Evaluating the Carbon Degradation Potential of Marine Plasmids

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Marine ecosystems are rich in carbon, an element whose processing and degradation is mediated by bacteria. Bacteria utilize CAZymes (carbohydrate active enzymes) to degrade complex carbohydrates and the presence of these enzymes within the chromosome of many marine bacteria has been well studied. However, whether these enzymes are harbored on the plasmids (non-chromosomal DNA capable of engaging in horizontal gene transfer) of marine bacteria remains unstudied. This study analyzes the potential for movement and diversity of CAZymes within the marine microbial populations. Specifically, we ask: do plasmids of marine origin harbor carbohydrate utilization genes, and if so, what is the distribution and abundance of these genes within plasmids and across the population of marine plasmids? Utilizing 125 complete plasmids from marine origin, a bioinformatic analysis evaluating the quantity, type, and distribution of CAZymes across marine plasmids was conducted. 48% of marine plasmids carried a CAZyme, representing 213 individual CAZymes, 56 CAZyme types, and all six major CAZyme families. The target substrates of these CAZymes were also diverse, representing a diversity of enzymatic functions within the population. These results of this study highlight the immense potential for carbon degradation within marine plasmids and leave many open questions regarding the selective pressures which have acted on marine plasmid populations to conserve CAZymes. To my knowledge, this is the first paper analyzing the CAZyme repertoires of marine plasmids.

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