

## ITS1 amplicon sequencing of feline gut mycobiome of Malaysian local breeds using Nanopore Flongle

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### ABSTRACT

The gut mycobiome exhibits major influence on the gastrointestinal health and disease but received less attention due to low abundance. This study characterizes the fungal community and compares the microbial diversity between indoor and outdoor cats. Genomic DNA was extracted and sequenced by targeting the Internal Transcribed Spacer 1 (ITS1) region using Flongle flow cell on MinION™ sequencing platform. Results show the phylum Ascomycota and genus *Peniophorella* were numerous in indoor cats, whereas the Basidiomycota and *Pichia* were abundant in outdoor cats. *Peniophorella* formed the core mycobiome in both feline populations. Furthermore, alpha ( $p$  value = 0.0207) and beta diversities ( $p$  value = 0.009) results showed significant differences between the two groups. Overall, indoor cats have greater amounts of *Peniophorella*, whereas outdoor cats have higher *Trichosporon* and unclassified Sordariaceae. The study also suggests that keeping a cat indoors or left as a stray will affect their respective gut mycobiome.

### KEYWORDS

Feline gut; Flongle; Fungi; Malaysia; Mycobiome

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