



BIOLOGY COLLOQUIUM

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Population Genomics and informed breeding aid species conservation



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Population genomics enabled by next-generation sequencing has allowed studying the genetic diversity not only of the human, but also several endangered species. Knowledge of a species genetic diversity aids breeding programs that aim at boosting the remaining population size. One among several examples given will be the California condor project. This highly endangered species was brought back from the brink of extinction in the mid 1980's when the only remaining 22 birds were captured in order to start an ambitious breeding program. The success of the breeding program has manifested itself by today's population of ~ 400 individuals, 200 of which are living in the wild. We have sequenced the genomes of 33 individuals including the founders and the F1 offspring, resulting in the first complete map of the allelic diversity of any species. In order to accurately assess genomic diversity, we sequenced and assembled the complete genome of one bird using 454 long reads, MiSeq stitched read pairs, as well as Moleculo read data with up to 27 kb length, resulting in a 1.2 GB assembly. The combination of de novo assembled genome and in-depth population genomic data allows for a detailed assessment of the remaining genetic diversity and lets us help direct breeding pairings in a collaboration with the breeding program at the Institute for Conservation Research in San Diego. Further results give insights into the natural history of this species by identifying population bottlenecks by means of PSMC analysis. We further describe candidate genes for the disease chondrodystrophy, a form of dwarfism that is lethal to hatchlings and negatively impacts the breeding program. Finally we report the first genomic proof of parthenogenesis in two cases, with one trio and one mother/parthenode pair sequenced. This fascinating naturally occurring phenomenon might be a factor in species conservation in instances of less than sufficient population density, while at the same time giving insights into the architecture of haploid vertebrate genomes.