Opportunity Title: Research Opportunity in Animal Genetics
Opportunity Reference Code: ARS-AGIL-2017-888-0047

Organization U.S. Department of Agriculture (USDA)

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How to Apply A complete application package consists of:

- An application
- Transcript(s) – [Click here for detailed information about acceptable transcripts]
- A current resume/CV
- Two references - While two references are requested, applications will be considered without reference information. It is preferred that a complete application package contains a minimum of one reference.

All documents must be in English or include an official English translation.

Description The successful applicant be mentored by Dr. John B. Cole in the USDA Animal Genomics and Improvement Laboratory (AGIL) in Beltsville, MD. Research activities will focus on a project titled "Identification and characterization of DNA sequence variants associated with immune response in Holstein cows from a long-term selection experiment", but participation in other Laboratory projects is possible, as well. Scientists at AGIL have access to the National Dairy Database, which is the largest collection of phenotypic, genetic, and genomic information about dairy cattle in the world. This project will include collaboration with a team of scientists at AGIL, University of Minnesota (St. Paul), the US Dairy Forage Research Center (Madison, WI), National Animal Disease Center (Ames, IA), and the Pirbright Institute (UK). The University of Minnesota has cows that are part of a long-term selection experiment to compare animals with 1960s-level genetics with animals selected for improved production.

A recent study using animals from that herd found that the control-line animals have a more robust immune response to a lipopolysaccharide challenge than did selection-line animals, particularly in the TL4 pathway. Supporting data include measures of immune response, as well as proteomic, RNAseq, and micro-RNA assays. We propose to conduct whole-genome sequencing of the animals used in the immune response experiment on AGIL's Illumina NextSeq DNA sequencer. The resulting data will be aligned against a new reference assembly with higher-quality coverage of immune genes than the current University of Maryland or Baylor assemblies. Single nucleotide polymorphism genotypes for each animal will be generated from the sequence data. The control and selection lines will be compared against the existing immune response, proteomic, micro-RNA, and RNAseq data to identify differences between the lines that may explain the difference in immune response. The immune gene alleles present in each population will be identified and changes in diversity quantified. The results of this study will provide a comprehensive overview of how the immune gene regions of Holstein cows under selection for greater productivity have changed since the 1960s.

Research opportunities are full-time, normally for one year, and may be renewed for up to four additional years upon recommendation of the ARS. Appointments are contingent on the availability of funds. The selected applicant will receive a stipend as support for their living and other expenses during this appointment. Stipend rates are determined by ARS officials, and are based on the applicant's academic and professional background. The participant must show proof of health and medical insurance. Health insurance can be obtained through ORISE. The participant will not enter into an employee/employer relationship with ORISE, ORAU, USDA, ARS, or any other office or agency. Instead, the participant will be affiliated with ORISE for the administration of the appointment through the ORISE appointment letter and Terms of Appointment.

While participants will not enter into an employment relationship with ARS, this position requires a pre-appointment check and a full background investigation.

This opportunity is available to U.S. citizens, Lawful Permanent Residents (LPR), and foreign nationals. Non-U.S. citizen applicants should refer to the **Guidelines for Non-U.S. Citizens Details** page of the program website for information about the valid immigration statuses that are acceptable for program participation.

For more information about the ARS Research Participation Program, please visit the **Program Website**.

Qualifications Candidates should have a doctoral degree in animal breeding and genetics, quantitative genetics, population genetics, computational biology, or a similar field with experience in the analysis of whole-genome DNA sequence data, SNP genotype data, and related data (e.g., RNAseq or methylation data); bioinformatics; computational biology; statistical analysis; and mammalian biology.

Preferred Skills:

- Demonstrated experience with analysis of whole-genome DNA sequence data, SNP genotype data, and related data (e.g., RNAseq or methylation data)
- Bioinformatics skills, including the use of scripting languages to automate repetitive tasks and/or development of computational pipelines.
- Statistical skills preferably to include the analysis of mixed linear models using SAS or R.
- Population genetics, particularly characterization of variation in a population at the genomic level (e.g., analysis of ROH, EHH, etc.)
- Knowledge of livestock production systems and biology is desirable, but not required.

Eligibility Requirements

- **Degree:** Doctoral Degree.
- **Discipline(s):**
  - **Computer, Information, and Data Sciences** (1 👁)

- **Life Health and Medical Sciences** (12 👁)