

Time-series metatranscriptomics reveals differential salinity effects on the methanogenic food web in paddy soil

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Abstract

Sea level rise and saltwater intrusion threaten coastal agroecosystems, yet their impact on the methanogenic food web in rice paddies remains virtually unknown. Using ‘double-RNA’ metatranscriptomics (rRNA, mRNA), we investigated salinity effects on the methanogenic community in straw-amended slurries. Our results demonstrate that salt stress significantly inhibits methane (CH₄) production, with the degree of inhibition varying by the community successional stage. Salinity fundamentally shifted the methanogenic food web towards *Clostridiaceae* dominance, altering key metabolic pathways including polymer breakdown, glycolysis, pyruvate metabolism, ethanol fermentation, and acetogenesis. Notably, the overaccumulation of acetate under salt stress fueled acetoclastic methanogenesis by *Methanosarcinaceae*, preventing CH₄ production inhibition after a 14-day preincubation. While the strong salinity inhibitory effect on the expression of the hydrogenotrophic methanogenesis pathway by *Methanocellaceae* diminished with preincubation time, syntrophic propionate oxidation activity was highly suppressed after 14-day preincubation. Additionally, methanol-dependent methanogenesis by *Methanomassiliicoccales* increased with prolonged preincubation time. These findings provide critical insights into the resilience of the anaerobic food web under salinity stress, with broader implications for understanding the impacts of sea level rise on global biogeochemical cycles.

Keywords: CH₄, methanogenesis, CAZyme, metatranscriptomics, salt stress