

NORUSCASA seminars:

"Functional Metagenomics for discovery of bioactive compounds"

Date and time: December 13, 2021; 17:00-19:00 CET

Venue: Teams; [Click here to join the meeting](#)

In the frame of Research Council of Norway project NORUSCASA, SINTEF and NTNU cordially invite interested students and researchers to the second seminar occasion in the NORUSCASA seminar series.

We are looking forward to welcoming you to 3 exciting lectures and vivid discussions!

17:00h CET - Prof Mark R. Liles, Auburn University, USA



Disease control using microbial cultures and metagenomes

This talk will discuss research on identifying and expressing biosynthetic gene clusters (BGC) from soil microbial cultures and metagenomes. The use of *Bacillus* spp. that can enhance plant growth and/or prevent disease has been enhanced through the use of pectin-rich prebiotic amendments as a seed coating and studies are ongoing to evaluate specific *Bacillus* strains to prevent seedling damping off due to fungal and oomycete pathogens. While culture-dependent approaches have great applicability in agriculture, the BGC rediscovery rate is very high, so a metagenomic approach has also been used to identify BGCs from diverse soil microorganisms. Over 1500 BGCs were identified by next-generation sequencing of a soil metagenomic library with an average insert size of 113 Kb in a broad host-range bacterial artificial chromosome (BAC) vector. 399 BGCs encoding polyketide synthases and non-ribosomal peptide synthetases derived from a large-insert soil metagenomic library were conjugally transferred to *S. coelicolor* M1154 and screened for antibacterial activity against multidrug-resistant pathogens. A subset of metagenomic BGCs were subcloned into a dual-promoter bacterial artificial chromosome vector and assayed for inducible expression of antibacterial activity. Structural elucidation of *Bacillus*- and metagenome-derived secondary metabolites has revealed diverse bioactive compounds with the ability to inhibit animal and plant pathogens.

17:40h CET – Ass. Prof. Laura Hug, University of Waterloo, Canada

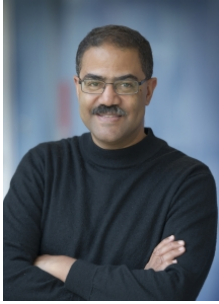


Mining shotgun metagenomes for novel PHA depolymerases

Polyhydroxyalkanoates (PHAs) are a family of microbially-made polyesters commercialized as biodegradable plastics. PHA production rates are predicted to increase as concerns around environmental plastic contamination and limited fossil fuel resources have increased the importance of biodegradable and bio-based plastic alternatives. Microbially-produced PHA depolymerases are the key enzymes mediating PHA biodegradation, but only a few PHA depolymerases have been well-characterized and screens employing metagenomic sequence data are lacking. Here, we used 3,078 metagenomes to analyze the distribution of PHA depolymerases in microbial communities from diverse aquatic, terrestrial and waste management systems. We significantly expand the recognized diversity of this protein family by screening 1,914 Gb of sequence data and identifying 13,869 putative PHA depolymerases in 1,295 metagenomes. Our results indicate that PHA depolymerases are unevenly distributed across environments. We predicted the highest frequency of PHA depolymerases in wastewater systems and the lowest in marine and thermal springs. In tandem, we screened 5,290 metagenome-assembled genomes to describe the phylogenetic distribution of PHA depolymerases, which is substantially broader compared to current cultured representatives. The Proteobacteria and Bacteroidota are key lineages encoding PHA depolymerases, but PHA depolymerases were predicted from members of the Bdellovibrionota, Methylophilota, Actinobacteriota, Firmicutes, Spirochaetota, Desulfobacterota, Myxococcota and Planctomycetota.

18:20h CET – Prof. Trevor Charles, University of Waterloo, Canada:

Functional metagenomics-enabled bacterial genome engineering for production of bioplastics from food wastes



Intracellular polyhydroxyalkanoate (PHA) granules are produced naturally by many bacteria as carbon and energy storage molecules. They can be extracted and used as fully biodegradable bioplastics. The monomer composition of the polymer determines techno-functional properties of the material and can be influenced by both cultivation conditions and the genetics of the production strains that drive the metabolic pathways. PHAs have the potential to replace currently used petroleum-based synthetic plastics that are not biodegradable, but a major challenge is higher production costs. Widespread adoption of bioplastics is hindered by the lack of reliable, predictable and inexpensive methods to produce a broad variety of PHA bioplastics. To address this challenge, we are using functional metagenomics-enabled bacterial genome engineering for the efficient vaporization of food waste and side streams into PHA bioplastics. We will focus on the engineering of lactose and galactose utilization pathways into *Pseudomonas putida*, coupled with modified PHA synthesis pathways, to convert lactose-rich waste from dairy production to a variety of PHA polymers.