

Investigating the genetic diversity, population structure and demography of Baja and Pacific *Odontodactylus scyllarus*

Ethan Holleman

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

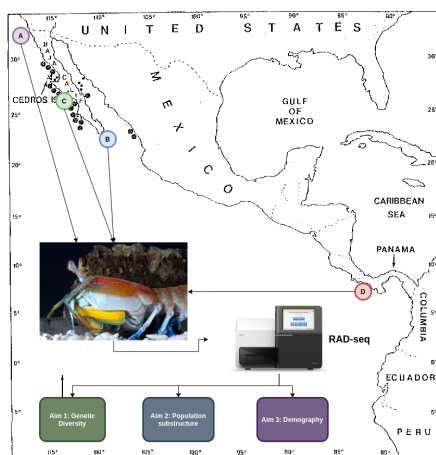


Figure 1: Proposed *Hemisquilla californiensis* collection locations shown as colored dots. Image adapted from Basch et al, 93

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 heterozygotes due to genetic differentiation among sub-populations)). F_{is} (inbreeding coefficient reduction in H_i due to non-random mating within a sub-populations) Bayesian sub-population assignment possibly admixture analysis here as well

Aim 3: Determine demographic history of two sub-populations of these bugs

Hypothesis recent decline in mantis shrimp that coincides with human activity. Mantis shrimp are sensitive to oceanic changes that effect them directly and habitat.

Evaluate the effect of selection on the observed site frequency spectrum gleaned from RAD-seq data collected as a part of aim 1.

- 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.
 - Historical demography of a population
 - * Step 1 determine allele frequency spectrum of a population by sampling individuals and determine what that is
 - * Neutral site freq spectrum has predictable decay but when looking at actual population and determine allele freq spectrum which might differ greatly from neutral expectation
 - * Step 2 is build some demographic model
 - Pop size on y and time on x axis
 - Shows how population size has changed over time
 - s is the strength of the decline (or more generally the change in population size)
 - * Step 3 Determine the parameters that we are going to vary
 - Might want to determine the
 - Strength of decline
 - Timing of decline
 - Rate of expansion
 - Some combination
 - These are the things that we are trying to determine.
 - * Step 4: Simulate data with different model parameter values.
 - Get a simulated SFS sSFS
 - DO many many simulations where you change the variables of interest and compare simulated SFS to observed SFS to try and find the parameter valeus that produce a simulated SFS to the population we are interested in.
 - This is ABC approximate Bayesian computation
 - Requires defining a prior distribution that will define the parameter space
 - Simulate with the same amount of data that we collected and get gene copies sequences (simulated) which allows for calculating the simulated allele frequency spectrum

References

- [1] Cara Van Der Wal, Shane T. Ah Yong, Simon Y.W. Ho, and Nathan Lo. The evolutionary history of stomatopoda (crustacea: Malacostraca) inferred from molecular data. *PeerJ*, 5:e3844, September 2017.
- [2] S. N. Patek, W. L. Korff, and R. L. Caldwell. Deadly strike mechanism of a mantis shrimp. *Nature*, 428(6985):819–820, April 2004.
- [3] S. N. Patek and R. L. Caldwell. Extreme impact and cavitation forces of a biological hammer: strike forces of the peacock mantis shrimp *odontodactylus scyllarus*. *Journal of Experimental Biology*, 208(19):3655–3664, October 2005.
- [4] Thomas W. Cronin, Michael J. Bok, N. Justin Marshall, and Roy L. Caldwell. Filtering and polychromatic vision in mantis shrimps: themes in visible and ultraviolet vision. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 369(1636):20130032, February 2014.
- [5] Susan Milius. Life: Mantis shrimp flub color vision test: Results suggest alternate way of detecting wavelengths. *Science News*, 182(6):11–11, September 2012.
- [6] Mei Yang and Xinzhen Li. Population genetic structure of the mantis shrimp *oratosquilla oratoria* (crustacea: Squillidae) in the yellow sea and east china sea. *Journal of Oceanology and Limnology*, 36(3):905–912, May 2018.
- [7] P.J. Antony, S. Dhanya, P.S. Lyla, B.M. Kurup, and S. Ajmal Khan. Ecological role of stomatopods (mantis shrimps) and potential impacts of trawling in a marine ecosystem of the southeast coast of india. *Ecological Modelling*, 221(21):2604–2614, October 2010.
- [8] Brant K. Peterson, Jesse N. Weber, Emily H. Kay, Heidi S. Fisher, and Hopi E. Hoekstra. Double digest RADseq: An inexpensive method for de novo SNP discovery and genotyping in model and non-model species. *PLoS ONE*, 7(5):e37135, May 2012.
- [9] Hye-Eun Kang, Jung Nyun Kim, Tae-Ho Yoon, Kyeong Dong Park, Won gyu Park, Hyun Park, and Hyun Woo Kim. Total mitochondrial genome of mantis shrimp, *squillaoides leptosquilla* (brooks, 1886) (crustacea: Stomatopoda: Squillidae) in korean waters. *Mitochondrial DNA Part A*, 27(4):2842–2843, July 2015.
- [10] Xiaojun Zhang, Jianbo Yuan, Yamin Sun, Shihao Li, Yi Gao, Yang Yu, Chengzhang Liu, Quanchao Wang, Xinjia Lv, Xiaoxi Zhang, Ka Yan Ma, Xiaobo Wang, Wenchao Lin, Long Wang, Xueli Zhu, Chengsong Zhang, Jiquan Zhang, Songjun Jin, Kuijie Yu, Jie Kong, Peng Xu, Jack Chen, Hongbin Zhang, Patrick Sorgeloos, Amir Sagi, Acacia Alcivar-Warren, Zhanjiang Liu, Lei Wang, Jue Ruan, Ka Hou Chu, Bin Liu, Fuhua Li, and Jianhai Xiang. Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. *Nature Communications*, 10(1), January 2019.
- [11] Kristina Mead and Roy Caldwell. Mantis shrimp: Olfactory apparatus and chemosensory behavior. In *Chemical Communication in Crustaceans*, pages 219–238. Springer New York, 2010.