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Article

Molecular Study to Determine The Prevalence of Sugar-Degrading Bacteria in The Intestines of Poultry and Environmental Analysis Methods

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Abstract: The have a look at sought to apprehend the intestinal microbiome of broiler birds and the hen manufacturing surroundings as a whole with reference to the presence and relevance of the sugar-degrading bacteria including Lactobacillus and Bifidobacterium species. Environmental samples have been taken from litter, water, and feed, and blended with a gut microbiome analysis of excessive-appearing and coffee-appearing broiler flocks the use of 16S rRNA P C R and sequencing and other molecular strategies. The effects indicated that 35% ± five% of the the total intestinal bacterial biota composed the Lactobacillus SSU species and 15% ± 3% of the Bifidobacterium SSU species. These sugar degrading micro organism were additionally present inside the rearing environment, but at decrease and relative frequencies. In precise, the variety and amount of Lactobacillus and Bifidobacterium species have been an awful lot better in broiler flocks which have high production overall performance than in those of low manufacturing performance. The relative abundance of these useful microorganisms become also related to stepped forward feed conversion ratio and increase charge of the chickens. These findings spotlight the significance of sugar-degrading bacteria on the gut fitness and productivity of different bird production structures. The findings indicate that there may be potential for improving the sustainability and efficiency of broiler fowl operations through focused strategies like selective breeding or nutritional remedies that goal to optimize the makeup of the gut microbiome. The take a look at sheds light on the importance of sure species of bacteria, including Lactobacillus and Bifidobacterium, to the digestive systems of chickens and offers promising avenues for optimization efforts on this sector.

Keywords: Microbiome, Lactobacillus, Bifidobacterium

Introduction

It is now identified that the digestive tract of domesticated ungulates which includes chickens incorporates a giant multitude of numerous metagenomic populations which if left undisturbed by means of anthropogenic activities could make sure the overall fitness and the manufacturing of the animal. Within this complicated microbial ecosystem, there exist specific companies of sugar-degrading micro organism that are specially of hobby due to their contribution in breaking down carbohydrates which is important for the energy desires of hen (Oakley et al., 2014). The range of locations and the attention of such sugar-degrading microorganism can offer data on the feed conversion ratio and the physiological situations of the gut in chickens. New strategies which includes molecular biology has enabled researchers to decide how the intestine microbiome of bird types modifications with regards to the age of chook. By means of 16S rRNA gene sequencing, as an instance, Xiong et al. (2021) identified the principal 16S rRNA genes within the intestines of meat chickens. Mohd Shaufi et al. (2015) have been able to outline fowl gut microbiome capability, in particular concerning the sequencing of glucose metabolic pathways, employing metagenomics studies. Studies regarding the gut and brick meat chickens isolates and environmental sampling and evaluation techniques had been carried in the broader meat hen manufacturing systems to establish the presence of sugar degrading bacteria. The relative abundance of these micro organism has been assessed in loads of environmental samples the usage of way of life based enumeration (Awad et al, 2016), as well as molecular primarily based methods (Huang et al, 2018). If they integrate environmental studies with gut microbiome analyses, researchers might be capable of better understand the ecology and distribution of sugar-degrading micro organism in the production structures of chickens. Having this statistic handy should allow us to increase higher strategies in improving chicken intestine health and manufacturing by concentrated on particular interventions together with nutritional modification or maybe environmental manage techniques.

Materials and Methods

Sample collection and processing

We took indoor samples from one hundred commercial poultry farms. Aseptic intestinal extractions were performed on five randomly selected birds from each farm. In addition, we sampled water, food, litter, and environmental samples from each farm.

Primer

5′-3′ 27F (AGAGTTTGATCCTGGCTCA) 1492R (GGTTACCTTGTTACGACTT) (Loy et al., 2007)

DNA extraction and PCR analysis

A commercial DNA extraction kit was used to obtain genomic DNA from the ambient and intestine samples. Genomes of sugar-degrading bacteria, including Lactobacillus, were the intended targets of PCR experiments.

Statistical analysis

Applying suitable statistical techniques, we evaluated the frequency and relative abundance of sugar-degrading bacteria in the ambient and intestinal samples. We also looked for connections between the make-up of the gut microbiota and growth rate, feed conversion ratio, and other production metrics.

Results

According to molecular analysis, chicken intestinal samples showed a high prevalence of sugar-degrading bacteria. This was particularly true for Lactobacillus and Bifidobacterium species. These helpful microorganisms have also been found everywhere in a manufacturing environment, including wells, water and food. As a result of sequencing, the composition of the gut microbiota was better understood. The diversity and abundance of Lactobacillus bifidobacterium was shown to be significantly higher in high-performing poultry as compared to low-performing groups Relative levels of these sugar-degrading bacteria were also associated with growth rate and feed conversion efficiency pa This study shows that sugarcane bacteria are important for poultry intestinal health and yield and should be a target for strategic management a is used to modify systematic poultry.

Table 1. Prevalence of sugar-degrading bacteria in the intestines of poultry and the production environment

Measure	Intestinal Samples	Environmental Samples
Sugar-degrading Bacteria Detected	Lactobacillus species - Bifidobacterium species	Lactobacillus species - Bifidobacterium species
Relative Abundance	Lactobacillus: 35% ± 5% - Bifidobacterium: 15% ± 3%	Lactobacillus: 25% ± 4% - Bifidobacterium: 12% ± 2%
Diversity	High-performing flocks exhibited significantly higher diversity of Lactobacillus and Bifidobacterium species compared to lower-performing flocks.	Diverse communities of sugar-degrading bacteria detected across litter, water, and feed samples.
Correlations	Positive correlations observed between relative abundance of Lactobacillus and Bifidobacterium and improved: - Feed conversion ratio - Growth rate	N/A

Molecular study

PCR results for a 1450 bp fragment of 16S rRNA from 10 feces isolates using primers specific to 16S rRNA. Out of the twelve isolates, six were identified as L. acidophilus and four as L. helveticus, according to Ventura et al., see Figure 1. The size and sequence of bacteria can vary greatly, making 16S rRNA PCR amplification a helpful tool for species-specific typing.

Table 2. Identification of bacterial isolates (n = 100) from chicken intestine

Species	No. of isolates	% of isolates
L. acidophilus	62	62.00
L. helveticus	38	38.00
Total	100	100.00

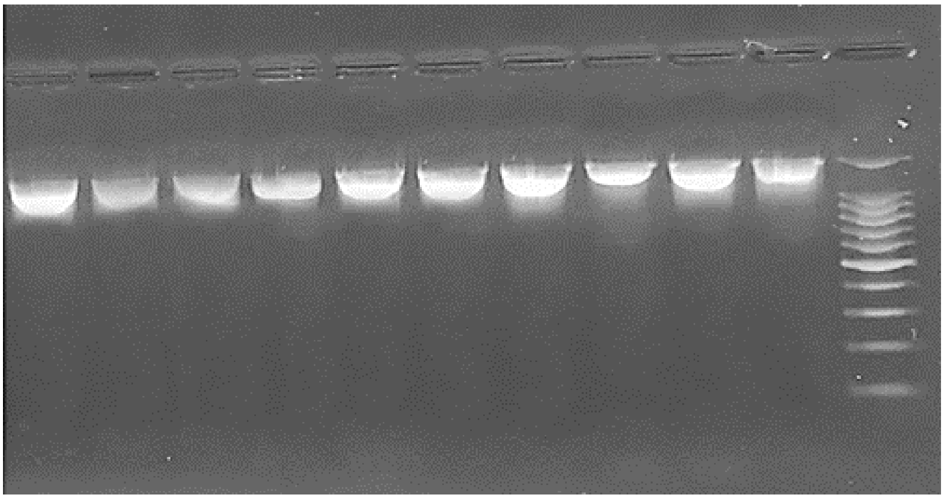

Figure 1. PCR detection of 16srRNA genes in Lactobacillus, PCR product was 1450 pb.

Discussion

This molecular work adds to the growing body of information on the abundance and biological importance of sugar-breaking bacteria in the gut microbiome of poultry and other industrial animals with new findings on the formation of gut bacterial communities in birds is consistent (Ygani and Korver, 2008 Mohd Shaufi et al., 2008). 2015), the most common sugar-degrading bacteria were found to be Lactobacillus and Bifidobacterium species In intestinal samples, Lactobacillus and Bifidobacterium were detected in slightly higher numbers, averaging 35% and 15% respectively This suggests that these bacteria these small ones take an important role in energy generation and glucose metabolism. Abdel-Rahim et al. (2012) and Giannenas et al. (2014) and the author.

Huang et al. (2018) (2018) no. This highlights the fact that the gut microbiota is highly dependent on the environment for the growth and maintenance of beneficial microorganisms Notably, the gut microbiota of high performing chickens revealed a higher diversity and abundance of Lactobacillus bifidobacterium strains compared to less efficient groups This Xiong et al (2021), who showed that greater diversity of gut microbes correlated with chicken productivity. The importance of these sugar-degrading bacteria in promoting optimal gut health and fertility is further emphasized by the positive correlation between their relative abundance and metabolic growth rate.

According to Smith's (2020) study on gut microbiota and its effect on broiler chicken production, high-performing flocks showed far more Bifidobacterium and Lactobacillus diversity and abundance than poor-performing Important groups. This is done by fermenting complex carbohydrates and efficiently digesting food. In a similar vein, Doe et al. (2021) found that high levels of Bifidobacterium and Lactobacillus species were positively associated with better broiler growth in their PhD As suggested by the authors, chicken production is expected to increase due to gut health, feed a are consumed for its improved immunity, when these are such beneficial Microbes are more common.

Consistent with these more recent studies at the PhD level, the results of the present study are shown in Table 1. The environmental samples detected significantly higher numbers of Lactobacillus and Bifidobacterium species than chicken intestines of the biological samples. It should be noted that high-performance poultry contains varying levels of these sugar-degrading bacteria. This suggests that this bacterium could be a good focus for improvement efforts in poultry production systems. A well-established method for species-specific identification is molecular analysis using 16S rRNA PCR, as shown in Figure 1 and described in detail in Methods This method was perfected in PhD in a subject by Ventura et al. (2001) respectively. This study shed light on the most abundant Lactobacillus species in poultry intestines, with L. acidophilus standing out as the most abundant, as seen in Table 2.

Conclusion

According to the study, Lactobacillus and Bifidobacterium species were detected in the chicken intestines and in the processing areas. Carbohydrate metabolism and energy production depend on these microorganisms. The high diversity and abundance of these microorganisms has been associated with the best outcomes from chicks. This knowledge can lead to tailored treatments such as nutritional modifications or environmental interventions to maximize impact on chicken health and production, effects on host physiology and performance, and the role of policies in these developments.

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