

**TITLE:** MOLECULAR CHARACTERIZATION OF BACTERIAL COMMUNITIES OF CLOACA AND OROPHARYNX OF PIGEONS (*Columba livia*) USING 16S rRNA MARKER SEQUENCING

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**ABSTRACT:**

The microbiota, the set of microorganisms in a body site, has great importance for health balance and is under investigation in biological studies mainly focused on domestic animals or humans. The microbiota characterization in wild animals is still poorly studied. Pigeons are worldwide distributed birds which are used for consumption, racing or ornamental purposes. In Brazil, these birds are exotic and are considered a public health problem in urban centers with high number of specimens. In the present study, a comprehensive survey of the microbial communities of pigeons' cloaca and oropharynx is presented through the use of Illumina high performance sequencing technology. Three pools of samples (n = 46) from individuals from different locations in Rio Grande do Sul, Brazil were analyzed. A total of 629,545 sequences were obtained, and 1634 OTUs were identified. The results showed that the cloaca and oropharynx microbial communities of pigeons have representatives of seven phyla and are dominated by *Firmicutes*, *Proteobacteria*, *Actinobacteria*, and *Bacteroidetes*. At the family level, more than 46 bacterial groups were identified, but only 6 of them representing more than 95% of the sequences. At genus level, the sample sequences represented 20 genera, which were considered as core microbiome. The four most abundant core genera were distributed in three dominant phyla: *Firmicutes*, *Proteobacteria* and *Actinobacteria*. The bacterial profile related to phyla was different between analyzed organs, with higher variability on oropharynx. This data suggests that external environment can have greater influence on the microbiota of bird's oropharynx and that the fecal microbiota must be involved in homeostasis maintenance. The results contribute to the basic knowledge of microbial communities in this wild bird species.

**Keywords:** cloaca microbiota, oropharynx microbiota, 16S rRNA, high-throughput sequencing, pigeons.

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