DTL FOCUS MEETING: WATER METAGENOMICS
June 2nd, 2014 - Utrecht, The Netherlands

Jery Baan, Detmer Sipkema, Claudia Lüke, Charlotte Vavourakis, Johanna Gutleben, Andrew Stubbs, Robert Kraaij, Cornelia Welte, Ali May, Eric Kuijt, Jonathan den Boer, Marten Boetzer, Geert Cremers, Szymon M. Kielbasa, Ulisses Nunes da Rocha, Daan Speth, Lex Overmars, Martijn Vermaat, Emily D. Melton, Tom Berben, and Bas E. Dutilh

During the DTL Focus Meeting: Water Metagenomics, three speakers presented their work in using metagenomics to study the microbiology of different aquatic environments.

First, Detmer Sipkema (Wageningen UR) discussed his research on the marine sponge-associated microbiota. Depending on the sponge species, up to 50% of the organism weight may be made up by microbes, with varying compositional complexities. The aim of his research is to characterize this niche, e.g. by finding out which bacterial species are sponge-specific, and what they do inside the sponge. One of the issues with studying this niche is the low amount of material one can obtain from a single sponge, resulting in a low amount of microbial DNA fit for sequencing. Culture-based approaches were unsuccessful in enriching certain microbial species of interest in order to obtain their genomes. Currently, the metagenome and metatranscriptome of a bacterial fraction of the sponge *Crambe crambe* have been sequenced, but the data were not sufficient yet to reconstruct the (partial) genome of the most abundant bacterial symbiont. One potential solution offered in the following discussion was obtaining multiple sponge samples for sequencing, and then using differential read coverage binning to recover such microbial genomes. This technique has been shown to be valuable in retrieving the genomes of low-abundant species [1-3].

Second, Claudia Lüke (Radboud University Nijmegen) talked about her work on the metagenomics of marine bacterioplankton. Contrary to simple, enriched environments where an assembly-based approach is feasible for genomic/transcriptomic characterization, environmental samples are more complex and require a reference-based analysis in order to achieve accurate characterization. High quality reference databases of functional genes are required to but still largely lacking. People at the Radboud University Microbiology Department in Nijmegen are currently creating such curated databases. The database of the *pmoA* gene (that encodes methane monooxygenase) was used as an example of how to explore metagenomic data and to find new diversity. These databases are a significant amount of work to set up but once they are completed, the upkeep is relatively simple. As such, more of these high quality, curated gene-specific databases will be necessary to improve metagenomic data analysis.

Last was Charlotte Vavourakis (IBED, University of Amsterdam), who is looking at the microbiota in the double-extreme environment of soda lake brines. Despite the extremes of this environment, they harbor a variety of microbial communities, depending largely on the salinity of the environment. One of the issues encountered was the relatively low-resolution taxonomy provided by using 16S to identify microbial species present in these environments. A good suggestion to help this project forward is to also look at other functional genes to improve resolution, such as specific genes required to survive in these double-extreme environments, or genes specific to, e.g. halophylic clades.

A healthy discussion accompanied all three of these talks. Questions and helpful suggestions were exchanged between the speakers and the audience members. Depending on their expertise, members of different Dutch research departments as well as members of industry weighed in on specific issues, aiming to improve research methods and achieve better results. All in all, it was a fruitful meeting for everyone involved.

The next metagenomics meeting will take place on September 3rd 2014. Please keep checking our website for updates at: http://www.metagenomics.nl.

References

[1] Albertsen et al.: "Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes." Nat Biotechnol 2013, 31(6):533-538.
[2] Sharon and Banfield: "Microbiology. Genomes from metagenomics." Science 2013, 342(6162):1057-1058.
[3] http://ggkbase.berkeley.edu/