

Comparative study of poultry gut and litter microbiota through a metagenomic approach - Pandolfi J.R.^{1*}, Silva V.S.¹, Kramer B.¹, Peixoto J.O.¹, Cantão M.E.¹, Loyola W.¹, Coldebella A.¹, Voss-Rech D.¹, Trevisol I.M.¹, Esteves P.A.¹, Jaenisch F.R.F.¹, Klein T.¹, Vaz C.S.L.¹, Caron L.¹, Schiochet M.F.¹, Lopes L.S.¹, Ibelli A.M.G.¹, Tessmann A.L.¹, Morés M.¹, Brentano L.¹, Santos F.B.O.¹, Ledur M.C.¹, Ianiski F.¹, Silva M.L.B.¹

1 - *Embrapa Swine and Poultry - Concordia, SC - Brazil*

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Metagenomic studies applied to animal gut content have made possible the discovery of microbiota composition and the identification of novel microorganisms, including some uncultivable and their relationship to diseases and environment. The interrelationship between litter and avian microorganisms influences the immunity and poultry production, leading to economic and sanitary impacts. Understanding such interaction may increase broiler production and reduce losses from culling and due to other diseases related to broiler gut disorders such as salmonellosis. Thus the aim of this study is to evaluate the gut microbiota from healthy and diseased broiler flocks and their litter before and after litter treatment. Each broiler group (healthy and diseased, of same sex, age, fed and bred under the same management conditions) will be composed of pools containing ceca samples from 15 individuals of each flock. The litter 4 groups will be formed of 10 representative broiler facility sub samples, two pre and 2 post litter treatment. Nucleic acids will be isolated from samples by commercial kits and then they will be sequenced on Illumina platform. The sequence analysis will be performed by Galaxy platform, an interactive tool for analysis of genomic sequences in large scale. In addition to the tools pre-installed, new scripts will be developed and inserted to perform specific analyses. After assembly, the genes identified will be annotated by the same platform. This study will base additional research on poultry and litter health and can point to microorganisms with potential biological use, as probiotics, litter inoculum, bacteriocins and bacteriophages.

Key-words: metagenomics, broiler litter, poultry production

Embrapa project number:



Ministry of
Agriculture, Livestock
and Food Supply



Comparative study of poultry gut and litter microbiota through a metagenomic approach.

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Introduction

Metagenomic studies applied to animal gut content have made possible the discovery of microbiota composition and the identification of novel microorganisms, including some uncultivable and their relationship to diseases and environment. The interrelationship between litter and avian microorganisms influences the immunity and poultry production, leading to economic and sanitary impacts. Understanding such interaction may increase broiler production and reduce losses from culling and due to other diseases related to broiler gut disorders such as salmonellosis. Thus the aim of this study is to evaluate the gut microbiota from healthy and diseased broiler flocks and their litter before and after litter treatment.

Material & Methods

Animals

Each broiler group (healthy and diseased, of same sex, age, fed and bred under the same management conditions) will be composed of pools containing caeca samples from 15 individuals of each flock.

Litter

The litter 4 groups will be formed of 10 representative broiler facility sub samples, two pre and 2 post litter treatment.

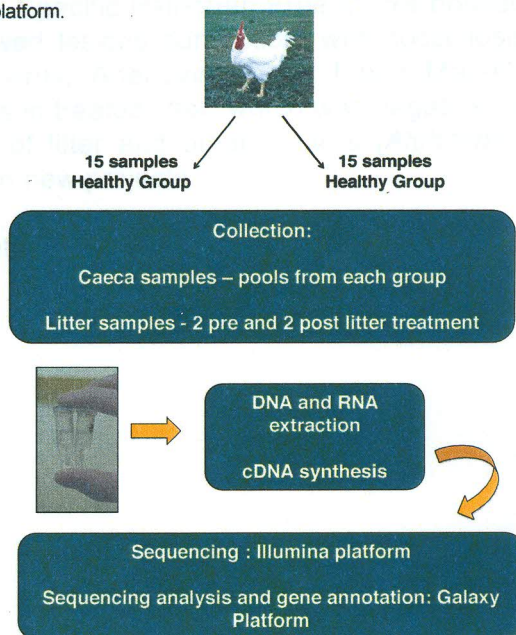


Nucleic acid isolation and sequencing

Nucleic acids (DNA and RNA) will be isolated from samples by commercial kits. cDNA will be produced from RNA and then cDNA and DNA samples will be sequenced on Illumina platform.

Bioinformatics

The sequence analysis will be performed by Galaxy platform, an interactive tool for analysis of genomic sequences in large scale. In addition to the tools pre-installed, new scripts will be developed and inserted to perform specific analyses. After assembly, the genes identified will be annotated by the same platform.



Future Directions

This study will base additional research on poultry and litter health and can point to microorganisms with potential biological use, as probiotics, litter inoculum, bacteriocins and bacteriophages.

