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Determining the Fecal Microbiome of Healthy Cockatiels (*Nymphicus hollandicus*) Fed Seeds vs Formulated Pelleted Diets Using Next-Generation DNA Sequencing

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Abstract: Fecal samples were collected from 34 clinically healthy cockatiels (*Nymphicus hollandicus*), with 15 consuming a commercially available seed diet and 19 on a formulated pelleted diet. Next-generation DNA sequencing was used to analyze the samples, revealing a diverse microbial landscape. A total of 179 bacterial species from 94 genera and 244 fungal species from 156 genera were identified across both diet groups. Although no significant differences in microbial diversity were observed between the 2 groups, distinct microbial compositions were noted. Notably, *Corynebacterium kroppenstedtii* and *Enterococcus durans/faecium* were enriched in the pellet-fed group, whereas *Lactobacillus oris* and a species in the Brevinemataceae family were more abundant in the seed-fed group. In the mycobiome, *Aspergillus penicillioides*, *Meyerozyma* sp, and *Fusarium* sp were enriched in the pelleted diet group, whereas *Bulleribasidium oberjochense* was more prevalent in the seed diet group. These findings highlight the nuanced effects of diet on the fecal microbiome of cockatiels, providing valuable insights for avian health management and potential probiotic interventions.

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