

# Connectivity of *Scylla serrata* in Kenya and the Indian Ocean

Mascaux Nemo<sup>1</sup>, Sara Fratini<sup>2</sup>, Stefano Cannicci<sup>2</sup>, Jared O. Bosire<sup>3</sup>, Mohd. Lokman Husain<sup>4</sup>, Carine Bourgeois<sup>1</sup>, Javy Zhang<sup>5</sup>, Farid Dahdouh-Guebas<sup>1,6</sup> and Marc Kochzius<sup>6</sup>

<sup>1</sup> Laboratory of Systems Ecology and Resource Management, Université Libre de Bruxelles (ULB), Avenue F.D. Roosevelt 50, B-1050 Bruxelles, Belgium

<sup>2</sup> Department of Evolutionary Biology, Faculty of Mathematical, Physical and Natural Sciences, Università degli Studi di Firenze – UNIFI, Via Romana 17, I-50125 Firenze, Italy

<sup>3</sup> Kenya Marine and Fisheries Research Institute (KMFRRI), PO Box 81651, Mombasa, Kenya

<sup>4</sup> Institute of Oceanography (INOS), University Malaysia Terengganu, 21030 - Kuala Terengganu, Malaysia

<sup>5</sup> Administration Bureau of Zhanjiang Mangrove National Nature Reserve (ZMNNR), Huguang township, Mazhang District, Zhanjiang City, 524088 Guangdong Province, PR China

<sup>6</sup> Vrije Universiteit Brussel (VUB), Pleinlaan 2, B-1050 Brussels Belgium.

Most of the studies conducted on the genetic population structure and gene flow of marine organisms have been focused on the genetic analysis of mitochondrial markers. Fratini *et al.* (2002, 2010) studied the genetic differentiation of *Scylla serrata* in the east African coast and found that the populations were genetically not homogenous. To better understand the population structure and the gene flow of *Scylla serrata* in and around the Indian Ocean, we propose to take more samples in Eastern Africa (Kenya) and to add more sequences from the entire Indian Ocean. The study area is located in the Southern part of the Kenyan coast. Samples were taken in Lamu Archipelago, Mida Creek, Kilifi, Mombasa, Gazi Bay and Shimoni. More samples were also received from South Africa, Madagascar, Zanzibar, Malaysia, Indonesia and China. On one hand, the results of this study will be compared with the results of Fratini *et al.* (2002 and 2010) in order to determine boundaries of populations and verify whether those genetic patterns are stable over time at a local scale (e.g. in Kenya). In the first analysis, no significant differences have been reported between the three periods of sampling (2000, 2009, 2011). Which could mean that the patterns are stable over time. However tests of deviation from neutral molecular evolution seemed to indicate a departure from the neutral hypothesis for five of the six stations, which could involve population expansion or selection. Haplotype diversity shows high values, unlike the nucleotide diversity, which could be a sign of a recent population expansion. Finally, the populations seem to be homogenous along the Kenyan coast and no structure has been detected. On the other hand, more samples from the wider Indian Ocean will be added into the database to better document the global geographic distribution (larger scale) of *Scylla serrata* around the Indian Ocean.

## References

- Fratini S. and M. Vannini. 2002. Genetic differentiation in the mud crab *Scylla serrata* (Decapoda: Portunidae) within the Indian Ocean. *Journal of Experimental Marine Biology and Ecology* 272:103– 116.
- Fratini S., L. Ragionieri and S. Cannicci. 2010. Stock structure and demographic history of the Indo-West Pacific mud crab *Scylla serrata*. *Estuarine, Coastal and Shelf Science* 86:51–61.