

Population structure and genetic connectivity of *Lutjanus russelli* (Lutjanidae) in Thailand.

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Abstract. Peninsular Thailand divides the South China Sea (SCS) from the Andaman Sea. Coastal fishes of Thailand are thus located in two oceans separated by a geographic barrier. The west coast of Thailand, however, is linked to the water mass of the SCS by a connection through the Straits of Malacca. Sources of larvae of fishes in the Andaman Sea can thus potentially come from both the SCS and Indian Ocean. However, within the Andaman Sea, surface currents flow from opposite directions, converging around Phuket; both water currents and geography may be barriers that separate population connectivity. In this study, we focused on examining distinctions in population structure of *Lutjanus russelli* (Bleeker) between the Gulf of Thailand and the Andaman Sea, and also between the northern and the southern Andaman Sea. A study of 182 individuals using 8 microsatellite loci showed that the *L. russelli* population in the Gulf of Thailand is genetically distinct from the populations in the Andaman Sea. Although not statistically significant, the populations in the northern and the southern Andaman Sea indicated a trend of population differentiation. This study demonstrates potential differences in population genetics that may imply the existence of hitherto unsuspected geographical barriers between the Gulf of Thailand and populations within the Andaman Sea, which has important consequences for stock management of a vital food fish.

Key words: Population, Genetic connectivity, *Lutjanus russelli*, Thailand

Introduction

Russell's Snapper, *Lutjanus russelli* (Bleeker, 1849) also called Moses Perch, are a moderate-sized lutjanid snapper that occur in tropical marine waters of the Indo-West Pacific, from the Red Sea and East Africa, north to Japan, south to Australia and east to Fiji. It is a common component of fish assemblages in nearshore habitats (seagrass and mangroves) and on coral reefs. Lutjanid fishes form an important component of the local fisheries of the Andaman coast of Thailand and the Gulf of Thailand, although they are not especially valuable commercially. Throughout their range in South East Asia, they are important in terms of food security for the millions of coastal villagers who rely on marine ecosystem goods and services for their livelihood. Several authors (e.g. Allen, 1985; Satapoomin, 2011) have reported consistently different color morphs in Indian Ocean and Pacific Ocean populations of *L. russelli*, hinting that the species may be partitioned into discrete stocks. It is important, then, to establish estimates of population connectivity and stock resilience in order to appropriately manage local fisheries. Since the artisanal fishers who most rely on lutjanids in their catch tend not to range far from home, depletion of local stocks represents a serious threat to their food security.

Peninsular Thailand's coasts front on two oceans. The Gulf of Thailand (east coast) faces the South China Sea, which is influenced from the western Pacific Ocean; the Andaman Sea (west coast) forms the eastern-most margin of the Indian Ocean. Superficially, the biota of the two coasts are not completely distinct, because of the existence of a connection via a persistent northwesterly flow through the Straits of Malacca (Kimura et al., 2009; Satapoomin, 2011). However, the water current from Malacca Straits does not flow throughout the entire Andaman Sea (Wyrтки, 1961 (in Rizal et al., 2010)). Current modeling and observation indicate that the water current from the South China Sea will influence organisms only in the southern part of the Andaman Sea; organisms in northern part of the Andaman Sea will be more influenced by water currents from Indian Ocean via the northern Bay of Bengal.

Surface water currents are one of the most factors that controls the dispersal of marine fish larvae. The convergence zone where the two opposing currents meet may function as a barrier to dispersal between northern and southern stocks and also the gentle current flowing westward from the South China Sea may effectually prevent eastward connectivity between the Gulf of Thailand and the Andaman Sea. Knowledge about the population structure of *L.*

russelli may enhance understanding of the degree of larval migration between biogeographic provinces. It may also highlight differences in population genetics that imply the existence of unsuspected geographical barriers.

In this study, we examine population differentiation of *L. russelli* between the Gulf of Thailand and the Andaman Sea, and also between the northern and the southern Andaman Sea. In seeking to establish whether the populations in each biogeographic area represent distinct genetic stocks or components of a larger metapopulation, we note that there are further consequences of stock isolation due to potential dispersal barriers for fisheries management and conservation of marine resources.

Materials and Methods

Adult *L. russelli* tend to inhabit coral reefs and rocky areas. They occasionally enter estuaries; however, reproductively mature adults are found only offshore (Sheaves, 1995). Most previous studies have classified *L. russelli* from estuaries in the tropical Indo-Pacific as juveniles (Allen, 1985; Sheaves, 1995). Juvenile Moses Perch are often seen in mangrove estuaries, and are commonly caught by local fishermen in seagrass meadows. *Lutjanus russelli* have a planktonic larval stage, but the duration and vagility of this phase is not well known; recruitment appears to be exclusively coastal. For this reason, we chose to collect fish along inshore-offshore transects to capture the full size range of *L. russelli* in each locality.

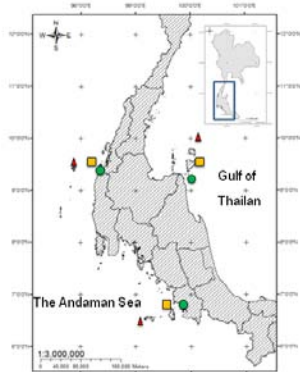


Figure 1: Site study; consist of Gulf of Thailand, the Northern part of Andaman Sea and the Southern part of Andaman Sea

The study sites are in both the Andaman Sea and Gulf of Thailand (GT) (Fig.1). The Andaman Sea is separated into 2 locations: northern part of The Andaman (NAD) and southern part of the Andaman (SAD), on either side of the Andaman convergence zone near Phuket.

The target fish were collected from May to November in 2011 by members of the local artisanal fishery. For genome analysis, the pelvic fin of each sample was clipped and preserved in 100% acetone. DNA extraction from the fixed

samples was achieved using the Phenol-Chloroform extraction method (Sambrook and Russell, 2001). Eight microsatellite loci, namely Lru01, Lru02, Lru10, Lru11, Lru14, Lru25, Lru30, and Lru43 (Guo *et al.*, 2007) were used to evaluate genetic compositions of each population sample. The amplified PCR products were examined by polyacrylamide gel electrophoresis and visualized using a silver staining (Sambrook and Russell, 2001).

Number of alleles, allelic richness and estimates of genetic diversity by allele frequencies were computed using the FSTAT (Goudet, 2001) and GDA program (Lewis and Zaykin, 2001). Deviations from the Hardy-Weinberg equilibrium, were tested for each microsatellite locus and for each population using the Markov chain method (Bagley *et al.*, 1999) implemented in the Genepop program version 4.1 (Ovenden and Street, 2003). To test for population structure, pairwise F_{st} was calculated and tested using Fisher's method based on exact G test implemented in the Genepop program version 4.1 (Ovenden and Street, 2003). A standard Bonferroni correction was applied to establish the stage of significance for multiple tests. (Salini *et al.*, 2006)

Result

We obtained a population sample of 25 fishes from the Gulf of Thailand (GT), 86 fishes from the northern Andaman Sea (NAD), and 71 fishes from the southern Andaman Sea (SAD). The number of alleles of the microsatellite loci studied ranged between 17 (Lru02) to 44 (Lru14). Allelic richness varied between population; that is, from 12.172 to 20.000 for the GT population, 7.318 to 22.324 for NAD population, and 7.485 to 22.885 for SAD population. The average gene diversity across loci is similar in all three populations; GT = 0.927, NAD = 0.911 and SAD = 0.915.

Table 1: F-statistics estimated from each microsatellite locus of the northern and the southern Andaman Sea populations. Probability values are shown in parentheses; F_{st} the proportion of genetic diversity due to allele frequency differences among populations; F_{is} inbreeding coefficient.

Locus	F_{st}	F_{is}
Lru01	0.0019 (0.137)	0.072 (0.013)
Lru02	-0.0006 (0.163)	-0.072 (0.339)
Lru11	0.0023 (0.269)	0.025 (0.395)
Lru10	-0.0028 (0.840)	0.217 (<0.001)
Lru14	0.0009 (0.500)	0.052 (0.079)
Lru25	-0.0005 (0.937)	0.158 (0.033)
Lru30	0.0066 (0.002)	0.218 (<0.001)
Lru43	0.0041 (0.096)	0.092 (0.001)
All	0.0016 (0.020)	0.098 (<0.001)

Averaged across samples, four of the eight microsatellite loci studied (Lru10, Lru14, Lru30, and Lru43) showed significant heterozygote

deficiencies, which could be explained by the presence of null alleles. The tests of population differentiation showed that the *L. russelli* population in the Gulf of Thailand is genetically distinct from the populations in both the southern Andaman Sea ($P < 0.001$) and the northern Andaman Sea ($P < 0.001$). The southern Andaman Sea population was also found to be significantly differentiated from the northern Andaman Sea population ($P = 0.026$). However, the probability value is low and not significant after Bonferroni correction. However, when evaluated locus by locus, a single microsatellite locus (Lru30) suggested the existence of incipient sub-populations ($P = 0.002$, Table 1)

Discussion

The population of *L. russelli* in the Gulf of Thailand is genetically separated from the populations in both the southern and the northern Andaman Sea. Within the larger Andaman Sea region, there is an indication of population disjunction, although not statistically significant using the microsatellite markers employed. Although it is possible that the Bonferroni correction over-corrects the test (Nagawa, 2004), the low but significant population differentiation between the northern and the southern Andaman Sea populations could be a result of the presence of null alleles in some of the microsatellite markers used. It is important to employ more microsatellite loci which do not contain null alleles to investigate population differentiations in the larger Andaman Sea region. Importantly, however, the distinction between South China Sea (Gulf of Thailand) and Indian Ocean (Andaman Sea) stocks may have important biogeographic implications. The genetic differences reported here agree well with published accounts of differences in colour morph between Indian and Pacific Ocean populations of *L. russelli* (e.g. Allen, 1985; Satapoomin, 2011). 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. Voris's (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) does not seem to have greatly diluted genetic differences between the eastern and the western populations. This relatively late event may explain the comparatively small differences between northern and southern Andaman populations, while hinting at a potential tool by which to measure the rate at which genetic drift occurs in these fishes. The present patterns of surface water current may eventually cause a separation of stocks of this fish within the Andaman Sea. The northern part of the Andaman Sea that

above Phuket province have less influence by the South China Sea that flow through Malacca Straights than the southern part of the Andaman Sea (Satapoomin, 2007). In addition, the northern part of the Andaman Sea appeared to be principally influenced by currents from the Indian Ocean and northern Bay of Bengal; populations in the northern part of the Andaman thus appear to retain representative characters of the Indian Ocean biota. However, information about larval behavior and dispersal is not well known; it is difficult to speculate exactly how this water current limits dispersal of active swimming larvae – if at all. There appear to be several factors separating this metapopulation into different groups that may be blurred by unknowns such as the degree to which larval fishes migrate along the nearshore margins unaffected by the offshore surface currents.

It is apparent that the stocks of Russell's snapper – a fish that supports the livelihoods of many thousands of local fishers in coastal Thailand – is not simply a homogeneous and ubiquitous resource. 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. Moreover, the explicit partitioning of *L. russelli* into discrete SCS and Andaman populations indicated by our research suggests that this species (and perhaps genus) may be overdue for taxonomic re-evaluation.

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