

USDA-NRSP8 Report for Horse Genome Committee for January 1, 2014 to December 31, 2014

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

Workshop Chair for 2015 PAG meeting: Scott Dindot (Texas A&M University)

Workshop Chair for 2016 PAG meeting: Ted Kalbfleisch (University of Louisville)

Workshop Chair for 2017 PAG meeting: Carrie Finno (University of California, Davis)

The workshop participants met on Saturday and Sunday, January 10-11, 2015 at the Plant and Animal Genome Conference in San Diego. Approximately 80 people attended the sessions with participants from at least 10 countries (USA, Brazil, China, Japan, Korea, Denmark, United Kingdom, Italy, Argentina, Ireland). Scott Dindot served as chair of the 2015 workshop. He will step down after this year and the next chair will be Ted Kalbfleisch. At the meeting, Carrie Finno was elected as vice-chair and will assist Ted Kalbfleisch in 2016 and assume full leadership of the workshop in 2017.

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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.

New Reference Genome Assembly

Ted Kalbfleisch announced that the Morris Animal Foundation had selected for funding a proposal crafted by Ted, Jamie MacLeod and Ludovic Orlando for creating a new assembly of the reference sequence, the putative Ecab 3.0. Partial support for a postdoctoral student will come from 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.

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 Cornell laboratory (Doug Antczak and Don Miller) have continued to provide samples to other scientists from TWILIGHT, the horse providing DNA for the reference sequence and from BRAVO, the horse that provided DNA for the CHORI 241 BAC 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.

New SNP assay tool

The 670K SNP chip is now available for research use on horses. This was an initiative proposed and driven by Dr. Molly McCue of the University of Minnesota with support of students, co-workers and funding from several agencies including the USD-NRSP8 coordinators' fund. Bob Schaefer (UMN) gave a presentation describing the considerations in designing the tool. Geneseek (NE) is a commercial laboratory offering testing and has agreed to coordinate testing among laboratories to help reduce costs. Workshop scientists contributed data from whole genome sequencing of more than 200 horses to discover SNPs for use on this assay tool.

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.

A consortium was established to annotate functional elements in the genome responsible for regulating phenotypic traits for all animal species. The group is called Functional Annotation of Animal Genomes (FAANG) and is patterned after the ENCODE program that has been successful for studying functional genomics in humans. Dr. Jamie MacLeod (University of Kentucky) has been invited to serve on the guiding committee to represent the interests of horse genomics. Dr. MacLeod has invited participation in a subgroup focusing on horses, called E-FAANG, for Equine – FAANG.

List of publications:

- Al-Jaru A, Goodwin W, Skidmore J, Raudsepp T, Khazanehdari K. 2014. Male Horse Meiosis: Metaphase I Chromosome Configuration and Chiasmata Distribution, *Cytogenet Genome Res*, Published online: August 29, 2014.
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Funding Sources Summary for 2014

(summaries provided by scientists from 14 participating laboratories and therefore represent a partial account of research funds obtained for horse genomics research in 2014)

Federal Funding:	\$ 4,272, 590
Industry:	\$ 677, 587
<u>Local/Institutional:</u>	<u>\$ 220, 000</u>
Total	\$ 5, 170, 177

Impacts

1. Identified a mutation that enhances the ability of horses to perform certain gaits, especially pacing or running walk and which can be used for early selection of “gaited” horses.
2. Determined significant heritable contributions to developmental bone diseases, muscle disease, bone fracture and laryngeal neuropathy which imply benefits for selection and the possibility of developing a prognostic test.