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Department of Marine Sciences Presents a Seminar By

Martin Polz

Parsons Laboratory for Environmental Science and Engineering Massachusetts Institute of Technology

Ecology and Evolution of Bacterial Populations in the Ocean

Many bacterial and archaeal lineages have a history of extensive gene acquisition and loss, evident as large genome content differences even among otherwise closely related isolates. Explaining the resultant vast diversity of genotypes within microbial communities remains one of the biggest challenges in microbial biology. Using marine vibrios as a model, we show that in spite of such high gene turnover, it is possible to define genotypic clusters, which also represent ecologically cohesive populations. These display many hallmarks of animal and plant populations, including speciation, shared gene pools, and social interactions. Population genomics shows that frequency dependent interactions among genotypes, e.g., via public good production and cheating, and via predator-prey relationships, e.g., via variation of surface antigens, lead to gene content variation among closely related genotypes. Overall, these observations provide a functional explanation for the observed high genomic diversity.

Host: Senjie Lin

Time & Date: 11:00 am, Friday, December 9, 2016 **Place**: Marine Sciences Building, Seminar Room 103

Please see this <u>page</u> for cancelations and additional seminar information, email <u>marinesciencesseminars@uconn.edu</u>, or call 860-405-9152 or 860-405-9151