HIGHLANDS IN CHEMISTRY SEMINAR SERIES

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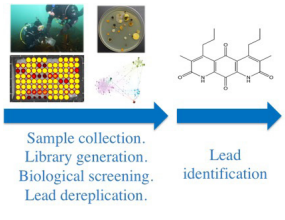
2:30PM ET

ZOOM

FACULTY HOST:
EMILY MEVERS

"Toward antibiotic discovery from a bacterial colony: A primer for academia"

The question of whether culturable microorganisms – a cornerstone of drug discovery since the 1930s – will continue to be a viable source of new drug leads is inherently married to the strategies used to collect samples from the environment, the methods used to cultivate microorganisms from these samples, and the processes used to create microbial libraries. An academic microbial natural products (NP) drug discovery program with the latest innovative chromatographic and spectroscopic technology, high-throughput capacity, and bioassays will remain at the mercy of the quality of its microorganism source library. To address this, we sought to design a discovery pipeline that maximized the amount of information obtained from a single bacterial colony. We designed a MALDI-TOF mass spectrometry (MS) data acquisition and bioinformatics pipeline (IDBac) to integrate data from both intact protein and NP spectra directly from bacterial cells grown on agar. This technique organizes bacteria into highly similar phylogenetic groups and allows for comparison of NP differences of hundreds of isolates in just a few hours. This technique, in combination with our design of a custom, 3D-printed multi-well bioassay plate, allows for high-throughput microbial competition assays from libraries with minimal NP overlap. Herein we present our vision of antibiotic discovery by showing that from a single bacterial colony, we can derive taxonomic, NP, and bioassay information in high throughput and use these to streamline what has traditionally been a laborious and serendipitous process.



Can we make front end microbial discovery efforts more efficient?

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