# AMERICAN SOCIETY OF MAMMALOGISTS

## 92<sup>nd</sup> ANNUAL MEETING

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**PROGRAM & ABSTRACTS** 

#### American Society of Mammalogists 92<sup>nd</sup> Annual Meeting—Reno, Nevada

**202 Technical Session 15: Genetics, Tuscany Ballroom 9, Tuesday 26 June 2012** <u>Jacob A. Esselstyn</u><sup>1,2</sup>, Anang S. Achmadi<sup>3</sup>, Maharadatunkamsi<sup>3</sup>, Cameron D. Siler<sup>4</sup>, Ben J. Evans<sup>1</sup> <sup>1</sup>Biology Department, McMaster University, Hamilton, Ontario Canada; <sup>2</sup>Field Museum of Natural History, Chicago, IL USA; <sup>3</sup>Museum Zoologicum Bogoriense, Cibinong, Bogor, Indonesia; <sup>4</sup>Biodiversity Institute, University of Kansas, Lawrence, KS USA

**Multilocus Species Delimitation Reveals Pleistocene Speciation in Javanese Shrews (Crocidura)** The shrews of Java Island, in Indonesia, have a tortuous taxonomic history involving small sample sizes, typographical errors, and a failure to designate type specimens. The most recent revision recognized only 3 species (*Crocidura brunnea*, *C. monticola*, and *C. orientalis*) among the 8 published names. We use recent collections from Java and sequences of 9 independently evolving loci to test these taxonomic hypotheses. Our results indicate that Javan *C. monticola* includes 2 closely related sister species, referable to *C. maxi* and *C. monticola*. Genetic data also support the recognition of *C. brunnea* and *C. orientalis*. In the tradition of naming shrews based on single specimens, we note evidence that a single specimen from West Java represents a 5<sup>th</sup> species endemic to the island. The speciation event that produced the sympatric *C. maxi* and *C. monticola* appears to have happened recently, around 200 Kya.

### 203 Technical Session 15: Genetics, Tuscany Ballroom 9, Tuesday 26 June 2012 Jorge Luis Pino<sup>1</sup>, Marina Ascunce<sup>1</sup>, David Reed<sup>1</sup>, Jean-Pierre Hugot<sup>2</sup>

<sup>1</sup>*Florida Museum of Natural History, University of Florida, Gainesville, FL 32611 USA;* <sup>2</sup>*Muséum National d'Histoire Naturelle, Origine, Structure et Evolution de la Biodiversité, Paris, France* 

### Microsatellite-DNA Evidence Population Structure in the Endangered Laotian Rock-Rat (*Laonastes* aenigmamus)

The Laotian rock rat, locally known as the kha-nyou (*Laonastes aenigmamus*), is considered a living fossil due the ancient divergence of its lineage within the order Rodentia. Although there is scarce information on the species boundaries, its distribution is mainly known from Southeast Asia, more specifically from a karstic region in Laos Republic. The affinity of *Laonastes* to karstic-uplifts suggests that its populations will show high population structure and potentially substantial genetic differentiation across their known distributional range. Here we developed and tested microsatellite markers *de novo*, and used microsatellite DNA variation to assess the population structure of *Laonastes* along a geographic range in Central Laos. We found evidence that indicates the presence of 3 major clusters or populations along the surveyed range and some degree of admixture among populations. These data are of importance for future explorations of the species boundaries. The microsatellite markers we developed offer a venue for studying demographic aspects of this threatened species.

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Karla Pelz Serrano<sup>1</sup>, Charles van Riper III<sup>2</sup>, David L. Bergman<sup>3</sup>, Melanie Culver<sup>4</sup>

<sup>1</sup>Departamento de Ciencias Ambientales, CBS Universidad Autonoma Metropolitana-Lerma, Lerma, Estado de México 52006 México; <sup>2</sup>USGS/SBSC/ Sonoran Desert Research Station, University of Arizona, Tucson, AZ 85721 USA; <sup>3</sup>USDA APHIS, Wildlife Services, Phoenix, AZ USA; <sup>4</sup>School of Natural Resources and the Environment, University of Arizona, Tucson, AZ 85721 USA

The Impact of Harvesting and Reintroductions on the Genetic Diversity of the American Beaver (*Castor canadensis*)

The American beaver is considered an ecosystem engineer due to the modification this mammal does to its environment. However, in the 1600's the beaver was also considered an important fur-trading item that resulted in the overexploitation and near eradication of the species in the late 1800's. By the beginning of the 20<sup>th</sup> century pelt traders and biologist conducted translocations and reintroductions to restore beaver populations. The purpose of this study was to assess if there was an impact of overexploitation and different management actions on the genetic diversity of the beaver in 7 areas across North America. We used 9 microsatellite loci to assess genetic diversity measures of 153 individuals from Alabama, Arizona, Maine, Minnesota, South Carolina, Texas, and Wisconsin. Our results show high genetic diversity (average observed heterozygosity was 0.613, and expected heterozygosity was 0.740), and high genetic differentiation (average  $F_{ST}$  =0.128, 95% CI from 0.093 to 0.182; average  $R_{ST}$  =0.199, P <0.001) across populations. No evidence of past population bottlenecks or isolation by distance could be detected.