# ASM 2004: CHANGES TO THE FINAL PROGRAM

## CANCELLATIONS

- **65.** EVOLUTION WITHIN THE BARE-BACKED FRUIT BATS, *DOBSONIA* (PTEROPODIDAE). DG Byrnes. (Tech 3: Gen-Evol 1)
- **104.** EFFECTS OF SITE FAMILIARITY ON MOVEMENT PATTERNS OF BRUSH MICE (*PEROMYSCUS BOYLII*). KE Mabry & M Breuer. (Poster 1)
- **116.** VARIATION IN MOVEMENT PATTERNS: IMPLICATIONS FOR ANALYSIS OF HABITAT SELECTION IN BIGHORN SHEEP. LK Svancara, JL Rachlow & EF Cassirer. (Poster 1)
- **184.** TAXONOMIC, FUNCTIONAL, AND BIOGEOGRAPHIC PERSPECTIVES ON THE COMMUNITY ECOLOGY OF BATS FROM THE SEMIARID TROPICS. MR Willig and RD Stevens. (Tech 6: Com Ecol 4)
- **254**. THE IMPLICATIONS OF PELVIC DIMORPHISM IN THE CARNIVORA. Heidi Schutz. (Poster 1)
- **281.** GENETIC MATERNAL EFFECTSANDTHE POTENTIAL FOR INTERNALLY DRIVEN POPULATION CYCLES. AG McAdam.(Tech 7: Pop Ecol 3)
- **288.** MICROCLIMATIC CHARACTERISTICS OF ENDANGERED MT. GRAHAM RED SQUIRREL MIDDENS AND THEIR EFFECT ON CONE STORAGE. MA Yurenka and JL Koprowski. (Tech 7: Pop Ecol 3)—**Replaced by talk 15**
- **301.** MOLECULAR ECOTOXICOLOGY AND THE DISCOVERY THAT *APODEMUS SYLVATICUS* IS COMPOSED OF AT LEAST TWO WIDE SPREAD SPECIES. YV Dunina-Barkovskaya, JK Wickliffe, BE Rodgers, CJ Phillips, RK Chesser, M Asakawa, S Gaschak & RJ. Baker (Tech 8: Gen-Evol 3).
- **329.** DISTRIBUTION AND PREVALENCE OF FACIAL TUMOR DISEASE IN TASMANIAN DEVILS. M Restani & N Mooney. (Tech 10: Conservation 5)
- **332.** COUGAR-HUMAN INTERACTIONS: MOVEMENT PATTERNS AND BEHAVIOR ALONG THE URBAN-WILDLAND INTERFACE. ML Wolfe & DC Stoner. (Tech 10: Conservation 5)

## TIME CHANGES

- ***Talk 15*** "SPACE USE AND SOCIAL ORGANIZATION OF ENDANGERED MT. GRAHAM RED SQUIRRELS: IT'S LONELY AT THE TOP. John L Koprowski and Sarah R King. Wildlife and Fisheries Science School of Natural Resources University of Arizona Tucson, AZ, USA" **has been switched to *slot 288*: 5:15 pm, Tuesday, June 14th,** Technical Session 7 (Pop Ecol 3).
- ***Slot* 15 has been filled by *Talk* 360 "**MOUNTAIN LION ACTIVITY AND MOVEMENT PATTERNS RELATIVE TO HUMAN ACTIVITIES IN THE REDWOOD CREEK BASIN OF NORTHWEST CALIFORNIA. J Ellingson, H Quigley, RT Golightly, CW Meinke and T Hofstra (full abstract below).
- ***Talk* 36.** "REDUCED MTDNA DIVERSITY IN ENDEMIC PHILIPPINE FRUIT BATS ON SMALL, ISOLATED ISLANDS. Trina E Roberts. Committee on Evolutionary Biology University of Chicago Chicago, IL , Field Museum of Natural History Chicago, IL" **has been moved to 8:45am, Tuesday, June 15th,** Technical Session 6 (Sys/Zoog 3).
- ***Talk 87.*** "CO-OCCURRENCE OF BAT FLIES ON NEOTROPICAL BATS: A NULL MODEL ANALYSIS. Carl W Dick . Department of Biological Sciences, Texas Tech University Lubbock, TX, USA **has been moved to 8:00 am, Tuesday, June 15th,** Technical Session 6 (Com Ecol 4). ***This is slot 178***. There is no longer a no. 87 in Poster Session 1.
- **No. 178 is a poster in Poster Session 2:** THE TINY GIANT: DISJUNCTION IN EVOLUTIONARY SIZE CHANGE OF A CENTRAL AMERICAN SHREW. N Woodman. USGS Patuxent Wildlife Research Center, National Museum of Natural History.
- ***Talk 306*** "POPULATION GENETICS OF *NEOTOMA MICROPUS* IN SOUTH TEXAS. Francisca M Mendez-Harclerode , John D Hanson , Charles F Fulhorst and Robert D Bradley" **moved to 4:30 pm, Monday, June 14th, Technical Session 5** (Gen-/Evol 2).
- ***Talk 309*** "TAXONOMIC STATUS OF THE GENUS *STURNIRA* (CHIROPTERA: PHYLLOSTOMIDAE) IN VENEZUELA. Cornelio Sánchez-Hernández, M. Lourdes, Romero-Almaraz and José Antonio Guerrero-Enríquez. **has been moved to Sunday, June 13th, *Poster Session 1*.**

## ADDITIONS

### 360.

***9:45am June 16th--Kate Buchanan Rm. (Tech. Sess. 9: Genetics/Evolution 3)***

**DEVELOPMENT OF *PEROMYSCUS* GENOMICS.** Julie L Weston[1], Clifton M Ramsdell[1], Stephanie C Napier[1], Rebecca Bullard-Dillard[2], Chantal Braithwaite[2], Hermes Exeter[2], Travis C Glenn[3], and Michael J Dewey[1]. [1]*Peromyscus* Genetic Stock Center, U of S Carolina, Columbia, SC; [2]Dept Biol, Claflin U, Orangeburg, SC; [3]Savannah River Ecology Lab, Aiken SC.

Aptly called “The Drosophila of North American Mammalogy”, peromyscines are considered to be an ideal genetic model for studying 1) the genes responsible for reproductive isolation and speciation, and 2) the genes enabling the physiological and behavioral adaptation to changing environmental conditions, adaptation to other species, adaptation to each other, and adaptation to microbial and other parasites. Full exploitation of the research potential of *Peromyscus* depends on the ability to define and analyze the genes involved in these processes. Therefore, our goal is to develop a linkage map with PCR-based markers of *P maniculatus* that will allow identification of candidate genes affecting particular traits of interest. Markers are being developed and mapped at sufficient density, ~5-10 cM, to permit identification of major genomic segments syntenic with the reference species, *Mus musculus*. Such markers consist of 1) Type I (protein coding genes), important for synteny identification, and 2) Type II (microsatellites), which are highly polymorphic and will ultimately be used for QTL analysis. Thus far, for Type I markers, about 1500 Expressed Sequence Tags (ESTs) from a placental cDNA library have been characterized (www.biol.sc.edu/~dewey/Peromyscus/EST.html) and over 100 microsatellites are available for the project. The linkage analysis panel was selected for maximizing utilizable polymorphism and is composed of interspecific meiotic segregants of crosses between the sister species *P m bairdii* and *P polionotus*. Results thus far have established substantial synteny between *Mus* chrm 11 and *Peromyscus* chrm 13. Furthermore, loci have been tentatively identified that reside in the region of chrm 13 inverted between *P m bairdii* and *P polionotus*.

## 360.

***11:15 am June 13th—Goodwin Forum (Tech. Sess. 1: Behavior 1) – This is slot 15 in your program***

**MOUNTAIN LION ACTIVITY AND MOVEMENT PATTERNS RELATIVE TO HUMAN ACTIVITIES IN THE REDWOOD CREEK BASIN OF NORTHWEST CALIFORNIA**. Jennifer Ellingson[1], Howard Quigley[2], Richard T Golightly[3], Cara W Meinke[3] and Terry Hofstra[4]. [1]Dept. of Wildlife and Fisheries Resources, University of Idaho, Moscow, ID; [2]Global Carnivore Program, Hornocker Wildlife Institute/WCS, Bozeman, MT; [3]Wildlife Dept., Humboldt State University, Arcata; [4]Redwood National and State Parks, Orick, CA.

Increases in mountain lion - human conflicts in the western United States have created a need for quantitative assessment of mountain lion (*Puma concolor*) activity and habitat selection at multiple scales. The potential of interactions between mountain lions and humans in Redwood National and State Parks (RNSP) was examined by quantifying mountain lion movements, activity levels, and habitat use patterns. Mountain lion movement and activity patterns were monitored to examine mountain lion-human interaction in and around RNSP from September 1998 to April 2001. Nine adult mountain lions were radio-collared and subsequently monitored to obtain 632 Euclidean distance movement events and 1368 activity readings; ten diel tracking sessions were also performed and analyzed to describe 24-hr movement and activity. Mean daily distance moved was greater for males than for females ($Z$ = 6.167, $P$ = 0.0001). Activity rates show a decline in activity during mid-day and an increase in activity around sunrise and sunset. There were no significant differences in movement ($P > Z$ = 0.1279) or activity ($P$ = 0.703) levels when examined by visitor and non-visitor seasons, indicating mountain lions are not affected by the influx of visitors (tourists) to the area. However, individual behaviors indicated mountain lions modify their behavior to avoid interaction with humans. We also tested the hypothesis mountain lions use RNSP habitats in proportion to availability through analysis of 259 mountain lion telemetry locations. Mountain lions do not use RNSP habitats in proportion to availability. Radio-collared mountain lions used south facing aspects (181-270$^{o}$) and moderate slopes (31-50$^{o}$) at mid-range elevations (401-600 m) more than expected. Mountain lions did not use habitats within 0-150 m of roads, trails, and human use areas in proportion to availability, while sites 0-150 m to streams were used more than expected. Mountain lions preferred the oak woodland habitats of the Bald Hills management area while avoiding coastal and old growth habitats.

## 361.

**4:00pm June 13th -- Kate Buchanan Rm (Tech Sess 3: Genetics/Evolution 1) - *This is slot 65 in your program***

**GENETIC AND MORPHOLOGICAL COMPARISONS OF CERVID SPECIES FROM THE YUCATAN PENINSULA.** Michael H. Smith[1], Crista Royal[2], Rick Purdue[3], James M. Novak[4], Taras Oleksyk[5], and Manuel Weber[6]. [1]Savannah River Ecology Laboratory, Aiken, SC; [2]Medical College of Georgia, Augusta, GA; [3]Illinois State Museum, Springfield, IL; [4]University of South Dakota, Vermillion SD; [5]Laboratory of Genomic Diversity, Frederick, MD; [6]ECOSUR, Campeche, MX.

Morphology and genetics of three species of cervids, *Mazama americana* (red brocket), *M. pandora* (Yucatan Peninsula brown brocket), and *Odocoileus virginianus* (white-tailed deer) were studied. There were significant differences among skulls of the three species and among sequences for cytochrome b and D-loop of mtDNA. There were significant differences among skulls calculated from a series of 43 landmarks located on the ventral surfaces of the skulls. The skull of the white-tailed deer was the most different from those of the other two species and most of the difference was due to size. Sequence data were also taken from GenBank for out groups and used with ours to construct phylogenetic trees. *M. americana* clustered more closely with *O. virginianus* than with *M. pandora* using D-loop data. The same was true for cytochrome b, but O *hemionus* was more distant from whitetails than were the brockets. The split between the two brockets is about as old as that between *Odocoileus* and *Mazama* based on these data.

## 362.

***June 13: Poster Session 1: University Center Depot***

**SUCCESS OF MOOSE HUNTERS: A NEW APPROACH FOR ASSESSING CPUE.** Jennifer Schmidt[1], Jay M. Ver Hoef[2], Julie A. K. Maier[1,] and R. Terry Bowyer[1,3]. [1]Institute of Arctic Biology and Department of Biology, University of Alaska Fairbanks, Fairbanks, AK; [2]Alaska Department of Fish and Game, 1300 College Road, Fairbanks, AK; [3]Department of Biological Sciences, Idaho State University, Pocatello, ID.

The relationship between hunters and their environment is a key component in managing wildlife populations. Characteristics, motivations, and effort by hunters are crucial to understanding whether a hunt will be successful. In addition to characteristics of hunters, we predicted that landscape characteristics and moose (*Alces alces*) densities would effect success of hunts. Modeling responses from harvest tickets returned by moose hunters in interior Alaska between 1997 and 2001 indicated that location of a hunt (Game Management Unit), mode of transportation, type of hunt (e.g., general, registered, draw, or Tier II), use of commercial services, year, density of roads, hunter to moose ratio, moose density, and residency of hunters were important predictors of success. In addition, we determined that a linear-regression approach to measuring catch per unit effort (CPUE) was inappropriate, because it produced and inverse relationship between hunting effort and success. This outcome occurred because of the nature of most hunts, particularly for many large mammals, where the harvesting of an animal ends the hunt. Likewise, modeling of hunter success with logistic regression similarly was biased by measures of hunter effort. Consequently, we used a time-to-event Weibull regression that provided a substantial improvement over standard models of CPUE. This model accurately illustrated the positive relationship between effort and success, and can be used to model length of hunt along with other covariates related to hunters and landscape characteristics for predicting success.