Colleen Hui
Merchant Group

“Iron storage and transport in the green alga Chlamydomonas reinhardtii”

ABSTRACT. For decades, the unicellular green alga Chlamydomonas reinhardtii has been used as a model organism for the study of trace metal metabolism in the plant lineage. Algae, like higher plants, require a substantial amount of iron (Fe) as cofactors for the proteins involved in photosynthesis. Fe homeostasis therefore fundamentally impacts yield, growth-rate, and productivity of these organisms, which are widely used in the study of biofuel production and other biotechnological applications. The Fe content in Chlamydomonas cells can be altered by the nutrient availabilities in the environment as well as other growth parameters affecting the Fe quota, including growth stage, carbon/energy source, soil/water pH, and aeration. To understand the potential impact of these growth parameters on trace metal homeostasis in Chlamydomonas, we have completed a systematic analysis of cellular trace metal content as a function of six different cultivation variables using ICP-MS/MS. These variables include 1) cell density/sampling time, 2) growth medium pH, 3) photon flux density, 4) aeration via variation on vessel size, culture volume, and shaker speed, and 5) carbon source. Significantly, we have discovered that alkaline pH under photoheterotrophic growth condition induced hyperaccumulation of Fe in cells up to 10- to 20- fold higher than cells grown in the neutral pH medium. Other parameters like aeration and photon flux density have relatively minor impact on Fe quota. To identify the cause of the Fe accumulation, we have undertaken a comparative transcriptome analysis of cells grown at pH 8.5 versus pH 7.0. We observed that 2523 genes (~14%) are differentially regulated between cultures grown at alkaline vs. neutral pH. In particular, fea2, which encodes a high affinity extracellular Fe assimilation protein, was induced 138-times more at alkaline pH than at neutral pH condition. In order to identify the location of the excess Fe within the cells, we visualized Fe distribution in cells sampled at pH 8.5 by nanoSIMS. Fe was evenly distributed within the cell when grown in neutral pH media. In comparison, imaging of cell sections sampled at pH 8.5 showed most Fe in distinctive hotspots that colocalized with calcium and phosphorus. This suggests that the excess Fe was stored in acidocalcisomes, a lysosome-related organelle.

Orlando E. Martinez
Clubb Group

“The Structure and Mechanism of the Essential Glycosyltransferase, TagA”

Abstract. Wall teichoic acids (WTA) are abundant glycopolymers embedded in the Gram-positive bacterial cell wall that have numerous essential functions, including cell morphogenesis, division, host-pathogen interactions, and antibiotic resistance. The first committed step in the WTA pathway, catalyzed by TagA, can be inactivated to produce viable, WTA-devoid cells resensitized to antibiotics. We recently discovered the high-resolution crystal structure of TagA, revealing a novel GT fold, termed GT-E. Cellular fractionation studies suggest a unique molecular mechanism in which membrane association activates TagA by triggering a dimer to monomer quaternary structural change that facilitates substrate recognition and formation of a catalytically competent active site. Through the employment of NMR and crystallography, we aim to further understand the interaction of TagA with its substrates and the peripheral association to the cell membrane by its C-terminal tail. Our findings will guide rational drug design of antimicrobial compounds to combat antibiotic resistance and promote study of the new GT-E superfamily.

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3440 Molecular Sciences
3:30 p.m.

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