

U.S. Poultry Species Coordination Activities
Supported by Allotments of Regional Research Funds, Hatch Act
January 1, 2014 to December 31, 2014

FACILITIES AND PERSONNEL: Mary Delany, Dept. of Animal Science, UC Davis, served as Coordinator with Hans Cheng, USDA, ARS, ADOL, as Co-Coordinator.

OBJECTIVES 1. Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest. 2. Facilitate the development and sharing of animal populations and the collection and analysis of new, unique and interesting phenotypes. 3. Develop, integrate and implement bioinformatics resources to support the discovery of genetic mechanisms that underlie traits of interest.

Progress toward objective 1. Shared genomic tools and reagents and sequence information.

Reference linkage map. Linkage mapping is now primarily via high throughput SNP assays. Very high density SNP mapping (ca. 600,000 SNP) panels have been developed and are being employed in genome-wide association studies (GWAS) and genomic selection (GS). Plans will begin soon to help resolute unmapped sequence contigs through genetic mapping of selected SNPs on the East Lansing reference panel.

Chicken genome sequence. Efforts are ongoing to improve the chicken genome sequence, which is being led by Wes Warren, The Genome Institute at Washington U. The latest build, Galgal5.0, will incorporate information from 30x PacBio coverage from a 10 Kb library (funded by Cobb-Vantress), which has improved the N50 contig size from 250 Kb to 1.79 Mb and cut about half of the number of unplaced scaffold gaps (1722 to 965). Unfortunately, even with these efforts and the use of 6x Moleculo sequence, the new build has still not captured the roughly 5% of missing sequence (believed to be predominantly on the microchromosomes). Future planned efforts include PacBio sequencing of a 20 Kb library and, as discussed above, integration with an improved genetic map.

Progress toward objective 2. Shared animal populations and phenotypes.

DNA from the East Lansing international reference mapping population has been sent to many laboratories throughout the world. Similarly, DNA from the junglefowl used to generate the reference sequence assembly has been widely distributed, especially for copy number variant studies.

Progress toward objective 3. Database resources.

Database activities are led by the NRSP-8 Bioinformatics Coordinator, Jim Reecy, and Susan Lamont, along with Shane Burgess, represent poultry interests on the advisory committee for this group. Poultry bioinformatics has also benefitted from support at several other locations. We maintain a homepage for the NRSP-8 U.S. Poultry Genome project (<http://poultry.mph.msu.edu>) that provides a variety of genome mapping resources, including our newsletter archive. The Poultry Genome Newsletter is published quarterly and is distributed through our Homepage and on the angenmap email discussion group.

Meetings: Over 3,000 scientists attended the joint Plant and Animal Genome XXII meeting last January, held jointly with the annual NAGRP meeting. Coordination funds helped support attendance at PAG-XXII:

- Travel support for John Hsieh, Iowa State U. graduate student (Lamont, PI); Melissa Monson, Recipient of Neal Jorgenson Genome Travel Award, U. Minnesota graduate student (Reed, PI); Dr. Michael Romanov, U. Kent, UK
- Dr. Rachel Hawken, Cobb-Vantress, NRSP-8 workshop speaker

Impact: This project is generating tools through which the genome sequence can be used to locate inherited production trait alleles and apply the DNA sequence to ascertain the physiological basis for those traits. It has resulted, among other things, in the generation of the complete sequence of the chicken and now the turkey genome. Commercial breeders are using the sequence and SNP we generated to characterize and improve production lines using GS. In simpler terms, we are now moving closer to understanding the cause of phenotypic variation that is relevant to the agricultural use of poultry.