In a previous work, we have observed that the phyllosphere of different plant species, select for distinct bacterial communities, and that each phyllosphere may harbor a substantial number of unknown bacterial species. Our estimates point from 2 to 13 million of new bacterial species in the canopy of the Atlantic Forest. In another work, developed in a 10 ha permanent plot at the Carlos Botelho State Park, we have observed that the bacterial communities in the phyllosphere of plants phylogenetically closer, were more similar to each other than in the phyllosphere of plants phylogenetically more distant. Also relevant is the fact that, even considering the spatial variability of the bacterial community structure in the phyllosphere of plants of the same species at different geographical positions, such variation is smaller than that observed among individuals of different species. Our data suggest that the bacterial populations in the phyllosphere are selected by the plant species, and that each plant species harbor a unique bacterial community in its phyllosphere. The analyses of the bacterial community associated to the bark of the same plant species revealed low bacterial species richness, with the dominance of few genera, as compared to the phyllosphere, and community structures defined by the plant species as well. In contrast, the soil under the canopy of the tree species sampled showed bacterial communities with higher species richness, as compared to phyllosphere and bark, with lower spatial variability and less dependency on the plant species. In general, our data points to a new paradigm in microbial ecology: the microbial diversity associated to the plant surfaces may be as high as the diversity in the soil, considered the environment with the highest known microbial diversity. Understanding the functional roles of these microorganisms in the phyllosphere and the soil of the Atlantic Forest is not a trivial task, even though the advances in the analytical techniques have significantly contributed to that. Hence, establishing a relationship between phylogeny and metabolic function is crucial for determining which microbial groups are essential for ecosystem sustainability, in particular for the C and N cycles. In the proposed project, we aim to evaluate the bacterial and fungi diversity in the phyllosphere and soil, respectively, in four 10 ha permanent plots of the Biota program, at Cardoso Island State Park (High Restinga Forest), Carlos Botelho State Park (Dense Ombrophylous Forest) and Assis Ecological Station (“Cerradão”), and their possible relationships with biochemical processes relevant for the functionality of forest ecosystems, using metaproteomics. In addition, we aim to quantify the biological nitrogen fixation and the diversity of diazothrophs in 1 ha permanent plots of a Dense Ombrophylous Forest at the Serra do Mar State Park.
SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

We have confirmed, using pyrosequencing, that the bacterial community structure in the phyllosphere of plants of the same species are more similar to each other than to plants of different species. Additionally, we have observed that the bacterial community structure in the phyllosphere of phylogeneticaly related plants are more similar, suggesting that bacterial communities co-evolved with their plant hosts. In addition, we have observed that the bacterial communities in the phyllosphere of M. robusta show geographical patterns of organization, with similarity in community structure decreasing with geographical distances. The bacterial community structure in the phyllosphere is also affected by organic volatile compounds released by the leaves, which might be important determinants of bacterial survival in such environment. Analyzing the meta proteome of the microbial community in the phyllosphere of several plant species, we have identified several microbial proteins putatively involved in transport, biofilm formation, stress responses, anti-oxidative responses, and nitrogen fixation. Biological nitrogen fixation has been measured in the phyllosphere and dermosphere of several plant species and seems to contribute with a significant part of N input in the Atlantic Forest.

MAIN PUBLICATIONS