APPENDIX ES-5

ADAPTIVE GENETICS OF HAWAIIAN TREE SNAILS & CLIMATE CHANGE

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Accomplishments
Whole mitochondrial genomes have been compared across the range of Achatinella mustelina. These results suggest the same management approach as COI alone (Holland and Hadfield’s 2002 paper), suggesting no change to the current management approach of 5 or 6 discrete ESUs, with populations grouping along the Waianae ridgelines.

However, when nuclear evidence was considered (a scan/survey of thousands of sites across the entire genome), we observed a more nuanced picture. For example, Makaha (ESU D) always groups with Koiahi and Ohikilolo (ESU B). Puu Hapapa (ESU D) groups with Ekahanui (ESU E) about 50% of the time. On the other hand, some populations are very much the same for both nuclear and mitochondrial markers. ESU C (Haleauau and Skeet Pass) always groups together, separate from the others. The populations on the three ridges that meet on top of Mt. Kaala (from ESUs B, C, D) separate out from one another with both mitochondrial and whole-genome approaches.

Based on these initial results, populations that are far apart geographically, even though they are lumped in the same ESU based on mitochondrial gene sequences, should NOT be lumped into the same enclosure simply because they are in the same ESU, particularly for ESUs B and D, which stretch a considerable distance. Unsurprisingly, total DNA evidence suggests that snail populations that are closer together geographically are more closely related genetically, and things that are farther apart are less related. Pulling nearby populations into enclosures should be enough to combat inbreeding, if that is the goal. In light of climate change, we still recommend ONLY moving snails to wetter, cooler locations, and never to locations that are warmer or drier than source locations.

GIS modeling has been scaled down to the level of ESUs. The climate-change modeling results, which have now been projected for both 25 and 60 years, suggest urgent management actions will be necessary in the near future, but we are not ready to make a specific recommendation. We may need to start intentionally mixing populations to help with adaptation to climate change. If populations are mixed for this purpose, individuals must ALWAYS be moved from drier, warmer environments to wetter, cooler environments, and not the other way around.
**Forecast**

Continued work with SNP identification and Fst-outlier analysis will be used to identify SNPs correlated with environmental variables. These data will be combined with the species’ current-range data, as well as forecast data, to predict where populations will be likely to tolerate warmer, drier conditions, and which populations should be combined to maximize adaptive ability.