Advancing the molecular understanding of growth in algae and plants

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Project Goals:

Research in the UCLA-DOE Institute for Genomics and Proteomics (IGP) includes major efforts in the area of algal and plant genomics. Green algae and plants are primary producers whose growth generates lipid and carbohydrate-based macromolecules for the production of biofuels and bioproducts. We have been working to advance our molecular understanding of algal and plant growth through the development and application of advanced 'omic' technologies. Our team is pioneering new techniques for scRNAseq in model algal species and advancing genome and transcriptome studies in non-model algal species. Our biological focus centers on optimizing growth in plants and algae in a changing environment.

Abstract:

The green unicellular alga *Chlamydomonas reinhardtii* has been a subject of study in the group and we have previously described how the bulk transcriptome responds to environmental changes. Here, we have applied single-cell RNA sequencing (scRNA-seq) to probe the heterogeneity of Chlamydomonas cell populations under three environments and in two genotypes differing in the presence of a cell wall. We demonstrate that single algal cells with and without cell walls can be used for scRNA-seq, offering the possibility to sample algae communities in the wild and the laboratory. We further show that single cells could be successfully separated into non-overlapping cell clusters according to their growth conditions; cells exposed to iron or nitrogen deficiency were easily distinguished despite a shared tendency to arrest cell division to economize resources. While these results mirrored our bulk RNA-seq results, they also revealed inherent heterogeneity that correlated with circadian responses.

Marine macroalgae also undergo growth in variable environmental conditions. We have produced a de novo transcriptome describing desiccation in lab and field conditions for *Fucus*, or rockweed. Since macroalgae are an emerging molecular system, our de novo transcriptome represents an incredible resource towards understanding novel desiccation tolerance mechanisms; our goal is to further dissect the molecular responses to desiccation in marine macroalgae and to apply this knowledge to improving drought tolerance in land plants. In parallel to this project, we are developing a draft genome for *Fucus* utilizing Illumina and Nanopore sequencing; this would be the third macroalgal genome available.

Future directions. Within the DOE IGP at UCLA we are working to accelerate the development of innovative genomics and structural biology tools for bioenergy-relevant plants. We are

developing technologies in two model species: the model grass, *Brachypodium distachyon*, and the model eudicot *Thlaspi arvense,* or pennycress. This approach allows for rapid technology development within our existing facilities which we can transfer to other DOE researchers for deployment in crops. Our plan will interrogate cell wall structure and function in these models, as it relates to growth. We will leverage our experience in scRNA-seq to develop methods that maintain tissue-context spatial information. Our program will examine the *in vivo* structural details of cell wall biosynthesis enzymes and their subcellular localization in cell-type-specific contexts. *In vivo* structures for cell wall modifying enzymes, within the cell wall, will be revealed as well as how such proteins interact with each other and their target carbohydrates under relevant physiological conditions.

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