

Baboon vaginal microbial flora

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Abstract

BACKGROUND:

Knowledge of the composition of vaginal microbial ecosystem is essential for understanding the etiology, prevention, and treatment of vaginal diseases. A baboon model has been used to provide detailed understanding of reproductive physiology and immunology applicable to women. However, little is known about the composition of its vaginal microbial ecosystem.

METHODS:

Gram stain and Nugent scores were used for assessment of baboon vaginal microbial flora. Biochemical identification and analysis of isolates were performed using the api(®) kits and identification software.

RESULTS:

Species of Lactobacilli, Staphylococci, Clostridia, Bacilli, Corynebacteria, Gram-negative rods, other Gram-positive rods, cocci and Candida, were isolated. Healthy vaginal microbiota consisted mainly of lactobacillus morphotypes. Animals with high Nugent scores had increased number of Gram-positive cocci and variable rods, with increased number of Gram-negative morphotypes.

CONCLUSIONS:

The baboon vaginal microbiota is heterogeneous in terms of species composition and is typified by a scarcity of lactobacilli.

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KEYWORDS:

Papio anubis; bacteria; culture; non-human primates; reproductive tract

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