TITLE: DISTRIBUTION PATTERN OF THE BACTERIAL COMMUNITY PRESENT IN HUMAN TONGUE

AUTHORS: NOVELLO, B.[1]; PEREIRA, R. S.[1]; DE LACERDA, J. R. M.[1]; LOPES, I. D. N.[1]; LANDIM, C. F. A. L.[1]; SELDIN, L.[1]; JURELEVICIUS, D. A.[1]

INSTITUTION: 1.UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, RIO DE JANEIRO, RJ (CENTRO DE CIÊNCIAS DA SAÚDE, AVENIDA CARLOS CHAGAS FILHO, 373, CIDADE UNIVERSITÁRIA, ILHA DO FUNDÃO, CEP 21941-902, RIO DE JANEIRO – RJ, BRASIL)

ABSTRACT:

Oral microbiome is one of the most diverse and complex of the human body. Among the different niches in human oral cavity, the tongue forms a unique ecological site that provides a large surface area favoring the accumulation of oral debris and microorganisms. Microbial community of tongue surface is easily influenced by personal habits such as diet, hygiene, among others. However, little is known about how individual habits may affect the structure of bacterial community present on tongue surface. Therefore, the aim of this study was to evaluate the distribution and the factors that shape the bacterial community on surface of human tongue. To this purpose, 3 groups of healthy individuals were analyzed: (i) 15 students from Odontology – coded as OD; (ii) 32 from Nutrition – NUT; and (iii) 4 students from the Laboratory of Microbial Biotechnology and Ecology – LABEM. All individuals were submitted to a qualitative and quantitative questionnaire about their habits of hygiene, diet and exercises. In addition, microbial community presented on their tongue surface was sampled with assistance of sterile swabs. Later, the bacterial community of each sample was analyzed by Polymerase Chain Reaction - Denaturing Gradient Gel Electrophoresis (PCR-DGGE).Further, PCR-DGGE bands profiles were compared using multivariate analysis and biostatistics. Additionally, the presence of genes related to bacterial resistance to ß-lactams (genes bla_{MOX} and bla_{CIT}) and vancomycin (gene *van*) was investigated using PCR. The questionnaire analysis did not showed the presence of a dominant behaviourof the groups OD, NUT or LABEM. However, the multivariate analysis of PCR-DGGE profiles demonstrated the structure of bacterial community present on tongue from individuals of OD group share more similarity between themselves than with bacterial community presentin individuals from NUT and LABEM. In addition, the PCR-DGGE analysis showed the richness and diversity of bacterial community present on surface tongue of OD group (Chao1=11±1,6 e Shannon H`= 2,8±0,1, respectively) were higher than observed in NUT (Chao1= 9,93±4,7e Shannon H`= 2,0±0,5, respectively). The results did not showed the presence of genes related to bacterial resistance to ß-lactams and vancomycin in the analyzed samples. The results suggest daily contact, more than the personal habits, are responsible to shape the bacterial community present in the human tongue.

Keywords: Oral microbiome; Personal habits; Tongue surface

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