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Population genetics of the southeastern beach mouse at Cape Canaveral Air Force Station.

INTRODUCTION AND METHODS

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The southeastern beach mouse (*Peromyscus polionotus niveiventris*) is native to coastal habitats in east Florida and was once abundant over about 280 km of coastline. Due to extensive coastal development, it is now restricted to 64 km of coastline in east-central Florida and is currently listed under both state and federal law as threatened. One of the few intact populations of this subspecies inhabits the Cape Canaveral Air Force Station in east-central Florida. Because the persistence of this population is critical for the sustained survival of the subspecies, we are:

- 1) documenting the genetic diversity, genetic structure, and effective population size within this population,
- 2) determining the relationship to geographically proximate populations of *Peromyscus polionotus*, and
- 3) describing the breeding patterns of this population.

Individuals were trapped using Sherman live traps and tissues were obtained by clipping a small portion of skin from distal end of the tail. We used ten polymorphic microsatellite loci to estimate the genetic diversity and genetic structure within this population, and estimated gene flow between eight geographically discrete sampling localities. This information will be critical for any reintroductions, translocations or other management efforts implemented in the future to promote the recovery of this subspecies.

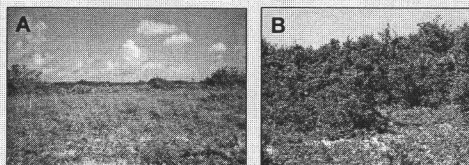


Fig 1. Sampling Habitats A) "primary dune habitat" typical of beach grids B) "scrub habitat" typical of inland grids

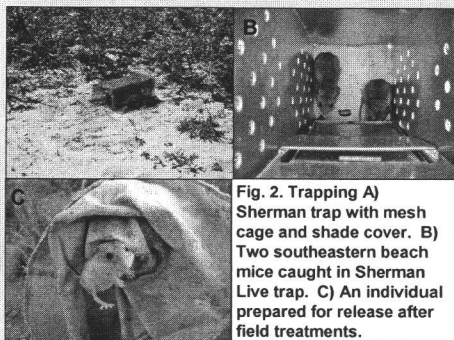


Fig. 2. Trapping A) Sherman trap with mesh cage and shade cover. B) Two southeastern beach mice caught in Sherman Live trap. C) An individual prepared for release after field treatments.

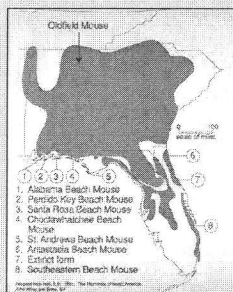


Fig 4. Approximate historic ranges of *Peromyscus polionotus* subspecies.

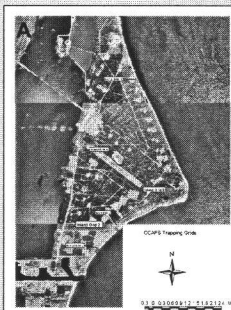


Fig 5. Aerial photos of A) Cape Canaveral Air Force Station and B) all of Merritt Island with sampling localities superimposed.

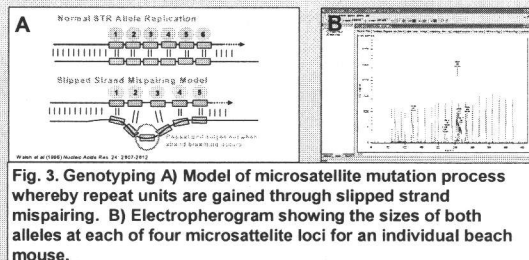
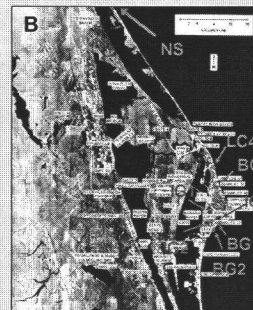


Fig. 3. Genotyping A) Model of microsatellite mutation process whereby repeat units are gained through slipped strand mispairing. B) Electropherogram showing the sizes of both alleles at each of four microsatellite loci for an individual beach mouse.

F_{st}

- Most commonly used measure of population differentiation for allelic data (although beginning to lose favor to less assumption-laden statistics)
- $F_{st} = 1/(4Nm+1)$ (Idealized)
- Generally
 - 0.0-0.05 "little divergence" >5 Migrants/gen (Nm)
 - 0.05-0.15 "moderate divergence" (1-5 Nm)
 - 0.15-0.25 "great divergence" (<1 Nm)

RESULTS

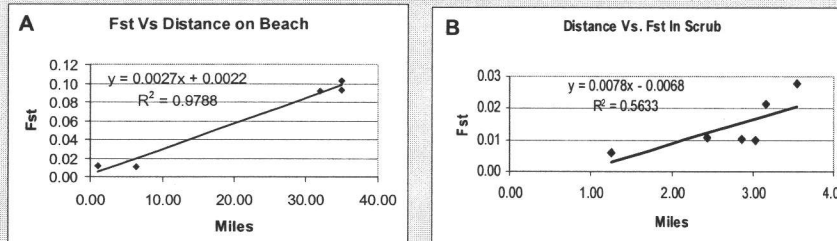


Fig 6. A) Statistically significant ($p < 0.05$, 100 permutations) pairwise F_{st} plotted against pairwise geographic distance for population pairs where the habitat matrix between the two was A) primary dune, and B) not primary dune habitat (i.e. it was scrub).

• Genetic diversity at these microsatellite loci is high and comparable to that seen in other beach mouse populations (Van Zant pers. comm.)

• There is no large-scale subdivision of genetic diversity on the Cape that is meaningful for conservation of specific areas so that sheer numbers and habitat suitability should be a conservation priority.

• However, on the finest scale, geographic distance, not beach-inland delineation, explains partitioning of genetic variation in the southeastern beach mouse. Further, the degree to which geographic distance effects genetic isolation seems to be greater in scrub habitat than in beach habitat.

FUTURE DIRECTIONS

Ongoing research at the University of Central Florida will

• Test hypothesis of differential dispersal on beach versus through scrub using more modern statistical techniques than F_{st} (e.g. maximum likelihood estimation of genetic marker genealogies)

• Expand scope to include true inland forms of *Peromyscus polionotus* – we have only "moderate divergence" over 35 miles of beach, is this true over 35 miles of scrub?

• Test for a relationship between individuals' inbreeding coefficient (using some correlated statistic, e.g. multi-locus heterozygosity) against components of fitness – adult weight, survivorship, etc.

• Use mitochondrial DNA to test hypotheses of sex-biased dispersal

• Use known sibling-parent relationships and these microsatellite markers to test long-standing doctrines of monogamy

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