Davenport East Seminar Room 3rd Floor, (Room 380), Lash Miller **Virtual Attendance:** https://utoronto.zoom.us/j/86092773171 Meeting ID: 860 9277 3171 Passcode: 802024	**Friday, March 22** **10AM** All are encouraged to attend!

Abstract: Directed evolution has enabled the development of extremely useful biocatalysts that have, in some cases, supplanted traditional organic chemistry in the industrial production of value-added commodity chemicals. Generally, mutations introduced into a protein scaffold to increase catalytic efficiency are accompanied by a compensatory destabilization of the enzyme. To circumvent this issue and allow a more thorough exploration of sequence space around naturally occurring enzymes, we have turned to sequence similarity networks (SSNs) to mine the genomes of thermophilic microorganisms to identify novel thermostable variants of enzymes with potential industrial utility. These networks allow for the exploration of whole protein families and the interrelatedness of every member sequence through an 'all-by-all' BLAST. Through the iterative construction of SSNs with varying sequence identity cutoffs, we have produced networks of putative isofunctional clusters that allow a single sequence with known catalytic function to reveal the role of thousands of unannotated PETase-like genes.

Our initial efforts in this arena have focused on the search for new thermostable plastic-degrading enzymes as a part of the OpenPlastic consortium's efforts to develop a circular plastics economy. Following the initial discovery of a cutinase-like enzyme from Ideonella sakaiensis that degrades polyethylene terephthalate (PET), there has been an explosion in research revolving around the biocatalytic degradation of PET and other plastics. While several engineered PETases have emerged that are sufficiently stable and catalytically efficient for industrial PET degradation, we opted to direct our initial efforts to exploit the wealth of PETase sequence-function relationships to mine the genomes of extremophiles for new PETases as starting points for further engineering efforts. Using the I. sakaiensis enzyme as a seed sequence, SSNs were constructed that led to the identification of 10 putative PETases from bacteria with optimal growth temperatures ranging from 50 °C to 80 °C. This presentation will detail our efforts to characterize these enzymes and their potential utility in the degradation of PET plastics. Similar bioinformatics-driven approaches to identify and characterize thermostable enzymes that degrade polyamides and polyurethanes will also be presented.

Website: https://www.thehowelab.com/

This seminar will be hosted by Prof. Ron Kluger and will be held in-person and virtual (hybrid).

If you are a student at UTM and UTSC and would be interested in attending this colloquium in person (travel expenses covered) and meeting Professor Howe, please send your request to chem.reception@utoronto.ca.

For additional information, contact: chem.reception@utoronto.ca

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