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<b>Título</b>	Microbiome analysis of sputum from patients with chronic lung disease in cystic fibrosis
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Microbiological communities in the airway of Cystic Fibrosis (CF) patients may be associated with clinical conditions and bacterial infections. The main aim of this study was to establish the correlation between the airway microbiome and the bacteriological culture. We also correlated the microbiome data with CFTR mutation and hospitalization status of CF patients. Sputum collected for routine bacteriological culture of 27 CF patients were submitted to microbiome sequencing. Library of 16S rRNA was prepared according to a standard protocol using a V3V4 region. The amplicon sequences variants (ASV) obtained from sequencing were compared with the CFTR mutation and laboratory parameters. Data of the CFTR mutation and hospitalization status were obtained from the hospital records of the patients. The genus *Staphylococcus* and *Pseudomonas* were detected by microbiome analysis in all 27 sputa while *Staphylococcus aureus* was identified in only 19 (70.4%) and *Pseudomonas aeruginosa* in only 9 (33.3%) sputa by bacteriological culture. In 14 specimens the genus *Burkholderia* (*Burkholderia*–*Caballeronia*–*Paraburkholderia*) was detected by microbiome analysis, however the *Burkholderia cepacia* complex was identified in only 8 sputa by bacteriological culture. A lower alpha diversity was directly correlated to the hospitalized patients. There was no significant difference in alpha diversity and CFTR mutations. Evaluation of the airway microbiome of CF patients plays an important role to better understand the pulmonary microbiota and to anticipate the detection of common CF pathogens.