

**TITLE:** Insights into the genomic potential of a *Methylocystis* sp. from Amazonian floodplains sediments

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Although floodplains are recognized as important sources of methane (CH<sub>4</sub>) in the Amazon basin, little is known about the role of methanotrophs in mitigating CH<sub>4</sub> emissions in these ecosystems. Our previous data reported the genus *Methylocystis* as one of the most abundant methanotrophs in these floodplain sediments. However, information on the functional potential of these organisms living under seasonal flooding is still missing. As an alternative, the use of culture-independent methods based on the reconstruction of microbial genomes from metagenomes (MAGs) allow access to the not-yet-cultivated microbial taxa. Here, we describe the first MAG of a *Methylocystis* sp. recovered from two Amazonian floodplains located in Pará State, Brazil. Metagenome data from 12 sediment samples collected during wet and dry seasons were processed on the Kbase platform, using Trimmomatic for trimming and filtering and MEGAHIT for assembly. The binning step were performed by MetaBAT2 and MaxBin2 and optimised by DASTool. The quality control was carried out using CheckM. MAGs were classified using GTDB-Tk and annotated with DRAM. Among the 45 medium and high-quality MAGs assembled, we selected the high-quality *Methylocystis* MAG (96% of completeness and 2.7% of contamination). The fasta output from DRAM and 8 public genomes of *Methylocystis* from NCBI was used as input for Pangenomics analysis using Anvi'o. Both GTDB-Tk classification and Pangenome identified the closest placement taxonomy as *Methylocystis parvus*. As Type II methanotrophs, the Core Pangenome confirmed the presence of genes related to CH<sub>4</sub> oxidation and serine pathway for formaldehyde assimilation. Furthermore, the Core Pangenome also indicates the nitrogen fixation and assimilatory sulphate reduction capabilities. Interestingly, the singletons cluster from the Amazonian *Methylocystis* MAG revealed the presence of unique genes related to nitrogen metabolism and cell motility. However, additional investigations are needed to understand the survival strategies for its predominance in our studied floodplains sediments. Considering the predicted CH<sub>4</sub> emission rises in a climate change scenario, our data highlights the need for further efforts in extending the knowledge about the methanotrophs roles in Amazonian floodplains.

**Key-words:** MAGs, methane, methanotrophs, pangenome, tropical wetlands

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