**Havemeyer/USDA-NRSP8 Report for Horse Genome Committee for January 1, 2015 to December 31, 2015**

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Workshop Chair for 2017 PAG meeting: Carrie Finno (University of California, Davis) cjfinno@ucdavis.edu

Workshop Chair for 2018 PAG meeting: Jessica Petersen (University of Nebraska)

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NRSP8 Horse Coordinators: Ernest Bailey (University of Kentucky); Molly McCue (University of Minnesota), Samantha Brooks (University of Florida)

The workshop participants met on Saturday and Sunday, January 9-10, 2016 at the Plant and Animal Genome Conference in San Diego. TheUSDA-NRSP8 meeting was held in conjunction with the Dorothy Russell Havemeyer workshop activities. Approximately 80 people attended the sessions with participants from at least 10 countries (USA, Brazil, China, Japan, Korea, Denmark, United Kingdom, Italy, Argentina, Ireland). Ted Kalbfleisch served as chair of the 2016 workshop. He will step down after this year and the next chair will be Carrie Finno. At the meeting, Jessica Petersen was elected as vice-chair and will assist Carrie Finno in 2017 and assume full leadership of the workshop in 2018.

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The workshop meeting at PAG followed a July 2015 Havemeyer Conference. During the Havemeyer Conference there were 42 podium presentations and 26 poster presentations over 3 days ranging in topics from studies of ancient DNA, comparison of extant populations, investigation of structural variations among horses, discovery of mutations affecting disease and performance and the use of genomics to better understand the quantitative genetics underlying performance and diseases of horses. In addition there were reports on development of infrastructure tools.

During the PAG conference (January 2016) two workshop sessions were held on horse genomics with 14 podium presentations. At the PAG meeting the focus of the meeting was on development of infrastructure and specifically, use and development of databases, creation of a new genome assembly and development of tools for investigating gene expression more effectively. In addition, scientists present podium talks on discoveries related to horse genomics and 36 posters were presented related to horse genomics.

**Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.**

The section below is duplicated in the coordinators’ report. However these activities were the product of discussions held by the workshop participants during the 2015 PAG meeting and during a July Workshop meeting held in Hannover, Germany.

New Reference Genome Assembly

Ted Kalbfleisch, Jamie MacLeod and Ludovic Orlando were funded by the Morris Animal Foundation to create a new assembly of the reference sequence, the putative Ecab 3.0.  Partial support for a postdoctoral student is provided by USDA-NRSP8 coordinators’ funds.  The grant proposal and work is underpinned by data provided by workshop participants including whole genome sequence information from TWILIGHT (reference horse) and from horses of other breeds. The work began in 2015 and is planned for completion in August 2016.

Whole Genome Sequences

In connection with research projects, many of which are cited in the reference section, over 200 horses have had their whole genomes sequenced. Many of those sequences are being used for the new assembly described in the previous paragraph and were used to identify SNPs for construction of the 670K SNP assay tool described below.

Access to reference DNA

The primary CHORI 241 BAC library was moved from the Children’s' Hospital of Oakland to the laboratory of Samantha Brooks (co-coordinator) at the University of Florida. This action was necessitated by the closing of the commercial operation of the BAC library. This move ensures continued research access to the library.

**Objective 2: Develop strategies to identify and exploit genes and allelic variation that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.**

The section below is duplicated in the coordinators’ report. We anticipate that discoveries in the future will be based on use of this newer higher density SNP chip. However during 2015 the molecular basis was discovered for many horse diseases affecting muscle, nervous system, respiratory system and immune system. Genetic signals were identified for yet other disease genes. Furthermore, progress was made in identifying the effect of genes previously shown to influence racing performance (MSTN) and gait (DMRT3). Other studies reported approaches to identifying estimated breeding values for performance of Thoroughbred, harness racing horses and warmblood horses.

New SNP assay tool

The 670K SNP chip was made available in late 2015 for research on horses.   This initiative was driven by Dr. Molly McCue (co-coordinator) of the University of Minnesota with support of students, co-workers and funding from several agencies including the USD-NRSP8 coordinators‘ fund.  Geneseek (NE) is a commercial laboratory offering testing .

**Objective 3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.**

The section below is duplicated in the coordinators’ report.

During 2015, the horse workshop group was invited to join the FAANG initiative. Jamie MacLeod of the University of Kentucky serves on the guiding committee for FAANG and also oversees cooperation among scientists studying the horse. During 2015, three scientists (Carrie Finno of UC Davis, Rebecca Bellone of UC Davis and Jessica Peterson of the University of Nebraska) applied for funds to collect tissues and begin conducting assays associated with the FAANG program. We are waiting to hear the results of that application. Regardless, we have committed NRSP8 coordinator funds to collection of tissues to benefit this or future applications. A meeting of the horse genome workshop committee is being planned for the ISAG meeting to be held in Utah in July 2016 to make plans.

**Impacts 2013-2015**

1. Mutations responsible for horse diseases involving muscle, nervous system, respiratory system and immune system were identified and diagnostic tests created for use by veterinarians and horse owners.
2. The diverse use of horses, the diverse methods for measuring performance and the small population sizes present problems for applying quantitative genetic approaches to evaluation. With the advent of SNP assays, the developments of genomic selection assays for performance are being investigated for use by horse breeders.