation within *Sillago sihama* inferred from genetic analysis.