

An International Genomic Conservation Plan for African Wildlife

Introduction: Conservation genomics is the use of biotechnology for the conservation and restoration of biodiversity. Levels of genetic diversity are directly proportional to a species ability to adapt, survive and thrive. Therefore, loss of genetic diversity is detrimental to overall population health and long-term survival. To date, one of the most detailed conservation genomics studies of any wildlife species focused on American bison. This species experienced severe and well documented population declines between 1800 and 1900 that reduced the census size of this species by over 99%. The spectacular recovery to over 700,000 animals present today is a testament to their genetic constitution and represents one of the most significant accomplishments in modern conservation biology. We propose, using the bison studies as a model, to expand the use of these genomic technologies for the benefit of African wildlife species. These efforts will be based on developing a network of professionals to collect genetic materials and health information from captured or killed animals and archive this material with museums, zoos and universities. This archive of genetic material and health information will then form the foundation for a number of proposed genetic investigations of specific species.

Objectives. (In ascending order of complexity and cost). *Working collaboratively with likeminded international researchers, veterinarians, conservationist, sportsmen, professional hunters and wildlife managers that may already be engaged in some of these efforts, we propose to:*

- 1) Establish a network of professional for the systematic **collection of genetic samples and associated health data** from harvested or captured wildlife species in Sub-Saharan Africa. In addition, we plan to collect living cells from selected individuals and establish tissue banks that will be eventually frozen in liquid nitrogen. These tissue banks will provide a permanent source of DNA and a repository of viable nuclei for cloning. *(This first objective is required as the foundation material for all other listed objectives).*
- 2) Fully develop rapid and economical individual **species/subspecies identification technologies** from multiple mitochondrial and nuclear genes. These genotyping procedures will be designed so that they can be conducted in any moderately outfitted laboratory.
- 3) Fully develop population level **technologies to access biodiversity** levels within and between populations of selected species for indices such as geographic variation within species, inbreeding, parentage testing and overall genetic fitness estimations. These technologies will be based on information from domestic animal and livestock genomic sequencing projects and will use highly variable polymorphic marker analyses.
- 4) Produce detailed **gene maps of selected species** using high throughput 3rd generation sequencing and/or microarray genotyping / gene expression technologies to identify genes that confer important heritable traits such as those involving body and horn size, behavior, fertility, overall fitness and disease resistance. Again, these gene maps will be based on the genome databases derived from genomic sequencing projects.

Project Description. The first step as outlined in objective 1 is to develop the networks for the collection of health and genetic material. Through these relationships, we will provide training, expertise, collection and data record materials and arrange for in country archiving or import/export permits and shipping of genetic materials. This genetic material will include: whole blood samples deposited on room temperature filter paper blood cards (Whatman FTA™) and hair follicles. In addition, the living tissue banks will be frozen in liquid nitrogen in appropriate facilities. This repository of genetic material and the associated information will be catalogued and archived for genetic evaluation. Eventually, these genetic samples will be made available to suitable laboratories, universities or museums for future molecular genetic analysis. *(Working with PHASA, NAPHA and ZPHGA, the first two years of this project are expected to cost \$200,000 per year for collection supplies, travel, communications and shipping and sample archiving materials, in subsequent years the cost will be reduced).*

Objectives 2 through 4 are studies using the genetic samples collected in objective 1 to address a number of important issues involving the conservation, propagation, and over-all health of these species.

Objective 2 will focus on developing and validating the use of genetic biotechnology to unequivocally identify the species of origin from biological samples. These technologies are being developed for many pathogens, insects, plants and animals around the world with the objective of developing a global genetic identification system for all species. There are a few groups of researchers developing these technologies for wildlife, but no systematic plan has been established for the species of concern in this proposal. This objective will require salary support for one graduate student and related laboratory expenses, *(estimated cost is \$150K for 3 years)*.

Completion of objective 3 will provide highly detailed population genetics information from selected species in order to develop scientific based management plans. Developing the technologies for accessing inbreeding, population sub-structuring, geographic differences among isolated populations and as well as overall genetic health will be a valuable resource for organizations, governments, wildlife managers and land owners that are required to make decisions that affect these animals. Specific species and populations to be studied will be addressed in collaboration with funding agencies and groups and the cost will depend on the selected species and required technology development. *(These studies will require funding for at least 1 student (\$35k / year) and associated expenses per species estimated at \$100K / year)*.

Objective 4 will be a series of studies using high resolution DNA sequencing, gene identification and mapping, gene function and expression analyses to discover the underlying genetic components that govern these genetic traits. These studies are currently underway in humans, livestock and laboratory animals as well as many agriculturally important plant species. The successful use of these cutting edge biotechnology tools will provide answers and understanding to many biological mysteries and open new and exciting avenues for species conservation, preservation and utilization. *(These studies will require funding for at least 1 student (\$35k / year) and associated expenses per species estimated at \$200K / year)*.

Species of Interest: Collection of genetic material will include members of the mammalian orders, Carnivora, Proboscidea (elephants), Perissodactyla (uneven toed ungulates), and Artiodactyla (even toed ungulates). These four orders include the majority of the African wildlife species commonly taken by hunters and represent the majority of the economically important African wildlife species.

Deliverables: These proposed studies are designed with the idea of partnering sportsmen associations, species conservation groups and in-country scientists to develop archived collections of genetic material and then use powerful new genomic technologies to help insure the long-term conservation of healthy wildlife populations. **Therefore, the ultimate goal is to develop resources and molecular biology technologies to provide for conscientious stewardship of African game species.**

The initial timeline for objective 1 is two years. At the end of that time we plan to have collected a large number of genetic samples from multiple African species across many regions and populations. In addition, we will have developed numerous contacts with individuals and organizations in Africa to facilitate continued collection of these genetic resources into the future and identify funding sources for the specific research projects. Finally, the Texas A&M University College of Veterinary Medicine is developing a new and comprehensive program in Conservation Medicine. This program will focus on instruction; extension and research will require extramural funding through public and private sources and could develop into a major area for education and research in the College of Veterinary Medicine at this University. Moreover, extension of this genomic conservation effort to wildlife species worldwide is should be a priority.

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