

Assessing the Taxonomic Status of the Red Wolf and the Mexican Gray Wolf

Committee

Joseph Travis

Chair

Joseph Travis is the Robert O. Lawton Distinguished Professor of Biological Science at Florida State University. Dr. Travis' research and expertise is on understanding the interplay between ecological processes and how these processes influence population variation in animal and plant phenotypes and density. His current work focuses on the ecology and evolution of livebearing fishes such as guppies and mosquitofish, and how demography (location of habitat) results in unique, localized traits. Dr. Travis began his career at Florida State as an assistant professor in 1980 and was promoted through the ranks, eventually serving as Department Chair (1991-1997) and Dean of the College of Arts & Sciences (2005-2011). He teaches the undergraduate course in evolution for majors in biological science and a graduate course in population ecology. He has served on the editorial boards of the Journal of Evolutionary Biology, Oecologia, Annual Review of Ecology and Systematics, and The American Naturalist, and served as editor of The American Naturalist from 1998 to 2002. Dr. Travis served as Vice-President (1994) and President (2005) of the American Society of Naturalists and is currently serving as President of the American Institute of Biological Sciences. He has also served on advisory boards for the National Science Foundation, the National Oceanic and Atmospheric Administration, and on the National Academies committee on the responsible conduct of gene drive research and practice. Dr. Travis was a member of the National Academies Committee on Gene Drive Research in Non-Human Organisms: Recommendations for Responsible Conduct (2015 to 2018). He is a fellow of the American Association for the Advancement of Science and the American Academy of Arts & Sciences. He received his undergraduate degree from the University of Pennsylvania and his doctoral degree from Duke University.

Fred W. Allendorf

Member

Fred Allendorf is a Regents Professor Emeritus of Biology at the University of Montana. He was a Professorial Research Fellow at Victoria University of Wellington (New Zealand, 2005-2012). He is an evolutionary geneticist who has spent much of his career applying the theory and molecular techniques of population genetics to problems in conservation. Much of his work in evolutionary genetics has been devoted to understanding the genetics of salmonid fishes following a whole genome duplication event (tetraploidy). He was a postdoctoral scholar at the University of Aarhus in Denmark, and a NATO Fellow at Nottingham University in England. He was Program Director of Population Biology at the National Science Foundation in 1989-1990, a Senior Fulbright Fellow in New Zealand in 2000-2001, and a Senior Fulbright Specialist at the University of Western Australia in 2013. He was elected Fellow of the AAAS in 1987, elected President of the American Genetic Association in 1997, and has served on the editorial boards of several international journals (e.g., *Evolution*, *Conservation Genetics*, *Molecular Ecology*, and *Conservation Biology*). From 1992-1996, Dr. Allendorf served on the NRC Committee on the Protection and Management of Pacific Northwest Anadromous Salmonids, which reviewed information concerning the seven species of the genus *Oncorhynchus* in the Pacific Northwest. He received the American Fisheries Society's Award of Excellence in recognition of his outstanding contributions to fisheries science and aquatic biology in 2011, and the Molecular Ecology Prize for lifetime achievements in the fields of molecular ecology and conservation genetics in 2015. He received a B.S. in zoology from Penn State University, and his M.S. and Ph.D. in fisheries and genetics from the University of Washington.

Diane K. Boyd

Member

Diane K. Boyd is the Wolf and Carnivore Specialist at Montana Fish, Wildlife & Parks in Kalispell, Montana. Dr. Boyd has more than four decades of expertise on behavior and conservation of vertebrates, with a focus on wild wolf populations. She began her career in 1977 with Dr L. David Mech. Since then, she has conducted and collaborated on research on wild wolf populations in four countries. She moved to Montana in 1979 to study gray wolf recovery in the Rocky Mountains, and followed the population growth from 1 wolf to 2000 wolves at present in Montana, Idaho, and Wyoming. She has also collaborated on wolf behavior and conservation research in Minnesota, Montana, Michigan, Arizona, New Mexico, British Columbia, Alberta, Italy, Romania, and Ellesmere Island. From 1997 to 1998, she worked for the Mexican Gray Wolf Recovery Program. Dr. Boyd received her B.S. in wildlife management from the University of Minnesota, St. Paul, and her M.S. in wildlife biology and Ph.D. in fish and wildlife biology from the University of Montana, Missoula.

Liliana Cortes Ortiz

Member

Liliana Cortés Ortiz is a Research Associate Professor in the Department of Ecology and Evolutionary Biology at the University of Michigan. Before starting her career at the University of Michigan she was a Professor at the Universidad Veracruzana in Mexico. She serves as Vice President for the Neotropics of the Primate Specialist Group of the International Union for Conservation of Nature. Dr. Cortés Ortiz's research focuses on the evolution and systematics of Neotropical primates. She uses molecular genetics and genomics approaches to address questions related to the diversification of Neotropical primates and the implications of natural hybridization in the origin and maintenance of primate diversity. Her work ranges from field-based data and sample collection to laboratory-based genetic work, and integrates different disciplines such as phylogenetics and systematics, biogeography, morphology, behavioral ecology, and genomics to provide an integral framework to examine primate evolution. Some of this work is implemented in collaboration with scientists in Latin America, England, and the United States. Dr. Cortés Ortiz received a B.Sc. in Biology from the Universidad Veracruzana in Mexico, a M.Sc. in Neuroethology also from the Universidad Veracruzana, and a Ph.D. in Biological Sciences from the University of East Anglia in England.

Lori S. Eggert

Member

Lori S. Eggert is a professor in the Division of Biological Sciences of the University of Missouri-Columbia. She and her students use genetic and genomic methods to address basic and applied questions in ecology, evolution, and conservation biology. At the historical level, studies in her lab use molecular data to determine the patterns of diversity within and among closely related species. By mapping those patterns onto the geographic distribution of species, she seeks to understand the relative roles of evolutionary processes such as geographic isolation, gene flow, natural selection, and genetic drift on patterns of speciation. Current projects include a study of the taxonomic distinctiveness and distribution of species and subspecies of smallmouth bass in the Central Interior Highlands of the United States. At the contemporary level, landscape genetic studies in her lab use molecular data to understand the role of environmental variables on the current distribution of and diversity within species. Current projects include a study of population sizes, sex ratios and connectivity of Asian elephants in Laos. Her research has involved a wide variety of taxa, including mammals, amphibians, birds, and fish, focusing primarily on species of conservation concern. Previously, Dr. Eggert had been a research and postdoctoral associate at the Smithsonian Institution National Museum of Natural History in Washington, DC. Dr. Eggert was a member of the NRC Committee on the Review of Land Management (BLM) Wild Horse and Burro Management Program from 2011 to 2013. She received her B.S. in biology from the University of California, San Diego, her M.S. in ecology from San Diego State University and her Ph.D. in biology from the University of California, San Diego.

Diane P. Genereux

Member

Diane P. Genereux is a research scientist in Vertebrate Genomic Biology at the Broad Institute of MIT and Harvard. She develops mathematical and statistical methods to address questions in population genetics, epigenetics, and genomics. She is the scientific manager of the 200 Mammals Project, an international collaboration that is using comparative genomics to identify genomic variants that underlie human disease. Her earlier work uncovered population genetic factors that shape the global distribution of fragile X syndrome, and yielded new approaches to track epigenetic stability and change across mammalian development. She has also contributed to identification of genetic variants associated with canine-compulsive disorder in pet dogs. She is currently collaborating on a project comparing epigenetic and behavioral data from dog and wolf pups, with the goal of identifying genes and pathways associated with social development. Dr. Genereux has taught undergraduate courses in evolution, genetics, epigenetics, molecular biology, and mathematical modeling, and has written about genomic approaches in several undergraduate and medical textbooks, and in the popular literature. She received her B.A. in history and biology from Brown University in 1999, and her Ph.D. in mathematical genetics from Emory University in 2005.

Michael Lynch

Member

Michael Lynch is the Director of the Biodesign Center for Mechanisms of Evolution, Arizona State University. His research interests focus on the genetic mechanisms of evolution, particularly at the genomic and cellular levels, and on the development of methods for population-genomic analysis. The lab focuses on a number of model systems, most notably the microcrustacean *Daphnia*, the ciliate *Paramecium*, and numerous other unicellular prokaryotic and eukaryotic species. Current research foci are: the 5000 *Daphnia* genomes project; the evolution of replication and transcription error rates; the consequences of genome duplication; the evolution of the transcriptional vocabulary; the evolution of multimeric protein structure; and long-term microbial evolution under regimes differing in population size, mutation rate, and degree of nutrient replenishment. All of this work is integrated with theory development. He has previously held faculty positions at the University of Illinois, University of Oregon, and Indiana University. He is a member of the US National Academy of Sciences, and of the American Academy of Arts and Sciences; and is past president of the Genetics Society of America, the Society for the Study of Evolution, the Society for Molecular Biology and Evolution, and the American Genetics Association. Dr. Lynch was a member of the NRC Committee on Scientific Issues in the Endangered Species Act (1993 to 1995) and the Ecosystems Panel (1997 to 2000). Three widely cited books that he authored are *Genetics and Analysis of Quantitative Traits* (with Bruce Walsh, 1998), *The Origins of Genome Complexity* (2007), and *Evolution and Selection of Quantitative Traits* (with Bruce Walsh, 2018). He received his undergraduate degree in biology from St. Bonaventure University, and a Ph. D. in ecology and behavioral biology from the University of Minnesota.

Jesus E. Maldonado

Member

Jesus E. Maldonado has been a research geneticist at the Center for Conservation Genomics at the Smithsonian Conservation Biology Institute since 1998. His research applies molecular genetics tools to answer basic and applied questions in conservation and evolutionary biology in mammals. Much of his research involves assessment of genetic variation within and among populations and species to document levels of inbreeding and determine units of evolutionary, taxonomic and conservation significance. He developed a research program that follows an academic model, and most of his projects over the past several years are based on collaborations established with students, postdoctoral fellows and research scientists/curators at the Smithsonian and other academic institutions and conservation communities in Latin American, India, South East Asia and Africa. This allowed him to build a strong conservation genomics program that is international in scope. Beyond theoretical aspects of his research, outcomes from many studies have direct applications to helping address critical conservation issues in a variety of threatened and endangered mammals. He is also interested in studying micro-evolutionary processes that shape genetic variation and evolutionary trajectories, as well as landscape genetics and genomics. During the past 19 years, he has developed and utilized non-invasive genetic techniques and ancient DNA technologies for obtaining reliable information to study many elusive endangered mammal species, such as deer, squirrels, black bear, island fox, maned wolves, African wild dogs, and sea otters among many other species. Maldonado has over 100 peer reviewed publications in scientific journals and has served in the editorial board of several journals including the Journal of Mammalogy, Conservation Genetics, PLoS ONE, Zookeys and Theria. He received his B.S. in biology and M.S. in zoology from Shippensburg University of Pennsylvania and Ph.D. in organismic biology, ecology and evolution from the University of California, Los Angeles.

Ramus Nielsen

Member

Rasmus Nielsen is the Raymond and Beverly Sackler Chair of Computational Biology at the University of California, Berkeley. He is a professor in the Department of Integrative Biology and in the Department of Statistics and has served as the chair of the Center of Computational Biology at UC Berkeley. He is also a professor at the Museum of Natural History at the University of Copenhagen. His work is on statistical and population genetic analyses of genomic data, in particular methods for describing population and species level processes such as migration and introgression, and for inferring natural selection and the demographic histories of populations. Much of his current research concerns statistical analysis of next-generation sequencing data in population genetics. Many of the methods he has developed have been used extensively by other researchers, including the phylogeny based methods for detecting positive selection implemented in phylogenetic analysis by maximum likelihood (PAML), the methods for inferring demographic histories implemented in the "Isolation with Migration" (IM) and IMa programs, the method for detecting selective sweeps implemented in SweepFinder, and the methods for analyzing Next Generation Sequencing (NGS) data implemented in Analysis of Next Generation Sequencing Data (ANGSD). He has published over 300 peer reviewed papers, invited book chapters, and review papers, which have been cited more than 50,000 times by other researchers. He received his M.S. from University of Copenhagen in 1994 and his PhD from UC Berkeley in 1998.

Keegan Sawyer

Staff Officer