

Genetic analysis of an invasive house mouse population on Southeast Farallon Island

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On the Farallon Islands, the house mouse (*Mus musculus*) is an invasive species that endangers the largest seabird breeding colony in the continental US. Currently, land managers are considering options to eradicate the house mouse ~~to protect~~~~while conserving~~ native flora and fauna. Understanding the genetics and population dynamics of an invasive species is important in designing effective eradication programs. For example, genetics can provide information about invasion rates and history, and identify potential resistance to eradication tools like rodenticide. Using the high-density Mouse Diversity Array, we genotyped mice from Southeast Farallon Island and from across the world. We found that all Southeast Farallon mice shared the same mtDNA haplotype, and all male mice shared the same Y-chromosome haplotype. However, their mtDNA and a majority of their autosome were derived from northern UK mice, whereas their Y-chromosome haplotype is only found in Mediterranean populations. Our phylogenetic analysis

suggests that the Farallon Islands were colonized in two historical waves by genetically distinct *M. m. domesticus* populations, but appear resilient to re-invasion. This is consistent with recent studies of other invasive island house mouse populations that show a considerable adaptive advantage for the first colonizers. In addition, recent studies have suggested that gene flow has occurred in the wild between *M. spretus* and *M. m. domesticus*, including the transfer of the *Vkorc1* anticoagulant resistance gene to mice from the same geographic origin as the likely colonizers of the Farallon Islands. The presence of the resistance gene in the Farallon mice could impact the choice of eradication strategies. We are currently sequencing *Vkorc1* in our sample and will report on these results.