TITLE: FILLING THE GAP BETWEEN RARE AND ABUNDANT BIOSPHERES: CONSIDERATIONS ABOUT THE FREQUENCY OF OCCURRENCE OF MICROBIAL COMMUNITIES.

AUTHORS: JONCK, C.R.¹²; PELLIZARI, V.H.²

INSTITUTION: 1-CENTRO DE PESQUISAS LEOPOLDO AMERICO MIGUEZ DE MELO (CENPES). R. Horácio de Macedo 950, Rio de Janeiro, RJ. CEP 21941598. 2-INSTITUTO OCEANOGRÁFICO DA UNIVERSIDADE DE SÃO PAULO (IO-USP). Praça do Oceanográfico 191, São Paulo, SP. CEP 05508120.

ABSTRACT:

The definition of "frequency of occurrence" (FO) categories for microbial species has always been confused. Abundant organisms, for example, are considered to have more than 1% of the total number of cells in a sample, a cut-off defined by the sensitivity of fingerprint techniques. The definition of rare species are even more subjective, being defined by different cut-offs (0.1, 0.01%) or a random number of sequences. These definitions co-evolve with the available detection technology. The only constant in these definitions is the arbitrariness. However, they end up creating a knowledge gap in the structure of the microbial communities surveyed, the often overlooked intermediate section. Using NGS of the 16S gene, we characterized the microbial communities of eight streams located in the four major Brazilian biomes (Amazon, Atlantic Forest, Cerrado and Caatinga). Considering that species abundance distribution of microbial communities are skewed, we use the Gini inequality index projected into Lorenz curve to define a limit above which the organisms would be considered abundant (g/2 projected in L) and another limit below which organisms would be considered rare (g+(1-g)/2) projected in L). We define the gap between them as the intermediate biosphere. We evaluated community's dissimilarity (Bray-Curtis) and taxonomic profiles (phylum-level) for each FO segment (abundant, intermediate and rare) and compared their results to the profile of full communities. Abundant segments share more than 90% of species while rare segments share less than 40%. The intermediate segment shows more than 75% coincidence, a value closer to the full community similarity (60%). Taxonomic profiles are highly dominated by Proteobacteria in the abundant segments. This dominance is gradually replaced with increasing diversity of phyla in the intermediate and rare segments. Again, the profile of the intermediate segment was the closest to the full community profile. The confusion in the definition of FO categories is evidenced by the amount of unassigned sequences in each segment. While the abundant has none and the rare ones have about 5%, the intermediate biosphere has near 20% of unassigned sequences in all ecosystems surveyed. Therefore, the intermediate biosphere can be an important source of news regarding the discovery of new organisms. In addition, it can become a good source of ecological data, since it is the segment that best represents the full microbial community.

Keywords: frequency of occurrence, microbial communities, intermediate biosphere, rares, abundants.