Letter to the Editor

Verrucomicrobia in Brazilian Atlantic Forest Soil

The Brazilian Atlantic forest is one of the main biodiversity hot spots in the world (4). This biome stretches along the Brazilian Atlantic coast, from the state of Rio Grande do Norte to Rio Grande do Sul, with an original area of 1,233,875 km² that has been reduced to less than 8% of its original cover (Fig. 1). Also included in this hot spot is the offshore archipelago of Fernando de Noronha and several other islands off the Brazilian coast. In fact, the Atlantic forest is a continental biome; it extends inland to eastern Paraguay, into northeastern Argentina, and narrowly along the coast into Uruguay.

Recently, Faoro et al. (2), using a culture-independent approach based on 16S rRNA gene sequences to survey the bacterial community of the southern Atlantic forest soils, presented the first work on the bacterial biodiversity in this biome. Samples were collected along the PR 410 highway in the state of Paraná, Brazil, which traverses 28.5 km of an area of Atlantic forest between 25°19.181’S and 25°32.515’S and 48°43.028’ to 48°55.654’W. Overall, the phylogenetic analysis, based on 894 partial 16S rRNA gene sequences, showed an overlap in the bacterial community composition with the previous scenario demonstrated in the Southeast Atlantic forest soil (2). For instance, Acidobacteria and Proteobacteria were the most frequent phyla on both ecosystems. Interestingly, contrasting with the data of Faoro et al. (2) the Verrucomicrobia phylum, apparently absent in the South Atlantic forest, was one of the most abundant groups in the Southeast Atlantic forest soil, with a prevalence ranging from 6% to 14%, depending on the soil sample (1). Verrucomicrobia is a recently described phylum abundant in soils (3), which comprises only a few described species. The difference in the bacterial phylum’s prevalence and composition in the two surveys can be due to specific contributions of physicochemical, geographic, and anthropogenic factors in the ecosystems of this biome. This scenario is just starting to reveal the extraordinary level of bacterial biodiversity in this almost unexplored reservoir.

Almost at the same time, our group published the second work on the same topic, bacterial biodiversity of the Atlantic forest soil (1). Our study used an approach similar to that used by Faoro et al. (2) to survey the bacterial community of the Southeast Atlantic forest soil. Samples were collected in another ecosystem, the Serra dos Orgãos National Park (PARNASO) in Rio de Janeiro state. This park is located ca. 150 km from Rio de Janeiro city in the Serra do Mar mountain range, reaching up to 2,263 m above sea level in some locations, between 22°52’ and 22°54’S and 42°09’W. Nonetheless, the phylogenetic analysis, based on 894 partial 16S rRNA gene sequences, showed an overlap in the bacterial community composition with the previous scenario demonstrated in the South Atlantic forest soil (2). For instance, Acidobacteria and Proteobacteria were the most frequent phyla on both ecosystems. Interestingly, contrasting with the data of Faoro et al. (2) the Verrucomicrobia phylum, apparently absent in the South Atlantic forest, was one of the most abundant groups in the Southeast Atlantic forest soil, with a prevalence ranging from 6% to 14%, depending on the soil sample (1). Verrucomicrobia is a recently described phylum abundant in soils (3), which comprises only a few described species. The difference in the bacterial phylum’s prevalence and composition in the two surveys can be due to specific contributions of physicochemical, geographic, and anthropogenic factors in the ecosystems of this biome. This scenario is just starting to reveal the extraordinary level of bacterial biodiversity in this almost unexplored reservoir.

We thank Heloisa Diniz from the Image Treatment and Production Service (IOC/FIOCRUZ) for technical support.

REFERENCES


Cristiane Carneiro Thompson
Erica Lourenço da Fonseca*
Ana Carolina Paulo Vicente
Laboratory of Molecular Genetics of Microorganisms
Oswaldo Cruz Institute, FIOCRUZ
Avenida Brasil 4365, Manguinhos
Caixa Postal 926, CEP 21040-360
Rio de Janeiro, RJ, Brazil

*Phone: 55-21-3865-8168
Fax: 55-21-2260-4282
E-mail: ericafon@ioc.fiocruz.br

Authors’ Reply

The distribution of the Verrucomicrobia phylum in soils is variable and apparently extremely sensitive to changes in the environment. This is exemplified by two recent works that analyzed the bacterial biodiversity in the Brazilian Atlantic Forest.
forest based on the 16S rRNA gene sequence. One of these was conducted in the Atlantic forest located in the southern region (3) and the other in the southeastern region (1), about 850 km distant. The major difference observed was the absence of the Verrucomicrobia phylum in soils of the southern region (3), while in the second study, the occurrence of this phylum ranged from 0.6 to 14% (1).

A comprehensive work conducted by Roesch and coworkers (6) used pyrosequencing for large-scale biodiversity analyses of soil from four regions of the Americas: southern Brazil (Rio Grande do Sul), the United States (Florida and Illinois), and northwestern Canada (Ontario). Verrucomicrobia was found only in soils from Illinois and represented 2% of the 16S rRNA gene sequences. Representatives of this phylum were not found at the other three sites. In other work conducted in Germany, sequences belonging to Verrucomicrobia were rare (<1% of 598,962 sequences) and had a variable distribution between forest and grassland soils, showing more abundance in the latter environment (5).

Lipson and coworkers (4) also analyzed 16S rRNA gene sequences from soils and showed that the Verrucomicrobia phylum was sensitive to seasonal changes, being more strongly represented in the summertime. Similar seasonal effects were detected by Buckley and coworkers (2) in soils from Michigan. Moreover, in that work, the authors showed that soil characteristics and vegetation did not affect the distribution of Verrucomicrobia, but the depth of the soil had a stronger effect on the abundance of this phylum.

In conclusion, the occurrence of Verrucomicrobia in soils can be influenced by a multitude of factors, including the poorly analyzed seasonal effect, all of which may help to explain the different distribution of this phylum in the Brazilian Atlantic forest.

REFERENCES


Fábio de Oliveira Pedrosa*
Emanuel Maltempi de Souza
Helisson Faoro
Department of Biochemistry and Molecular Biology
Federal University of Paraná
Caixa Postal 19046
CEP 81531 980-Curitiba, PR, Brazil

*E-mail: fpedrosa@ufpr.br