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METHANE METABOLISM ASSOCIATED GENES AND THEIR MICROBIAL SPECIES IN ANAEROBIC INCUBATED AMAZONIAN FLOODPLAIN SOILS WITH FOUR DIFFERENT CARBON SOURCES

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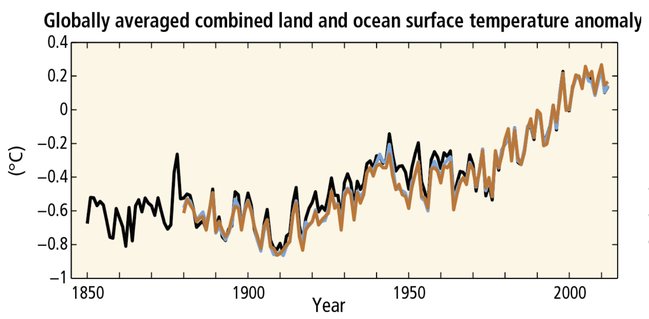
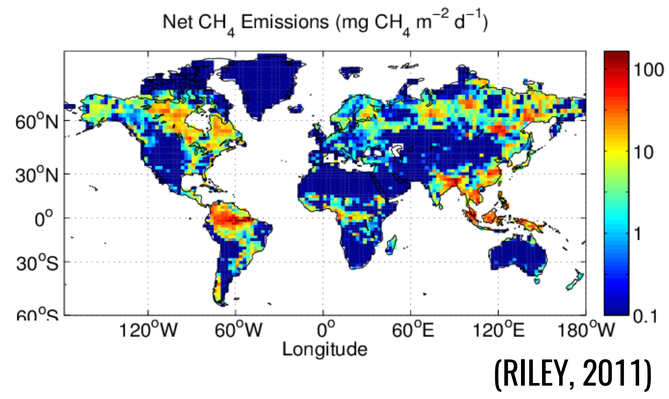
INTRODUCTION



(IPCC, 2021)



(RILEY, 2011)

(1) In a climate change scenario, what are the main pathways for methanogenesis?
(2) Who are the microorganisms responsible for methanogenesis in this scenario?

METHODOLOGY

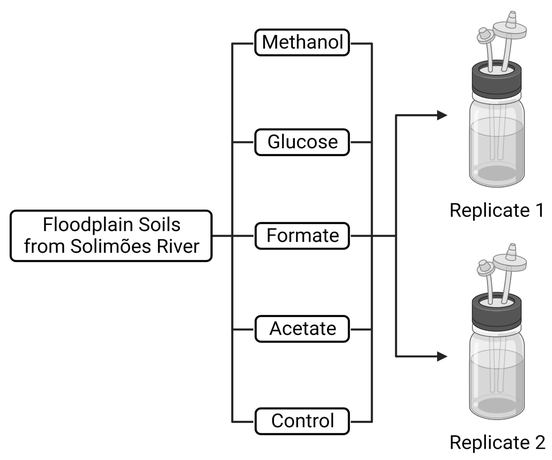


Figure 1. Experimental scheme of the anerobic incubation of the floodplain soils with different carbon sources

Soils were incubated anaerobically in Zinder culture media supplemented with the designated carbon sources and with a 2°C increase in the mean temperature to simulate global warming

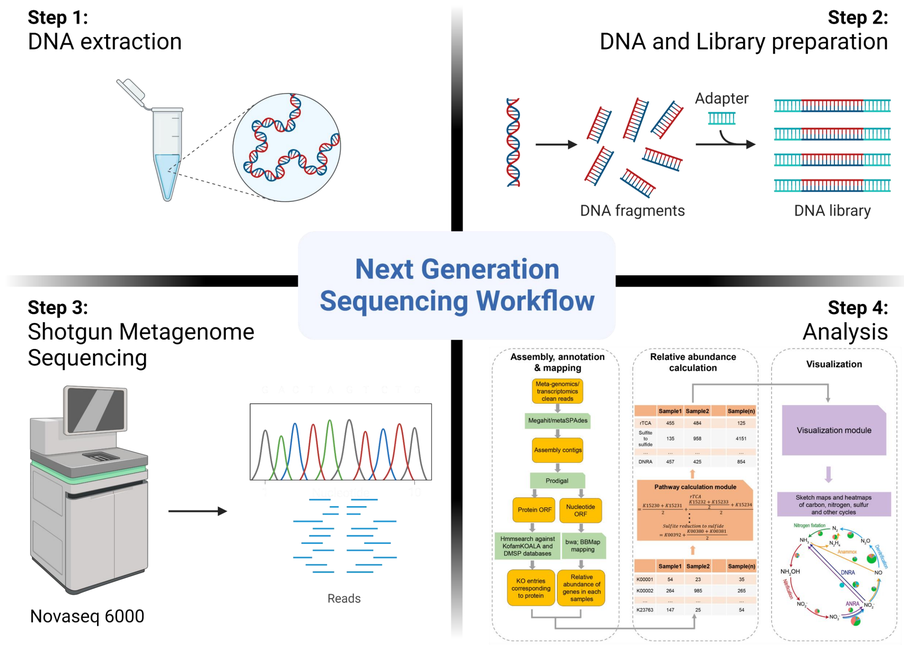


Figure 2. Molecular biology workflow for DNA extraction and shotgun metagenome sequencing, followed by data processing and bioinformatic workflow

RESULTS AND DISCUSSION

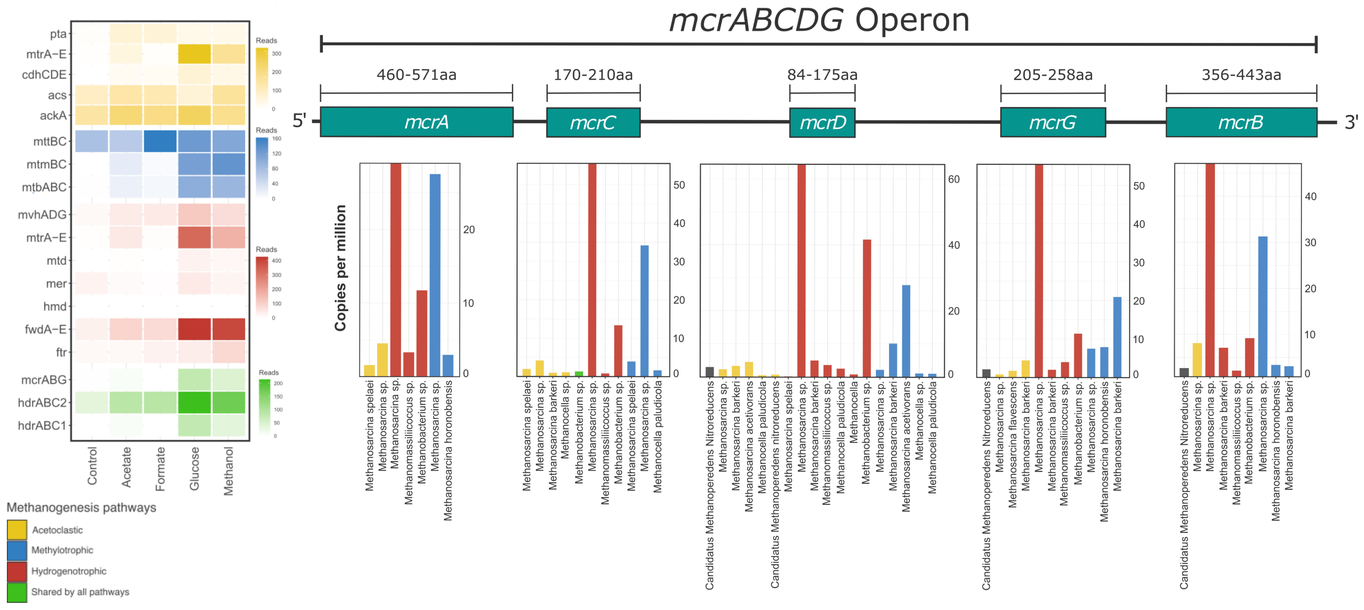


Figure 3. Read-based analysis of the normalized abundance of genes related to the acetoclastic, methylotrophic, and hydrogenotrophic methanogenesis pathways followed by the taxonomic classification of assembled contigs belonging to the *mcrABCDG* operon.

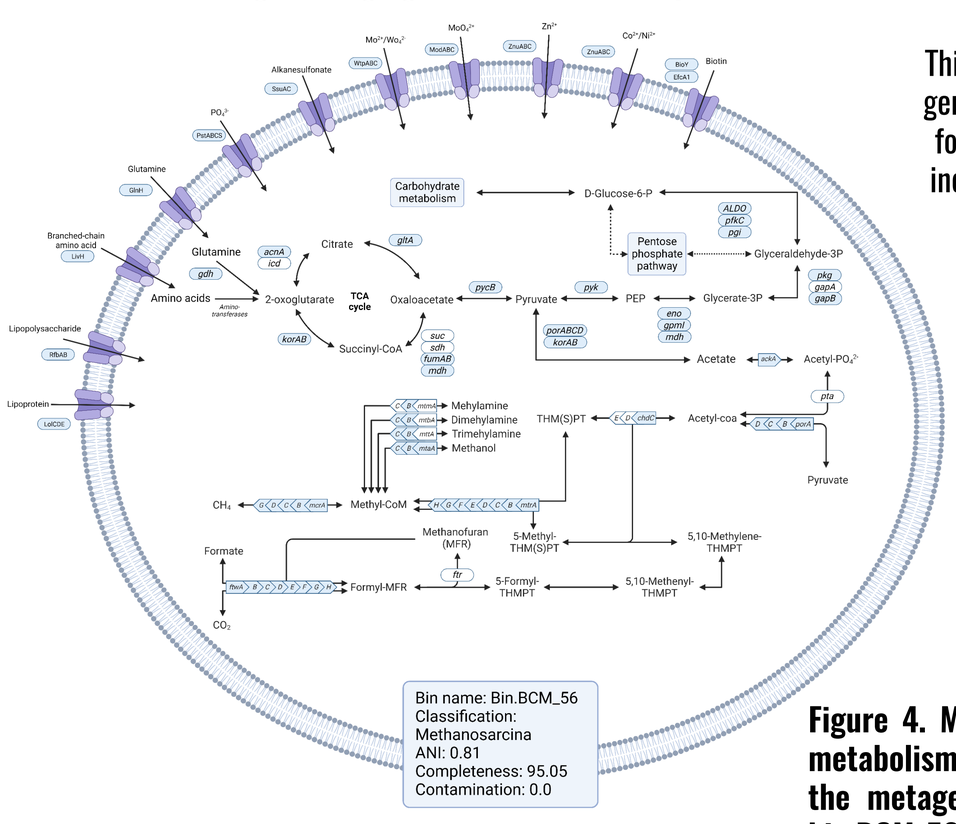


Figure 4. Model prediction for the central metabolism based on the genes present on the metagenome-assembled genome from bin.BCM_56.

This specific metagenome assembled genome presented all three pathways for methanogenesis and its genome indicate a possible new specie as its ANI is 0.81.

CONCLUSION

- The analysis of both reads and contigs from the anaerobic reactor highlighted the role of different members of the *Methanosarcina* genus in the methanogenesis of the floodplain soils of the Solimões river. As global warming increases the mean global temperature, it is estimated that all methanogenesis pathways will increase as the production of these substrates can fuel all three pathways of CH_4 production.

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ACKNOWLEDGEMENTS

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