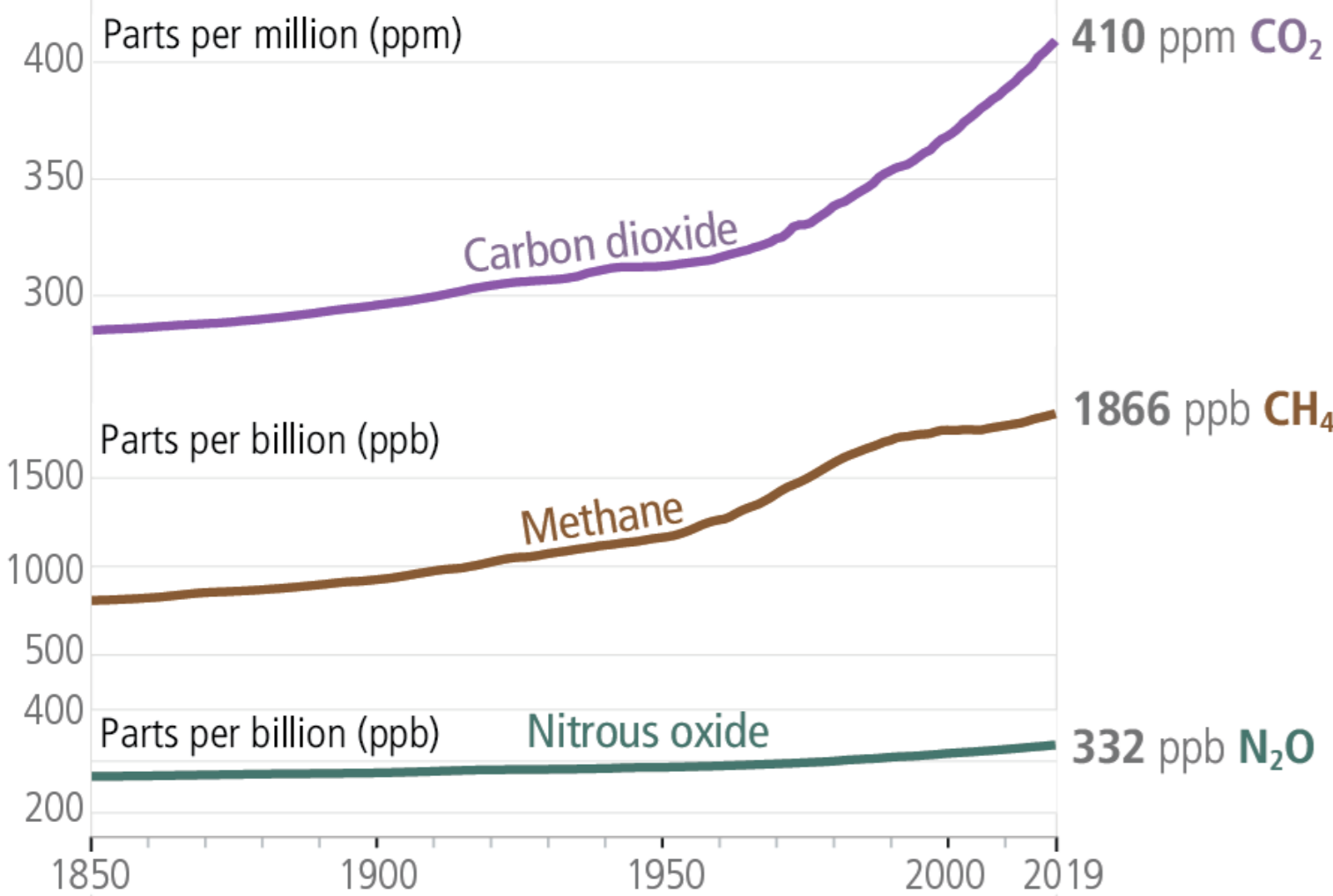


Gabriel G. T. N. Monteiro ^{1*}; Barros, D. J ²; Thierry A. Pellegrinetti ¹; Venturini, A. M ¹; Neu, V. ³; Siu Mui Tsai ¹ Navarrete, A. A. ⁴

¹ Center for Nuclear Energy in Agriculture - CENA, University of São Paulo, Piracicaba – SP; ² Federal University of Tocantins – TO; ³ Socio-Environmental and Water Resources Institute – ISARH, Federal Rural University of the Amazon, Belém – PA; ⁴ Graduate Program in Environmental Sciences, University Brazil, Fernandópolis - SP
*E-mail: guto.monteiro@usp.br

BACKGROUND

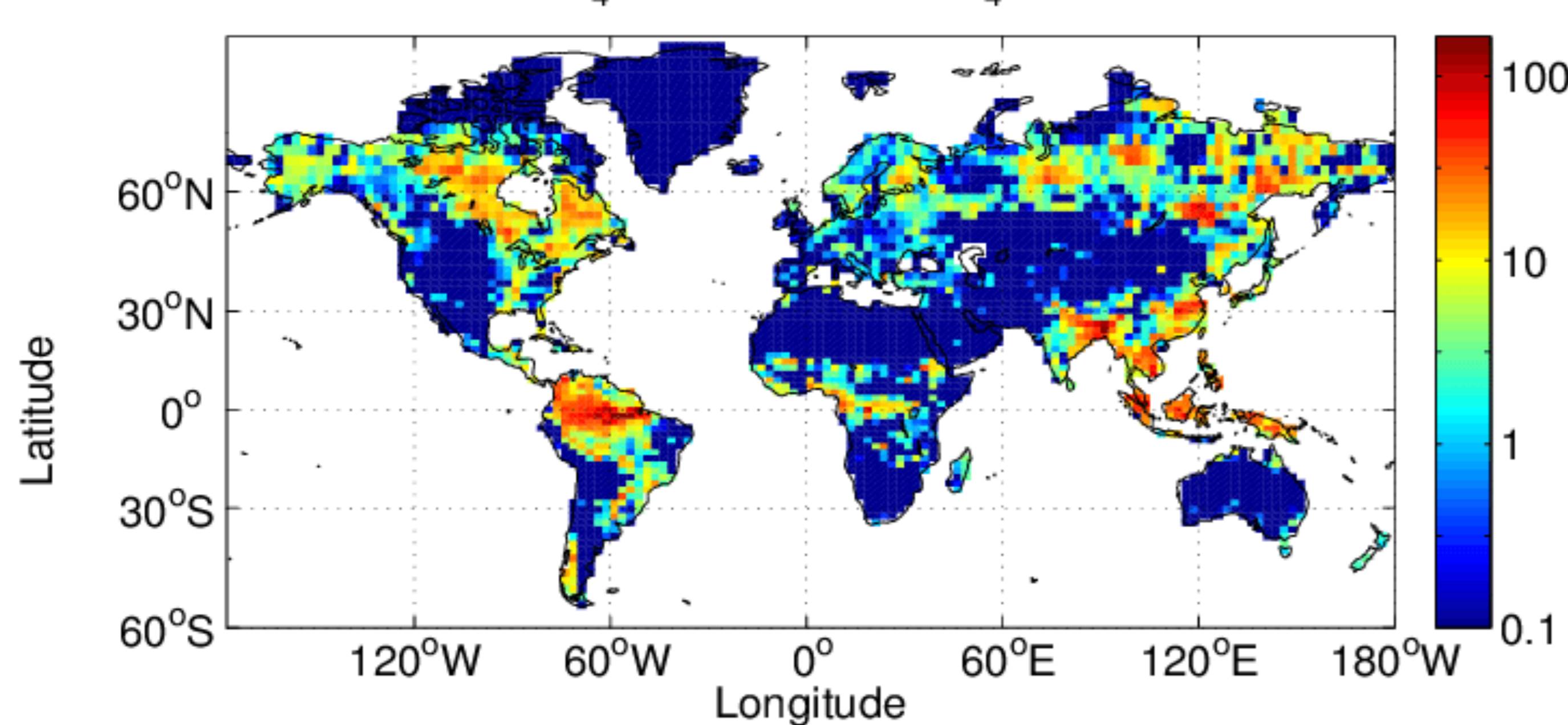
Concentrations of GHGs have increased rapidly since 1850 (scaled to match their assessed contributions to warming over 1850–1900 to 2010–2019)



Methane (CH₄) is a greenhouse gas with an approximately 34 times greater global warming potential over 100 years than carbon dioxide (CO₂).

Tropical and subtropical wetlands are important sources of CH₄ because of their elevated net primary productivity and high temperatures, producing 50–60% of all wetland CH₄ emissions.

Net CH₄ Emissions (mg CH₄ m⁻² d⁻¹)



(1) The type of rivers is the major driver of changes in the chemical profile of these soils; (2) Both seasonal shifts in the soil water saturation and changes due to the chemical profile of each floodplain can modulate the methanotrophic/methanogenic microbial communities.

METHODS

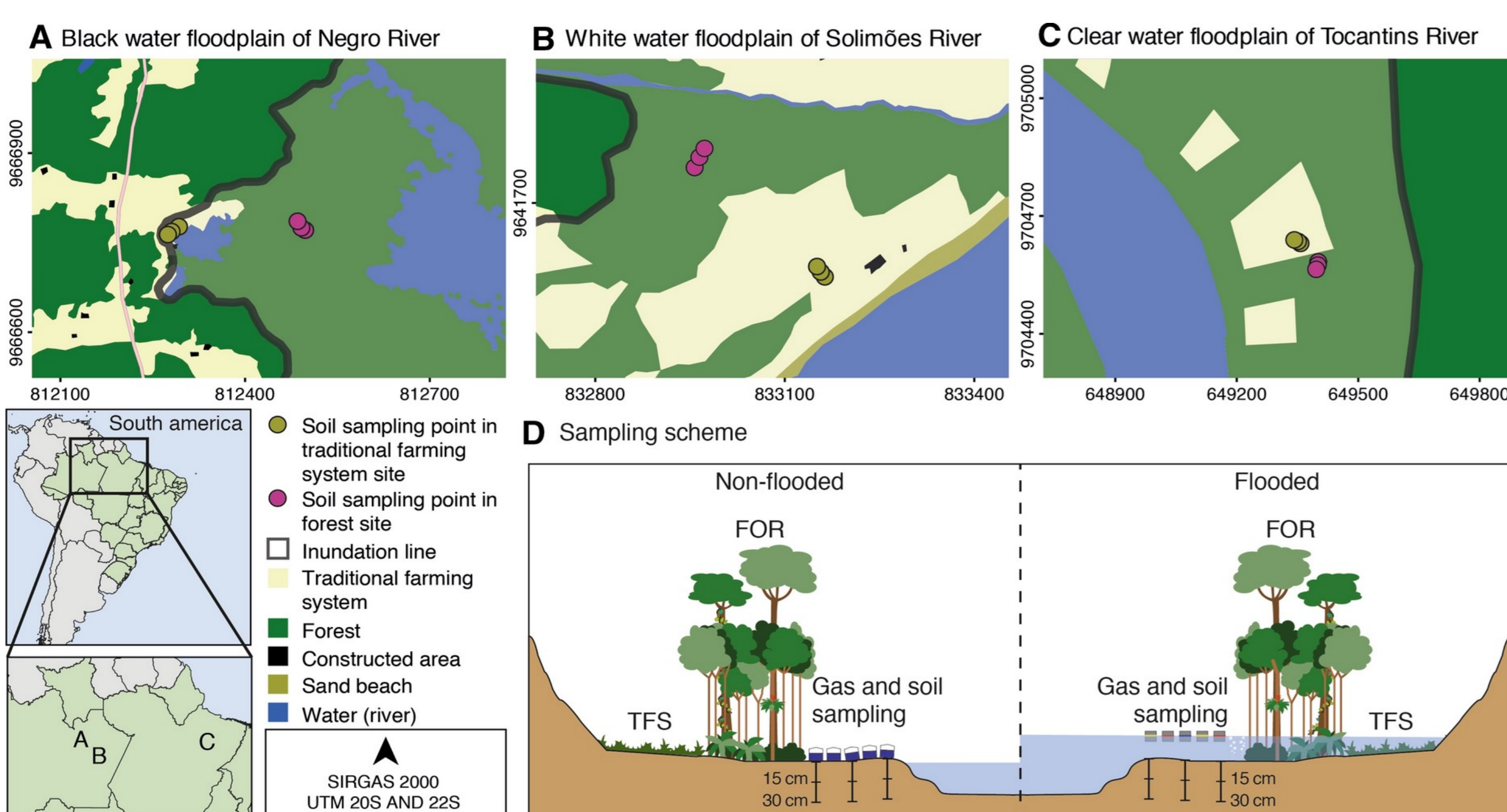


Figure 1. A, B, and C Location of the sampling sites in the Brazilian Amazon, and land use/land cover classification and inundation line in the three study areas seasonally flooded with black water, white water, and clear water. D Sampling scheme for gas and soil samples collection in the non-flooded and flooded periods

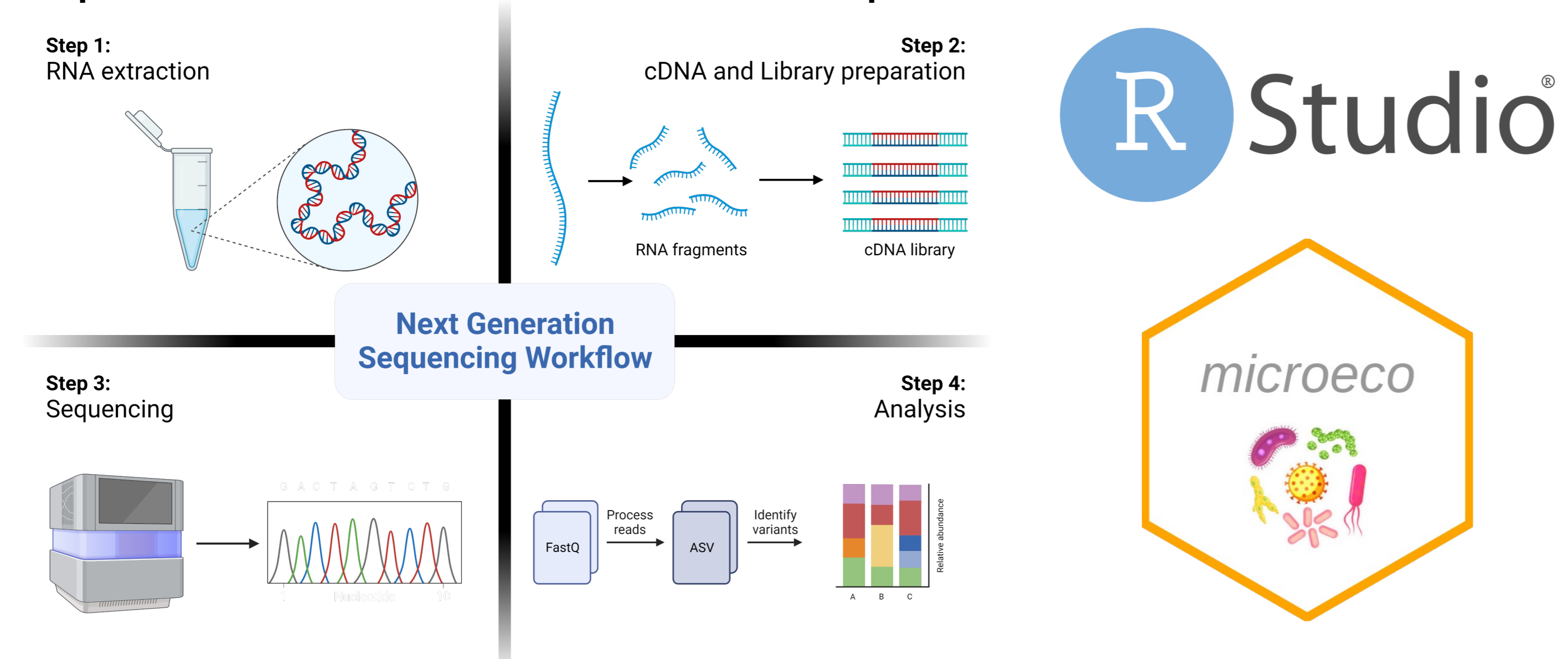
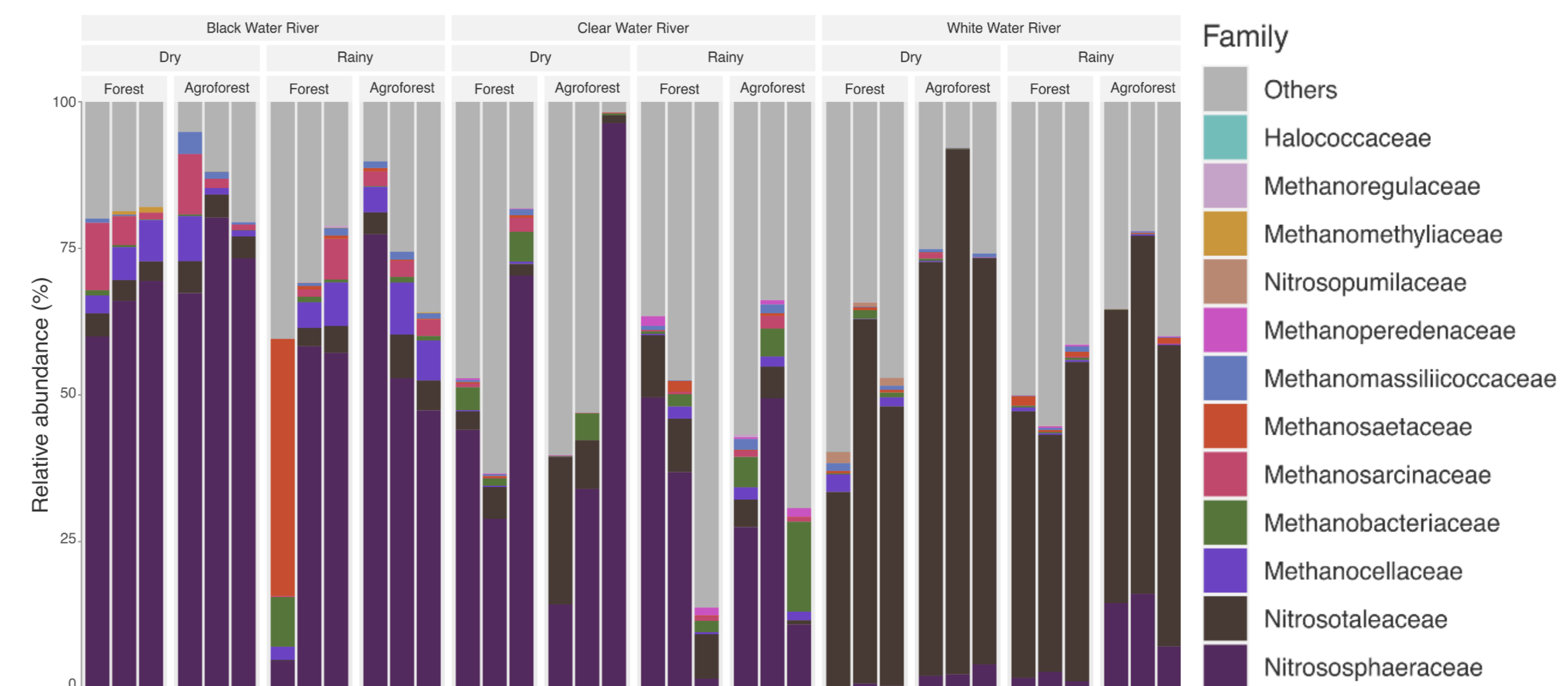


Figure 2. Molecular biology workflow for RNA extraction, cDNA synthesis and amplification of archaeal and bacterial 16s rRNA followed by data analysis

RESULTS



The microbial community was dominated by the ammonia-oxidizing (AOA) members of the Nitrososphaeraceae and Nitrosotaleaceae family in both seasons

Figure 4. Relative abundance of the archaeal community of the floodplain soil from different Amazonian rivers

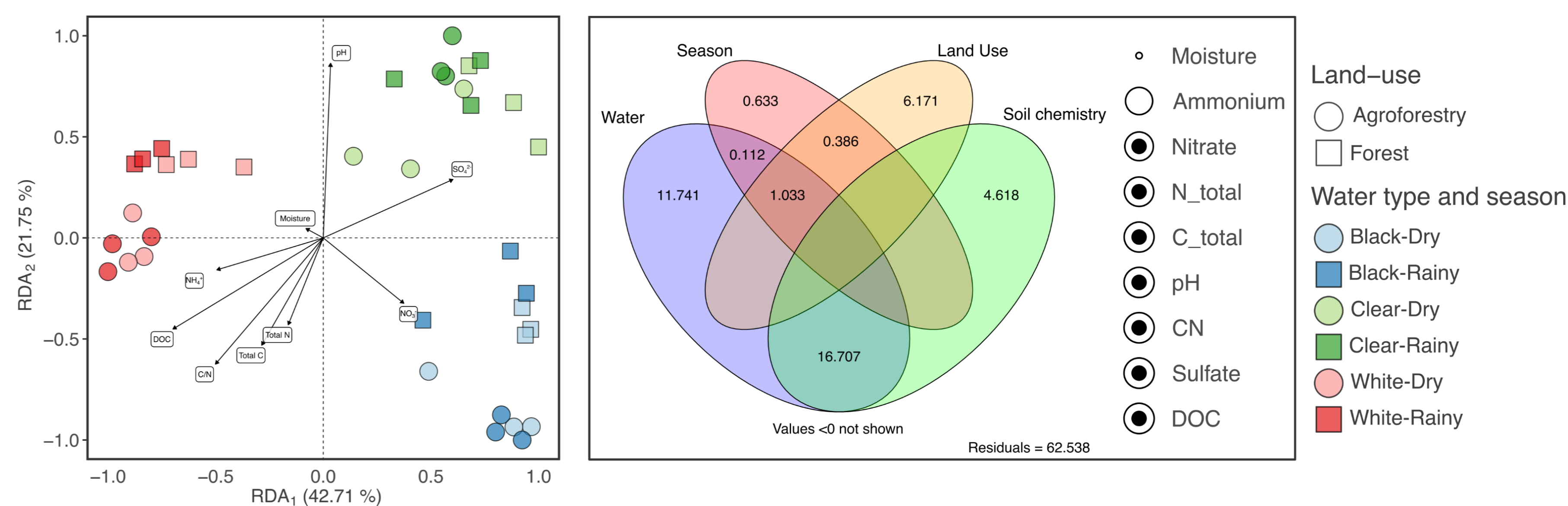


Figure 3. Redundancy analysis (RDA) followed by variance partitioning and permutational analysis of variance (PERMANOVA) of the archaeal community of the floodplain soil from different Amazonian rivers

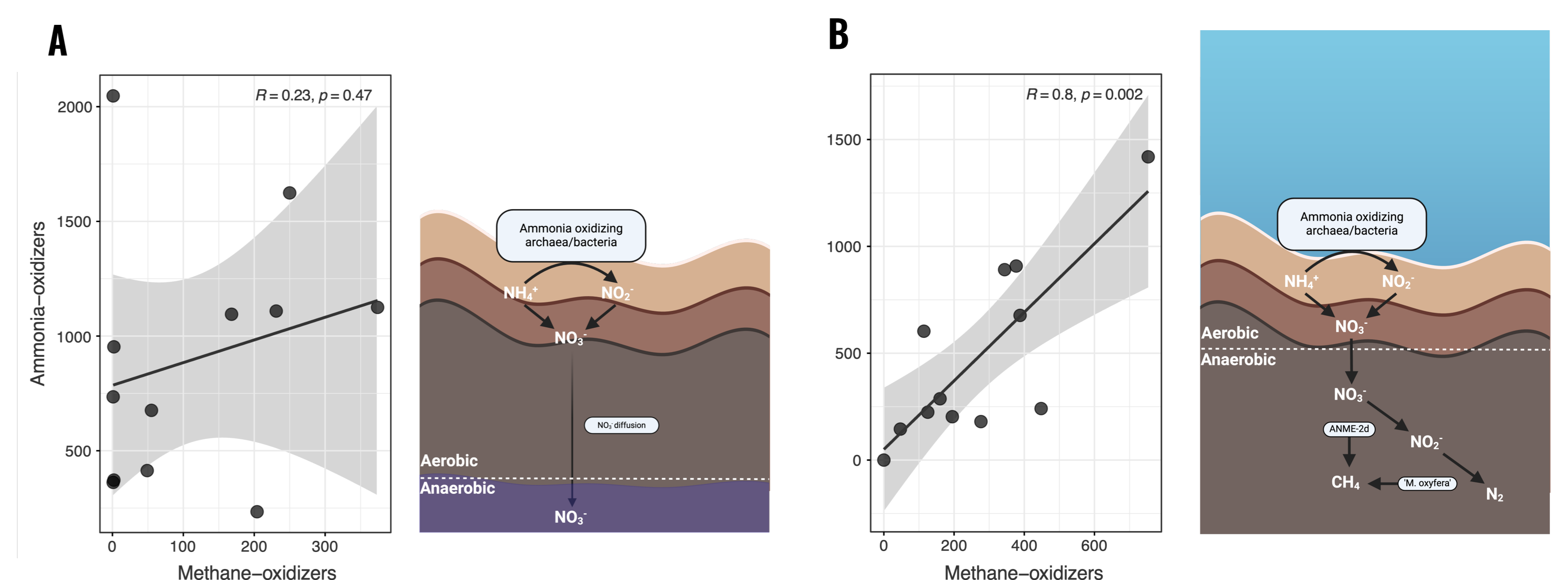


Figure 4. Correlation of the archaeal methanotrophic and ammonia-oxidizing community in the (a) dry season and (b) rainy season. Schematics indicate the putative biogeochemical process that might occur with the rise of the water table of the floodplain soils.

HIGHLIGHTS

- Our data indicates that the flood pulse and the hydrology of these areas are the main drivers of the microbial dynamics in these soils and are correlated not only to the microbial community shifts but also to the chemical dynamic in the floodplains. Each river (white, clear, and black water) has distinct properties, which can impact the microbial dynamics, favoring, for example, ammonia-oxidizing archaea communities that are adapted to acid conditions.
- Also, the data suggested a possible interaction between ammonia-oxidizers and methanotrophs in these acidic soils, with a possible link between the carbon and nitrogen cycles through the methanotrophy coupled with the reduction of both NO₃⁻ and NO₂⁻.
- Although the present study only presents circumstantial evidence, it provides one of the first reports of the active presence of these microbes in Amazon soil, highlighting the possible interaction between distinct biogeochemical cycles in these areas depending on the season.
- Further research is needed to provide in-depth insights into the proposed relationships



References and other information about our research are available in the QR code!