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| Nota di contenuto | (1) Introduction on different applications of molecular tools to answer novel questions in the field of population genetics/genomics of endangered mammals (Mike Bruford, School of Biosciences, Cardiff University, UK) -- (2) Climate change impact at the genetic level: patterns in the Couesi's rice rat <i>Oryzomys couesi</i> (Ella Vázquez Domínguez, Instituto de Ecología, UNAM, Mexico) -- (3) Use of molecular and demographic data to prioritize populations of black-tailed prairie dogs (<i>Cynomys ludovicianus</i>) from Chihuahua, Mexico for conservation (Luis Eguiarte Fruns, Instituto de Ecología, UNAM, Mexico) |

-- (4) Anthropogenic and Historic Movements of American Black Bears Shape Contemporary Population Structure (Emily Puckett, Division of Molecular Sciences, University of Missouri, USA) -- (5) How many ESUs are of conservation interest within some species of Neotropical carnivores (Felidae, Canidae, Ursidae, Mustelidae and Procyonidae)? : Individual mitochondrial genes versus mitogenomics (Manuel Ruiz García, Departamento de Biología, Pontificia Universidad Javeriana, Spain) -- (6) Phylogeographic footprint of armadillo colonization in North America (María Clara Arteaga, Departamento de Biología de la Conservación, Mexico) -- (7) Koala conservation in Queensland: a role for a living genome bank in genetic rescue? (Jenny Seddon, School of Veterinary Science, The University of Queensland, Australia) -- (8) Noninvasive genetics sheds light on the status, phylogeography, and evolution of the most elusive carnivores: The case of the snow leopard (Jan Janecka, Department of Biological Sciences, Duquesne University, USA) -- (9) Documenting genetic diversity in changing populations for management and conservation (Jennifer Leonard, Conservation and Evolutionary Genetics, Estación Biológica de Doñana, Spain) -- (10) Conservation genetic of gray brocket deer (*Mazama gouazoubira*) in the southern of the distribution range (Susana González, Departamento de Biodiversidad y Genética, Universidad de Uruguay) -- (11) Noninvasive Genetic Monitoring of the Elusive European Wildcat as a Tool for Science-Based Wildlife Conservation (Katharina Steyer, Seckenberg Research Institute, Germany) -- (12) Conservation genetics in bats: current progress and future prospects (Serena Dool, University of Greifswald, Germany) -- (13) From dung to demography: Using noninvasive methods to study elephants inside and outside protected areas (Lori Eggert, Division of Biological Sciences, University of Missouri, USA) -- (14) Effect of the habitat connectivity in the genetic variability of the Volcano rabbit (*Romerolagus diazi*) (Jorge Ortega/Leslie Montes/José Antonio Guerrero, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional) -- (15) Different immune system diversity for city life: comparing major histocompatibility complex alleles in San Joaquin kit fox (*Vulpes macrotis mutica*) (Jesus Maldonado/Tammy R Wilbert, Masoumeh Sikaroodi, Brian Cypher, Christine Van Horn Job, Katherine Ralls, and Patrick M. Gillevet, Center for Conservation Genomics, Smithsonian Institute, Washington, DC, USA) -- (16) Conclusion: current state and future prospects of conservation genomics in mammals (Jorge Ortega, Jesus Maldonado).

Sommario/riassunto

This book focuses on the use of molecular tools to study small populations of rare and endangered mammals, and presents case studies that apply an evolutionary framework to address innovative questions in the emerging field of mammalian conservation genomics using a highly diverse set of novel molecular tools. Novel and more precise molecular technologies now allow experts in the field of mammalogy to interpret data in a more contextual and empirical fashion and to better describe the evolutionary and ecological processes that are responsible for the patterns they observe. The book also demonstrates how recent advances in genetic/genomic technologies have been applied to assess the impact of environmental/anthropogenic changes on the health of small populations of mammals. It examines a range of issues in the field of mammalian conservation genomics, such as the role that the genetic diversity of the immune system plays in disease protection and local adaptation; the use of noninvasive techniques and genomic banks as a resource for monitoring and restoring populations; the structuring of population by physical barriers; and genetic diversity. Further, by

integrating research from a variety of areas – including population genetics, molecular ecology, systematics, and evolutionary and conservation biology – it enables readers to gain a deeper understanding of the conservation biology of mammals that are at increasing risk of extinction at local, regional and global scales. As such, it offers a unique resource for a broad readership interested in the conservation biology of mammals and conservation management strategies to better preserve biodiversity.
