

# EquinePrimer

S1094 UPDATE WINTER 2023

## Coordinator Corner

Welcome to the first newsletter for multistate project S1094 “Genomic tools to improve equine health, wellbeing, and performance.” We hope that you will not only consider joining this multistate as a member, but will also recruit others who have an interest in using genetics and genomics tools to promote health, welfare, and performance in horses across breeds and discipline. Please do not hesitate to reach out to us with questions or suggestions! We can be reached any time at: [horsegenomeworkshop@gmail.com](mailto:horsegenomeworkshop@gmail.com)

Annette McCoy,  
University of Illinois

Elaine Norton, University  
of Arizona

Michael Mienaltowski,  
University of California-  
Davis

S1094 Co-Coordinators



Photo of participants at the 13<sup>th</sup> International Havemeyer Foundation Horse Genome Workshop courtesy of Doug Ancyzac and Don Miller

## this issue

Get to Know S1094 P.1

PAG30 Recap P.2

Research Highlights/Photo Gallery P.3

Industry Partnership Profile P.4

## Get to Know S1094

With the sunset of NRSP-8, the National Animal Genome Research Program, in 2023, the equine genetics community identified the need to develop a new umbrella multistate program that would support our collective efforts at developing shared resources and educational tools. A writing committee was identified at the Havemeyer Horse Genome Workshop in summer 2022 (Ernie Bailey, Samantha Brooks, Stephen Coleman, Sian Durward-Akhurst, Ted Kalbfleisch, Annette McCoy, Michael Mienaltowski) and submitted a multistate proposal through the south region later that fall. This proposal was approved and has been designated S1094 “Genomic tools to improve equine health, wellbeing, and performance.”

Multistate awards are a great opportunity to network with colleagues and provides the community with a collaborative structure. Depending on the insitution, some funds for research or travel may be available on a competitive or non-competitive basis to multistate members.

Multistate proposals are designed to “address regional or national agricultural issues through multidisciplinary research.” S1094 has four specific objectives:

**OBJ 1. Improve detection, curation and annotation of pan-genomic variability for genetic selection, as well as stewardship of genetic diversity, across horse breeds and exotic or feral populations.**

**OBJ 2. Apply and improve genomic resources to increase our understanding of equine performance and disease.**

**OBJ 3. Expand the availability of genetic diagnostic testing and education on its use.**

**OBJ 4. Create platforms for broad sharing of data, technology, and resources to enhance continued development and application of genomics tools in the industry.**

## Join S1094!

If you are at an academic institution in the United States, join by filling out Appendix E in NIMSS. The details of how you do this will vary by institution! If you are located internationally or are a member of the equine industry, then join the Horse Genome Workshop (QR code below) and contact the program administrator (Cindy Morley, [cmorley@uark.edu](mailto:cmorley@uark.edu)) for NIMSS membership.

<https://tinyurl.com/horsegenome>



## Upcoming Events

Equine Sciences Society meeting, June 6-9, Grapevine, TX

International Society for Animal Genetics meeting, July 2-7, Cape Town, South Africa



Photo of PAG30 equine poster session courtesy of Annette McCoy

## PAG30 Recap

Laura Patterson Rosa, Sul Ross State University

The equine genetics community was back together in person at the Plant and Animal Genome meeting in San Diego in January 2023!

## WORKSHOP SPEAKERS

Ancient Segmentally Duplicated *LCORL* Retrocopies in Equids (Bannasch et al)

New Genomic Insights into the Conformation of Horses from Shape Space Data (Gmel and Neuditschko)

Whole-Genome Sequencing Identifies Candidate Missense Variants in Several Genes As Potential Causes of Feathering in Horses (Sawicki et al)

A De Novo 2.3 Kb Deletion in *MITF* Explains a Novel Splashed White Phenotype in Thoroughbreds (Bellone et al)

Cners: Circular Nucleic Acid Enrichment Reagents for Targeted Sequencing (Sundararaman et al)

Evaluation of Candidate Gene Prediction Programs in Equine Disease (Hughes et al)

Tissue-Specific Distribution and Complexity of Small Non-Coding RNA Expression in the Horse (Cullen et al)

RNA Sequencing Detects Genes Implicated in Hoof Strength to Withstand Barefoot Racing in Standardbreds (Alameddine et al)

Identification of a Global Gene Expression Signature Associated with the Genetic Risk of Catastrophic Fracture in Thoroughbred Horses (Lago et al)

More than 70 members of the Horse Genome Workshop community and other participants from around the globe met at the 30<sup>th</sup> annual Plant and Animal Genome Conference (PAG30) January 14-15 at the Town and Country Resort in San Diego, CA. This meeting served as the final official meeting for the equine NRSP-8 members and the first meeting of S1094. The meeting was chaired by Dr. Felipe Avila (University of California-Davis) and co-chaired by Dr. Elaine Norton (University of Arizona). Scientists, trainees, and guests from 35 different universities and organizations were given the opportunity to hear about research advances from the past year from 15 diverse speakers. This work highlighted the varied applications of genomic and transcriptomic tools and resources developed by the Equine Genome community for investigation of horse physiology and disease over the two decades of NRSP-8 support.

The workshop's keynote address was given by Dr. Sue Stover, from the University of California-Davis, a world-renowned expert in the mechanisms of orthopedic injury in racehorses. Her talk highlighted the ways in which genomics tools could be applied to a wide variety of equine health, welfare, and performance issues and illustrated the need for cross-disciplinary collaboration and involvement of partners from the equine industry to move equine research forward.

# Research Highlights from PAG30

Research into the genetic variants associated with an autosomal recessive **spinocerebellar ataxia** discovered in Quarter Horse foals is currently ongoing. Causative variants discovered during the course of this research will be useful for diagnostic testing of Quarter Horse foals with neurological disease and may be important when making future breeding decisions in Quarter Horses. (Carrie Finno, University of California-Davis)

**Proteomic analysis** of peritoneal fluid in horses with colic identified differentially expressed proteins between strangulating and non-strangulating intestinal disease. Data collection and further analyses are ongoing, but results suggest that protein variations may be useful to distinguish between strangulating and non-strangulating intestinal disease, and could therefore serve as candidate biomarkers to assist in identification of colic patients at increased risk of post-operative complications (Rebecca Bishop, University of Illinois).

A SINE insertion and a SNP variant in the **myostatin (MSTN) gene** are associated with optimum racing distance in Thoroughbred horses. The MSTN-SINE insertion was found in Turkoman as well as Thoroughbred horses. DNA sequencing showed more variation in the region for the Turkoman than the Thoroughbred suggesting a more ancient origin in Turkoman horses. Further investigation is ongoing to find out if the Turkoman horse was the source of the SINE-S variant in Thoroughbreds (Navid Mashouf, University of Kentucky).

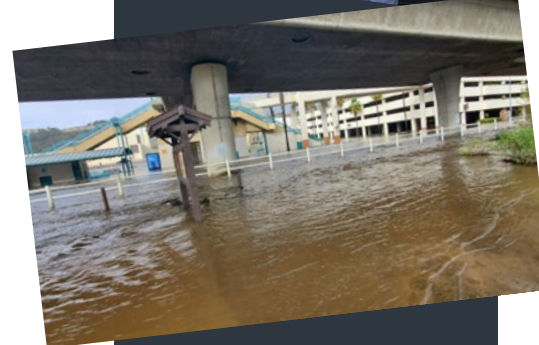
In addition to the workshop speakers, **more than 25 posters highlighting equine genetics research** were presented at the two poster sessions on January 16.

## Horses and Donkeys and SnakeMake, oh my!

One of the major goals of the Horse Genome Workshop is to make the tools and resources that have been developed easily accessible to the broader community. To this end, a hands-on workshop was held the evening of January 16 to demonstrate the containerized workflows developed for use with an array of equine genomics data. It also introduced the FAANG data and resources available at [equinegenetics.uky.edu](http://equinegenetics.uky.edu).



## Photo Gallery



We won't forget the impressive flooding any time soon!



A special thank you to the Havemeyer Foundation and Gene M. Pranzo for once again sponsoring the Hospitality Suite at PAG.

## Industry Partnership Profile: Shining a Light on Night Blindness

Rebecca Bellone, UC-Davis

An astute owner of a 13-year-old Tennessee Walker Horse gelding noticed he was having trouble finding his feed bucket, but only at night. The horse was taken to North Carolina State University to be examined by veterinary ophthalmologist Dr. Brian Gilger. After performing a complete ocular exam, including electroretinography, Dr. Gilger confirmed that the horse was not able to see in low light conditions. Dr. Gilger then reached out to Dr. Rebecca Bellone at the University of California-Davis and together they explored the genome of this night blind horse. After sequencing the genome of the horse, genes that were good biological candidates for playing a role in the disease were examined. A recessive missense mutation (a change in the DNA causing the protein product to be altered) was found in *GRM6*, a glutamate receptor known to be important for proper cell signaling in night vision. The frequency of this mutation was reported by Hack and colleagues in 2020 to be 10%, suggesting that 1 in 100 Tennessee Walking Horses may be night blind! Genetic testing can now be used to help select mates so that affected horses are not produced. However, the story doesn't stop there. With the help of the United States Trotting Association, Cal Expo Harness Racing Association, and owners of horses from three horse breeds, this same genetic variant has now been identified as a cause of night blindness in other breeds. The latest stage of this research was presented at the 2023 Plant and Animal Genome (PAG) conference and is currently under review for publication. While we still have lots to learn about inherited eye disease, passionate owners and committed industry partners are helping to unravel the mechanisms of vision issues in horses.

Have a partnership story to share? Have an idea for a newsletter feature? Contact us at [horsegenomeworkshop@gmail.com](mailto:horsegenomeworkshop@gmail.com).



### We want YOU to join our herd!

Calling all equine industry stakeholders! This multistate project needs your involvement! We are looking for anyone who is interested in sharing their thoughts about needs related to horse genetics, whether that's genetic testing or working to unravel the genetic mechanisms behind a disease. Your expertise is valued. Within the S1094 multistate group we hope to bring together scientists, veterinarians, breed registries, and other stakeholders to help us achieve our goal of healthier horses. Contact us at [horsegenomeworkshop@gmail.com](mailto:horsegenomeworkshop@gmail.com).