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Revising the Endangered Species Act

How might genomic advances inform ESA decisions?

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The Endangered Species Act (ESA), signed into law in 1973, is a framework to conserve and protect endangered and threatened species implemented by the U.S Fish and Wildlife Service (USFWS) and U.S. National Oceanic and Atmospheric Administration (NOAA) Fisheries Service. The ESA and its implementation is continually evolving through amendments and executive orders. Following Executive Order 13990 from the Biden administration, the USFWS and NOAA Fisheries Service are proposing regulatory revisions to the ESA. These revisions are aimed at providing greater clarity and consistency on key decisions about species listing, permitting, recovery, and other protections, a long-standing request from experts and stakeholders.

Similarly, the science informing determinations under the ESA is also evolving in an effort to use the most representative and best scientific data available. Since federal agencies have recently relied on genetic information to objectively inform ESA decisions,[1] increasingly available genetic data will likely become an essential component underlying decision-making, assessment, and enforcement under a reinvigorated ESA.

Recent advances in DNA sequencing technologies and bioinformatics have made it more affordable to generate large, high-resolution genomic datasets for any species from across the globe. There are now large and diverse types of genomic data available for thousands of species and these resources continue to grow rapidly. Most existing genomic datasets are openly available and may represent the best available scientific information regarding species' taxonomy, life history, and habitat, upon which ESA decisions are based.

Informing the "3 Rs"

Genomic data provide essential insights into each of the three main principles of the Species Status Assessment (SSA) Framework, developed by the USFWS to guide all ESA decisions: *representation, resiliency,* and *redundancy* (collectively known as the "3 Rs"):

- ***Representation*** describes the ability of a species to adapt to changing environmental conditions. Higher diversity increases the probability that a species' gene pool will contain genes suitable to an altered environment, supporting population persistence. Genomics can improve the accuracy of metrics used to quantify representation, which include gene diversity, heterozygosity, or alleles per locus. Moreover, genomic data allows the identification of genes underpinning adaptions to changing environmental conditions.
- ***Resiliency*** refers to the species' ability to withstand stochastic disturbances in demographics or environmental conditions. Genomic tools can be used to measure proxies of resiliency that increase the likelihood of survival and reproduction in spite of stochasticity, such as effective population size and connectivity among populations.
- ***Redundancy*** describes the ability of a species to withstand catastrophic events, such a fires and extreme weather, and can be assessed using genomic methods to identify populations or distinct population segments, delineate spatial extent and critical habitats, and assess degree of population connectivity.

By shedding light into the 3 Rs, genomics can help governmental agencies, NGOs, and businesses engaged in ESA-related activities reach more informed

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[1] See "Genetic Data and the Listing of Species Under the U.S. Endangered Species Act," "Improving conservation policy with genomics: a guide to integrating adaptive potential into U.S. Endangered Species Act decisions for conservation practitioners and geneticists," "The Use of Population Genetics in Endangered Species Act Listing Decisions," and "Genomics and conservation units: The genetic basis of adult migration timing in Pacific salmonids."

decisions that maximize a species' likelihood of sustaining wild populations over time. Mining companies could leverage genomics to assess the conservation status of listed species or populations occurring within their areas of operation and use this information to mitigate impacts and design management actions. Industries like fisheries or solar and wind farms could gain insights into the minimum population size required to maintain sufficient genetic diversity in a given population and use this knowledge to define catch limits or tolerable incidental takes. Stakeholders involved in water use conflicts or large infrastructure siting projects could also use genomic methods to identify threatened populations and delineate critical habitat. Genomic data may also play a role in informing the National Environmental Policy Act (NEPA), environmental assessments, the development of agency biological opinions, candidate conservation agreements, and Conservation Bank Agreements.

It Comes Down to Genomics

At the end of September, the USFWS proposed delisting 23 species from protection under the ESA, declaring them extinct. These proposed delistings by extinction show that loss is occurring and highlight the importance of the ESA, which according to the USFWS has protected 99% of listed species from the same fate. Genomics is one of the best available tools to help apply ESA protections more effectively to prevent future biodiversity loss. Recent petitions to list species as threatened or endangered have relied heavily on genetic information. Examples include the Atlantic bluefin tuna, the loggerhead sea turtle, and the polar bear. Likewise, the recent delisting of populations from the Steller sea lion to the gray whale and the canary rockfish also relied on genetic information.

How Exponent Can Help

Exponent's scientists have used genetic and genomic tools in the assessment of a broad range of organisms that include bacteria, plants, and animals, as well as to inform clients' complex litigation and business concerns involving agricultural property rights, genetically modified organisms (GMOs), invasive species, restoration management, and product contamination and identification. Genomic datasets for many endangered species already exist (e.g., NCBI, VGP, NIES), and Exponent scientists can leverage these genomic datasets and other data to inform the 3 Rs of SSA. The scientific tools at the forefront of genomic technologies are evolving quickly, and our experts track and understand both the advantages and limitations of these tools and can help clients plan, undertake, and interpret genetic species status assessment.

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