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bioinformatics.udel.edu

BIOINFORMATICS SEMINAR

PRISCILLA HEMPEL

PhD Student, Department of CEEG UNIVERSITY OF DELAWARE

TRANSCRIPTIONAL RESPONSE OF ACTINOBACTERIA IN LIGHT/DARK CYCLING

Light is an environmental cue and energy source that is readily available in surface environments. While the conversion of light to energy is well understood in prokaryotes, the conversion of light to signaling information and the associated cellular response(s) has only been characterized in a few microbial species. Actinobacteria in the Luna1 and acII lineages are ubiquitous in surface freshwater environments and we aim to characterize the transcriptional response of two species to changing light regimes. Previously, we showed these heterotrophic Actinobacteria grow faster in light, even without functional photosystems and that this is likely due to upregulation of sugar transport and metabolism in constant light. Here I will present immediate and delayed transcriptional responses of *Rhodoluna laticola* and *Aurantimicrobium* sp. strain MWH-Mo1 to light/dark cycling that simulate a 24 diel cycle. Their ability to sense light and upregulate carbohydrate transport could allow them to coordinate maximum organic carbon uptake with the time of maximum organic carbon production by primary producers. The ability to regulate uptake of organic carbon without needing to constitutively express carbohydrate transporters at a high energy cost or waiting to detect organic carbon allows these species to grow efficiently during the day. This suggests that in surface freshwater environments, light increases the heterotrophic activity that converts organic carbon to CO₂ and biomass, and therefore changes the balance between carbon burial and CO₂ release. Understanding how light signals organic carbon transport and conversion to energy is therefore crucial to understanding how organic carbon cycling changes from night to day and the biochemical mechanisms within the carbon cycle.

RITA HAYFORD

PhD Student, Department of CIS UNIVERSITY OF DELAWARE

UNDERSTANDING PLANT STRESS RESPONSES: USING SYSTEMS BIOLOGY APPROACHES AND TEXT MINING METHODS

One of the most significant challenges in the 21st century is the issue of changing climatic conditions which make research into stress tolerance in plants of utmost importance. Developments in the area of "omics", in the last ~25 years including genomics, transcriptomics, proteomics, and metabolomics has provided a good platform to conduct complex studies to understand the molecular mechanisms underlying stress responses in plants. These studies which can provide understanding of what is happening at a global, whole genome scale in response to external stimuli such as stress, can also produce very large amounts of data that can be difficult to analyze to derive meaningful conclusions. Therefore, development of tools and resources that help to comb through this data will help in the understanding of plant responses to stress. This study combines high throughput technologies, bioinformatics tools, and use of text mining systems to extract stress responsive genes and their relationship with biological processes. Such knowledge will eventually be useful to create a resource for the plant biology, and broader biological community; additionally, in the long-term, this will aid in helping design better crops which can better withstand environmental stresses.

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