ARCHAEAL METABOLIC DIVERSITY IN THE RHIZOSPHERE OF TOMATO (*SOLANUM LYCOPERSICUM* VAR RÍO GRANDE) UNDER LOW-NUTRIENT CONDITIONS

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Tomato (*Solanum lycopersicum* L.) is a model for plant–microbe interaction studies. While most research has focused on bacterial communities, the metabolic diversity and functional roles of archaea in the tomato rhizosphere remain unexplored. We studied tomato plants metagenomes grown on multiple soils and hydroponics to investigate the assembly and metabolic potential of the rhizosphere microbiome. Metagenomic and 16S rRNA analyses, although primarily targeting bacteria, revealed archaeal sequences with diverse metabolic capabilities at low abundance. Consistent with previous reports[1,2], the archaeal community was dominated by Thaumarchaeota and Euryarchaeota, including ammonia-oxidizing archaea, halophiles, and methanogens as key representatives. These groups possess metabolic pathways for nitrogen cycling, for example, ammonia oxidation and nitrification, as well as carbon fixation and methane production, indicating their potential contribution to nutrient transformations in the rhizosphere under nutrient-limited conditions. Notably, the metabolic profile of the archaeal community appeared more influenced by plant genotype than soil type, as previously observed in other tomato cultivars[1]. This suggests a selective recruitment of archaea with specific metabolic functions that may act as functional partners within the plant holobiont, enhancing nutrient acquisition and plant resilience. Although archaea were less abundant than bacteria, their consistent presence and metabolic versatility across treatments highlight their potential ecological and functional relevance.

References

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