Testimony of Dr. L. Scott Mills

House Resources Committee Meeting Regarding The National Lynx Survey

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(Representing myself and not any organization)

Mr. Chairman and Members of the House Resources Committee,

I thank the Committee for inviting me to testify before you today.

I am a Wildlife Biology Professor in the School of Forestry at The University of Montana. My research and teaching expertise centers on understanding the population dynamics of wildlife species; to this end my students and I use field studies, mathematical models, and genetic analyses to address questions in applied biology (see attached abbreviated Biographical Sketch).

In 1998, I began to collaborate on issues related to lynx surveys with Dr. Kevin McKelvey, the lead scientist who developed and implemented the National Lynx Survey for the US Forest Service. This is one of numerous productive collaborations that I have had with research scientists of the Forest Service and other state and federal agencies. My role in the collaboration was to identify to species the hair samples collected, using a DNA-based species identification protocol developed in my laboratory and subsequently peer-reviewed and published (see Mills et al. 2000, attached). The heart of this species identification protocol involves polymerase chain reaction (PCR) amplification of short (about 400 base pair) segments of mitochondrial DNA found in the hair samples. We next use restriction enzymes to produce species-specific fragments of DNA. These fragments are consistent across the range of a species and are not shared by other species. Hair samples can be amplified via PCR (allowing a species determination) in approximately 80% of the samples.

In developing this protocol we tested it using 95 known samples collected across the range of the species involved, to make sure, for example, that a lynx was always identified as a lynx, a bobcat as a bobcat, and so on. Before the protocol was published or instituted as a diagnostic tool in the National Lynx

Survey we also instituted extensive blind tests -- whereby the technician performing the analysis did not know the identity of the sample –on a total of 87 samples both within our lab and at an external lab (USFWS National Fish and Wildlife Forensics Laboratory in Ashland, Oregon). Species identification was correct in all 95 geographic range tests and all 87 blind tests. We continue to obtain known samples to validate this and other species-identification protocols we have developed: to date we have analyzed 465 known-species samples including 151 blind test samples. These validation controls have provided 465 chances for us to obtain the wrong species identity, yet no samples have been misidentified. Furthermore, we consistently detect lynx in geographic areas where they are known to occur.

In addition to the validation procedure, we have other appropriate laboratory controls to minimize the probability of inaccurate species identification via either false positives (calling the source of a sample lynx when it is not) or false negatives (calling the source of a sample a species other than lynx when it is actually a lynx). Every set of samples we analyze includes “positive controls” to ensure that test conditions are appropriate for species identification and “negative controls” (pure water) to detect contamination. We also extract DNA from hairs in a separate building from where other laboratory activities occur to control against contamination.

We consulted extensively with the USFWS Forensics lab concerning preserving the chain-of-evidence associated with forensic samples. Records of all of the gels we have run are kept in lab books, all of the extracted DNA samples are preserved in 20-below-zero freezers, and all hair samples are held in sealed, dessicant-filled vials in locked cabinets in the hair extraction lab. If there are any issues associated with a specific sample, we can readily access the DNA analyses, extracted DNA, and the original hair sample.

The National Lynx Survey has relied on field personnel in 12 states to follow pre-defined, detailed, rigorous instructions developed by Dr. McKelvey and me to guide all aspects of initiating the survey, collecting the data, and sending us the samples. The mislabeling of National Lynx Survey samples by a few field personnel was wrong, and cannot be defended on any scientific merit (see correspondence items by Mills and by Buskirk on page 471 of the Jan. 31 issue of Nature).

That said, I believe that the National Lynx Survey retains integrity to inform land management and to provide credible scientific insights on lynx distribution. Although the mislabeled samples could have led us to report 3 false lynx detections, and the few mislabeled samples have created problems for perception of the project as a whole, two important components built into this study provide a firewall that protects the integrity of the study for evaluating lynx distribution. First, the lead scientists (McKelvey and I) are population biologists whose training would lead us to interpret the results appropriately to the scientific community and to management. Although mislabeled samples could have led us to report false lynx detections on 2 National Forests, we would have simultaneously noted that *a detection is not the same as a population*.

Secondly, and most importantly, the hair collection in the National Lynx Survey was only the first step in evaluating lynx presence. As I am sure Dr. McKelvey will describe, follow-up snow tracking and trapping efforts are built into the study to separate actual lynx populations from transient individuals, fur farm escapees, or (as we have learned) mislabeled samples.

Therefore, I do not believe that the scientific validity of this study to contribute to land-management decisionmaking was compromised by the mislabeling of samples.

Finally, the question arises as to the motivation of those who mislabeled samples. I do not know those individuals, nor do I know their motivations. My experience throughout my career in working with hundreds of biologists and field personnel -- including employees of USFWS, USFS, NPS, state Wildlife Departments, private groups, and several Universities – is that they have exceptionally high ethical standards in their pursuit of knowledge. Although inappropriate actions may occur on an individual and rare basis, my opinion is that these instances do not invalidate the larger body of biology, in the same way that inappropriate actions by a few physicians does not mean that we should shut down the practice of medicine.

In summary, I believe those few who mislabeled samples have no legitimate excuse for their actions. However, I also believe that their actions should not compromise the role of biological studies in policy decisionmaking. I hope that the actions of these few do not taint the excellent work of biologists across this country, who strive toward the highest ethical standards as they carry out a public mandate to understand the critical needs of wildlife species.

L. SCOTT MILLS ABBREVIATED BIOGRAPHICAL SKETCH

PROFESSIONAL PREPARATION and ACADEMIC APPOINTMENTS

North Carolina State University, Raleigh	B. S., Zoology	May 1983
Utah State University, Logan	M. S., Wildlife Ecology	July 1987
University of California, Santa Cruz	Ph. D., Biology	July 1993

ASSOCIATE PROFESSOR; Wildlife Biology Program, School of Forestry, University of Montana (Since Sept. 1999), ASSISTANT PROFESSOR (June 1995-Sept. 1999): research and teaching emphasis on population ecology.

VISITING ASSISTANT PROFESSOR/Post-Doctoral Fellow Fisheries & Wildlife Department, University of Idaho. Aug. 1993-May 1995

B. SELECTED JOURNAL PUBLICATIONS [Past 3 Years]

Schwartz, M.K., L.S. Mills, K.S. McKelvey, L.F. Ruggiero, and F.W. Allendorf. 2002. DNA reveals high dispersal synchronizing the population dynamics of Canada lynx. Nature 415:520-522.

Mills, L. S. 2002. False samples are not the same as blind controls. Nature 415:471.

Biek, R., W. C. Funk, B. A. Maxell, and L. S. Mills. In Press. Amphibian Population Declines: Insights from Ecological Sensitivity Analysis. Conservation Biology.

Tallmon, D. A., H. M. Draheim, L. S. Mills, and F. W. Allendorf. In Press. Ecological insights into fragmented vole populations from combined genetic and demographic data. Molecular Ecology.

Hoekman, S. T., L. S. Mills, D. W. Howerter, J. H. Devries, and I. J. Ball. In Press. Sensitivity analysis of the life cycle of mid-continent mallards. Journal of Wildlife Management.

Biek, R., L. S. Mills, and B. Bury. Salamander responses to forest edges. In Press. Northwest Science.

Reed, J. M., L. S. Mills, P. Miller, K. S. McKelvey, E. S. Menges, R. Frye, J. B. Dunning, Fr., S. R. Beissinger, and M-C Anstett. In Press. Use and emerging issues in population viability analysis. Invited Paper, Conservation Biology.

Mills, L. S., K. L. Pilgrim, M. K. Schwartz, and K. McKelvey. 2000. Identifying lynx and other North American felids based on mtDNA analysis. Conservation Genetics 1:285-288.

Mills, L. S., D. F. Doak, and M. J. Wisdom. 2000. Elasticity analysis for conservation decision-making: Reply to Ehrlen et al. Conservation Biology 15:281-283.

Mills, L. S., J. J. Citta, K. Lair, M. Schwartz, D. Tallmon. 2000. Estimating animal abundance using non-invasive DNA sampling: Promise and Pitfalls. Ecological Applications 10:283-294.

Wisdom, M. J., L. S. Mills, and D. F. Doak. 2000. Life-stage simulation analysis: estimating vital rate effects on population growth for conservation. Ecology 81:628-641.

Mills, L. S., D. F. Doak, and M. J. Wisdom. 1999. The reliability of conservation actions based on sensitivity analysis of matrix models. Conservation Biology 13:815-829.

Jules, E., E. Frost, D. Tallmon, and L. S. Mills. 1999. Ecological consequences of forest fragmentation in the Klamath region. Natural Areas Journal 19:368-378.

Citta, J. J., and L. S. Mills. 1999. What do demographic sensitivity analyses tell us about controlling brown-headed cowbirds? Studies in Avian Biology 18:121-134.

Soulé, M. E., and L. S. Mills. 1998. No need to Isolate Genetics. Science 282:1658-1659.

C. SELECTED OTHER PUBLICATIONS [Past 3 Years]

Mills, L. S., M. K. Schwartz, D. A. Tallmon, and K. P. Lair. In Press. Measuring and interpreting changes in connectivity for mammals in coniferous forests. Editors C. Zabel and R. Anthony. Conservation of mammals in western coniferous forests.

Mills, L. S., and M. Lindberg. In Press. Sensitivity Analysis to Evaluate the Consequences of Conservation Actions. S. R. Beissinger and D. R. McCullough, editors. Population Viability Analysis. University of Chicago Press.

Mills, L. S. In Press. Genetics, Demography, and Viability of Fragmented Populations (Book Review). Quarterly Review of Biology.

Mills, L. S., and D. Tallmon. 1999. Genetic issues in forest fragmentation. In Forest Fragmentation: Wildlife and Management Implications. J. Rochelle, L. A. Lehmann, and J. Wisniewski, eds. Brill Publishers (Netherlands).

Dobson, A., K. Ralls, M. Foster, M. E. Soule, D. Simberloff, D. Doak, J. A. Estes, L. S. Mills, D. Mattson, R. Dirzo, H. Arita, S. Ryan, E. A. Norse, R. F. Noss, and D. Johns. 1999. Connectivity: maintaining flows in fragmented landscapes. Pages 129-171 In Soulé, M. E. and J. Terborgh, editors. Continental Conservation: Scientific Foundations of Regional Reserve Networks. Island Press.

Groom, M., D. B. Jensen, R. L. Knight, S. Gatewood, L. Mills, D. Boyd-Heger, L. S. Mills, and M. E. Soule. 1999. Buffer zones: benefits and dangers of compatible stewardship. Pages 191-198 In Soulé, M. E. and J. Terborgh, editors. Continental Conservation: Scientific Foundations of Regional Reserve Networks. Island Press.

D. SELECTED SYNERGISTIC ACTIVITIES

- Co-PI for Wildlife response portion (Montana) of $1.1 million grant from the Joint Fire Sciences Program to investigate response to fire and thinning. The study is occurring at 14 sites across the US. At each site, there are PI’s for wildlife, soils, insects/disease, and silviculture. June 2000 – 2005.
- 1997-98 “Most Inspirational Professor” at University of Montana.
- Collaborator with USDA Rocky Mountain Research Station in development and application of methods in conservation genetics for carnivore conservation. 1998-present.
- Mentor/Advisor: I strongly believe in involving undergraduate students in research. In the last 5 years I have mentored 18 students on Honors or Senior Thesis projects. Eleven of these students have received University research awards totaling $24,850.

E. MAJOR GRANTS (Past 3 years)

- Mills, L. S. Genetic Analysis of lynx and other mammals. National Park Service.
- Goodburn, J. M., and L. S. Mills. Calibrating models of landscape models of spatially structured snowshoe hare populations. U.S.D.A. McIntire-Stennis.
- Mills, L. S. Effects of precommercial thinning on snowshoe hare abundance. Plum Creek Timber Co.
- Kukuk, P., L. S. Mills, and F. Allendorf. Acquisition of instrumentation for research in evolutionary and conservation genetics. National Science Foundation.

- Mills, L. S. Comparison of pellets to hare densities. USDA Rocky Mountain Research Station.
- Mills, L. S. Supplemental Funding to support Undergraduate Research. National Science Foundation.
- Mills, L. S., and R. Redmond. Highways as potential barriers to movement and genetic exchange in small vertebrates. Montana Department of Transportation.
- Mills, L. S. Snowshoe hares and lynx in a fragmented landscape: merging demographic and genetic approaches. National Science Foundation CAREER grant.
- Mills, L. S. Quantifying an ecosystem perturbation: forests, mycorrhizae, and red-backed voles. USDA Competitive Grants Program.
- Mills, L. S. and S. Cox. Dispersal and metapopulation dynamics of Olympic marmots. EPA STAR Fellowship Program.