

Title:

Small-scale biogeography of biofilms

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Abstract (300 words maximum):

Biofilms hold the majority of the microbial biomass not only in natural and anthropic environments, but also within hosts. However, biofilms monitoring is often limited to small surface areas, potentially providing limited information on larger fractions of these ecosystems. In this study, we use shower hoses as a model system to assess the degree of small-scale biogeography and community structure in macroscopically homogeneous or heterogeneous environments, as well as the possibility to upscale their diversity estimates. Two datasets were composed of 16S amplicon sequences and flow cytometric counts obtained from 200 pieces (1.2 cm long; top and bottom section) from two shower hoses in controlled and real-usage conditions representing, respectively, macroscopically homogeneous and heterogeneous environments. A third dataset consisted of 16S sequences from 85 shower hoses installed in a single building (i.e., heterogeneous environment with physical disconnection). While a non-uniform bacterial community was expected along the real-usage hose due to environmental conditions heterogeneity, both community structure and composition changed significantly also along the control hose where no macroscopic heterogeneity was present. Despite this, only around 10% of the total area was sufficient to accurately estimate the overall diversity. Conversely, this percentage increased to 60% and 66% in the case, respectively, of the real-usage hose and different shower hoses within a building, suggesting that a similar degree of heterogeneity was present despite the different connectedness of the two types of environments. Finally, local diversity estimates highlighted that only a very limited fraction of OTUs (<10%) are present at distances compatible with metabolic interactions (5 – 20 μm), indicating the limited opportunities for interaction of single bacteria arising due to the biofilm spatial structure. These results provide useful insights regarding biofilm community assembly important, not only, to understand community function, but also to design reliable biofilm monitoring campaigns.