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Decoding the Gut Microbiome; Providing Solutions for Poultry Production

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Decoding the Gut Microbiome; Providing Solutions for Poultry Production

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Introduction

The term “microbiome” refers to all the micro-organisms within a particular environment. In poultry, the microbiome is influenced by the barn, diet, and age of the birds and is believed to modulate immunity and inflammation. In the past, culture methods were primarily used to evaluate the presence of the various micro-organisms present in the microbiome; however, recent technological advances in genomic sequencing have revolutionized sample analysis. This technology has opened new avenues of research in poultry production and our understanding of the associated health challenges. Turkey cellulitis has been a major economic and health concern for many years. Traditional bacterial culture methods indicate that multiple species may be involved in this disease with most studies implicating either *Clostridium septicum* or *Clostridium perfringens* as the primary pathogens. A recent study by Luisa de Oliveira et al. indicates that avian pathogenic *Escherichia coli* may also play an important role in the development of cellulitis. The purpose of this presentation is to share the results of a study conducted to further understand the microbiome of turkeys with cellulitis.

Research Findings

A turkey producer in the mid-west with a history of cellulitis flocks was identified for evaluation. Samples were collected from three different tom flocks all approximately 18 weeks of age. The first flock had no history with cellulitis (Control). The second flock regularly broke with cellulitis and had cellulitis related mortality at the time of sample collection. Both cellulitis negative (Cell -) and cellulitis positive (Cell +) birds were sampled. The third flock (Cell + Ab) was actively being treated for cellulitis with penicillin. Samples were taken from the gastrointestinal tract, skin, and subcutaneous tissue for microbiome analysis. *Clostridium* spp.

were found in high abundance in the subcutaneous tissue collected from Cell + and Cell + Ab birds when compared to birds without cellulitis (Control and Cell -). In the ileum, *Clostridium spp.* and *Escherichia-Shigella spp.* were the predominant bacteria found in the Cell + birds, whereas *Lactobacillus spp.* and *Romboutsia spp.* were the predominant bacteria found in the other sample groups. Samples from gastrointestinal loops and spleens collected from Cell + birds and grown in selective media yielded multiple isolates of *Clostridium perfringens*; while both *C. septicum* and *C. perfringens* isolates were found in the serosanguinous fluid collected from lesions. Whole genome sequencing on individual *C. perfringens* isolates indicated that most contained genes that confer antibiotic resistance for tetracycline and lincosamide. Interestingly, three of the *C. perfringens* isolates also contained the Beta-lactam gene which confers antibiotic resistance to penicillin. Many virulence factors were present in the *C. perfringens* isolates, with relatively fewer found on the *C. septicum* isolates. Further evaluation of gastrointestinal samples collected from these flocks also yielded multiple isolates of avian pathogenic *Escherichia coli*.

Summary

Cellulitis is a major economic and health concern to the commercial poultry industry. Studies evaluating the causative agent of cellulitis have indicated that multiple pathogens may be involved in this disease; however, to our knowledge, this is the first microbiome study conducted to evaluate the microbiome of turkeys with cellulitis. Microbiome data indicates that *Clostridium spp.* can be found in the lesions at high proportions. We also found that *Clostridium spp.* and *E. coli-shigella spp.* were highly elevated and *Lactobacillus spp.* were depressed in the ileum of birds with cellulitis. Culture identification by whole genome sequencing and PCR confirmed the presence of both *Clostridium perfringens* and *Clostridium septicum* in lesions and avian pathogenic *Escherichia coli* and *Clostridium perfringens* in the gastrointestinal tract. Taken together, these data confirm the findings of past reports and support the involvement of multiple pathogens in turkey cellulitis. This study also highlights the utility of microbiome technology for evaluating complex diseases that affect the poultry industry and will bring about new opportunities for improving poultry production.

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