

Notes and Comments

Intra and inter-monkey transmission of bacteria in wild black capuchins monkeys (*Sapajus nigritus*): a preliminary study

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Black capuchin monkeys (*Sapajus nigritus*) are characterized by presence of robust capuchin monkeys, which have adornments or tufts on the head. Monkeys live in a social structure involves hierarchies of dominance between males and females, which results in different behaviors, such as agonistic, affiliative, and cooperative (Valença-Silva et al., 2014; Back et al., 2019). Some authors have even suggested that pro-social and affiliative behaviors (grooming, licking or kissing) might have been in part, evolved in the microbial transmission (Ezenwa et al., 2012). The gastrointestinal microbiota of primates is composed by a diverse microbial community, including *Enterococcus* sp (Lebreton et al., 2014). The idea of interaction between microbiota and behavior have stimulates the development of novel research to analyze the social contact and acquisition/exchange of commensal and symbiotic microbial. Thus, our aim was to investigate if there is a correlation between oral and fecal enterococci isolated from wild black capuchins monkeys.

Paired oral and rectal swabs were collected from five wild black capuchin monkeys living in a forest fragment in Santa Cruz do Sul – Brazil (29° 43' 03" S; 52° 25' 33" W). Wild capuchin monkeys were captured and manipulated using conventional methods according to the protocol for sample collection described by Instituto Chico Mendes de Conservação da Biodiversidade [ICMBio] using Tomahawk-type cages. The sample collection was approved by Information Authorization System in Biodiversity number 56640. Isolation of enterococci was performed as previously described by Santestevan et al. (2015). Collected bacteria were identified by MALDI-TOF MS and PCR amplification. Similarity between RAPD fingerprints was calculated using the simple association coefficient and cluster analysis, applying the Unweighted Pair Group Method with Arithmetic Mean (UPGMA). The strains grouping coefficients of similarity of $\geq 75\%$ for RAPD typing were applied.

A total 114 *Enterococcus* spp. were isolated from paired samples, being *E. faecalis* (n=96) and *E. casseliflavus* (n=14) detected in both cavities, and *E. hirae* (n=4) only in one oral cavity. Using RAPD, we assessed the genetic relationships between oral and rectal strains, and the results showed an inter- or intra-transmission of enterococci among the monkeys. Clusters IV, V and XVII were composed by oral and rectal strains isolated from the same monkey, suggesting that autocoprophagy as mechanism of enterococci transmission. The clusters XI and XI were also formed by oral and rectal strains; however, these were isolated from different monkey suggesting that allocoprophagy as another mechanism of enterococci transmission. Two other clusters were formed by enterococci species isolated from rectal swabs from different monkey, suggesting that these bacteria might be transmitted through affiliative behavior (Figure 1). There are good evidences that gut microbial manipulate the food cravings in hosts to optimal resource for bacterial growth and induce host social interaction to facility the bacterial transmission. In addition, Schmidt et al. (2019) demonstrated the oral-fecal transmission and suggested that this transmission is an important process that shapes the gastrointestinal microbiota in health and disease.

Therefore to our knowledge, this is the first study that reports the genetic relationships between oral and rectal enterococci isolated from wild black capuchin monkeys. In conclusion, despite of the fact that a low number of samples were used for comparison- justified by the difficulties to find and capture wild monkeys- this preliminary analysis suggest that coprophagy and affiliative behaviors might have an important role in shaping and maintenance of enterococci in wild monkeys. In addition, to exploring of interactions of social dynamics and microbiota in wild populations, could be an insight for future research.

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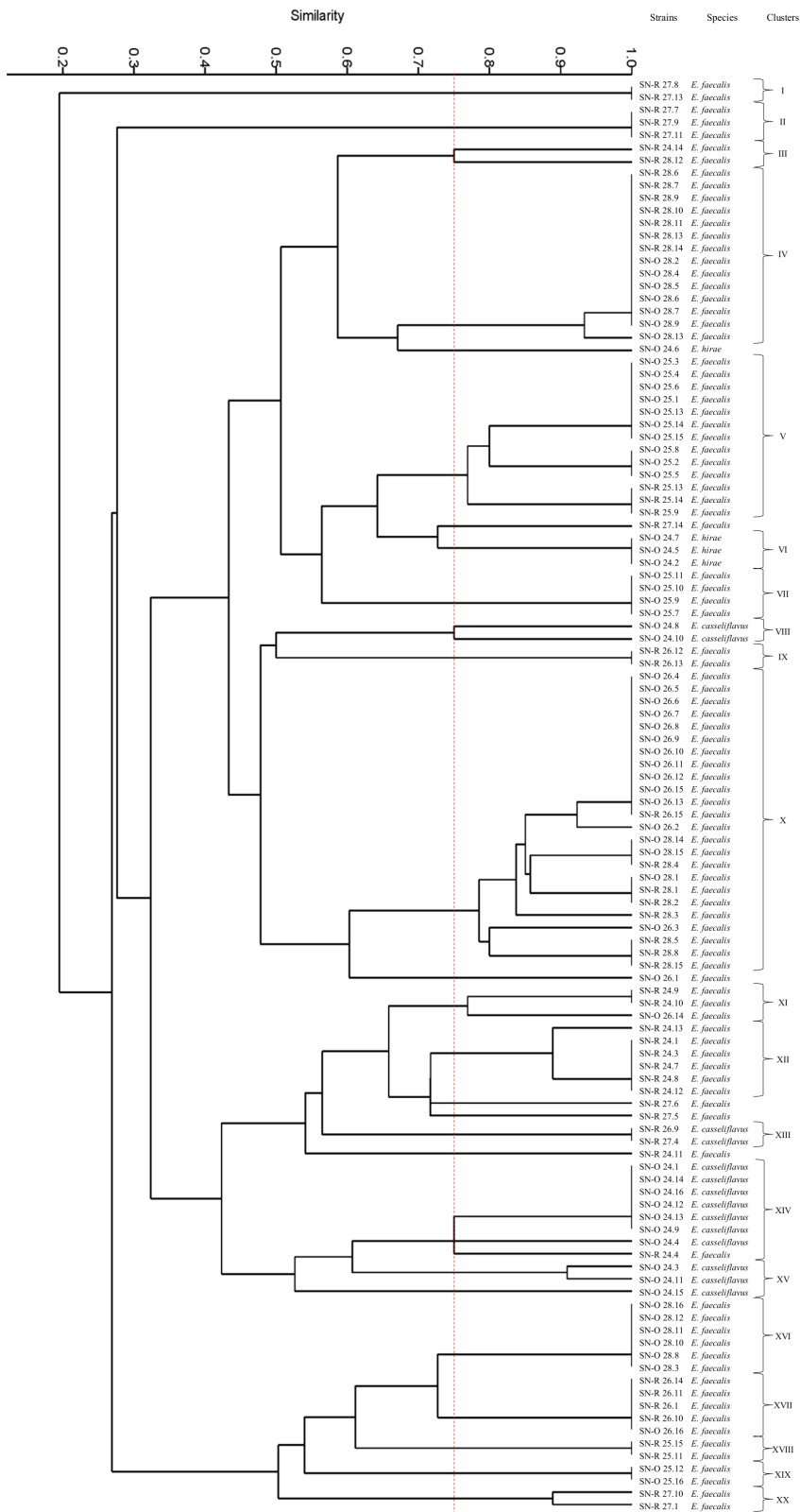


Figure 1. Unweighted Pair Group Method with Arithmetic Mean-dendrogram showing clustering pattern for 26 genotypes of enterococci isolated from paired oral (O) and rectal (R) swabs of black capuchin monkeys (*Sapajus nigritus*-SN). UPGMA using Sorensen-Dice coefficients of similarity (> 75%).

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References

- BACK, J.P., SUZIN, A. and AGUIAR, L.M., 2019. Activity budget and social behavior of urban capuchin monkeys, *Sapajus* sp. (Primates: cebidae). *Zoologia*, vol. 36, pp. 1-10. <http://dx.doi.org/10.3897/zoologia.36.e30845>.
- EZENWA, V.O., GERARDO, N.M., INOUYE, D.W., MEDINA, M. and XAVIER, J.B., 2012. Animal behavior and the microbiome. *Science*, vol. 338, no. 6104, pp. 198-199. <http://dx.doi.org/10.1126/science.1227412>. PMID:23066064.
- LEBRETON, F., WILLEMS, R.J.L. and GILMORE, M.S., 2014. *Enterococcus* diversity, origins in nature, and gut colonization. In: M.S. GILMORE, D.B. CLEWELL, Y. IKE and N. SHANKAR, eds. *Enterococci from commensals to leading causes of drug resistant infection*. Boston: Massachusetts Eye and Ear Infirmary, pp. 1-52.
- SANTESTEVAN, N.A., ANGELIS ZVOBODA, D., PRICHULA, J., PEREIRA, R.I., WACHHOLZ, G.R., CARDOSO, L.A., DE MOURA, T.M., MEDEIROS, A.W., AMORIN, D.B., TAVARES, M., D'AZEVEDO, P.A., FRANCO, A.C., FRAZZON, J. and FRAZZON, A.P., 2015. Antimicrobial resistance and virulence factor gene profiles of *Enterococcus* spp. isolates from wild *Arctocephalus australis* (South American fur seal) and *Arctocephalus tropicalis* (Subantarctic fur seal). *World Journal of Microbiology & Biotechnology*, vol. 31, no. 12, pp. 1935-1946. <http://dx.doi.org/10.1007/s11274-015-1938-7>. PMID:26347323.
- SCHMIDT, T.S., HAYWARD, M.R., COELHO, L.P., LI, S.S., COSTEA, P.I., VOIGT, A.Y., WIRBEL, J., MAISTRENKO, O.M., ALVES, R.J., BERGSTEN, E., DE BEAUFORT, C., SOBHANI, I., HEINTZ-BUSCHART, A., SUNAGAWA, S., ZELLER, G., WILMES, P. and BORK, P., 2019. Extensive transmission of microbes along the gastrointestinal tract. *eLife*, vol. 8, no. e42693, pp. 1-18. <http://dx.doi.org/10.7554/eLife.42693>. PMID:30747106.
- VALENÇA-SILVA, G., MACIEL, F.G., ZAGANINI, R.L., LUCINDO, A.S., CARAMASCHI, S. and PAULA, H.M.G., 2014. Reporting social behaviours of mixed-species troops formed by *Callithrix jacchus* and *Callithrix penicillata* (Primate, Callitrichidae). *Brazilian Journal of Biology = Revista Brasileira de Biologia*, vol. 74, no. 3, pp. 607-611. <http://dx.doi.org/10.1590/bjb.2014.0091>. PMID:25296209.