Ecological Strategies of Surface Ocean Bacterioplankton: A Tale of Ecology and Evolution

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The r- and K-selected taxa embody a fundamental division of ecological strategies of surface ocean bacterioplankton. The r-strategists have large genomes, versatile metabolic capacities, and rapid responses to nutrient enrichment, while K-strategists have streamlined genomes, the ability to grow in oligotrophic environments, and the inability to respond to nutrient patchiness. Ecological strategies thus have consequences for spatial and temporal coupling of carbon cycles. I use computational methods to study ecological strategies of marine Roseobacter, a dominant alphaproteobacterial clade in ocean surface. The talk will focus on a recently developed computational approach, which uses computed patterns of non-synonymous nucleotide substitutions to provide high-confidence identification of metagenomic reads from uncultivated Roseobacters. The wild Roseobacters differ systematically from their cultured representatives in gene stoichiometry of several genomic traits, including fewer genes for signal transduction and cell surface modifications but more genes for Sec-like protein secretion systems, anaplerotic CO2 incorporation, and phosphorus and sulfate uptake. Several of these trends match well with characteristics previously identified as distinguishing K- versus r-selected ecological strategies in marine bacteria, suggesting that the r-strategist model assigned to cultured roseobacters may be less applicable to their oceanic counterparts. In the remaining of the talk, I will discuss the evolutionary origin of r-selected ecological strategy using ancestral reconstruction of genome content and molecular dating techniques.

Reference:

H. Luo, A. Loytynoja, and M.A. Moran. 2012. Genome content of uncultivated marine roseobacters in the surface ocean. *Environ Microbiol*. 14 (1): 41-51