

# Characterization of the skin microbiome of dogs with strong body odor and the effect of a spot-on product

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**Abstract:** Next-generation sequencing (NGS) has been used to evaluate the cutaneous microbiota. This study investigated the bacterial and fungal microbiota on the skin of healthy dogs with and without strong body odor and how the use of Dermoscent Essential 6<sup>®</sup> spot-on (Bayer, Shawnee Mission, KS, USA) influenced body odor and the microbial communities. We hypothesized that dogs with strong body odor would have dysbiosis of their skin microbiota with increased abundances of *Staphylococcus* and *Corynebacterium* spp. Skin swab samples were collected on day 0 and week 4 from two body regions (axilla and dorsum) of eight dogs without, and 16 with strong body odor. Dogs with strong body odor were randomly divided into a placebo or treatment group, and received four weekly topical applications. DNA was extracted and the bacterial 16S rRNA was amplified and sequenced using NGS. Additionally, quantitative PCR for *Malassezia*, *Staphylococcus* spp., and *Staphylococcus pseudintermedius* was performed. Average body odor grading was higher in the strong body odor groups compared to the control group at day 0. Body odor was significantly reduced at week 4 in the treatment group ( $P < 0.05$ ), but not the placebo group. NGS analysis demonstrated significant differences in bacterial communities between study groups ( $P < 0.05$ ). Increased abundances of *Malassezia*, *Staphylococcus* spp., and *Staphylococcus pseudintermedius* in strong odor dogs at day 0 by quantitative PCR ( $P < 0.05$ ) expanded upon NGS findings. Healthy dogs with strong body odor had reduced diversity of their skin microbiota. Further investigations are needed to better identify microorganisms responsible for body odor in dogs.

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