
Title

16s gene metagenomic characterization in healthy stallion semen

Abstract

Studies on the bacterial composition of seminal samples have primarily focused on species isolated from semen and their effects on fertility and reproductive health. Culture-independent techniques, such as 16S rRNA gene sequencing and shotgun metagenomics, have revolutionized our ability to identify unculturable bacteria, which comprise >90% of the microbiome. These techniques allow for comprehensive analysis of microbial communities in seminal samples, shedding light on their interactions and roles. In this study, we characterized the taxonomic diversity of seminal microbial communities in healthy stallions using 16S rRNA gene sequencing. Semen samples were collected from four stallions during the reproductive season, and DNA was extracted for sequencing. The results revealed a diverse array of bacterial taxa, with Firmicutes, Bacteroidota, and Proteobacteria being predominant phyla. At the family and genus levels, significant variations were observed among individuals, with individual variability in microbial richness and diversity standing out. Moreover, each stallion showed a distinct microbial fingerprint, indicating the presence of a characteristic microbial core for each stallion. These results underscore the importance of considering individual microbial profiles in understanding reproductive health and fertility outcomes. © 2024 Elsevier Ltd

Authors

Núñez-Montero K.; Leal K.; Rojas-Villalta D.; Castro M.; Larronde C.; Wagenknecht L.; Contreras M.J.

Author full names

Núñez-Montero, Kattia (57195945450); Leal, Karla (57188866192); Rojas-Villalta, Dorian (57996798300); Castro, Macarena (58533449900); Larronde, Carolina (59011564000); Wagenknecht, Lisbeth (58837416200); Contreras, María José (57214328539)

Author(s) ID

57195945450; 57188866192; 57996798300; 58533449900; 59011564000; 58837416200; 57214328539

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Affiliations

Facultad de Ciencias de la Salud, Instituto de Ciencias Aplicadas, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Instituto de Ciencias Aplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Biotechnology Research Center, Department of Biology, Instituto Tecnológico de Costa Rica, Cartago, 30101, Costa Rica; Doctorado en Ciencias Aplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Facultad de La Salud, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Haras La Gloria, Vilcún, Chile

Authors with affiliations

Núñez-Montero K., Facultad de Ciencias de la Salud, Instituto de Ciencias Aplicadas, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Leal K., Instituto de Ciencias Aplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Rojas-Villalta D., Biotechnology Research Center, Department of Biology, Instituto Tecnológico de Costa Rica, Cartago, 30101, Costa Rica; Castro M.,

Doctorado en Ciencias Aplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Larronde C., Facultad de La Salud, Universidad Autónoma de Chile, Temuco, 4810101, Chile; Wagenknecht L., Haras La Gloria, Vilcún, Chile; Contreras M.J., Instituto de Ciencias Aplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Temuco, 4810101, Chile

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Correspondence Address

M.J. Contreras; Universidad Autónoma de Chile, Temuco, Avenida Alemania #1090, Chile; email: maria.contreras@uautonoma.cl

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