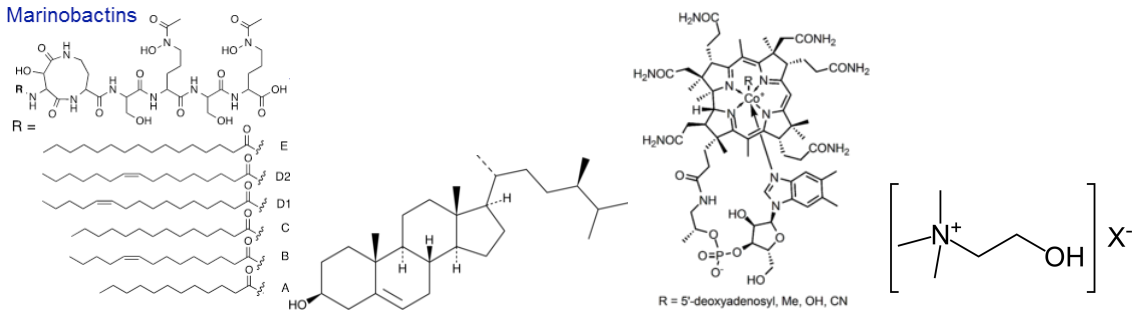
2017 Microbial Diversity Course at MBL, Woods Hole, MA

Symposium I - July 22, 2017 – Lillie Auditorium,

MICROBES AND SMALL MOLECULES



Opening remarks

9:00am-9:30am **Roberto Kolter, Ph.D.**
Department of Microbiology and Immunology
Harvard Medical School

Iron-Clad Strategies of Microbial Growth: Variations in the Biosyntheses of Siderophores

9:30am -10:30am **Alison Butler, Ph.D.**
Department of Biochemistry and Microbiology
UC Santa Barbara

10:30am -11:00am COFFEE BREAK

Discovery of a fourth canonical sterol biosynthesis pathway exclusive to bacteria

11:00am -12:00pm **Paula Welander, Ph.D.**
Environmental Earth System Science, Biology
Stanford

12:00pm -1:30pm LUNCH BREAK

Corrinoids in Communities: Nutrient Sharing in the Microbial World

1:30pm -2:30pm **Michi Taga, Ph.D.**
Plant and Microbial Biology
University of California, Berkeley

2:30pm -3:00pm COFFEE BREAK

Gut reactions: understanding and controlling chemical interactions in the human microbiome

3:00pm -4:00pm **Emily Balskus, Ph.D.**
Chemistry and Chemical Biology
Harvard

Closing remarks

4:00pm -4:30pm **Roberto Kolter, Ph.D.**
Department of Microbiology and Immunology
Harvard Medical School

TALK ABSTRACTS

Alison Butler, PhD

Iron-Clad Strategies of Microbial Growth: Variations in the Biosyntheses of Siderophore

Nearly all bacteria require iron to grow, and thus iron is an object of competition among microbes. Microbes often produced siderophores - small molecules with high ferric ion affinity - to sequester and facilitate transport of Fe(III) into and within bacteria. In marine bacteria – which face an extreme paucity of iron in surface ocean water – we have identified two striking classes of siderophores: a) large suites of fatty acyl siderophores which self-assemble and partition into membranes and b) a-hydroxy-carbocylic acids which when complexed by Fe(III) are photoreactive. Through recent genomic screening we have identified a class of tris catechol siderophores defined by combinatoric library of D- and L-amino acids which are produced by marine and pathogenic microbes. We are interested the biosynthesis and evolution of siderophore structures, as well as the process of iron uptake.

Paula Welander, PhD

Discovery of a fourth canonical sterol biosynthesis pathway exclusive to bacteria

Sterols, like cholesterol, are often thought of as an exclusively eukaryotic feature where they play critical roles in membrane fluidity,stress responses, cell signaling and development in multi-cellular organisms. In my group, we've been challenging this dogma by using a combination of bioinformatics, microbial genetics, biochemical and physiological approaches to identify bacterial sterol producers. We have demonstrated that sterol production by bacteria is more widespread than previously thought, and, in this seminar, I will present how we uncovered a distinct biosynthetic pathway that bacteria use to synthesize their sterols.

Michi Taga, PhD

Corrinoids in Communities: Nutrient Sharing in the Microbial World

Nearly every environment on earth is populated with a diverse community of microbes. Microbial communities are major drivers of environmental processes such as carbon cycling, and they provide important nutritional, reproductive, and immune functions to animal and plant hosts. One aspect of microbial communities that remains poorly understood is how microbes share nutrients. We are studying mechanisms of nutrient sharing in bacteria by focusing on a specific family of shared cofactors, corrinoids (which include vitamin B12 and related molecules). Corrinoid cofactors are used by over 80% of bacteria, yet they are produced by less than 40%. Furthermore, corrinoids produced by different microbes have differences in structure, creating specificity in corrinoid use. We use a combination of genetic, biochemical, and bioinformatic approaches to investigate corrinoid biosynthesis and requirements for particular corrinoid structures in order to develop new ways to understand and predict corrinoid-based metabolism in microbial communities. In the long term, a greater understanding of corrinoid crossfeeding may lead to improved strategies for targeted manipulations of microbial communities.

Emily Balskus, PhD

Gut reactions: understanding and controlling chemical interactions in the human microbiome

The human gut is colonized by trillions of microbes that provide functional capabilities that extend beyond those of host cells, including the ability to make and modify small molecules. There is growing evidence that gut microbial chemical processes affect host biology. However, we still do not understand the vast majority of the molecular mechanisms underlying this phenomenon. This is due to the difficulty of linking gut microbial activities to specific microbial genes and organisms, as well as an inability to selectively control individual activities in complex communities. This talk will discuss my lab's efforts to discover and characterize gut microbial enzymes and metabolic pathways, with a focus on transformations of drugs and dietary compounds. Gaining a molecular understanding of these activities is not only helping us to elucidate the mechanisms by gut microbial metabolism affects host biology, but will also aid future efforts to manipulate gut microbial communities to treat and prevent disease.