

United States Department of Agriculture
Project Initiation

Project Data for Accession Number 1034086

Project Title

Quantifying The Role Of The Microbiome On Turkey Growth Through Cecal Microbiota Transplantation

Project Details

Sponsoring Institution National Institute of Food and Agriculture	Project Status ACTIVE
Funding Source NIFA Non Formula	Grant Year 2025
Grant No. 2025-77045-45286	Cumulative Award Amt. \$449,020.00
Proposal No. 2023-06329	Multistate No. (N/A)
Project Start Date Sep 15, 2025	Project End Date Sep 14, 2028
Program Code [LHTR] Laying Hen and Turkey Research Program	

Project Director

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Recipient Organization

PURDUE UNIVERSITY
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Performing Department

(N/A)

Non Technical Summary

The overall goal of this project is to determine the underlying mechanism by which subtherapeutic antibiotics promote animal growth, specifically the role that commensal gut microbiota play in the growth-promoting effect of subtherapeutic antibiotics. We will usececal microbiota transplantation (CMT) to systematically control the composition of the microbiome. To do this we will harvest the digesta from the cecum (a portion of the intestinal tract between the large and small intestines) and give the bacteria from the digesta to other young turkeys. We will keep birds that recieve the transplant from control birds separate from bird receiving bacteria from birds fed antibiotics. Human microbiome research relies heavily on this same method. They observe contrasting phenotypes in human populations, transplanting human feces from each population to germ-free mice, and then determining if the same phenotype is observed in the mice as their fecal donors. If the expected phenotype is observed, the hypothesis is confirmed and that the microbiota plays a role in establishing the phenotype. Without this method, incorrect

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assumptions might be made that the microbiota plays an important role in a phenotype. This method also removes confounding factors that are common in antibiotic feeding trials. The commensal intestinal microbiota are surely not the sole cause of the animal growth phenotype, but a contributing factor among many that lead to the growth phenotypes. The key is that we will isolate the effect of the commensal microbiota via CMT to turkey poults to determine the role of the corresponding microbiota in the absence of the other factors. This project is relevant to the Laying Hen and Turkey Research Program because it will establish a controlled and reproducible method to experimentally isolate the microbiota to either confirm or refute the initial assumption of the importance of the microbiota to animal growth phenotypes.

Animal Health Component

Animal Health Component: 100%

Research Effort Categories

Basic	75%
Applied	25%
Developmental	0%

Classification

Knowledge Area (KA)	Subject of Investigation (SOI)	Field of Science (FOS)	Percent
305	3230	1100	100%

Knowledge Area

[305] Animal Physiological Processes

Subject Of Investigation

[3230] Turkey, live animal

Field Of Science

[1100] Bacteriology

Keywords

gut microbiota, cecal microbiota transplantation, subtherapeutic antibiotics, turkey growth

Goals / Objectives

While fecal transplants from humans to germ-free mice is a common practice to determine the role of the commensal microbiota on human phenotypes, a similar approach is rarely used in agricultural animal research. The goal of the proposed project is to provide new evidence of the role of the intestinal microbiome on the growth of turkeys, by employing methods that have been championed in human microbiome research. Specifically, we will transplant the microbiota from high and low performing turkeys into day of hatch turkey poults (gnotobiotic turkeys) to more specifically test the role of the complex intestinal microbial community on turkey growth and health, while controlling confounding factors of diet and antibiotic treatment side-effects. To meet this goal, we will complete the following

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objectives: Objective 1: Determine the response of the cecal microbiome succession, growth-rate phenotypes, to subtherapeutic antibiotics. Objective 2: Determine if cecal microbiota transplantation from turkeys with or without antibiotics in their diets replicates the growth-rate phenotype in recipient birds, and examine health and welfare benefits of cecal microbiota transplantation.

Project Methods

A variety of methods will be used during the execution of this project. During Objective 1, an animal experiment will be carried out in which turkeys will be raised either with or without growth promoting antibiotics. The body weights, feed consumption and welfare of the animals will be collected at least weekly. The microbiome will be analyzed by both 16S rRNA gene amplicon sequencing, a common method to determine the membership of microbial communities, and by RNA sequencing, a method to determine the genes expressed by the microbes, which provides insight into what function the microbes are performing. We will also perform a variety of analyses to determine how the microbiome changes over time and how the microbiome in antibiotic fed animals is different than the microbiome in animals not fed antibiotics. We assume that the microbiome will be most different between the two groups 1-2 weeks after introduction of the antibiotic diet, based on our previous research. Appropriate statistical testing will be used. Cecal samples from both the antibiotic group and the non-antibiotic groups will be collected and preserved appropriately for use during Objective 2. In Objective 2, cecal contents from Objective 1 will be selected for further study. The target sample will come from a timepoint when both the microbiome and the animal growth performance are different between the control and antibiotic-fed groups. The cecal contents from the two groups will be given to one day old turkey poults and kept separate as control or antibiotic-fed recipients. Recipient birds will be housed on pre-sterilized wood shavings, given autoclaved water and fed sterilized feed in attempts to reduce their exposure to contaminating bacteria. The microbiome will be analyzed from multiple timepoints of the recipient bird's life as in Objective 1, by 16S rRNA gene sequencing and RNA sequencing. We expect a change in intestinal performance as a result of cecal transplantation, so gut immune response, gut barrier function, and production of short chained fatty acids in the cecum. Again a comparison between control and antibiotic-fed recipient groups will be made to determine if simply the colonization of the digestive tract with bacteria alters animal performance and validates the importance of the microbiome on animal performance.