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**W741****Whole Genome Sequencing of California Condors is Now Utilized for Guiding Genetic Management***Date: Saturday, January 9, 2016**Time: 5:00 PM**Room: Pacific Salon 3**Oliver Ryder , San Diego Zoo Institute for Conservation Research, Escondido, CA**Webb Miller , Pennsylvania State University, Pennsylvania, PA**Katherine Ralls , Smithsonian Conservation Biology Institute, Washington, DC**Jonathan D. Ballou , Center for Conservation and Evolutionary Genetics, Washington, DC****Cynthia C. Steiner** , San Diego Zoo Institute for Conservation Research, Escondido, CA**Anna Mitelberg , San Diego Zoo Institute for Conservation Research, Escondido, CA**Michael Romanov , University of Kent, Canterbury CT2, United Kingdom**Leona G. Chemnick , San Diego Zoo Institute for Conservation Research, Escondido, CA**Michael Mace , San Diego Zoo Safari Park, San Diego, CA**Stephan Schuster , Pennsylvania State University, University Park, PA*[PDF file](#)

The California condor is a critically endangered avian species that, in 1982, became extinct in the wild. Its survival has persevered through a captive breeding program and reintroduction efforts within its former range. As of April, 2015, 421 California condors, including 204 flying in the wild constituted the extant population. Concern regarding preservation of genetic diversity and inbreeding, have led to intensive population management supported by molecular genetics research and, more recently, the application of genomic methodologies. 36 complete California condor genomes, representing the whole gene pool of the species, have been sequenced identifying about 4 millions polymorphic sites (SNPs). This has allowed reassessment of kinship among the founder birds, which is now being applied to selecting breeding pairs for the ongoing captive propagation effort. A genetic disease, chondrodystrophy, is inherited consistent with an autosomal recessive mode of transmission in condors. Utilizing whole genome sequencing of affected chicks and their carrier parents, a series of linked markers localized in a 1 Mb region of the condor genome have been employed to detect carrier condors heterozygous for the lethal mutation. This information can be incorporated into population management to reduce the risk of reproductive failure, as reintroduced populations begin to expand.

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January 08 - 13, 2016

Where:

San Diego, CA