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Guelph Research and Development Centre

Seminar Series

Presents

SACCHARIS: A Bioinformatic Tool to Aid in the Discovery of Carbohydrate Enzymes for Diverse Applications in Plant and Animal Agriculture

By

Speakers: **Drs. D. Wade Abbott and Dallas Thomas**
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Date: *Thursday, September 13, 2018*
Time: *10:30 AM – 12:00 PM*
Place: *Lab Services Boardroom B,C*
95 Stone Rd West, Guelph, Ontario, Canada

Abstract

Carbohydrates represent the largest renewable energy resource in the biosphere and are integral for nearly every aspect of plant and animal agriculture. Understanding the processes by which complex carbohydrates are synthesized and dismantled by enzymes, therefore, is of high importance for discovery-based innovations in Canadian agriculture. Although mining available sequence datasets is a promising approach for enzyme discovery and characterization, bioinformatic and biochemical technologies to streamline these activities have become limiting in the '-omic' age. Deposition of new genetic sequences in online databases is expanding at an unprecedented rate. Recent totals on the CAZy website (www.cazy.org) boast 11,418 annotated 'CAZomes' (CAZome = total predicted proteins involved in glycan modification), and 528,755 predicted glycoside hydrolases, of which only ~2% are characterized. In this paradigm, the discovery of carbohydrate active enzymes (CAZymes) and carbohydrate binding modules (CBMs) with novel functions is hindered by high backgrounds of uncharacterized sequences particularly when the enzyme sequences cluster within sequence-related families that exhibit diverse functional specificities.

Therefore, to inform sequence-based discovery and characterization of CAZyme and CBM function we have developed an in silico pipeline entitled: Sequence Analysis and Clustering of CarboHydrate Active enzymes for Rapid Informed prediction of Specificity (SACCHARIS; from the Greek "sákkʰaris" meaning "sugar"). SACCHARIS trees built with known enzyme activities (i.e. EC numbers) can be embedded into user-defined datasets (e.g. genomics, metagenomics, and transcriptomics) to assist with prediction of CAZyme and CBM specificity, and identify sequences that possess uncharacterized, and potentially novel,

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catalytic functions. Most recently, we have automated SACCHARIS to generate "CAZome fingerprints", which provide a comprehensive picture of an organism's total saccharolytic potential; comparison of CAZome fingerprints now enables differential analysis of glycan metabolism between organisms with unprecedented resolution.
In summary, SACCHARIS provides a unique in silico tool that can be tailored for CAZyme bioprospecting in complex user datasets and for diverse applications in agriculture, such as cell wall engineering, plant-microbe symbiosis, and analysis of saccharolytic potential in microbial ecosystems. In this presentation we will describe how the pipeline was assembled and present some recent analyses that have been conducted using SACCHARIS.

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