

INFLUENCE OF SCAT AGEING ON THE GUT MICROBIOME

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Abstract

The study of the host-microbiome by the collection of non-invasive samples has the potential to become a powerful tool for conservation monitoring and surveillance of wildlife. However, multiple factors can bias the quality of data recovered from scats, particularly when field-collected samples are used given that the time of defecation is generally unknown and could have been as recent as hours, days, or weeks. Previous studies using scats have shown that exposure to aerobic conditions can compromise the microbial composition and that this rate of exposure differs between species. However, the impact that this aging process has on the relationship between the bacterial and fungal composition has yet to be explored. In this study, we measured the effects of time post-defecation on bacterial and fungal compositions and structures in a controlled experiment using scat sample from the endangered koala (*Phascolarctos cinereus*). We found that targeting the core of the scat for DNA extraction reduced the impact of oxygen exposure as we did not observe the previously reported reduction in obligate anaerobic bacteria nor an increase in facultative anaerobes even after aging for 10 days. We found that even though bacteria remain stable through the scat aging process, the fungal composition did not. We report a cluster of fungal taxa that colonises scats after defecation which can dilute the genetic material from the autochthonous mycoflora and inhibit recovery. Finally, we propose strategies to combat the effects of time and preserve the integrity of a scat sample collected in the wild.

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