**U.S. HORSE GENOME COORDINATION PROGRAM ACTIVITIES**

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**Overview:** Coordination of Horse Genome Coordination Program is under the National Animal Genome Research Program (NAGRP) and is the effort at the University of Kentucky. CSREES support is allocated from NRSP-8 and provided to the Agriculture Experiment Stations by off the top funding. The NAGRP is made up of the membership of the Animal Genome Technical Committee, including the Horse Species Subcommittee.

#### **Coordinators:**

Ernest Bailey, PhD; professor, University of Kentucky

Samantha Brooks, PhD; assistant professor, University of Florida

Molly McCue, DVM, PhD, DACVIM; professor, University of Minnesota

**Objectives:**

**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.**

**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.**

**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.**

**Objective 1:**

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:**

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:**

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.

#### **Database Activities:** Two databases compile published genetic data for horses: <http://locus.jouy.inra.fr/cgi-bin/lgbc/mapping/common/intro2.pl?BASE=horse>; <http://www.thearkdb.org/>. .

#### Several genome browsers have been developed at the University of California, Santa Cruz, ENSEMBL and NCBI: <http://www.genome.ucsc.edu/cgi-bin/hgGateway?hgsid=95987985&clade=vertebrate&org=Horse&db=0>; <http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?taxid=9796>; <http://www.equinegenome.org/Equinegenome.org.html><http://pre.ensembl.org/Equus_caballus/index.html>.

#### A SNP database is available: <http://www.broad.mit.edu/mammals/horse/>.

A RNAseq database: <http://macleod.uky.edu/equinebrowser/>

#### A major entry point for databases and other relevant information about the horse genome workshop and participants is the workshop website: <http://www.uky.ledu/AG/Horsemap>.

**International Efforts:** The horse genome technical committee is an international activity with approximately half of the participants coming from Europe, Africa and AustralAsia while the other half come from North America.

#### **Communication:** Communication within the horse genome workshop is facilitated by an email list for sharing information by the Horse Genome Coordinator and through the website: <http://www.uky.edu/AG/Horsemap>. One of the major aspects of the website is to increase its value for informing members of the horse industry about the scientists using horse genomics to solve important problems and to explain the value of horse genomics

#### **Travel and Meeting Support:** During 2014, travel awards were provided to 10 students, including one Jorgenson award, and travel support for two invited speakers to the Horse Genome Workshop and to the NRSP8 general meeting.

**Future Activities:** During 2015 a workshop on Horse Genomics will be conducted under the auspices of the Dorothy Russell Havemyer Foundation in conjunction with the USDA-NRSP8. The workshop will include discussions of applications of the horse genome tools to address issues of performance and health in horses. In addition, one session will be devoted to discussion of FAANG and activities to promote this program. Coordinator funding will be used for partial support of a postdoctoral fellow to work on the Morris Animal Foundation funded project to create a new assembly for the horse genome (Ecab 3.0).