

Results from mammal surveys at Pahrnagat Valley National Wildlife Refuge, August 7-11, 2006.

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Objective

Montane voles of the genus *Microtus* are distributed across high elevation sites in western and southwestern North America. Because of the species affinity for high elevation sites, low mobility and short generation times, *Microtus* voles are model organisms to study the influence of habitat alteration and climate change on the distribution, genetics, and long-term viability of the populations. The primary objectives of this research are to elucidate the influence of spatial structure on the ecology, genetics and persistence times of montane mammals using the long-tailed vole, *M. longicaudus* and *M. montanus*, the montane vole, as proxies for the montane community. Understanding the interplay among ecological, genetic and climatic parameters on species persistence is an integral step to managing present and future natural resource areas and the organism communities they support.

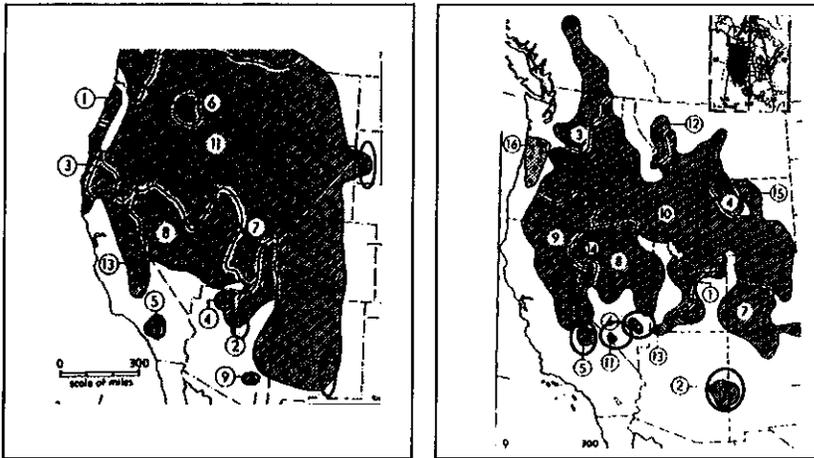
The extinction probability for a species is determined by a number of non-mutually exclusive factors, including body size (Marshall, 1988), population size (Lande, 1988; Diamond, 1984), genetics (Reed and Frankham, 2003; Schmitt and Hewitt, 2004), ecological tolerance (Martinez-Meyer et al., 2004), spatial structure, habitat area and degree of isolation. Studies of the contribution of determinants to species persistence, and their degree of interaction are motivated by an awareness of habitat change or loss from anthropogenic and/or climatic factors. A principal driver for these studies, particularly the latter four variables, is the increasing influence of recent global climate change on species distributions (Epps et al., 2004; Parmesan et al., 1999).

The spatial structure of a species population is a potentially significant predictor of species persistence, because it determines the presence and frequency of gene flow between populations. The concept of spatial structure in species distribution is a primary component of ecological and genetic models, such as the Theory of Island Biogeography, and the Island and metapopulation models of gene flow (Wright, 1930; Slatkin, 1977). A metapopulation is connected by levels of gene flow low enough that genetic differentiation is maintained even in the face of gene flow. Because of on-going gene flow, metapopulations are more likely to persist than non-connected populations. As such, identifying whether a species distribution meets criteria for a metapopulation has been a productive aspect of conservation and management strategies.

Materials and Methods

The distribution of montane voles is characterized by both peripheral and larger, more contiguous populations (Fig. 1). Gene flow for the populations has largely been uncharacterized, and therefore, whether the populations are connected by gene flow is unknown.

Figure 1. Distribution of (a), the long-tailed vole and (b), the montane vole as core (shaded) and peripheral populations (red circles). Modified from Hall, 1981.



Therefore, my initial primary objectives are:

1. assess the historical pattern of connectivity for each species,
2. elucidate genetic variation between peripheral and core populations,
3. elucidate whether peripheral and core populations are connected by gene flow using genetic and ecological data

To accomplish goals of the study, I will collect DNA samples from 20-40 voles per population. A sample size of 30-40 is recommended for population level studies of genetic variation. To date, I have acquired 303 tissues; I collected 63 and have access to the remainder through the Museum of Southwestern Biology Division of Genomic Resources (Table 1).

Notably absent from current DNA samples are populations of *M. montanus* from southern Nevada, particularly Ash Meadows National Wildlife Refuge and Pahranaagat Valley NWR (Fig. 1). The montane vole located within the White Mountains of New Mexico and adjacent Arizona is recognized as a distinct subspecies, *M. m. arizonensis*, and is listed as endangered by the State of New Mexico Department of Game and Fish. *M. montanus* populations in southern Nevada may be endangered (Christi Balbino, *pers. comm.*), but a comprehensive survey has not been conducted since 1933. The southern Nevada populations of

the species are likely to make a significant contribution to our understanding of the interplay among spatial structure, genetics, and ecology in species persistence. Trapping surveys for southern Nevada and other locations are needed to fill sampling gaps (Table 1).

To assess the historical connectivity between populations, I will first sequence the cytochrome *b* gene of mitochondrial DNA using primers L14724 and *cytbR*. I test for current gene flow by amplifying microsatellite loci and primers optimized for the species (Van De Zande et al., 2000). Using a hierarchical AMOVA, I will assess levels of genetic variation within and between populations (Excoffier, et al., 1992). I will elucidate presence and levels of current gene flow testing for correlation between geographic and genetic distance (microsatellites) (BAYESASS software, Wilson and Rannala, 2003). I will estimate geographic distance between populations using a GIS and genetic distances from molecular data.

Table 1. DNA samples from long-tailed vole and montane vole populations to be used in this study.

Species	Population	Samples acquired	Samples needed
Long-tailed vole	Peripheral populations	AZ White Mts. (2) AZ Pinaleno Mts. (16) AZ Kaibab Plateau (35) NM Sacramento Mts. (12)	AZ White Mts. (28) AZ Pinaleno Mts. (24) NM Sacramento Mts. (18)
	Core population	Southern Rockies (CO, WY) (140)	
Montane vole	Peripheral populations	AZ White Mountains (37) NM Catron Co. (7) NV Pahranaagat Valley (0) NV Ash Meadows (0)	NV Pahranaagat Valley (30) NV Ash Meadows (30)
	Core population	Southern Rockies (CO, WY) (54)	

Site Descriptions

Cottonwood log N 37deg 15.940 W 115deg 07.369 Elevation 1001.8m

GPS Accuracy 5.2m

20 traps for 4 nights

80 trapnights

Cottonwood Springs N 37deg 14.658 W 115deg 06.362 elevation 989.6m

GPS Accuracy 4.8m

170 trapnights

Middle Marsh N 37deg 15.149 W 115deg 06.345 Elevation 1007.6m

GPS Accuracy 7.3m

20 traps 3nights

60 trapnights

This site is characterized by a diverse assemblage of vegetation, including juncus, cattails, salt grass. Some runways, perhaps from *Microtus*, were noted.

Headquarters South pond N 37deg 15.960 W 115deg 07.316 Elevation 1002.2m

GPS Accuracy 6.4m

20 traps 1 night

20 trapnights

This site was dominated by juncus, bulrush, and some grasses. Of all the sites, this site exhibited the highest vertical and horizontal structure. Many runways were noted, including some that appear to have been made by *Microtus*.

Juncus south N 37deg 15.674 W 115deg 06.551 Elevation 999.4m

GPS Accuracy 4.3m

10 traps

2 nights

20 trapnights

Middle Marsh north N 37deg 15.149 W 115deg 06.345 Elevation 1007.6m

GPS Accuracy 7.3m

10 traps

2 nights

20 trapnights

This site was characterized by a mixed community of bulrush, cattails and juncus.

Cattail Line N 37deg 14.658 W 115deg 06.362 elevation 989.6m

GPS Accuracy 4.8m

10 traps 2 nights

20 trapnights

North End site N 37deg 18.164 W 115deg 07.879 Elevation 1022.6m

GPS Accuracy 4.8m

20 traps 3 nights

60 trapnights

This site is dominated by salt grass and bordered by cattails that line the shore of a large body of water. The site was largely xeric during surveys, and grass height averaged approximately 8cm. No runways or other possible vole sign were noted.

Survey Results

Surveys conducted from August 7-11, 2006 resulted in 32 captures out of 450 trapnights for a 7% total trap success (0.07x100). The most numerous species captured was *Mus musculus*, and the most productive site was Cottonwood log just south and west of the Refuge Headquarters. No montane voles were captured.

Table 1. Record of mammal captures for Pahrnagat Valley National Wildlife Refuge, August 7-11, 2006. The number of trap nights was approximately equal to 450.

Species	# Captures	# Recaptures	% Trap Success
<i>Mus musculus</i>	19	0	4.2
<i>Reithrodontomys megalotis</i>	10	0	2.2
<i>Peromyscus maniculatus</i>	3	0	0.6
Total capture success	32		7.1

Table 2. Summary of mammal captures per site for Pahrnagat Valley National Wildlife Refuge, August 7-11, 2006.

Site Name	Species captured	No. captured/site
Cattail Line	<i>Mus musculus</i>	2
	<i>Peromyscus maniculatus</i>	1
Cottonwood Log	<i>Mus musculus</i>	6
	<i>Reithrodontomys megalotis</i>	3
	<i>Peromyscus maniculatus</i>	1
Cottonwood Spring	<i>Mus musculus</i>	4
	<i>Reithrodontomys megalotis</i>	3
Juncus drainage	<i>Reithrodontomys megalotis</i>	2
Middle Marsh	<i>Mus musculus</i>	6
South Headquarters	<i>Mus musculus</i>	2
	<i>Reithrodontomys megalotis</i>	2

A more detailed report, documenting the August and October surveys, will be available later this year.

Literature Cited

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