

High throughput sequencing of deep sea metagenomes - Bi-Annual report VISTA: 1 January – 30 June 2011

by [Thomas Haverkamp](#) — last modified 2011-07-15 09:23

History

Action	Performed by	Date and Time	Comment
Submit Report	Thomas Haverkamp	2011-07-15 09:23	No comments.

Project title: High throughput sequencing of deep sea metagenomes

Project leader: Jakobsen, Kjetill S., Centre of Ecology and Evolutionary Synthesis (CEES), University of Oslo

Post-doc/ scholar: Haverkamp, Thomas
Project duration: 15.04.2009 – 14.12.2012

Technical contact person in Statoil: Collin-Hansen, Christian.
Division head: Kotlar, Hans Kristian
Project number: 6503

Objective

The objective of this project is to establish high throughput sequencing as a tool for metagenome investigations associated with oil and gas explorations in the deep sea northern regions, and make this competence accessible to other VISTA research groups through collaborations.

Our aims within the project are

- Comparison of microbial diversity at the sea floor and in oil reservoirs at different sites.
- Setting up competence around high throughput sequencing and bioinformatics analysis of metagenomic data and sharing this competence with collaborators around Norway. The Norwegian Sequencing Centre (NSC) is a central technology provider in this project.

Status:

- Collaboration with Othilde Håvelsrud (IMBV) and Anne Gunn Rike (NGI) to describe two metagenomes from the Coal Oil Point seep system found off the coast of California. A surface sample (0-4cm) and a deeper taken sample (10-15cm) were used to create the metagenomes. Both samples have very different community compositions with the surface sample being dominated by aerobic methanotrophs and the deep sample contains anaerobic methanotrophs of the archaeal ANME group. The results of this metagenomic comparison have been summarized in a manuscript that was recently submitted to a journal for review.
- Metagenomic comparison of Oslo Fjord sediment samples and Troll oil field sediment samples.

In 2009, DNA was extracted from 8 environmental samples in collaboration with Anne Gunn Rike, NGI. These samples were sequenced using 454 technology in the summer of 2010. The samples are used for comparative analysis in order to identify community and metabolic differences between the samples. The metagenomic sequence data contain between 600.000

and 1.5 million reads. The first results in the comparison of the Oslo Fjord and Troll Oil field samples indicate distinct community differences. E.g. the Troll Field sediments have an overrepresentation of Thaumarchaeota and an underrepresentation of Crenarchaeota and Euryarchaeota. One of the metabolic signatures of Thaumarchaeota is their ability to oxidize ammonia, and this metabolic signature is overrepresented in the Troll Fjord samples as well.

- Collaboration with Svein Valla, Mimmi Throne-Holst, Anna Lewin (NTNU) and Hans Kristian Kotlar (Statoil) on the analysis of an oil well metagenome. The analysis of the metagenome was finished in 2010 and the results were summarized into a manuscript that was submitted to a journal for review. The paper describes the unique way of sampling an oil field ecosystem and the unique community of the oil field. The paper got recently accepted in Environmental Microbiology Reports and is now in press.
- In collaboration with the LaMDa group (<http://Lamda.uio.no/lamda.html>) and the 454 sequencing platform at NSC (www.sequencing.uio.no) experience was gained in genome assembly of four Bacillus cereus group genomes. The various genome sequences were assembled into contigs. Using the LaMDa databases, which contain all available Bacillus sp. genomes we binned the contigs into three groups: chromosomal, plasmid derived, or the unknown group. These bins were then used to create artificial sequences, with the chromosomal contigs ordered based on the reference Bacillus genomes. At the start of 2011, the sequence data were annotated by the Joint Genome Institute. The genome annotations will be used in combination with various comparative genomics tools to compare the genomes to those of previously sequenced strains from the B. cereus group, and building up general competence in bacterial comparative genomics and annotation.
- The manuscript from the Troll and Oslo Fjord metagenomes project is currently being written up for publication.

Publications:

In press:

Hans K.Kotlar, et al., High Coverage sequencing of DNA from microorganisms living in an oil reservoir 2.5 km subsurface. Environmental Microbiology Reports (accepted)

Submitted:

Håvelsrud O.E , Haverkamp T.H.A, Kristensen T, Jakobsen K.S. and Rike A.G. (2011) A metagenomic study of methane oxidation in Coal Oil Point seep sediments” BMC Microbiol (submitted – in review)