Report on Lecture at St Petersburg State University
September 09, 2014

# Title: **Genomic Methods in Marine Microbiology**

**Introduction:**
In common with microbes in most settings, both bacteria and viruses in marine environments are poorly understood due to the difficulty in culturing them. Estimates are that the open ocean contains less than 0.1% of culturable microbial species. This means that molecular methods, and DNA sequencing in particular, are critical to gain an understanding of the functions of marine microbes and their contribution to the global cycling of matter.

The lecture introduced a short history of DNA methods and the roles of DNA and RNA sequencing and provided some background on the revolution in cost effectiveness brought about by the dramatic increase in efficiency of Next Generation sequencing techniques. The cost per finished base pair has dropped by four orders of magnitude since 2007. Thus many projects that involve metagenomic analysis and RNA sequencing are now feasible with relatively low sequencing cost. The burden of progress has shifted to the effectiveness of bioinformatics and the training of new cadres of bioimathematicians and biocomputation experts.

It is still critical to isolate and process DNA and RNA from marine and other samples, before sequencing and molecular analysis such as hybridization, cloning and expression of genes to study the proteins can be done with efficiency. Methods for nucleic acid handling and quality assurance were described. PCR amplification, the uses of ribosomal RNA analysis to understand phylogeny and the methods for staining target RNA and DNA in situ in cells by hybridization were discussed.

Fingerprinting analysis during population studies and the isolation of marine symbiotic bacteria were analyzed. Together with the application of quantitative PCR to determine absolute amounts target DNA sequences in complex samples.

Cloning techniques for extraction of large DNA molecules from vanishingly low amounts of extracted DNA were discussed, including the Single Amplified Genome (SAG) methods which are now on the cutting edge of technology. DNA sequencing methods that focus on single molecule sequencing reactions were described. The pyrosequencing, Illumina and PacBio platforms were described.

Finally the new developments of Stable Isotope Probing (SIP) to determine the identity of metabolizing cells in complex populations, and the latest revolution in low cost synthesis of DNA and subsequent ease of carrying out genome editing were described.