Mauricio Caraballo, PhD

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SHORT CV (MAX 200 WORDS)

Mauricio Caraballo received his Ph.D. (2017) and a M.S. (2013) in Sciences from University of São Paulo (Brazil) for his work on natural products from microbial interactions of endophytes at the laboratory of Prof. Mônica T. Pupo. He received a M.S. in Biosciences and Law from Universidad Nacional de Colombia (2011) for his work related to access to genetic resources and benefit sharing. He received his B. Sc. in Pharmacy from the same institution in Colombia (2006). He joined the laboratory of Prof. Pieter Dorrestein as Postdoctoral Researcher where he applied mass spectrometry approaches to understand symbiotic ecosystems, as well as animal, human and microbial metabolomes. Currently, he is Project Scientist at the Dorrestein Lab, Skaggs School of Pharmacy and Pharmaceutical Sciences - UC San Diego. Dr. Caraballo-Rodriguez directs the MScollaboratory (https://mscollaboratory.ucsd.edu/), an initiative supported by the Moore foundation, which focuses on democratizing molecular analysis of marine symbiosis and diverse ecosystems using mass spectrometry approaches. His expertise areas include detection, isolation, and structural characterization of small molecules by using Mass Spectrometry and Nuclear Magnetic Resonance. He is fascinated with understanding the role small molecules play in nature as they might be involved in driving animal and plant behaviour.

Title of the Lecture: From microbes to ecosystems, how to gain molecular insights through metabolomics analysis.

Abstract (MAX 200 WORDS)**:**

Keywords: metabolomics; mass spectrometry; microbes; small molecules

Background: The potential of discovering small molecules by applying recent metabolomics and computational approaches is huge. However, complete characterization of detected molecules is not a trivial task and requires high level of expertise. To accelerate the discovery of small molecules, untargeted mass spectrometry-based metabolomics approaches have gained popularity due to collaborative efforts, development of computational resources, and data availability. During this lecture, you will gain an overview about discovery of microbial molecules, how to contextualize them based on the biological source and/or producer and recent workflows to accelerate analyses that contribute to the understanding of the studied system at the molecular level; *Methods*: We apply liquid chromatography tandem mass spectrometry-based untargeted metabolomics, computational approaches such as molecular networking, and resources such as spectral libraries and MASST family tools (e.g., microbeMASST); *Outcomes*: Discovery of microbial molecules from symbiotic ecosystems will be provided to

demonstrate the use of recent computational tools to accelerate these analysis, enabling scientists to ask big questions that can be explored at repository scale. Contribution of curated microbial datasets that enabled us to build resources and tools such as microbeMASST will provide an overview of the available resources for investigating ecosystems at the molecular level.