

Michael John Mendiola, Rachel Ravago-Gotanco. Genetic differentiation and signatures of local adaptation revealed by RADseq for a highly-dispersive mud crab *Scylla olivacea* (Herbst, 1786) in the Sulu Sea.

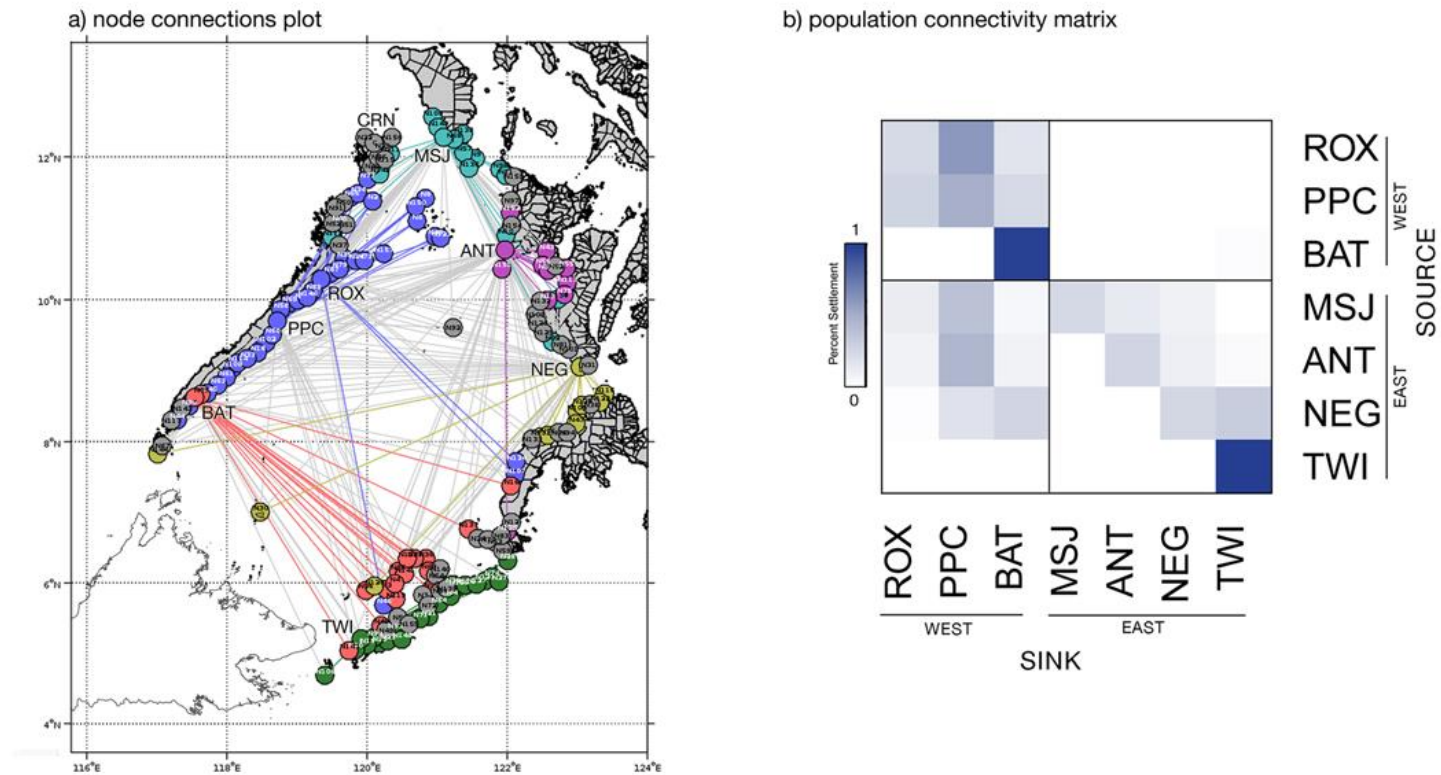


Figure 1. Estimated larval dispersal and connectivity of *S. olivacea* populations in the Sulu Sea basin from Lagrangian simulations. (a) Node connections plot generated from the larval dispersal estimates resulted in six population clusters indicated by the colored nodes and connections, gray links indicating connections between clusters. Site codes represent particles release sites and settlement nodes were labelled numerically. (b) Population connectivity matrix showing the proportion of larvae successfully settled from the source locations (y-axis) to settlement areas (x-axis). Sulu Sea populations were segregated according to their boundary location (east or west). See Table 1 for location codes.

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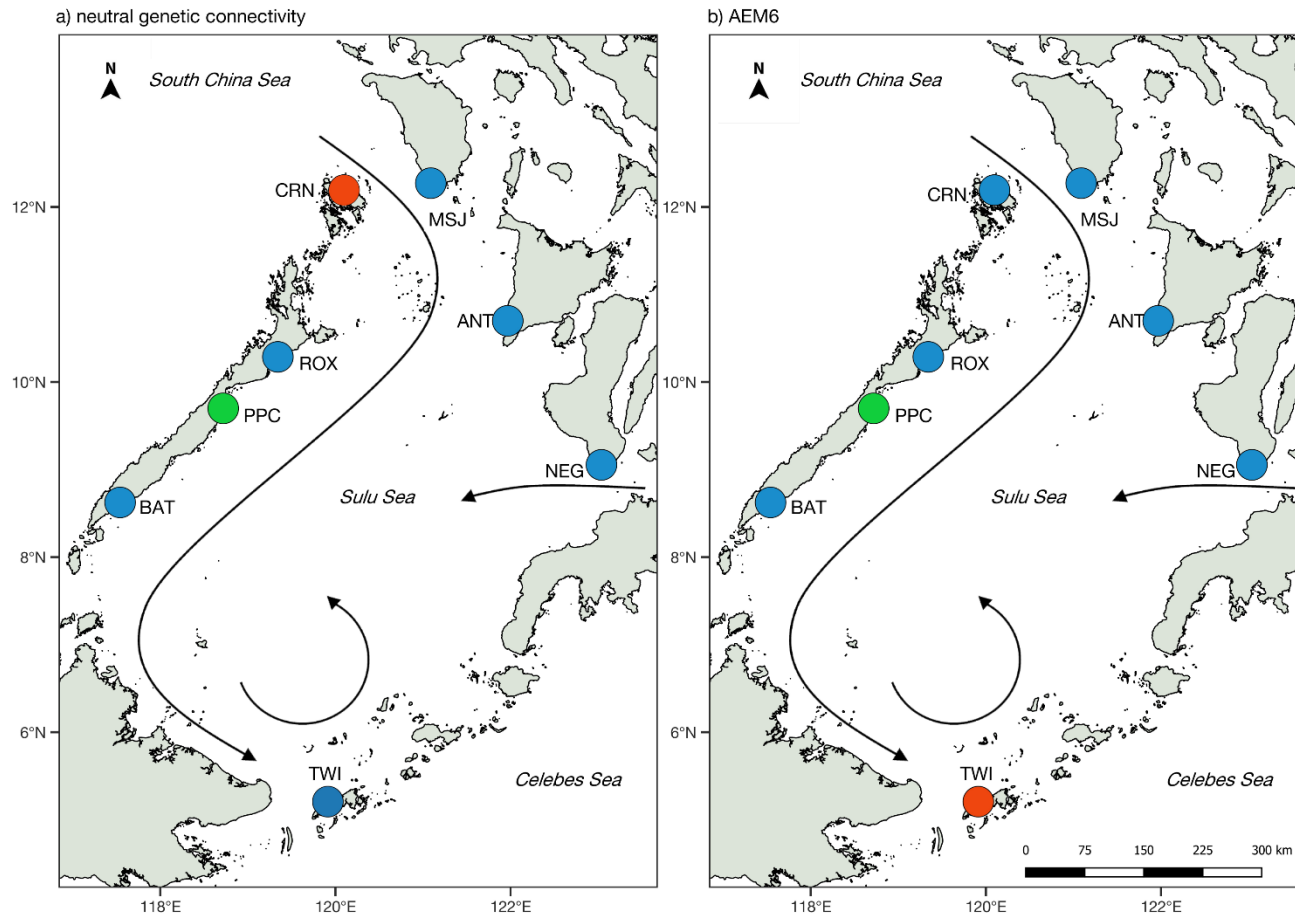


Figure 2. Spatial patterns of *S. olivacea* connectivity based on (a) empirical genetic estimates (pairwise F_{ST}) from the putatively neutral loci (1,643 SNPs); and (b) asymmetric larval dispersal estimates (AEM6) from the particle dispersal simulations in the Sulu Sea. Sampling points are colored according to their cluster assignment. Persistent surface currents in the Sulu Sea are shown.

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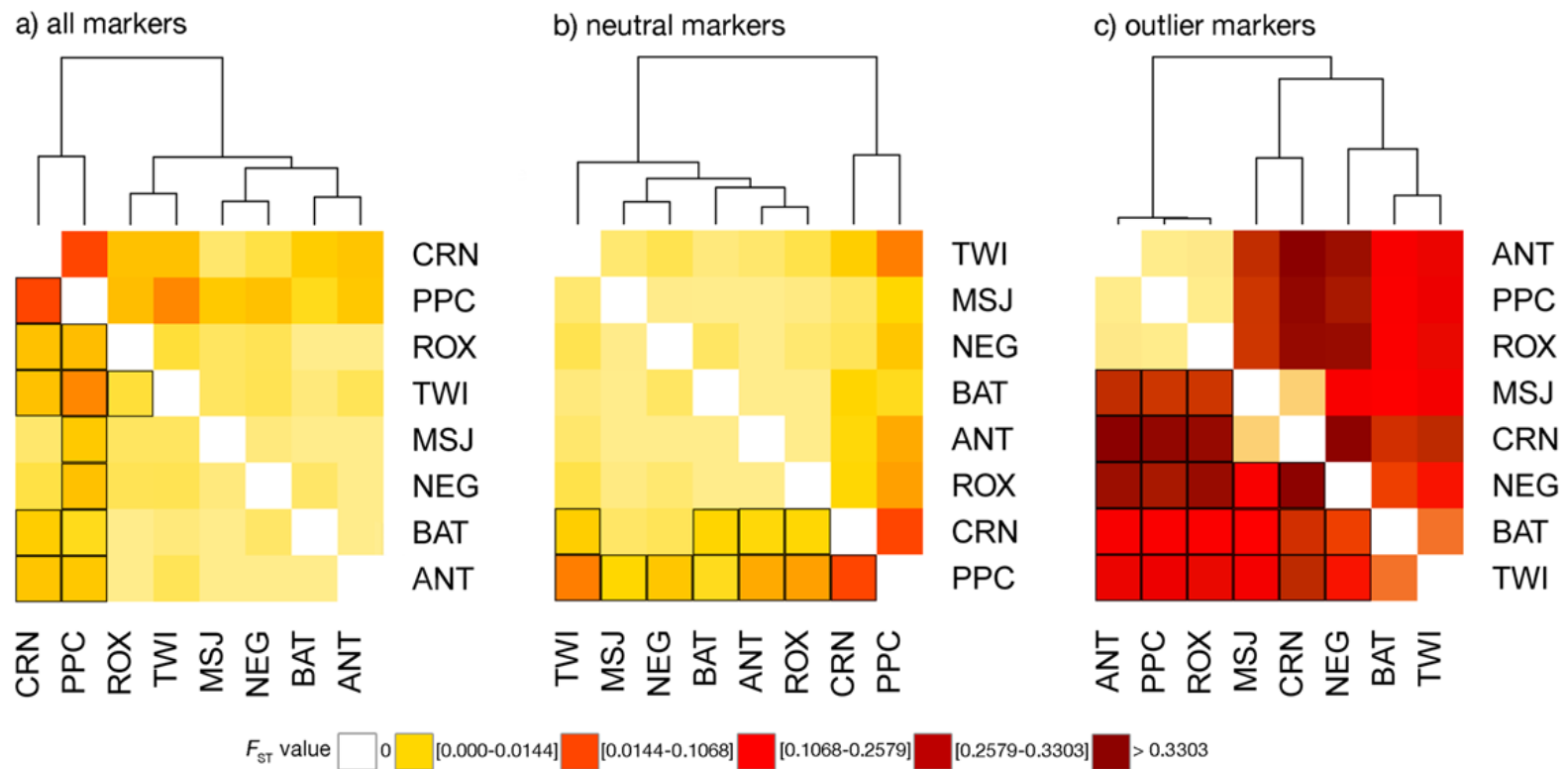


Figure 3. Heatmap of pairwise genetic differentiation (F_{ST}) of *S. olivacea* between sampling locations in the Sulu Sea, based on Weir and Cockerham weighted estimates using (a) all markers (1,655 loci), (b) neutral-only markers (1,643 SNPs), and (c) outlier only (12 SNPs). All points were clustered by pairwise F_{ST} values, based on classification and hierarchical clustering method. Site combinations (below diagonal) with boxed bold lines indicate significant genetic differentiation following FDR correction for multiple tests ($p < 0.05$).

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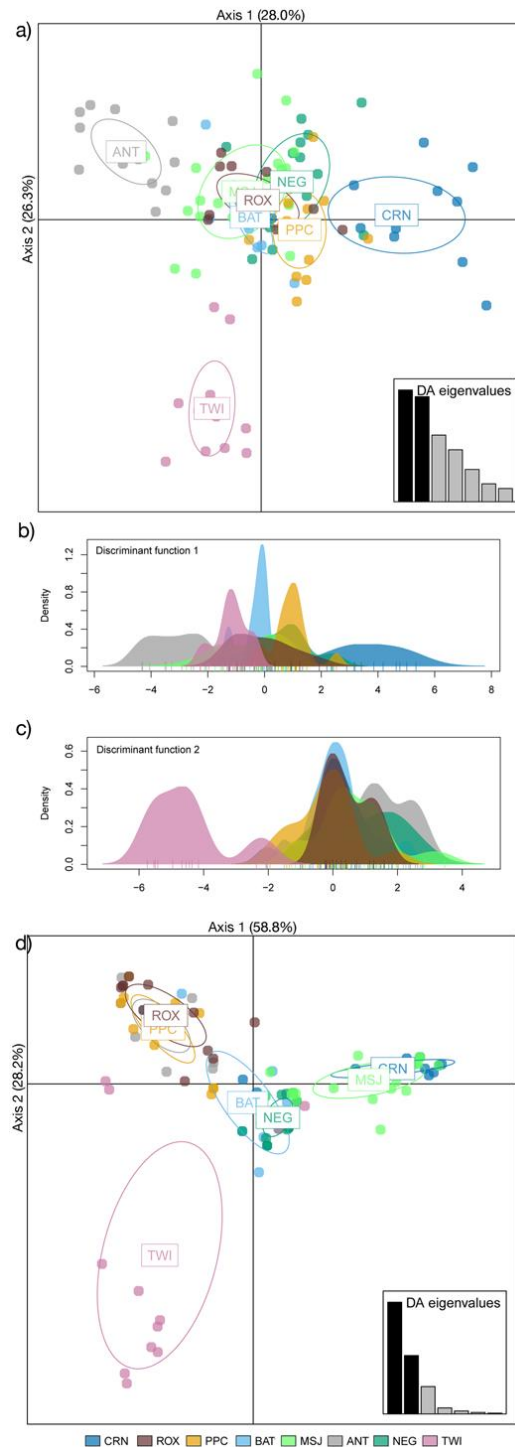


Figure 4. (a) Scatterplot of genetic clusters of Sulu Sea populations identified by DAPC based on neutral loci (1,643 SNPs) and sampling location information as a prior, with density plots for (b) the first and (c) the second discriminant axes. Genetic clusters identified using outlier loci (12 SNPs) and sampling location information as a prior (d).

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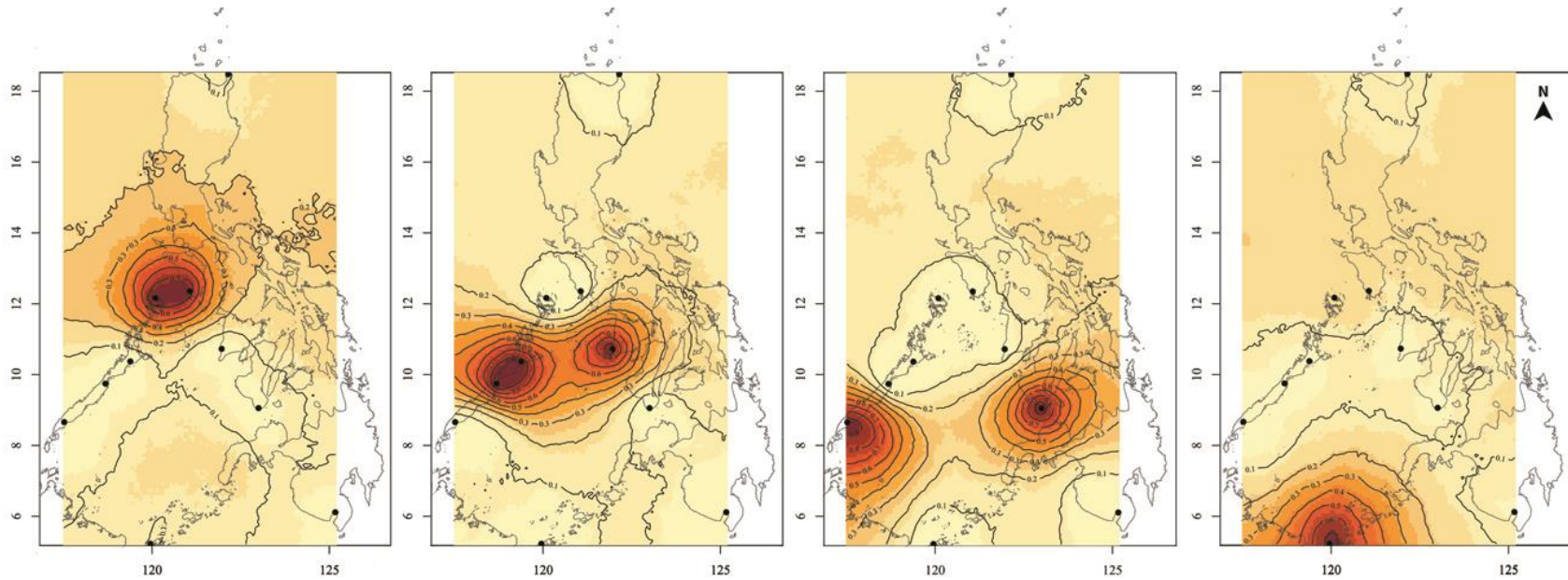


Figure 5. Distribution of genetic clusters of *S. olivacea* in the Sulu Sea based on outlier loci and Geneland analysis. Posterior probability isoclines illustrate putative genetic landscapes for the Sulu Sea domain, where sites are represented by black dots, and darker colors indicate higher probabilities of membership to each of the six clusters identified across all sampling sites. Isoclines for the outgroup populations representing two genetic clusters are not shown.