CHAPTER 4

GENERAL DISCUSSION

In this study, I aimed to establish the existence of geographic variants within *Lutjanus russelli* (Bleeker, 1849) by examining both external morphology and population genetic variability within the larger Thai Andaman Sea region and also between the Gulf of Thailand and the Andaman Sea. The target species of this study, commonly known as Moses perch, is a common fish in Thai coastal waters and is an important fish for local food security. Many lutjanids in this region are heavily targeted and have a vulnerable life history. While adults spawn in open water, are mostly solitary or associate only in small groups and can be difficult to locate, juveniles are found mostly in coastal estuary habitats where they are easily caught. It is likely that Moses Perch juveniles recruit into the adult fishery around the time of sexual maturity, which has been reported to occur at around 4-5 years old. Recruitment overfishing (the removal of juveniles before they can recruit into the reproductive replenishment pool) is less of a problem for marine fishes in an open system (reliant on geographically external sources of larvae/recruits) than for fishes such as these that recruit inshore and spend many years vulnerable to local fishers. Consequently, increasing fishing pressure due to economic necessity and growing coastal populations increases the risk of overexploitation for these fish. Very little is currently known about whether this and other lutjanid species are threatened by overfishing in the South East Asian region or Thailand in particular, mostly because of a critical paucity of population-level studies such as this one.

My examination of the external morphology of *L. russelli* from the two coasts of Thailand revealed consistent differences between the populations in terms of both stripe pattern and some other characters that were not used in the FAO description of this species (Chapter 2). All samples from Andaman Sea (AN) possessed 7 golden-brown stripes on each sides and black spot situated on or just above the lateral line, below the posterior soft dorsal fins. Conversely, fishes form the Gulf of Thailand (GT) exhibited no stripes on their sides, although retaining a black spot upper in the same position. This is consistent with the descriptions found in Allen (1985) and the FAO diagnostic characters description. In this study, it was apparent that most of the morphological characters in adult fish that differed between the Andaman Sea and Gulf populations were in and around the head area. In juvenile fishes, many new measurable characters were found that represent different proportions of body shape in the populations from east and west coasts. When measured appropriately, there is obviously distinctive morphology between populations from two coasts of Thailand.

Morphological variation can occur within many species because of phenotypic plasticity, differences in the expression of the same gene in varied environment conditions (such as temperature, salinity), or because of food availability, habitat use, life histories, flow regime, predator/prey interactions, etc. (Arbour *et al*., 2011; Remerie *et al.,* 2005). According to these factors, fishes would have different morphometrics, even in populations exhibiting strong genetic homogeneity, such as yellowtail snapper (*Ocyurus chrysurus*) (Vasconcellos *et al.,* 2008), and Arctic char (*Salvelinus alpines*) (Arbour *et al*., 2011). However, phenotypic plasticity is probably not the prime determinant of morphological variation in *L. russelli*, because the results of microsatellite comparison indicated that genetic composition of fish populations on the two coasts was absolutely different (Chapter 3).

This is a very early stage population genetic study of snappers to compare genomic markers between two oceans and the result revealed significantly different genetic structure across their ranges. Within the Andaman Sea, however, pairwise population comparisons indicated that fish have a degree of genetic homogeneity; that is, this study was not able to detect strong differences between the northern and southern Thai Andaman Sea populations. This indicates that either that the populations are connected by larval or adult migration, or that this study used markers that were not sensitive to fine scale population differences, The conjunction of opposing surface currents in the middle part of Andaman Sea (Wyrtki, 1961 (in Rizal *et al*., 2010)) was not apparently not a barrier to connectivity in this species. This should not be surprising, given that larval fishes are quite strong swimmers, and the larvae of this species recruit into inshore localities (Newman, 2002 and Sheaves, 1995), (thus avoiding the oceanic barrier)

Pleistocene variations in sea levels across Southeast Asia may have constituted an important factor in restricting gene flow of organisms from the Indian Ocean to the South China Sea, and thus may be a key factor in the apparent population disjunction identified here. Voris' (2000) models suggested that the east-west flow of water through the Malacca Straits occurred for only a small fraction of the past quarter of a million years. Holocene intrusion of SCS water (and potentially, larvae) into the Andaman Sea does not seem to have greatly diluted genetic differences between the eastern and the western populations of *L. russelli*. Previous studies examining species with populations potentially separated by the Sundaic barrier have revealed that the majority of examined species with Indo-Pacific distributions have some sort of genetic separation between populations on either side (Gaither et al, 2010). In those species with limited dispersal ability, this effect is exaggerated, and may lead to episodes of extinction or speciation in the Indo-West Pacific. It is likely that this is the primary driver or mechanism for the observed intraspecific genetic differentiation between oceans in *L. russelli* revealed by the current study.

Study of microsatellites in DNA can provide evidence of genetic divergence between recently or incompletely separated populations (Hellberg, 2009). Attempting to apply this method of divergent molecular markers to answer questions about particularly phylogeny or prove species classification is a misapplication of the technology, however, since it delivers very weak phylogenetic results. Other molecular markers such as mitochondrial genes (COI, COII and CYTB) and nuclear genes (RAG1, RAG2) can be used for examine genetic "distance: between populations and putative phylogenetic relationships would be required to develop a cohesive evolutionary story for this uncertainly-positioned species.

Intraspecific genetic differentiation and external morphology revealed strong geographic variation within this species in the waters around Thailand. Although, these results could not certainly separate this fish into different species, they provided important and reasonable evidence to improve the species' classification. Moreover, in many ways, this research points out how little is really known about non-commercial fishes in South East Asia. More research is needed, especially at larger scales, to determine the additional management needs to be implemented to safeguard resource security for coastal fishers. This includes knowledge about larval behaviour and vagility and whether implementation of closed seasons and marine reserves are justified to optimize fisheries productivity and resource conservation.

SUGGESTION

Although this study gained a lot of information regarding the extent of geographic variation within this species, I feel that further study is warranted on population connectivity and taxonomy of this fish in another region. To this end, I think samples from Strait of Malacca, Malaysia, Indonesia, Philippine, Vietnam, China, Eastern Pacific Ocean and Western Indian Ocean should be obtained to confirm geographic variation over its entire range; this may reveal historical patterns in the phylogeny of this species (and perhaps genus). It may also provide solid evidence to suggest that this species (and perhaps genus) should have taxonomic re-evaluation.

The existence of an unsuspected barrier within the Andaman Sea is still questionable. Increasing the number of microsatellite loci to establish finer-scale variations in the population genetics of this fish and expand the scope of examination in another marine species may be answer this complicated population pattern. Moreover, since the South Andaman Sea population is potentially a hybrid population between Andaman Sea and Gulf of Thailand groups; further study should clarify this possibility.