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Widespread methylphosphonate-driven methanogenesis from coastal to offshore waters in the South China Sea

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Methane (CH_4) supersaturation in oxygenated surface waters represents a “methane paradox”, as CH_4 production has traditionally been considered a strictly anoxic process. The microbial degradation of methylated compounds (e.g., methylphosphonate, MPn) via C–P lyase activity has been proposed as a key pathway contributing to CH_4 supersaturation in oxic waters, yet field investigations remain scarce and are mostly limited to oligotrophic oceans. In this study, we investigated aerobic methanogenesis across coastal-to-offshore systems in the South China Sea spanning contrasting trophic conditions. By measuring methane production in seawater samples amended with MPn, dimethylphosphinic acid (DMP), and methylamine (MN), we demonstrate that CH_4 produced from MPn lysis is ubiquitous across these diverse regions, including nutrient-rich coastal waters. Size-fraction experiments revealed that this methanogenic potential was associated with a broad range of plankton sizes, including nanoplankton (>3 μm), picoeukaryotes and picocyanobacteria (3-0.8 μm), and bacterioplankton (0.8-0.2 μm). In contrast, utilization of DMP and MN was not observed under various nutrient limitation conditions. We propose mechanisms driving this differentiation and discuss the potential controls on MPn utilization and aerobic CH_4 production.