

Development of Novel Approaches to Optimize Energy Crops

Dominique Loqué

Joint BioEnergy Institute, Environmental Genomics and Systems Biology, Lawrence Berkeley National Laboratory; Plant and Microbial Biology department, University of California, Berkeley
dloque@lbl.gov

Development of highly performant energy-crops is needed to provide sustainable and large resources of biomass to feed our biorefineries and to support cost-effective conversion of the biomass into biofuels and bio-products. Plant biomass is mainly composed of polymers made of fermentable sugars (cellulose and hemicellulose) that are embedded in a robust aromatic polymer called lignin. Recalcitrant to degradation, lignin inhibits efficient extraction and hydrolysis of cell wall polysaccharides and prevents low-cost lignocellulosic-biofuel production. Unfortunately, content and composition of these polymers cannot be drastically manipulated to the same extent in all tissues without causing deleterious consequences on plant productivity. Therefore, technologies allowing the precise manipulation of content and composition of various components of plant cell walls should be developed to facilitate the production of cheap and large quantities of fermentable sugars without compromising plant growth. Moreover, engineering plants with complex metabolic pathways or multiple traits is often inhibited by the number of genes that are required to reach the final product. It shows the need of synthetic biology tools to express multiple genes with controllable expression strengths and in specific tissues. Here we highlight our progress in synthetic biology to support plant engineering which includes *in vitro* and *in vivo* DNA assembly methods to stack multiple gene cassettes, promoter libraries developed for root specific expression, and novel devices to fine-tune gene expression in plants. We believe the development of these tools and approaches have the potential to support scientists and engineers who are looking at stacking and controlling multiple genes and interested in manipulating endogenous metabolic pathways.

This work was part of the DOE Early Career Award and the DOE Joint BioEnergy Institute (<http://www.jbei.org>) supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research; and U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U.S. Department of Energy.