

# PEROMYSCUS NEWSLETTER

NUMBER TWENTY-SEVEN



MARCH 1999

Cover: Cotton mouse (*Peromyscus gossypinus*).  
Photo by Clint Cook.

Due to budgetary uncertainties we were unduly late with the "September 1998" issue of *Peromyscus Newsletter* which wasn't mailed until early spring 99. Thus, the "March 1999" issue is also late. Hopefully we will be back on schedule by the next issue.

In the current issue the reader will find indices to the most recent updates of information summaries from previous issues (p. 16), e.g. the last update of the species list was in Issue # 17, page 18. For those readers who keep old issues of *PN*, with these indices tables of interest can be quickly located. Coming updates will soon be posted in *PeroBase*, making the index to *PN* redundant.

With reference to *PeroBase*, we are now getting into high gear. "Industrial strength" hardware has been purchased upon which the database will be mounted. SyBase software was purchased to manage the data and several grad students and a postdoc are working on specific categories of organization. A number of potential "datamasters" from the *Peromyscus* research community have been identified. The datamasters will serve as reviewers and advisors for specialized topics within *PeroBase*. What is currently on-line at <http://www.cs.sc.edu/research/perobase/perobase.htm> at this point still represents a much abbreviated mock-up version. This will be replaced shortly by parts of "the real thing". The first to come on line will be "Genetics" and "Taxonomy, Systematics and Evolution" followed by "Reproduction and Development" and "Behavior". In due course several other topical categories will be included. As it develops the amount of data will greatly increase for each topic, and the data will continually be reviewed to reflect current information.

Another major new feature of *PeroBase* is addition and expansion of the Bruce Buttler Bibliography. Many readers will recall that Bruce (Canadian Union College, Edmonton, AB) for about 15 years has been organizing *Peromyscus* literature references into topical areas and periodically making these lists available as loose-leaf volumes. Bruce has generously allowed us to purchase rights to his comprehensive electronic version of the bibliography. In recognition of the immense amount of effort he has devoted to this project, in *PeroBase* the 5000plus reference list will be referred to as the "Bruce Buttler Bibliography of *Peromyscus*."

Please continue to send entries for *Peromyscus Newsletter*. We think that, in spite of *PeroBase*, *PN* will continue to be relevant and useful, although, as we suggested in the past two issues, its focus will likely shift from an emphasis on genetics into other research areas.

W. Dawson  
Editor

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# C O N T E N T S

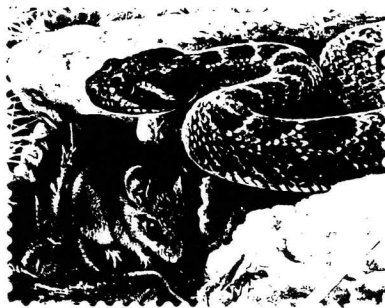
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**PEROMYSCUS ON U.S. POSTAGE STAMP --- AGAIN !!!**

A cactus mouse (*Peromyscus eremicus*) is one of 25 species of animals and plants native to the Sonoran Desert featured on a souvenir sheet of self adhesive 33 cent postage stamps. The sheet was issued in March 1999. Unfortunately (for the mouse) it shares the stamp with a western diamondback rattlesnake. This is the second U.S. stamp to feature *Peromyscus*. A 1988 stamp pictured a deer mouse (*P. maniculatus*).



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**BACK ISSUES.** Unfortunately our supply of original back issues of *PEROMYSCUS NEWSLETTER* is becoming depleted. The only issues we still have in adequate supply are Numbers 8, 13, 14, 17, 18, 19, 20, 21, 23 and 24. For others there are either no available copies or fewer than 5 on hand. We have good photocopies of scarce back issues (with covers in the original colors) that can be supplied for \$ 5 each. A complete set of *PN* (Numbers 1 thru 25), including some as the photocopied version, will be provided for \$ 50 including postage.

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Twenty-two presentations (papers and posters) on *Peromyscus* were given at the 1999 meeting of the American Society of Mammalogists. The meeting was held in Seattle at the University of Washington.

\* \* \* \* \*



New home of the *Peromyscus* Genetic Stock Center.  
The Graduate Science Center under construction  
at the University of South Carolina.



## PEROMYSCUS STOCK CENTER

**What is the Stock Center?** The deer mouse colony at the University of South Carolina has been designated a genetic stock center under a grant from the Special Projects Program of the National Science Foundation. The major function of the Stock Center is to provide genetically characterized types of *Peromyscus* in limited quantities to scientific investigators. Continuation of the center is dependent upon significant external utilization, therefore potential **users are encouraged to take advantage of this resource**. Sufficient animals of the mutant types generally can be provided to initiate a breeding stock. Somewhat larger numbers, up to about 50 animals, can be provided from the wild-type stocks.

A user fee of **\$17.50 per wild-type animal** and **\$ 25 per mutant or special stock animal** is charged. The user assumes the cost of air shipment. Animals lost in transit are replaced without charge. Tissues, blood, skins, etc. can also be supplied at a modest fee. Arrangements for special orders will be negotiated. Write or call for details.

### Stocks Available in the Peromyscus Stock Center

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| WILD TYPE SPECIES                                                      | ORIGIN                                                                                                                                       |
|------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| <i>P. maniculatus bairdii</i><br>(BW Stock)                            | Closed colony bred in captivity since 1948.<br>Descended from 40 ancestors wild-caught near Ann Arbor MI                                     |
| <i>P. polionotus subgriseus</i><br>(PO Stock)                          | Closed colony since 1952.<br>Derived from 21 ancestors wild-caught in Ocala Nat'l. Forest FL. High inbreeding coefficient.                   |
| <i>P. polionotus leucocephalus</i><br>(LS Stock)                       | Derived from beachmice wild-caught on Santa Rosa I., FL. and bred by R. Lacy.<br>Approximately ten generations in captivity.                 |
| <i>P. leucopus</i><br>(LL Stock)                                       | Derived from 38 wild ancestors captured between 1982 and 85 near Linville NC.<br>Approximately 20 generations in captivity.                  |
| <i>P. californicus insignis</i><br>(IS Stock)                          | Derived from about 60 ancestors collected between 1979 and 87 in Santa Monica Mts. CA.<br>Approximately twelve generations in captivity.     |
| <i>P. aztecus</i><br>(AM Stock)                                        | Derived from animals collected on Sierra Chincua, Michoacan, Mexico in 1986<br>Approximately ten generations in captivity.                   |
| <i>P. melanophrys</i>                                                  | Originated from a group of animals collected at Zacatecas Mexico during the 1970's.<br>Formerly maintained by R.W. Hill at Mich. State Univ. |
| <i>P. maniculatus</i> X <i>P. polionotus</i><br>F <sub>1</sub> Hybrids | Sometimes available.                                                                                                                         |

## MUTATIONS AVAILABLE FROM THE STOCK CENTER<sup>1</sup>

### Coat Colors

Albino *c/c*  
Ashy *ahy/ahy*  
Black (Non-agouti) *a/a*  
Blonde *bln/bln*  
<sup>2</sup>Brown *b/b*  
California blonde *cfb/cfb*  
Dominant spotting *S/+*  
Golden nugget *b<sup>gn</sup>/b<sup>gn</sup>* [in *P. leucopus*]  
Gray *g/g*  
Ivory *i/i*  
<sup>3</sup>Pink-eyed dilution *p/p*  
Platinum *plt/plt*  
<sup>2</sup>Silver *sil/sil*  
Tan streak *tns/tns*  
Variable white *Vw/+*  
White-belly non-agouti *a<sup>w</sup>/a<sup>w</sup>*  
Wide-band agouti *A<sup>Nb</sup>/a*  
Yellowish *yel/yel*

### Other Mutations and Variants

Alcohol dehydrogenase negative *Adh<sup>o</sup>/Adh<sup>o</sup>*  
Alcohol dehydrogenase positive *Adh<sup>f</sup>/Adh<sup>f</sup>*  
Boggler *bg/bg*  
Cataract-webbed *cwb/cwb*  
Epilepsy *ep/ep*  
<sup>3</sup>Flexed-tail *f/f*  
  
Hairless-1 *hr-1/hr-1*  
Hairless-2 *hr-2/hr-2*  
Juvenile ataxia *ja/ja*  
  
Enzyme variants.

### ORIGINAL SOURCE

Sumner's albino deer mice (Sumner, 1922)  
Wild-caught in Oregon ~ 1960 (Teed *et al.*, 1990)  
Horner's black mutant (Horner *et al.*, 1980)  
Mich. State U. colony (Pratt and Robbins, 1982)  
Huestis stocks (Huestis and Barto, 1934)  
Santa Cruz I., Calif., stock (Roth and Dawson, 1996)  
Wild caught in Illinois (Feldman, 1936)  
Wild caught in Mass. (Horner and Dawson, 1993)  
Natural polymorphism. From Dice stocks (Dice, 1933)  
Wild caught in Oregon (Huestis, 1938)  
Sumner's "pallid" deer mice (Sumner, 1917)  
Barto stock at U. Mich. (Dodson *et al.*, 1987)  
Huestis stock (Huestis and Barto, 1934)  
Clemson U. stock from N.C. (Wang *et al.*, 1993)  
Michigan State U. colony (Cowling *et al.*, 1994)  
Egoscue's "non-agouti" (Egoscue, 1971)  
Natural polymorphism. U. Mich. (McIntosh, 1954)  
Sumner's original mutant (Sumner, 1917)

### ORIGIN

South Carolina BW stock (Felder, 1975)  
South Carolina BW stock (Felder, 1975)  
Blair's *P. m. blandus* stock (Barto, 1955)  
From Huestis stocks (Anderson and Burns, 1979)  
U. Michigan *artemisiae* stock (Dice, 1935)  
Probably derived from Huestis flexed-tail (Huestis and Barto, 1936)  
Sumner's hairless mutant (Sumner, 1924)  
Egoscue's hairless mutant (Egoscue, 1962)  
U. Michigan stock (Van Ooteghem, 1983)

Wild type stocks given above provide a reservoir for several enzyme and other protein variants. (Dawson *et al.*, 1983).

<sup>1</sup>Unless otherwise noted, mutations are in *P. maniculatus*.

<sup>2</sup>Available only as silver/brown double recessive.

<sup>3</sup>Available only as pink-eye dilution/flexed-tail double recessive.

**OTHER RESOURCES OF THE *PEROMYSCUS* GENETIC STOCK CENTER:**

Highly inbred *P. leucopus* ( $I_{20+}$ ) are available in limited numbers as live animals or as frozen tissues. Several lines developed by George Smith (UCLA) are currently maintained by the Stock Center.

Limited numbers of other stocks, species, mutants, inbreds and variants are on hand, or under development, but are not available for distribution. Currently we can supply up to 10 each of the species *P. eremicus* and *P. melanophrys*.

Preserved or frozen specimens of types given in tables above.

Tissues, whole blood or serum of types given in tables above.

Flat skins of mutant coat colors or wild-type any of the species above.

Reference library of more than 2400 reprints of research articles and reports on *Peromyscus*.

Copies of individual articles can be photocopied and mailed. Please limit requests to five articles at any given time. There will be a charge of 5 cents per photocopied page after the initial 20 pages.

Materials are available through the *Peromyscus* Molecular Bank of the Stock Center. Allow two weeks for delivery. Included is purified DNA or frozen tissues from any of the stocks listed above. Several genomic libraries and a variety of molecular probes are available. (See next page.)

*For additional information or details about any of these mutants, stocks or other materials contact: Janet Crossland, Colony Manager, Peromyscus Stock Center, (803) 777-3107 or peromyscus@stkctr.biol.sc.edu*

**PLEASE CALL WITH INQUIRIES.**

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## Materials on Deposit in the *Peromyscus* Molecular Bank

| Accession<br>Number           | Item               | Description                     | Species                | Donor          | Location <sup>1</sup> |
|-------------------------------|--------------------|---------------------------------|------------------------|----------------|-----------------------|
| <b>Probes and Clones:</b>     |                    |                                 |                        |                |                       |
| Pr-01                         | LINE1              | pDK62                           | <i>P. maniculatus</i>  | D. Kass        | C                     |
| Pr-02                         | LINE1              | pDK55                           | <i>P. maniculatus</i>  | D. Kass        | C                     |
| Pr-03                         | ADH1               | pADH F72                        | <i>P. maniculatus</i>  | M. Felder      | B                     |
| Pr-04 <sup>2</sup>            | Mys                |                                 | <i>P. leucopus</i>     | (Requested)    |                       |
| Pr-05 <sup>2</sup>            | SAT                |                                 | <i>P. leucopus</i>     | (Requested)    |                       |
| Pr-06                         | 6PGD               | pB5 clones                      | <i>P. californicus</i> | S. Hoffman     | A                     |
| Pr-07                         | MHC <i>PeleI</i>   | 38dp2                           | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-08                         | MHC <i>PeleI</i>   | 52ap6                           | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-09                         | MHC <i>PeleI</i>   | 40Bgl                           | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-10                         | MHC <i>PeleI</i>   | 53Pv1                           | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-11                         | MHC <i>PeleI</i>   | 37B2                            | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-12                         | MHC <i>PeleI</i>   | 37B4                            | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-13                         | MHC <i>PeleII</i>  | $\alpha$ 3E23                   | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-14                         | MHC <i>PeleIII</i> | 17E2                            | <i>P. leucopus</i>     | M. Crew        | A                     |
| Pr-15                         | MHC <i>PemaI</i>   | pr44                            | <i>P. maniculatus</i>  | M. Crew        | A                     |
| <b>Libraries:</b>             |                    |                                 |                        |                |                       |
| Lb-03                         | lambda genomic     | testis                          | <i>P. leucopus</i>     | M. Crew        | A                     |
| Lb-04                         | cosmid genomic     | testis                          | <i>P. leucopus</i>     | R. Baker       | A                     |
| Lb-05                         | lambda genomic     | liver                           | <i>P. californicus</i> | S. Hoffman     | A                     |
| <b>Frozen Tissue for DNA:</b> |                    |                                 |                        |                |                       |
| S-01                          | bairdii (BW)       | liver, tail, other <sup>3</sup> | <i>P. maniculatus</i>  | Stk. Ctr.      | A                     |
| S-02                          | subgriseus (PO)    | liver, tail, other              | <i>P. polionotus</i>   | Stk. Ctr.      | A                     |
| S-03                          | leucopus (LL)      | liver, tail, other              | <i>P. leucopus</i>     | Stk. Ctr.      | A                     |
| S-04                          | wild-caught SC     | liver, other                    | <i>P. gossypinus</i>   | -              | A                     |
| S-05                          | aztecus (AM)       | liver, tail, other              | <i>P. aztecus</i>      | J. Glendinning | A                     |
| S-06                          | insignis (IS)      | liver, tail, other              | <i>P. californicus</i> | S. Hoffman     | A                     |
| S-07                          | inbred PmH1A       | liver, other                    | <i>P. maniculatus</i>  | Jackson Lab    | A                     |
| S-08                          | inbred PmH8        | liver, other                    | <i>P. maniculatus</i>  | Jackson Lab    | A                     |

<sup>1</sup>Location code: A = USoCar SAI 01; B = USoCar CLS 603; C = USoCar CLS 707

<sup>2</sup>Not currently available.

<sup>3</sup>kidney, spleen, testis, carcass.

## PROPOSED:

### TAXONOMY, SYSTEMATICS and EVOLUTION IN *PeroBase*

As we develop *PeroBase* content becomes important. What do potential users of peromyscines want to know? A significant number of queries involve the phylogenetic affinities, particularly the evolutionary distance, between or among species within *Peromyscus*, or between *Peromyscus* and *Mus* or *Rattus*. While general relationships are fairly well established, some cases, particularly those dating the most recent common ancestry, remain controversial. There also are differences of opinion regarding the taxonomy of peromyscines, usually concerning what taxa should and what should not be included in the genus *Peromyscus*, or what species should be assigned to a particular species group. We view these debates as useful, because they result in research that enlightens the evolutionary history of North American sigmodontine rodents. In view of this, we feel that *PeroBase* should reflect the existing state of systematics and evolutionary knowledge in the field, rather than attempting to provide absolutes.

So what do we have in mind? First, we will have the **taxonomic classification** currently recognized in the literature, specifically that of Carleton (1989) but with subsequent published changes. Our scope of "peromyscines" will include traditional "*Peromyscus*" (*sensu* Hall 1981) plus *Onychomys* and *Neotomodon*. The inclusion of peripheral genera (*Ochrotomys*, *Baiomys*) assigned to *Peromyscus* by Osgood (1909) and *Reithrodontomys* formerly included among peromyscines (Carleton, 1980) will not be included. Carleton's (1989) taxonomy does not include extinct species. The earlier classifications of Osgood and of Hooper (1968) will be accessible from the database, but not "up front". From the classification an account of any peromyscine species, as described in the next paragraph, can be accessed.

**Second**, there will be a **descriptive account of each peromyscine species**, based on those published in the *Mammalian Species* series. Each account will, if available, include a color photograph of the adult animal, a range map and a drawing or photograph of the skull and/or dentition. The account will include synonymy, identifying features, and much information about the biology of the species. At this time *Mammalian Species* accounts are available for fewer than half of the species. Where these accounts do not exist, we will provide information from other sources. (We greatly appreciate the cooperation of the American Society of Mammalogist for permitting us the use material from *Mammalian Species*). The individual species pages will have numerous "hot keys" permitting access to information elsewhere in the database.

**Third**, **reconstructed peromyscine phylogeny** will be presented diagrammatically. The need is for non-sytematists to quickly grasp the taxonomic and evolutionary structure of Peromyscini. This poses a particularly difficult problem since many phylogenetic trees have been published based widely different criteria (morphology, allozymes, chomosomes, molecular sequences, *etc.*) and the included taxa vary greatly. Various algorithms, philosophies (phyletic, cladistic) and assumptions are involved. Some of these, *e.g.* that of Stangl and Baker (1984), are more comprehensive and consistent with varying data sets

than are others. There is clearly a need for a consensus phylogeny. A major goal for *PeroBase* is to devise a consensus tree that best represents peromyscine phylogeny as we currently understand it. No doubt some subjectivity will be necessary to achieve this goal, but regular re-evaluation will be essential as additional data becomes available. Alternative trees based on specific criteria (e.g. allozymes, mtDNA restriction maps) will be accessible from the main phylogeny page.

**Fourth**, since *Peromyscus* has been long viewed as an ideal genus for speciation studies, **reproductive isolating mechanisms** operating among the species will be presented in tables, text and figures. The results of experimental hybridization attempts within and between species will be presented. Behavioral tests between species and behaviors in nature that are relevant to reproductive isolation will be described. Other relevant information, e.g. natural hybrid zones or evidence of hybrid dysgenesis, will also be accessible from this page.

**Fifth**, the **fossil record** of peromyscines and ancestral rodent taxa needs to be included in *PeroBase*. Fossils of extinct and extant species of *Peromyscus* and related sigmodontines are well represented in later Tertiary and Quaternary collections from North America (Hibbard, 1968). A list of fossil species with descriptions, accompanying figures, maps, and taxonomy will be inserted into *PeroBase*.

**Sixth**, a program of "**scenario-based evolution**" of peromyscines will be incorporated. Evolution of peromyscines has occurred against a backdrop of late Pliocene and Pleistocene events in North America with glacial advances and retreats, dramatic changes in climate, vegetation and sea level. Any meaningful interpretation of present-day distributions and adaptations in *Peromyscus* and closely allied genera needs to incorporate the paleohistorical events of the last five million years during which peromyscines are represented in the fossil record. Accounts of evolution of peromyscine taxa will be presented in the database as a sequence of scenarios reflecting stages in the process set against contemporaneous geological, climatic and vegetational events. These scenarios represent most probable "stories" (hypotheses, mini-paradigms) of how a given species evolved based on all available intrinsic and extrinsic evidence. The specific types of information will vary from scenario to scenario, and will have varying degrees weight or relevance. As additional information is obtained, a given scenario may be strengthened, weakened or refuted. In *PeroBase* a series of scenarios will be pictorially presented as a sequence of five or more maps of the continent at periodic intervals roughly corresponding to successive glacial and interglacials with hypothetical range map overlays. Accompanying text labels will address key events at various stages. For some species, particularly those in Mesoamerica, there is insufficient information available to present more than a very generalized scenario.

**Seventh**, there will be a category on **evolutionary processes**, e.g. selection, effective population number, drift *etc.* that will be included in "Population Biology" in another part of *PeroBase*.

The Taxonomy, Systematics and Evolution section will be comprehensively referenced from among the 6000+ titles in the *PeroBase* Buttler Bibliography.



**NOTICE**

**PEROMYSCUS NEWSLETTER IN NOT A FORMAL SCIENTIFIC PUBLICATION.**

Therefore ...

**INFORMATION AND DATA IN THE "CONTRIBUTIONS" SECTION SHOULD NOT BE CITED OR USED WITHOUT PERMISSION OF THE CONTRIBUTOR.**

**THANK YOU!**



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**Identification of the cotton mouse (*Peromyscus gossypinus*)  
in southern Illinois**

The cotton mouse (*Peromyscus gossypinus*) is on the northern periphery of its range in the five southernmost counties of Illinois (Alexander, Johnson, Pope, Pulaski, and Union) (Hoffmeister 1989), the Jackson Purchase Region of Kentucky (Barbour and Davis 1974), and southeast Missouri, which includes the bootheel (Hall 1981). This species is not listed as threatened or endangered in Illinois, but is considered rare in Missouri (Missouri Department of Conservation 1998) and threatened in Kentucky (Kentucky State Nature Preserves Commission 1998).

This species is sympatric with the white-footed mouse (*P. leucopus*) in Kentucky, Illinois, and Missouri (Hall and Kelson 1959; Hoffmeister 1989; Robbins et al. 1985). Sympatry among *Peromyscus* species is common in many geographic areas (Sternburg and Feldhamer 1997) and identification is difficult due to similar morphology (Wolfe and Linzey 1977; Schwartz and Schwartz 1981; Engstrom et al. 1982; McDaniel et al. 1983).

The cotton mouse had not been reported in Illinois since 1909 (Hoffmeister, 1977), until recent collections at Horseshoe Lake Conservation Area ( Feldhamer et al. 1998). Feldhamer et al. (1998) examined five cotton mice, all males, and 60 white-footed mice captured from Horseshoe Lake Conservation Area in 1996. They found the mean hind foot length (22.4 mm) and mean body mass (26.7 g) in cotton mice was significantly greater than the mean hind foot length (20.7 mm) and mean body mass (21.5 g) in male white-footed mice. Skull measurements were taken (i.e.,

condylobasal length, crown length of maxillary tooth row, and length of the nasals), analyzed, and were in the ranges of measurements reported by Hoffmeister (1977).

Using allozyme electrophoresis, Price and Kennedy (1980) and Robbins et al. (1985) found glucose-6-phosphate isomerase-1 (GPI-1; E.C. #5.3.1.9) to have diagnostic allelic differences between cotton mice and white-footed mice using internal tissues. The use of internal tissues mandates lethal sampling of the mice. We wanted to use a reliable, non-lethal technique to distinguish between these species in Illinois. We are taking a conservative approach to comply with wishes from the IDNR because this species may be a future candidate for listing in Illinois. Because toe-clips (non-lethal sampling) are taken for identification, we attempted to use this tissue for allozyme electrophoresis. A pilot study was conducted in Missouri where 32 *Peromyscus* sp. were sacrificed. Morphometric data were taken on cleaned skulls (Hoffmeister 1989) to accurately identify the species. Electrophoretic gel results (cellulose acetate) were compared to morphometric results to verify the accuracy of the technique. There was 100% compatibility between the two techniques.

We are interested if anyone else has had success using toe-clips for allozyme electrophoresis. Please e-mail your comments and/or ideas to: ([vabarko@siu.edu](mailto:vabarko@siu.edu)).

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**Recent progress in the ecology of the Sin Nombre virus – *Peromyscus maniculatus* system in a variable landscape: Towards a predictive model**

Initial field studies of Sin Nombre virus (SNV) and its primary rodent host, *Peromyscus maniculatus*, demonstrated the presence of a complex and quite variable system. Earlier suspicions of a simple link between disease prevalence and host density proved not to be universally true, and longitudinal studies have revealed that disease prevalence varies considerably over time within some sites. These difficulties, in addition to the well-known complexities of habitat use exhibited by *P. maniculatus*, have prevented researchers from easily predicting conditions likely to produce new outbreaks. However, by integrating ecological concepts such as threshold effects, scale-dependence, and population connectivity in our studies, we have made substantial progress in developing a predictive computer simulation model linked to GIS databases. Both longitudinal and spatially extensive data, in addition to published studies, were used to create model parameters. Further refinement of this model will not only potentially allow improved assessment of risk factors, but may foster the formulation of new hypotheses.

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### **Co-infection with *Borrelia burgdorferi*, *Babesia microti*, and the agent of HGE in field samples collected on Long Island, NY**

Since *Ixodes scapularis* is the vector for *Borrelia burgdorferi*, *Babesia microti*, and the agent of human granulocytic ehrlichiosis (HGE), it is likely that a single tick can harbor and transmit multiple pathogens to human and animal hosts. *Peromyscus leucopus* is considered the primary rodent reservoir for all three pathogens. To determine possible sources of tick infection, we examined the role of *P. leucopus* in the zoonotic cycles of these tick-borne pathogens on Long Island.

During peak larval tick activity in 1997, we conducted a mark-recapture field study in Wading River, NY, to monitor temporal aspects of these infections in mice. Twenty-eight *P. leucopus* recruits were captured and variously recaptured for a total of 48 captures. Traps were set weekly over a five week period so that sequential captures of a single animal were never less than one week apart. Blood and tissue samples were collected upon each capture. DNA was extracted from blood and tissue was cultured for *B. burgdorferi* in BSK media. Blood extracts were analyzed by PCR for all three pathogens. Additionally, animals were held for 24 hours during which time replete larval ticks that dropped off were collected. Ticks were allowed to molt and analyzed for infection by PCR.

Our findings indicate that the zoonotic cycles for all three of these pathogens exist and overlap considerably on Long Island. Blood and tissue samples from mice yielded PCR and culture data that indicate co-infection in the mouse population. *B. burgdorferi* was detected alone in 3/48 captures and in combination with at least one other pathogen in 7/48 captures. Likewise, *B. microti* was found alone in 16/48 and as a co-infection in 15/48 captures and HGE was found alone in 1/48 and as a co-infection in 10/48 captures. These data are striking in several respects. First, *B. microti* infection is present alone in one third of the samples, and in combination with other pathogens in nearly another third. *B. burgdorferi* and the agent of HGE are rarely found alone in any mouse and were never found together in the absence of *B. microti*. Analysis of *Peromyscus*-derived ticks showed infection rates of 45%, 10%, and 29% for *B. burgdorferi*, *B. microti*, and HGE, respectively as well as co-infections with every combination of these organisms. Finally, co-infection with all three pathogens did occur in at least 4% of captured mice and 7% of mouse-derived ticks. In conclusion, co-infection appears to play an important role in the zoonotic cycles of *Ixodes*-borne pathogens on Long Island.

In addition to the above, we have been evaluating host-targeted application of the acaricide permethrin to *P. leucopus* and other rodents to reduce tick populations since 1995. In these studies animals are treated during peak abundance of subadult ticks during the first summer and the efficacy measured by collection of free ranging ticks the following summer. While mechanical sprayers that delivered a single calibrated dose onto animals significantly reduced tick densities their cost for general use was prohibitive. Currently we are evaluating the use of commercially available bait boxes modified to passively apply liquid acaricides. This efficacy study is supported in part by a Cooperative Agreement from the Centers for Disease Control.

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#### **Microsatellite variation in deer mice**

In order to gain insight into the relationships between observed variation and genetic distance of population substructure it is essential to understand the mutational process. Most of the current estimates of these relationships were developed based on interpretations of allozymes and mitochondrial DNA (mtDNA sequence data). In allozymes most new mutations give rise to new distinguishable alleles, but evolution of these non-neutral markers is not rapid. In mtDNA the evolution is more rapid, but limitations exist because of its haploid nature and maternal inheritance. Developments in molecular genetics now enable analysis of characteristics that provide improved sensitivity in detecting and assessing genetic variation. Microsatellites as a method of analyzing genomic variation within and among species is considered superior to these other techniques not only because of its diploid characteristics and high mutation rate of 10<sup>3</sup> and 10<sup>5</sup> mutations per gamete, but they have the potential to be 60-90% polymorphic across subpopulations. Since microsatellites combine extensive hypervariability with somatic stability and a co-dominant inheritance pattern they are considered ideal genetic markers, including for the deer mouse. The deer mouse, *Peromyscus maniculatus*, has been, and continues to be one of the most important sentinel species for studies of ecology, environmental toxicology, epidemiology, adaptation, and population dynamics. Critical to the use of deer mice for each of these endeavors is a thorough understanding of the genetic variation throughout the species. The availability of these microsatellite markers should have a substantial impact on both applied and basic studies employing this species.

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**Evidence of multiple colonization of eastern North America by long-tailed  
*Peromyscus maniculatus* since the Wisconsin Ice Age.**

A study of electrophoretic variation in enzymes of long-tailed forms of the deer mouse, *Peromyscus maniculatus*, in eastern North America, revealed that the present geographic distribution of these in Michigan apparently is the result of at least two colonization since the Pleistocene Epoch. Samples of these forms to the west of Michigan were nearly fixed for the "b" allele of aspartate aminotransferase-1 (AAT-1; also know as, glutamate oxaloacetate transaminase-1, GOT-1), whereas the "c" allele was infrequent or absent. In contrast, Michigan, southeastern Ontario, and eastward at all latitudes the b allele of AAT-1 varies from 0-78% in frequency, and the c allele from 22-100%. The distribution of AAT-1 allele frequencies in the eastern (Appalachian) region indicates that following the Pleistocene there first was a northward expansion of long-tailed *P. maniculatus* that had resided in the southern Appalachians during the Wisconsin Ice Age; initially this population likely was fixed for the c allele of AAT-1. Independently, long-tailed deer mice inhabiting the Mississippi River valley area expanded northward, and also at a time subsequent to the initial expansion in the east. Subsequent expansion of the western population in the east extended at least as far south as western Tennessee, and at least as far north as southern Ontario, southern Quebec, the Gaspé Peninsula, and New Brunswick; population farther north do not possess the b allele, nor does a sample from western Virginia, in the extreme eastern region of the Appalachian. It is not known whether the western population is continuing to expand in eastern North America.

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### **Recuperation of *Peromyscus pseudocrinitus* population by eradication of feral cats**

Due to the presence of feral cats on many islands in the Gulf of California, Mexico, we visited Coronados Island in 1995. We made an evaluation of the populations of endemic rodents present on Coronados Island that have lower densities (*Peromyscus pseudocrinitus*, *Chaetodipus spinatus pullus*, *Neotoma bunkerii*). (Arnaud and Troyo, 1995)

With this information, we implemented an eradication program for the feral cats present on the island in 1998-1999. Our objectives are recovery and conservation of the native populations of rodents, reptiles and birds. During the eradication program, we also carried out a census of the populations of rodents in order to observe their eventual recovery due to the absence of their main predator.

The eradication program is part of a conservation project of natural resources in the islands of the Gulf of California, developed by the Center for Biological Research of the Northwest (CIBNOR) with support from the National Commission for the Knowledge and Use of the Biodiversity (CONABIO) and the Loreto Bay National Park.

For estimating the rodent populations, we used 4,482 Sherman traps in three different habitats: xerophyllous shrub, halophyte vegetation and volcanic rocky soils. There have been 225 mice trapped thus far of which 67 percent is *Chaetodipus spinatus pullus* and 33 percent is *Peromyscus pseudocrinitus*. *Neotoma bunkerii* was not captured and we assumed is extinguished.

In the trap sessions developed in June and October of 1998, and January and May of 1999, an increment increase of populations densities was observed in *Peromyscus* and *Chaetodipus*. This corresponds to the decrease and total eradication of feral cats from the island. We could affirm that their recovery was possible. The census of the populations of rodents will continue during the year 2000.

On the other hand, there are islands in the Gulf of California with eleven species and twenty-three sub-species of endemic mammals (Hall, 1981) where the presence of feral cats could threaten those rodents. (Rodríguez-Moreno, 1997) For this reason, we have an eradication program of feral cats on these islands to guarantee the survival and recovery of these populations.

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### **Analysis of blood-feeding ectoparasites as a possible mode of transmission for Sin Nombre Virus among *Peromyscus maniculatus* at Orange County, California**

Four distinct groups of hantaviruses have been identified through serological and epidemiological studies, one of which has been identified as Sin Nombre Virus (SNV). *Peromyscus maniculatus* (deer mice) are the primary reservoir for SNV and does not appear to cause illness to the host (CDC 1993; LeDuc 1987, Nichol et al. 1993; Glass et al. 1990; Pether 1994). This research is currently conducted in association with the Orange County Vector Control District (OCVCD) to help identify any correlation(s) between blood-feeding ectoparasites on *P. maniculatus* that are seropositive and negative for the virus. Based on the study conducted by Bennett et al. (1999), the hypothesis to be tested will be that SNV antibody positive deer mice will have a greater density of blood-sucking ectoparasites than non-infected mice. *P. maniculatus* used for this project were trapped for previous studies by OCVCD from March 1995 to 1999 from Newport Coast in Orange County, California. A total of 387 mice will be examined. Currently, 79 ticks, 180 lice, 71 mesostigmatid mites, and 82 fleas have been collected. This project will focus on increasing the data available for blood-feeding ectoparasites as a possible mode of transmission for hantavirus within a rodent population.

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**Demographic response of white-footed mice, *Peromyscus leucopus*, in a forest and adjacent secondary successional habitat**

A series of demographic characteristics of white-footed mice, *Peromyscus leucopus* were examined in two habitats: a forest and an adjacent 14-year old experimental fragmentation site in northeastern Kansas. *P. leucopus* colonized the fragmented habitat in 1994 and this study describes the demographic differences between the adjacent forest and the recently colonized fragmented habitat. Habitat preference and fitness differences were measured with a series of demographic characteristics, such as longevity, proportion of adults, proportion of breeding adults, population density, and movement patterns between habitats. The forest habitat appears to be superior to the fragmented habitat by all measures. *P. leucopus* in the fragmentation area had lower population densities, a higher proportion of non-adults, lower adult mass, shorter persistence among resident adult females combined with fewer bouts of reproduction. In addition fragmented adult males were less likely to be scrotal, and adult mice moved to the forest. White-footed mice living in the forest are more likely to be long-lived adults who reproduce more than once in their life and do not leave the forest. Forest *P. leucopus* had higher proportions of adults in the population in all years. Resident females in the forest lived significantly longer than resident females in the fragmentation area and these females also persisted longer than forest males. Transient forest mice are typically adult males, whereas transient mice in the fragmented habitat mice are predominantly pre-reproductive. Based on the patterns of movement and demography, white-footed mice living in the fragmented habitat may be excluded from the preferred forest habitat by dominant forest individuals.

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Most of the information listed in the *PN* Index will be edited, updated and inserted into *PeroBase*. Therefore, tables of gene lists, molecular sequences, etc. will appear less frequently in *PEROMYSCUS NEWSLETTER* consistent with the policy announced in our last issue (#26).