Opportunity Title: USDA-ARS Computational Plant Biology Fellowship
Opportunity Reference Code: USDA-ARS-2021-0235

Organization	U.S. Department of Agriculture (USDA)
Reference Code	USDA-ARS-2021-0235
How to Apply	*Connect with ORISE...on the GO!* Download the new ORISE GO mobile app in the Apple or Google Play Store to help you stay engaged, connected, and informed during your ORISE experience and beyond!

A complete application consists of:

- An application
- Transcript(s) – For this opportunity, an unofficial transcript or copy of the student academic records printed by the applicant or by academic advisors from internal institution systems may be submitted. All transcripts must be in English or include an official English translation. Click here for detailed information about acceptable transcripts.
- A current resume/CV, including academic history, employment history, relevant experiences, and publication list
- Two educational or professional recommendations

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

Application Deadline	12/3/2021 3:00:00 PM Eastern Time Zone
Description	*Applications will be reviewed on a rolling-basis.*

ARS Office/Lab and Location: A research opportunity is currently available with the U.S. Department of Agriculture (USDA), Agricultural Research Service (ARS) located in Ames, Iowa.

The Agricultural Research Service (ARS) is the U.S. Department of Agriculture's chief scientific in-house research agency with a mission to find solutions to agricultural problems that affect Americans every day from field to table. ARS will deliver cutting-edge, scientific tools and innovative solutions for American farmers, producers, industry, and communities to support the nourishment and well-being of all people; sustain our nation's agroecosystems and natural resources; and ensure the economic competitiveness and excellence of our agriculture. The vision of the agency is to provide global leadership in agricultural discoveries through scientific excellence.

Research Project: Many crop species have relatives that have also been domesticated, with selection independently being applied in the various species to modify traits such as seed size, dormancy, reduction of seed dispersal, changes in taste or toxic compounds, or changes in photoperiod sensitivity or plant architecture. Within the legume family, more than two dozen species have been domesticated, including plants such as pea, soybean, peanut, and common bean. The many related but independently domesticated species offer an opportunity to determine in which cases the domestications have occurred
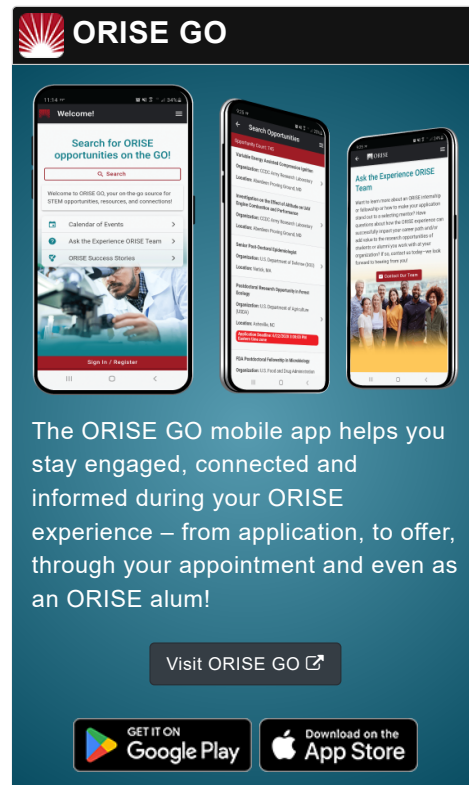
through modification of genetically corresponding (orthologous) genes, or via distinct, non-corresponding loci. This project will use a combination of analyses utilizing gene families, synteny relationships, genetic association results, and published gene functional information, to catalog and evaluate the genes involved in domestication in crops within the legume plant family. This research has applied value, through identification of genes that are likely to modify important domestication-related traits across many species. The research also addresses basic questions, such as whether domestication has preferentially operated on genes that have unusually high amounts of standing variation within wild populations.

This opportunity will involve developing and applying methods of gene family analysis in the context of the legume plant family. Use results to identify gene correspondences at several taxonomic levels – in particular, across genera, typically spanning several species of agronomic importance such as beans or chickpeas; and also across the plant family as a whole, to identify correspondences among agronomically important genes across many crop and model species in this large plant family. After identifying corresponding genes, genomic regions will be evaluated for features such as signatures of selection or diversifying or purifying selection, around genes and regions of agricultural importance.

Learning Objectives: The ORISE participant will learn and apply methods in computational biology and genetics, including: statistical methods of marker-trait association, methods for determining syntonic relationships and for calculating and representing pan-genome relationships, methods for inferring gene families and for inferring evolutionary events from large collections of gene families. The participant will also read, evaluate, and participate in writing scientific manuscripts in these areas of focus.

Mentor(s): The mentor for this opportunity is Steven Cannon (steven.cannon@usda.gov). If you have questions about the nature of the research please contact the mentor(s).

Anticipated Appointment Start Date: 2021. Start date is flexible and will depend on a variety of factors.

Appointment Length: The appointment will initially be for one year, but may be renewed upon recommendation of ARS and is contingent on the availability of funds.

Level of Participation: The appointment is full-time.

Participant Stipend: The participant will receive a monthly stipend commensurate with educational level and experience.

Citizenship Requirements: This opportunity is available to U.S. citizens, Lawful Permanent Residents (LPR), and foreign nationals. Non-U.S. citizen applicants should refer to the

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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.

ORISE Information: This program, administered by ORAU through its contract with the U.S. Department of Energy (DOE) to manage the Oak Ridge Institute for Science and Education (ORISE), was established through an interagency agreement between DOE and ARS. Participants do not become employees of USDA, ARS, DOE or the program administrator, and there are no employment-related benefits. Proof of health insurance is required for participation in this program. Health insurance can be obtained through ORISE.

Questions: Please visit our Program Website. After reading, if you have additional questions about the application process please email USDA-ARS@orau.org and include the reference code for this opportunity.

Qualifications

The qualified candidate should be currently pursuing or have received a master's degree in one of the relevant fields. Degree must have been received within the past five years.

Preferred skills:

- Graduate training in genetics and biology
- Coursework in statistics
- Experience with computer scripting languages and Unix command-line tools
- Computer programming and computational biology experience
- Training or experience in plant biology
- Experience in statistical methods related to genome-wide association analysis

Eligibility Requirements

- **Degree:** Master's Degree received within the last 60 months or currently pursuing.
- **Discipline(s):**
  - **Computer, Information, and Data Sciences** (4 👁)
  - **Life Health and Medical Sciences** (9 👁)
- **Veteran Status:** Veterans Preference, degree received within the last 120 month(s).