

Genetic diversity, population structure and demography of *Odontodactylus scyllarus*

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Include a brief background on your organism, and the populations that you propose to study. Describe how you would (1) characterize genetic variation, (2) determine population substructure, and (3) infer demographic history among two or more subpopulations within your species. In addition, describe how you would identify loci that have been influenced by selection, and how you would distinguish differences due to selection from other processes

1 Background

Odontodactylus scyllarus, or the Mantis shrimp are a unique group of carnivorous stomatopods that are believed to have diverged from the class Malacostraca around 340 million years ago [1]. Mantis shrimp are notable for both their unique mechanically driven raptorial smashing claws which are powerful enough to induce cavitation in the surrounding water [2, 3] and acutely sensitive visual system which is believed to be the most complex ever discovered in nature [4, 5]. Due to their extraordinary physiology the biology of Mantis shrimp species has been the subject of significant study but comparatively few studies have focused on the genetic structure of Mantis shrimp populations and have focused on Asian Mantis shrimp species in the Yellow and East China Seas [6]. Mantis shrimp are known to play an important role in marine ecosystems by acting as efficient predators of other crustaceans and oxygenating ocean sediments [7].

Main goal is to resolve the genetic diversity of *Hemisquilla californiensis* ranges from Santa Barba California to Bay of Panama population mapping efforts preceded the advent of next-generation sequencing technologies

In this effort we will pursue three specific aims.

Aim 1: Quantify genetic variation of the California Mantis shrimp

Hypothesis: *Odontodactylus scyllarus* will show significant genetic variation between sampling locations.

Locations, number of samples (N), percent amplification (

Use double-digest restriction site associated DNA sequencing (RAD-seq) [8]. Challenge will be the lack of reference genome for shrimp as non-model organism. Also utilize the a total mitochondrial genome of *Squilla leptocheila* [9], a mantis shrimp species closely related to *Odontodactylus scyllarus*.

Will rely on the closely related *Litopenaeus vannamei*, Pacific white shrimp, genome [10]

Aim 2: Evaluate sub-population structure within sampling locations

Mantis shrimp species are known to be mostly solitary creatures, rarely spending significant amounts of time outside of their sea floor burrows [11]. This small range is expected to give rise to significant population sub-structure within the four sampling locations.

- Fixation Index: reduction in genetic diversity of sub populations due to differentiation among sub populations.

– Access the reduction of differentiation to compare specific sub-populations using pairwise comparison.

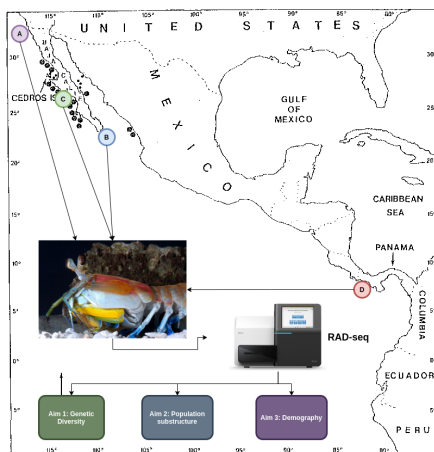


Figure 1: Proposed *Hemisquilla californiensis* collection locations shown as colored dots. Image adapted from Basch et al, 93

- How to define different sub populations? Blobs of areas / habitats
- High pairwise F_{st} to gauge the distinctness of populations. Do something where defining subpopulations at greater and greater distances to determine how quickly F_{st} will drop off at different sampling sites.

- Another entry in the list

Expected heterozygotes H_t (total population was randomly mating) Collect genotype data from a single locus A/T SNP and collect adults Determine allele frequencies of locus interested in This is where would look at mean F_{st} (fixation index which is mean reduction in H_s (expected heterozygosity due to genetic differentiation among subpopulations)). F_{is} (inbreeding coefficient reduction in H_i due to non-random mating within a subpopulations) Bayesian subpopulation assignment possibly admixture analysis here as well

Aim 3: Determine demographic history of two subpopulations of these bugs

- How to tell demography vs selection?
 - Wright-Fisher model predicts something. Neutral expectation. Constant size and no selection.
 - Selection
 - * Selective sweep
 - * negative selection
 - * balancing selection
 - * Any of these is occurring at specific loci that is under selection compared to a population (demographic level) change that should be observed genome wide because not specific to specific locus.

References

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