

**TITLE:** RESPONSE OF THE AMAZONIAN SOIL MICROBIAL COMMUNITY TO CLIMATE CHANGE

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## **ABSTRACT**

The Brazilian Amazon has undergone alterations, in addition to changes in land use, caused by global warming and its consequences on the global climate. Considering the global projection of temperature rise from 1.5 °C to 2 °C, an increase in the average temperature is expected for the region, as well as changes in the frequency, intensity, and amount of rainfall. Therefore, predicting the effects of climate change on Amazonian soils is a crucial task, which may further affect soil microbial communities. In this study, we investigate these microbial responses in forest, pasture, and reforestation sites in the Tapajós National Forest (PA) and adjacent areas in the Brazilian Eastern Amazon. We collected soil samples from a primary forest (F1), a secondary forest (F2) with 40 years of passive regeneration, and a pasture site (Pa) in November 2020. A soil microcosm experiment was set up and maintained for 30 days under two temperatures (27°C and 30°C) and moisture contents (60% and 100% of field capacity). Samples from days 0, 1, and 29 of the experiment were collected, DNA-extracted, and evaluated by quantitative PCR (16S rRNA genes of Archaea and Bacteria). At the beginning of the incubation (D0), the number of bacteria among soil types was similar, with changes only observed after 24 hours (D1), in which Pa had a higher abundance than F1 and F2. The abundance of Archaea differed among all three sites in both D0 and D1. At the end of the experiment (D29), the number of bacteria was affected by land use and its interaction with temperature, being this effect remarkably different comparing Pa and forest soils. In contrast, for Archaea, we observed this interaction with the soil moisture content. We can conclude that bacterial and archaeal communities are being altered by the warming factor. Land use is still a dominant driver of community change, but temperature and moisture will also interfere with the size and, consequently, the structure of these communities. Furthermore, our results revealed the importance of secondary forests as a recovery strategy since F2 exhibited an intermediate trend regarding microbial abundance, with results tending to be more similar to F1.

**Keywords:** Land-use change, Archaea, Bacteria, qPCR

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