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Abstract Book

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GUT MICROBIOTA CHANGES ON CANARIES WITH A *MACRORHABDUS ORNITHOGASTER* INFECTION IN AN AVIARY CENTER

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Introduction: Birds have an extreme morphological diversity, diets that vary widely and a complex ecosystem which contains a huge number of microorganisms, dominated by members of the Firmicutes, with *Actinobacteria, Bacteroidetes,* and *Proteobacteria* also commonly observed. In addition, a pathological process or a treatment with antibiotics can vary considerably the intestinal flora. At present there are no works about gastrointestinal (GI) microbiota of canaries. In this study, 16S rRNA gene amplicon target sequencing has been employed to assess the gut microbiota diversity of feacal sample from healthy canaries and birds infected with *Macrorhabdus ornithogaster,* an opportunistic avian gastric yeast (AGY) that cause proventriculitis, ulceration of the digestive tract, atrophy of the pectoral muscle.

Materials and Methods: A total of 36 animals, divided into three groups, coming from a single aviary center, were used for the study: 15 healthy birds (N), 12 symptomatic birds (S) and 9 asymptomatic birds (A). DNA directly extracted from feces of birds were used to assessed the microbiota by 16S amplicon based sequencing on an Illumina MiSeq platform.

Results: Comparing the relative abundance of the main OTUs across samples, it was possible to observe that the main OTUs drove the cluster separation according to the birds status ($p < 0.001$). Differences were further demonstrated by principal component analysis (PCA), based on the relative abundance of the main OTUs, clearly showing that N samples were well separated from S and A samples. Moreover, alpha-diversity also showed that there was a higher level of complexity ($p < 0.05$) in N samples when compared to S.

Comparing the relative abundance of the main OTUs across samples, it was possible to observe that the main OTUs drove the cluster separation. In details Acinetobacter, Pseudomonas, Lactococcus and Leuconostoc were found to be characteristic of N samples (FDR < 0.05), Candidatus arthromitus, Lachnospiraceae and Staphylococcus characteristic from S samples (FDR < 0.05) while Lactobacillus and Streptococcus characteristic for A samples (FDR < 0.05).

Conclusions: Modifications of the intestinal tract due to the presence of AGY can clearly affect the modification of the gut microbiota. Birds were reared together and fed in the same way so probably the seeds can be the source of contamination. It is possible that the yeast chemically modifies the digestive tract environment by pH modification. These data suggest a possible competition between yeast and bacteria. Moreover, the results of this research confirm a link between the amount of AGY and the clinical signs of Megabacteriosis.