

AMENDED EXECUTIVE SUMMARY - ACTION ITEM**ITEM 1.4: Request to Approve FY 2027 Regents' Research Grant: Genetic Testing of the Salt River Horse Herd**

Requested Action: The board office asks the committee to review and approve a TRIF Regents' Research Grant: Genetic Testing of the Salt River Horse Herd. A Regents' Research Grant to Northern Arizona University and the University of Arizona in response to the Arizona Department of Agriculture's Opportunity Statement, as described in this executive summary and supporting documentation.

Background/History of Previous Board Action

Arizona law established TRIF from Proposition 301 state sales tax revenue and gives ABOR the authority to administer the fund on behalf of Arizona State University (ASU), Northern Arizona University (NAU), and the University of Arizona (U of A). The board manages and administers the TRIF revenues through awarding and allocating revenues.

DiscussionPurpose

The purpose of Regents' Research Grants is to address and deliver solutions to critical issues facing the State of Arizona and its citizens, leveraging the skill sets resident at Arizona's three public universities. The Regents may award TRIF funding to Arizona public universities in the form of Regents' Grants to support:

- Academic research in areas of greatest need and interest to the State of Arizona and/or its citizens.
- Programs and initiatives aimed at having a large economic impact directly tied to the State of Arizona.

The Regents' Research Grants are designed to address and deliver solutions through academic research to critical issues facing the State of Arizona and its citizens by:

- Accelerating and delivering solutions to critical unmet needs for the State of Arizona;
- Bringing together and leveraging synergistic skill sets resident at multiple Arizona public universities; and
- Establishing centers of excellence that will generate sustainable future research funding.

Proposal evaluations were based on:

- Near-term Benefit to Arizona - The proposal's potential to impact Arizona citizens' most pressing unmet needs. Arizona agency feedback regarding potential impact of the proposal is a prime factor in the selection criteria.

- Additional criteria may be added depending on the nature of the proposal, e.g., practicality of implementation, technology readiness criteria, market information, proposal creativity, research team strength, etc.

Discussion

The proposal being submitted has the support from the Arizona Department of Agriculture.

The following table contains the project title with proposal link, suggested funding, term, and university team.

Project Title and Link	Funding and Term	University Team
Genetic Testing of the Salt River Horse Herd	\$325,000.00 over 2-years	Northern Arizona University and the University of Arizona

Supporting Document/s

- Salt River Horse Heard Genetic Testing Opportunity Statement
- Salt River Horse Heard Research Proposal

Statutory/Policy Requirements

- A.R.S. § 15-1626 (General Administrative Powers and Duties of Board)
- ABOR Policy 3-412 Administration of Technology and Research Initiative Fund.

Contact Information:

Sarah Harper, ABOR

sarah.k.harper@azregents.edu

602-229-2542

Ken Polasko, ABOR

ken.polasko@azregents.edu

602-229-2591

KATIE HOBBS
Governor



PAUL E. BRIERLEY
Director

Office of the Director

1110 W Washington – Suite 450, Phoenix, Arizona 85007
Mailing: 1802 W Jackson #78, Phoenix, Arizona 85007
(602) 542-0990

September 25, 2025

SUBJECT: Genetic Testing of the Salt River Horse Herd to aid in determining a sustainable, genetically diverse herd.

Arizona Board of Regents
ATTN: Ken Polasko
Ken.polasko@azregents.edu

Mr. Polasko:

The Arizona Department of Agriculture (AZDA) is charged with supporting farming, ranching and agribusiness in Arizona by protecting plants and animals, issuing agriculture and environmental licenses, inspecting farming practices and overseeing commerce standards and measurement devices.

The State of Arizona is proud of its western heritage represented by the Salt River Horse Herd (SRHH). Viewing these horses in a natural habitat is a joy for locals and visitors to our great state.

On May 11, 2016, Governor Ducey signed H.B. 2340 (Laws 2016, 2nd Regular Session, Chapter 136), which amends Arizona Revised Statute (A.R.S.) to add an article that protects the SRHH. This newly added article: a) protects the horses from being harassed, shot, injured, killed or slaughtered; b) requires written authorization from the AZDA or the Maricopa County Sheriff's Office (MCSO) before interacting with a horse from the herd; c) clarifies that horses from the SRHH are not considered stray livestock under Arizona law; and d) directs the AZDA to enter into an agreement with the U.S. Forest Service (USFS) to implement this article or to address any issues relating to the SRHH. Section 2 of H.B. 2340 requires the AZDA and USFS to enter into an intergovernmental agreement pursuant to A.R.S. § 11-952 for the law to become effective.

Upon inception of the statute, the SRHH has been managed by AZDA in cooperation with the USFS and a contracted third party.

Development and implementation of a Humane SRHH Management Plan (MP) is essential to: a) maintaining a healthy, age and genetically diverse herd; while b) addressing environmental sustainability as prescribed by the overall range ecology.

Speaking first to the overall range ecology, while the SRHH has been reduced from 400+ in 2017 to approximately 280 today, the current herd size exceeds the forage capacity of the SRHH management area (SRHHMA). To date, the herd reduction strategy has included a birth control program, natural attrition and humane adoption. Continuing drought conditions across the southwest have exacerbated the impact of the herd exceeding the carrying capacity of the SRHHMA, requiring daily supplemental feeding. [Judith Dyess, USFS, *Estimating Capacity for the Horses in the Lower Salt River Area August*

19, 2019, Sarah Noelle, Brett Blum and George Ruyle, University of Arizona, *Forage Assessment of the Lower Salt River Horse Recreation Area, Maricopa County, Arizona September 4, 2018.*]

As the drought conditions continue, the pressure to advance the reduction in herd size has increased. [University of Arizona, College of Agriculture and Life Sciences, Gila County Cooperative Extension, *Vegetation Assessment in the Salt River Horse Management Area*, April 2025.]

This requires AZDA to balance any such pressure with the need to ensure any MP maintains a minimum level of herd size and genetic diversity, determining minimum viable herd size, and which horses to remove, if necessary, whether done individually or in family unit(s) of 10 or more. Age, gender and genetic diversity in the departing and remaining horses must be fully considered.

To inform these management decisions, a comprehensive evaluation of the herd's current genetic diversity is desired, along with options for the minimum size and characteristics of a genetically sustainable herd maintained in the SRHH management area.

AZDA seeks an allocation from Arizona Board of Regents to leverage the genetic research capacity of Arizona Universities. The objective of this project would be to develop genetic science-based options on herd size and characteristics needed to: a) maintain the SRHH sustainably; and b) serve to guide genetically sustainable removal decisions if necessary.

Examples of scientific tools include:

- Simulation of genetic change under four removal strategies for a wild horse population. [Zimmerman, S.J., J.A. Fike, and S. J. Oyler-McCance. 2023. Administrative Report from USGS Fort Collins Science center to the BLM. Received August 2, 2022.]
- Fecal material genetic analysis is a peer reviewed, widely published process used by the Bureau of Land Management (BLM) and the USFS in managing wild burro and horse herds across the western United States [[Sarah R. B. King](#), [Kathryn A. Schoenecker](#), [Jennifer A. Fike](#), [Sara J. Oyler-McCance](#), *Wildlife Management*, February 2021].
- Advances in non-invasive sampling now enable isolation of host DNA from fecal material, eliminating the need for direct handling and reducing stress to the SRHH [[Sarah R. B. King](#), [Kathryn A. Schoenecker](#), [Jennifer A. Fike](#), [Sara J. Oyler-McCance](#) *Ecology and Evolution*, March 2018]. Low-throughput whole-genome sequencing of these samples will allow for precise assessment of individual and herd genetic variation, levels of inbreeding, and regions of homozygosity [Taylor et al, *Conservation Genetic Resources*, 2022 and [Gavriliuc et al](#), *Conservation Genetics Resources*, 2022]. This information would help guide decisions regarding optimal herd size and composition to ensure long-term genetic health, ecological sustainability, and compliance with statutory protections [[Kathryn A. Schoenecker](#), [Sarah R. B. King](#), [L. Stefan Ekernas](#), [Sara J. Oyler-McCance](#), *Wildlife Management*, May 2021].

Project Deliverables:

- Provide science-based options to support Executive decisions regarding management of the SRHH:
 - Genetic make-up, and diversity of the current SRHH.
 - Current gender diversity of the SRHH.
 - Define options for maintaining genetic diversity while minimizing SRHH population for long term herd sustainability.

- Information regarding appropriate gender diversity necessary for optimizing long term SRHH sustainability.
- Information or options for humane horse removal to maintain genetic and gender diversity of removed band(s) of the SRHH.
- Creation of a scoring rubric to aid in identifying individuals most beneficial to the long term health and welfare of a sustainable, genetically diverse SRHH.

AZDA expects this project to have a significant impact on its efforts to manage the SRHH in a humane and sustainable manner. During this 2-3 year project we expect the selected Arizona University(s) to work directly with AZDA and its SRHH vendor on a monthly basis or more often as necessary in identifying the statistically valid sample pool, collecting the samples, and reviewing of the results and release of the final report.

If you have any questions, please contact Paul Brierley at, pbrierley@azda.gov, or by calling 602-542-0990.

Sincerely,



Sheldon R. Jones
Deputy Director

This page intentionally left blank

Arizona Board of Regents & Arizona Department of Agriculture

Genomic Assessment of Genetic Diversity and Long-Term Viability of the Salt River Horse Herd

TEAM

Northern Arizona University: Drs. Jeffrey Foster, E. Anne Chambers, and Faith Walker

University of Arizona: Drs. Jessica Rick, Leigh Combrink, and Jacob Hennig

US Geological Survey–Fort Collins Science Center (USGS–FORT): Drs. Kate Schoenecker and Sara Oyler-McCance

Southern Arizona Experiment Station: Brett Blum

Salt River Wild Horse Management Group: Simone Netherlands

PROJECT SUMMARY

Our project will provide the Arizona Department of Agriculture with genetic data on the Salt River Horse Herd (SRHH) to inform science-based management that promotes herd health and maintains long-term genetic diversity. Using whole genomes generated from DNA from fecal samples, we will assess the genomic health of the SRHH at an unparalleled level of resolution. We will determine genetic diversity (measured as observed heterozygosity and allelic richness), genealogy (parentage), relatedness, degree of inbreeding, and effective population size of all horses in the herd. Finally, using forward-time simulations, we will provide genetic diversity estimates under different management scenarios to determine how to best maintain population viability into the future. Our team is composed of academic and government experts in wildlife genetics and genomics, including researchers with extensive experience studying wild horses and expertise in noninvasive genetic sampling from feces. We have partnered with a non-profit organization, the Salt River Wild Horse Management Group, who will assist with collecting fecal samples from every horse in the herd. Results will provide the Arizona Department of Agriculture with a science-based approach to determine management options for the SRHH.

OBJECTIVES

Our overall goal is to evaluate the genetic health, diversity, relatedness, and long-term viability of the SRHH wild horse population using modern genomic tools to inform science-based management and conservation decisions.

Aim 1. Characterize the current genomic health and demographic structure of the SRHH.

Objectives. Within the SRHH, we will **(1A)** quantify genomic diversity and population structure, **(1B)** estimate effective population size of the herd, and **(1C)** calculate inbreeding and relatedness.

Aim 2. Determine the minimum genetically sustainable herd size and composition.

Objectives. Using the data obtained from Aim 1, we will **(2A)** run forward-time genetic simulations parameterized using our genomic data and demographic variables, which will include birth and mortality rates, sex ratio, and age composition projected forward under different management scenarios, including contraceptive management and removal of particular individuals. Our team members have developed simulations for horses and

other wildlife populations [1–3].

Aim 3. Translate genomic findings to support the management of the SRHH.

Objectives. Using the results from Aims 1 and 2, we will **(3A)** synthesize genomic and modeling results to characterize the predicted genetic consequences of alternative herd sizes and removal scenarios, and **(3B)** communicate these findings to AZDA and relevant partners through regular meetings and reports.

APPROACH

Field data collection. In fall 2026, we will start collecting fecal samples from all 267 horses in the population, working in close collaboration with the SRWHMG, which has created a database to identify each individual in the population along with their demographic information. In this way, we will ensure that we do not collect duplicate samples from the same individuals. By employing the expertise and skillset of SRWHMG, we expect to collect samples within 4–5 months over fall and winter, assuring research progress is expedient. Simone Netherlands will supervise SRWHMG volunteers for field data collection, working in collaboration with UofA and NAU students, staff, and faculty.

Fecal samples will be collected by locating and identifying horses on foot and waiting for them to defecate, with a primary initial focus on horses at supplemental feeding stations to maximize efficiency. First, a sterile swab will be passed over the fresh bolus and stored in a tube prefilled with Zymo DNA/RNA shield preservation buffer. Additionally, we will use wooden tongue depressors to collect inner and outer sections of a fresh feces bolus. Samples will be placed in bags following [4] and stored temporarily in a cooler in the field and then transferred to a freezer for storage until lab analysis. Each sample will be labeled with the date, collector, an identifier for the specific horse (from SRWHMG), age class of individual, and its sex. All data will be recorded in a Survey123 database via smartphones or tablets to ensure that fecal information is paired with individual horse identification, all photos taken, sampling bout information, and any additional observations.

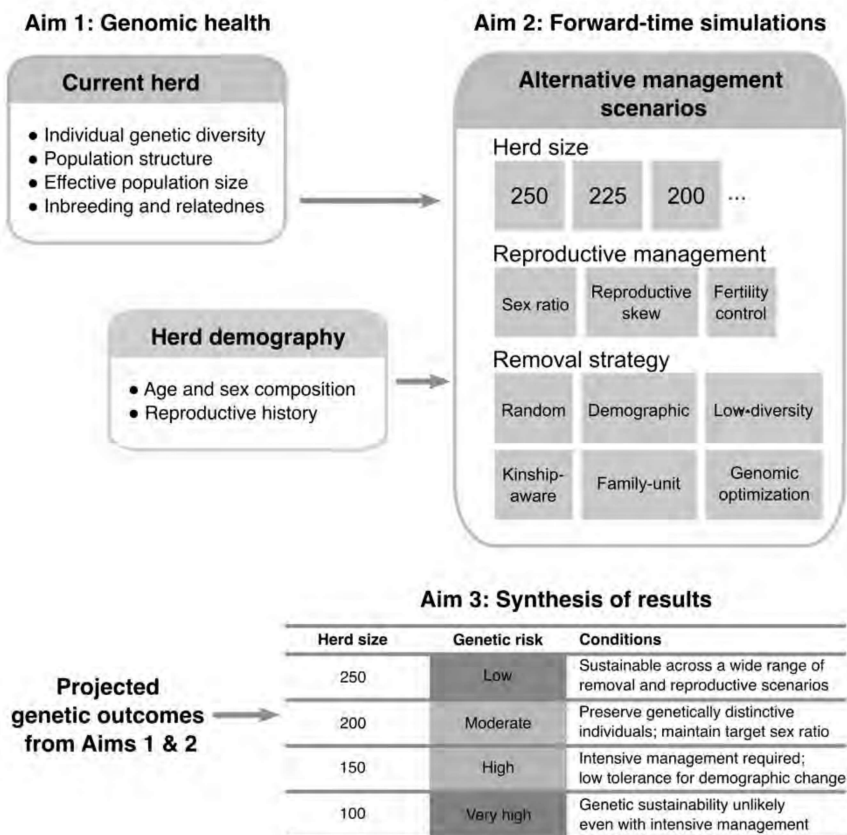


Figure 1. Schematic of the three project Aims.

Laboratory protocols, genomic sequencing, and bioinformatics processing. We will store samples and extract DNA following protocols previously described to have been successful for generating high-coverage whole genome data from caribou fecal samples [5]. We will submit samples for sequencing to University of Arizona's PANDA Genomics and Microbiome sequencing facility. A recent, high-quality reference genome was assembled for the domestic horse (EquCab3.0; [6,7]), which we will use for read mapping and variant calling of our samples. Assuming a genome size of 2.41Gb for the domestic horse [6], we aim to recover ~96.4M reads per sample at a depth of coverage of 10X using paired-end short-read sequencing (2x150 bp) on the NovaSeqX platform. We will use the snpArcher bioinformatic pipeline for variant calling, quality control, and filtering which has been successfully used for many other vertebrate species as part of the California Conservation Genomics Project [8,9]. Subsequent filtering, processing, and linkage disequilibrium pruning will be accomplished using Plink [10], vcftools [11], and bcftools [12].

Genomic health assessment

Individual-level genetic diversity. Different metrics of genetic diversity can help us understand different aspects of a population: variation that exists among individuals (observed heterozygosity) and the breadth of variation within the herd (allelic richness). The latter measure is particularly relevant when considering the loss of rare alleles with removals. We will calculate both metrics of genetic diversity: observed heterozygosity will be calculated using Plink's *het* function and allelic richness will be calculated using the *wingen* R package [13]. In this way, we will quantify both the distribution of genomic variation among individuals and the breadth of genetic variation represented across the herd.

Population structure. An additional measure of differentiation within the SRHH is population structure, which we will measure in two ways. The first is by conducting a genomic Principal Components Analysis (PCA) on our variant calls to uncover the major axes of variation. Secondly, we will run the likelihood-based method admixture [14] on a wide range of *K* values. The most suitable *K* value (*i.e.*, number of populations) will be selected based on a cross-validation analysis across all *K* values, identifying the population structure.

Effective population size. We will calculate the effective population size of the SRHH using a recently developed linkage-disequilibrium-based method, *currentNe2* [15]. This method is preferable to other commonly used estimators (e.g., NeEstimator v2; [16]) in scenarios where there is unequal reproductive contribution within a population, such as in the SRHH.

Inbreeding and relatedness. Because inbreeding results in a loss of heterozygous sites, the length and frequency of runs of homozygosity can indicate the degree and timeframe of inbreeding [17–19], which we will measure using the bcftools's *roh* function [20] using parameters that will detect inbreeding that has occurred within the last ~50 years. To understand relatedness among individuals in the herd, we will calculate pairwise genomic relatedness using the KING kinship estimator in Plink2 [10]. Finally, these genomic relationships will be integrated with available age, sex, reproductive, and social group information to identify the family structure of the herd using the *sequoia* package in R [21]. These metrics all help us understand how genetically distinctive each individual is relative to the rest of the herd and identify individuals whose removal could

disproportionately affect the herd's remaining genetic diversity. Although SNPs from genomic data can reliably determine pedigrees, in fact more reliably [21,22], a subset of the DNA samples (estimated at 75) will be genetically assessed using microsatellites to enable a comparison to other wild horse populations as well. Indeed, nearly all genetic research on wild horses in the US has been done using microsatellites but there is a growing acceptance that genomic approaches provide a more thorough, robust toolkit to analyze wild populations [23].

Genetic sustainability simulations. Simulations can provide a critical missing link in pairing demographic factors with genomic health to understand how different management strategies can affect the sustainability of a herd in the future. Individual-based, forward-time simulations can take in genomic and demographic data to project population trajectories under alternative management strategies. We will parameterize such a model using the results from Aim 1 using the *cgsim* package in R [1] which was initially developed for wild horse removal and has subsequently been successfully implemented in other herd wildlife [2]. We will provide the results from our genomic analyses with known demographic factors that are curated to the SRHH and examine trajectories of the herd in the future under iterations of three categories of management strategies. These categories include removal strategy (Table 1), resulting herd sizes (in increments of 25 individuals, ranging from a census herd size of 225 down to 50 individuals), and reproductive management strategy (Figure 1).

Removal strategy	Removal rule
Random	Individuals removed irrespective of genetics
Demographic	Optimize age/sex composition
Low-diversity	Preferentially remove individuals with high inbreeding and low diversity
Kinship-aware	Avoid removing genetically distinctive individuals; preferentially remove members of overrepresented families
Family-unit	Remove intact family groups
Genomic optimization	Select removals that minimize predicted loss of herd-wide genetic diversity

Table 1. Different removal strategies that will be tested using forward-time, individual-level simulations that incorporate genomic and demographic features of the Salt River Horse Herd.

DELIVERABLES

Decision-support products from genetic data:

- Observed heterozygosity, allelic richness, and the degree of inbreeding for sampled horses in the SRHH
- Effective population size of the SRHH

- Relatedness among all sampled horses in the SRHH (including a pedigree and parentage information)
- The reproductive contribution of sampled horses in the SRHH
- Population modeling outputs under different removal scenarios, including observed heterozygosity, allelic richness, and mean number of alleles (along with mean, standard deviation, and standard error) for every simulated time step

Genomic and analytical resources:

- Whole genome re-sequencing data (raw FASTQ reads) deposited in NCBI's Sequence Read Archive (SRA) database
- Variant calls (VCF file) and associated metadata deposited on Dryad upon publication
- Open-source analysis workflows and scripts uploaded to designated GitHub repository and on Dryad upon publication
- Archived analysis products (Dryad)

TIMELINE

In Year 1 of the project, months 1–6 will be devoted to obtaining all required fecal samples, performing lab work for DNA extraction, DNA quality quantification, library preparation, and whole genome sequencing. We will have a kickoff meeting in Phoenix with NAU, UofA, AZDA, USGS, and SRWHMG in month 2 of the project. Months 7–12 will involve running the bioinformatics pipeline to call variant sites. In Year 2, months 1–6 will be spent completing **Aim 1** analyses; months 4–9 will be devoted to **Aim 2** analyses. Finally, we will complete **Aim 3**, which is to communicate all genetics findings to the Arizona Board of Regents and the Arizona Department of Agriculture, during months 7–12.

PROJECT TEAM

Dr. Jeff Foster is a Professor and wildlife biologist at NAU, with a focus on wildlife genomics as well as livestock disease. He has successfully led dozens of genetics projects of comparable size and scope, with funding from NSF, DoD, USFWS, USDA, and NIH, leading to over 175 publications. Primary interests have been population and comparative genomics of the Hawaiian Honeycreepers to understand the evolution of resistance to avian malaria [24–29], population genetics of the introduced birds [30], as well as applying genomics for conservation [31]. He also has done extensive work on metabarcoding of fecal samples to assess animal diets [32–38] and his lab processes 1000s of fecal samples annually.

Dr. E. Anne Chambers is an Assistant Professor and wildlife biologist at NAU. She has extensive experience working with large-scale whole genome sequencing datasets as she is managing the landscape genomic analyses for ~20,000 whole genome sequences from 220 species for the California Conservation Genomics Project (CCGP [8]). The analyses included in the CCGP include all those in the current proposed project. She was also a co-developer of a new method (*wingen* [13]) to map genetic diversity, which we will use in this project to estimate allelic richness. Being a part of the CCGP has also enabled Chambers to lead working group meetings with state and federal agencies and policymakers to ensure that the results from the project can be translated into actionable management

practice [39].

Dr. Faith Walker is an Associate Research Professor and molecular ecologist at NAU whose research applies genetic tools to wildlife conservation and management. For more than 25 years, she has used noninvasively collected fecal samples to assess genetic diversity, population structure, relatedness, disease, and diet in wild and feral species. She leads the *Species from Feces* program [40–44], which develops and applies DNA-based approaches for extracting individual- and population-level information from noninvasively collected fecal samples of any species. Through the program, she has directed hundreds of wildlife genetics projects for tribal, federal, and state agencies, universities, NGOs, and private organizations using noninvasive genetic approaches to address conservation and management challenges. Relevant to this project, she has conducted genetic research on Arizona wild horse populations.

Dr. Jessi Rick is an Assistant Professor and wildlife biologist at the University of Arizona. She has been in the UofA's School of Natural Resources and the Environment (SNRE) since 2023 and is a specialist in population and conservation genetics of wildlife. Dr. Rick has over ten years of experience conducting population genomics and phylogenomic research across taxa including fish, herpetofauna, and mammals. Most relevantly, Dr. Rick has extensive experience generating and analyzing genomic sequencing data from wild populations, as well as working with state and federal management agencies to produce high-quality, interpretable scientific information for data-driven management decisions.

Dr. Leigh Combrink is an Assistant Professor and wildlife biologist at the University of Arizona. She joined SNRE in 2022 and is an expert in wildlife disease and conservation. With over 20 years of experience in wildlife conservation, she has focused her career on understanding factors affecting the health and wellbeing of wildlife particularly emphasizing the use of non-invasive sampling (fecal samples, feather samples etc.) combined with molecular techniques (DNA/RNA extractions, microbiome analyses, host genetics etc.). Much of her work relates to population recovery through reintroductions, and as such she is acutely aware of the role of genetics in determining the long-term sustainability of a wild population.

Dr. Jacob Hennig is an Assistant Professor and Cooperative Extension Specialist in Public Lands Grazing at the University of Arizona. Dr. Hennig started with SNRE in 2024 and is an expert in wild equid ecology. Dr. Hennig has over 10 years of experience working with wild horses and burros across the western United States. He has extensive experience in population size estimation and habitat selection of wild equids as well as elucidating the effects they have on semi-arid and arid ecosystems. Dr. Hennig has published >15 articles and given >30 presentations on wild equid ecology and is currently working with Tribal nations to develop wild horse and burro management plans. Hennig will guide fieldwork design and will ensure that our project deliverables are aligned with stakeholder priorities.

Dr. Kate Schoenecker is a Supervisory Research Wildlife Biologist and Branch Chief with USGS-FORT and is a world expert on wild horses. For more than two decades, she has led research on free-roaming horses and burros across the western United States, focusing on population ecology, management, and conservation [45]. Her work has included studies of horse genetics, genetic diversity, population structure, and the use of fecal DNA to assess

gene flow and herd health [4]. She has been a national leader in developing science-based approaches to wild horse management while balancing conservation, animal welfare, and public land stewardship.

Dr. Sara Oyler-McCance is a Supervisory Research Geneticist with USGS–FORT and is an internationally recognized conservation geneticist, using genetic and genomic tools to address wildlife management and conservation challenges across North America. Her work on wild horses has advanced the use of noninvasive DNA methods to assess population size, genetic diversity, population structure, and long-term herd viability. She has also contributed to research evaluating the genetic consequences of wild horse management strategies, providing critical science that informs conservation and stewardship of free-roaming horse populations.

Brett Blum, MS is an Interim Director at the Arizona Experiment Station and the Director of the Southern Arizona Experiment Station. Mr. Blum is an expert in wild equid and ungulate biology, with extensive experience in wildlife conservation and rangeland extension services. He will serve as an advisor to the project team regarding project deliverables, stakeholder communication, and wild horse biology, lending his prior experience working with the SRHH.

Ms. Simone Netherlands is the director of the Salt River Wild Horse Management Group, who are contracted by AZDA (CTR080640-2) to assist with management of the SRHH. She and her network of SRWHMG volunteers will help conduct fecal sampling. Their knowledge of the herd, daily monitoring, and ability to individually identify horses is crucial to the project.

LITERATURE CITED

1. Zimmerman SJ, Oyler-McCance SJ. Cgsm: An R package for simulation of population genetics for conservation and management applications. *Mol Ecol Resour.* 2025;25: e14081.
2. Zimmerman SJ, Geremia C, Oyler-McCance SJ. Predicted genetic consequences of alternative population control strategies for North American plains bison in Yellowstone National Park. *J Wildl Manage.* 2026;90. doi:[10.1002/jwmg.70207](https://doi.org/10.1002/jwmg.70207)
3. Zimmerman S, Fike JA, Oyler-McCance S. Simulation of genetic change under four removal strategies for a wild horse population. Bureau of Land Management; 2023. Available: <https://pubs.usgs.gov/publication/70241960>
4. King SRB, Schoenecker KA, Fike JA, Oyler-McCance SJ. Long-term persistence of horse fecal DNA in the environment makes equids particularly good candidates for noninvasive sampling. *Ecol Evol.* 2018;8: 4053–4064.
5. Taylor RS, Manseau M, Redquest B, Keobouasone S, Gagné P, Martineau C, et al. Whole genome sequences from non-invasively collected caribou faecal samples. *Conserv Genet Resour.* 2022;14: 53–68.
6. Kalbfleisch TS, Rice ES, DePriest MS Jr, Walenz BP, Hestand MS, Vermeesch JR, et al. Improved reference genome for the domestic horse increases assembly contiguity and composition. *Commun Biol.* 2018;1: 197.
7. Raudsepp T, Finno CJ, Bellone RR, Petersen JL. Ten years of the horse reference genome: insights into equine biology, domestication and population dynamics in the post-genome era. *Anim Genet.* 2019;50: 569–597.
8. Shaffer HB, Toffelmier E, Corbett-Detig RB, Escalona M, Erickson B, Fiedler P, et al. Landscape genomics to enable conservation actions: The California Conservation Genomics Project. *J Hered.* 2022;113: 577–588.
9. Mirchandani CD, Shultz AJ, Thomas GWC, Smith SJ, Baylis M, Arnold B, et al. A fast, reproducible, high-throughput variant calling workflow for population genomics. *Mol Biol Evol.* 2024;41: msad270.
10. Chang CC, Chow CC, Tellier LC, Vattikuti S, Purcell SM, Lee JJ. Second-generation PLINK: rising to the challenge of larger and richer datasets. *Gigascience.* 2015;4: 7.
11. Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, et al. The variant call format and VCFtools. *Bioinformatics.* 2011;27: 2156–2158.
12. Danecek P, Bonfield JK, Liddle J, Marshall J, Ohan V, Pollard MO, et al. Twelve years of SAMtools and BCFtools. *Gigascience.* 2021;10: giab008.
13. Bishop AP, Chambers EA, Wang IJ. Generating continuous maps of genetic diversity using moving windows. *Methods Ecol Evol.* 2023;14: 1175–1181.
14. Alexander DH, Novembre J, Lange K. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* 2009;19: 1655–1664.
15. Santiago E, Caballero A, Köpke C, Novo I. Estimation of the contemporary effective population size from SNP data while accounting for mating structure. *Mol Ecol Resour.* 2024;24: e13890.
16. Do C, Waples RS, Peel D, Macbeth GM, Tillett BJ, Ovenden JR. NeEstimator v2: re-implementation of software for the estimation of contemporary effective population size (N_e) from genetic data. *Mol Ecol Resour.* 2014;14: 209–214.
17. Kyriazis CC, Robinson JA, Lohmueller KE. Long runs of homozygosity are reliable genomic markers of inbreeding depression. *Trends Ecol Evol.* 2025;40: 874–884.

18. Ceballos FC, Joshi PK, Clark DW, Ramsay M, Wilson JF. Runs of homozygosity: windows into population history and trait architecture. *Nat Rev Genet.* 2018;19: 220–234.
19. Martin CA, Sheppard EC, Illera JC, Suh A, Nadachowska-Brzyska K, Spurgin LG, et al. Runs of homozygosity reveal past bottlenecks and contemporary inbreeding across diverging populations of an island-colonizing bird. *Mol Ecol.* 2023;32: 1972–1989.
20. Narasimhan V, Danecek P, Scally A, Xue Y, Tyler-Smith C, Durbin R. BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. *Bioinformatics.* 2016;32: 1749–1751.
21. Huisman J. Pedigree reconstruction from SNP data: parentage assignment, sibship clustering and beyond. *Mol Ecol Resour.* 2017;17: 1009–1024.
22. Whalen A, Gorjanc G, Hickey JM. Parentage assignment with genotyping-by-sequencing data. *J Anim Breed Genet.* 2019;136: 102–112.
23. Meek MH, Larson WA. The future is now: Amplicon sequencing and sequence capture usher in the conservation genomics era. *Mol Ecol Resour.* 2019;19: 795–803.
24. Neddermeyer JH, Cassin-Sackett L, Paxton EH, Campana MG, Fleischer RC, Foster JT. Evolution of resistance to avian malaria infection in an endemic Hawaiian honeycreeper. *Ecol Evol.* 2026;16: e73550.
25. Kyriazis CC, Venkatraman M, Masuda B, Steiner CC, Cassin-Sackett L, Crampton LH, et al. Population genomics of recovery and extinction in Hawaiian honeycreepers. *Curr Biol.* 2025;35: 2697–2708.e4.
26. Costantini MS, Videvall E, Foster JT, Medeiros MCI, Gillece JD, Paxton EH, et al. The role of geography, diet, and host phylogeny on the gut microbiome in the Hawaiian honeycreeper radiation. *Ecol Evol.* 2024;14: e70372.
27. Cassin-Sackett L, Campana MG, McInerney NR, Lim HC, Przelomska NAS, Masuda B, et al. Genetic structure and population history in two critically endangered Kaua'i honeycreepers. *Conserv Genet.* 2021;22: 601–614.
28. Navine AK, Paxton KL, Paxton EH, Hart PJ, Foster JT, McInerney N, et al. Microbiomes associated with avian malaria survival differ between susceptible Hawaiian honeycreepers and sympatric malaria-resistant introduced birds. *Mol Ecol.* 2023;32: 6659–6670.
29. Foster JT, Woodworth BL, Eggert LE, Hart PJ, Palmer D, Duffy DC, et al. Genetic structure and evolved malaria resistance in Hawaiian honeycreepers. *Mol Ecol.* 2007;16: 4738–4746.
30. Foster JT, Walker FM, Rannals BD, Sanchez DE. Population genetics of an island invasion by Japanese Bush-Warblers in Hawaii, USA. *Auk.* 2018;135: 171–180.
31. Garner BA, Hand BK, Amish SJ, Bernatchez L, Foster JT, Miller KM, et al. Genomics in conservation: Case studies and bridging the gap between data and application. *Trends Ecol Evol.* 2016;31: 81–83.
32. Hoffman BJ, Theimer TC, Holton PB, Foster JT. Diets of human-subsidized ringtails (*Bassariscus astutus*) at the Grand Canyon using isotopic niche and fecal analyses. *J Mammal.* 2026;107: 187–196.
33. Johnston EM, Mittelhauser GH, Foster JT, Mau RL, Gibson AA, Gillece JD, et al. Barnacles dominate the winter diet of *Calidris maritima* (Purple Sandpiper) in Maine: A bona fide dietary shift or molecular techniques revealing an unknown diet composition? *Ornithology.* 2025;142. doi:[10.1093/ornithology/ukaf005](https://doi.org/10.1093/ornithology/ukaf005)
34. Souza-Cole I, Ward MP, Mau RL, Foster JT, Benson TJ. Eastern Whip-poor-will

- abundance declines with urban land cover and increases with moth abundance in the American Midwest. *Condor*. 2022;124. doi:[10.1093/ornithapp/duac032](https://doi.org/10.1093/ornithapp/duac032)
35. O'Rourke D, Rouillard NP, Parise KL, Foster JT. Spatial and temporal variation in New Hampshire bat diets. *Sci Rep*. 2022;12: 14334.
 36. Maslo B, Mau RL, Kerwin K, McDonough R, McHale E, Foster JT. Bats provide a critical ecosystem service by consuming a large diversity of agricultural pest insects. *Agric Ecosyst Environ*. 2022;324: Not Available.
 37. O'Rourke DR, Mangan MT, Mangan KE, Bokulich NA, MacManes MD, Foster JT. Lord of the Diptera (and moths and a spider): Molecular diet analyses and foraging ecology of Indiana bats in Illinois. *Front Ecol Evol*. 2021;9. doi:[10.3389/fevo.2021.623655](https://doi.org/10.3389/fevo.2021.623655)
 38. O'Rourke DR, Bokulich NA, Jusino MA, MacManes MD, Foster JT. A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. *Ecol Evol*. 2020;10: 9721–9739.
 39. Chambers EA, Bishop AP, Wang IJ. Individual-based landscape genomics for conservation: An analysis pipeline. *Mol Ecol Resour*. 2023. doi:[10.1111/1755-0998.13884](https://doi.org/10.1111/1755-0998.13884)
 40. Westeen EP, Martínez-Fonseca JG, d'Orgeix CA, Walker FM, Sanchez DE, Wang IJ. Dietary niche partitioning of three Sky Island *Sceloporus* lizards as revealed through DNA metabarcoding. *Ecol Evol*. 2023;13: e10461.
 41. Sobek CJ, Walker FM. Square salads: exploring the diet of the southern hairy-nosed wombat (*Lasiornhinus latifrons*) via DNA metabarcoding. *Aust Mammal*. 2021;43: 104–109.
 42. Walker FM, Horsup A, Taylor AC. Leader of the pack: faecal pellet deposition order impacts PCR amplification in wombats. *Mol Ecol Resour*. 2009;9: 720–724.
 43. Walker FM, Williamson CHD, Sobek CJ, Sanchez DE, Chambers CL. Species from feces: reliably identifying global bat species with a DNA mini-barcode assay. *Genome*. 2015;58: 294–294.
 44. Walker FM, Williamson CHD, Sanchez DE, Sobek CJ, Chambers CL. Species from feces: Order-wide identification of Chiroptera from guano and other non-invasive genetic samples. *PLoS One*. 2016;11: e0162342.
 45. Schoenecker KA, King SRB, Ekernas LS, Oyler-McCance SJ. Using fecal DNA and closed-capture models to estimate feral horse population size. *J Wildl Manage*. 2021;85: 1150–1161.