

## 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 km<sup>2</sup> 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' to 25°32.515'S and 48°43.028' to 48°55.654'W. One of the conclusions was that the main difference between the Brazilian Atlantic forest and European forests would be the apparent absence of members of the *Verrucomicrobia* phylum in the Atlantic forest soil, suggesting that this group is much less well represented or absent in the latter environment.

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 Órgãos 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. 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 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 0.6 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.

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#### 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

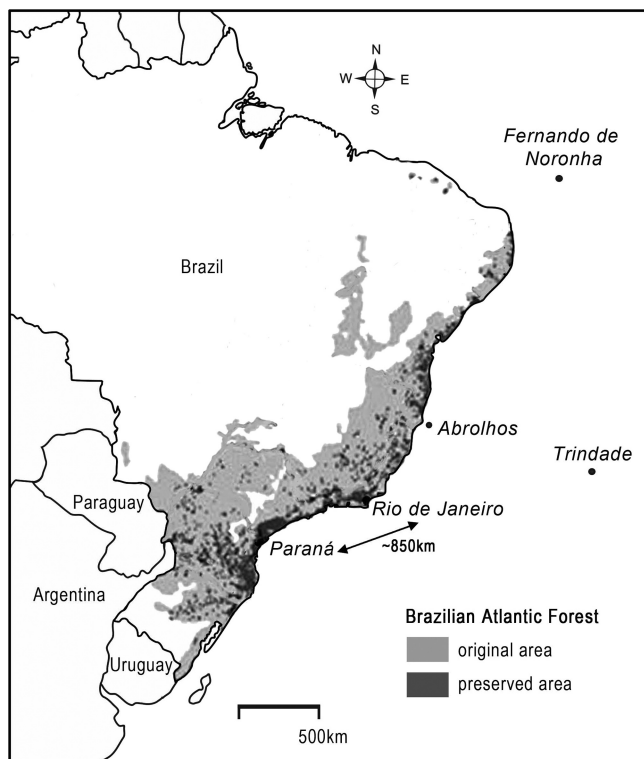


FIG. 1. Brazilian Atlantic forest map indicating its original area (light gray) and the remaining area (dark gray). The Atlantic forest sites studied by Bruce et al. (1) and Faoro et al. (2) and the distance between them are labeled.

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.

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