

Population genomics in the Hawaiian volcano shrimp: cryptic speciation and mitonuclear discordance

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Halocaridina rubra (H. rubra) is an atyd shrimp found exclusively in Hawaiian anchialine habitats¹, which are coastal pools with underground connections to both salt and freshwater aquifers, but no surface connection to the ocean. Early sequencing of mt-COX1 suggests that *H. rubra* is composed of at least eight divergent lineages across the Hawaiian islands². However, mitochondrial loci often have different histories than nuclear loci, and mitonuclear discordance is rampant in phylogenetics. We aim to uncover signatures of mitonuclear coevolution and mitonuclear genetic incompatibilities leading to reproductive isolation.





- In 2005, Santos et al. sequenced mt-COX1 in a collection of *H. rubra* samples from anchialine pools across the Hawaiian islands²
- The KBP population on Oahu (boxed in orange) shows mitotypes from the neighboring EWA and OWAI populations,

with OWAI being the predominant mitotype^{2,3}

2b-RAD sequencing of the nuclear genome identifies admixture and possible mitonuclear discordance



- 2b-RAD nuclear genome sequencing yields similar groupings of lineages and identifies instances of nuclear admixture
- The KBP population shares majority nuclear ancestry with the EWA population. This contrasts with the mt-COX1 sequencing done in 2005 showing that the KBP population predominantly carries mitotypes from the OWAI population²
- These data suggest that there may be mitonuclear discordance at play

Generating complete mitogenomes for *H. rubra* populations

Preliminary Mitochondrial Phylogeny Nuclear Phylogeny

• We are testing a new low coverage whole



genome sequencing library prep which is simple and low cost (\$3-4 per sample)

- Constructed a preliminary mitochondrial phylogeny derived from parallel mitogenomic sequencing of a subset of 23 samples that underwent 2b-RAD sequencing
- Mitochondrial and nuclear phylogenies were discordant, suggesting that mitochondrial introgression may be rampant in anchialine species



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Next Steps:

We plan to perform extensive genomic and mitogenomic sequencing on modern and historically collected samples from H. rubra across the range. These data will allow us to:

1) conduct holistic population genomics studies of *H. rubra* to identify instances of mitonuclear coevolution and mitonuclear discordance leading to reproductive isolation

2) evaluate the impacts of volcanism-induced thermal habitat changes on evolution and plasticity in H. rubra

Our findings have conservation implications for the management of this species and Hawaiian anchialine habitats, which are of cultural importance.

References

Acknowledgements

1. Holithus LB (1963) Zoologishe Mededelingen

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(Leiden)

2. Santos et al. (2006) *Molecular Ecology*

3. Craft et al. (2008) *Limnology* Oceanography

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