## 132. Universal expression tools to improve nutrient acquisition of energy crops

Nasim Mansoori Zangir1* (nmansoorizangir@lbl.gov), Carlos Hernandez-Garcia1, Patrick Shih1, Charlee Vuu1, Garima Goyal1, Sangeeta Nath2, Nathan J. Hillson1,2, Samuel Deutsch2, Dominique Loqué1

1Joint BioEnergy Institute, Physical Biosciences division, Lawrence Berkeley National Laboratory, 1 Cyclotron road, Berkeley, CA 94720, USA; 2DOE Joint Genome Institute, 2800 Mitchell Drive, B310-346A, Walnut Creek, CA 94598, USA

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**Project Goals**: The main goals of this research are the generation of "universal" expression tools for plant root engineering and to utilize them to improve nutrient acquisition in energy crops.

Plant growth and development relies on roots as a means to anchor the plant body as well as to absorb water and nutrients such as N, P and K. As deficiency in these nutrients negatively impacts photosynthesis, plant growth and yield, chemical fertilizers have been used to compensate and meet the growing demand for plant material. Unfortunately the excessive use of fertilizers has come at high environmental and economic costs; and its production utilizes a substantial proportion of worldwide energy consumption. The current development of growing crops on marginal land (low water content, low nutrient supply, vulnerability to erosion and heavy-metal pollution) for bioenergy will reduce competition with food crops and the pressure on high-quality arable lands utilization. As sufficient nutrient uptake by the plant root is vital especially when soil conditions restrict its availability, root systems in energy crops can be engineered to acquire/ accumulate the required nutrients.

Our focus is to design "universal" expression tools for plant root engineering functional across diverse plant species. Through targeted-cell engineering and synthetic biology we aim to engineer plant root systems to generate metabolic pathways and improve nutrient acquisition/accumulation in energy crops. This aim will be carried out through development and validation of a large set of root-specific and nutrient-responsive promoters. In house transcriptome analysis will help identify root specific genes that are constitutively expressed, induced or repressed through conserved metabolic responses to N, P and Fe starvation in hydroponic conditions across a widely diverse selection of plant species. Promoters from the identified genes will be isolated and characterized for spatiotemporal expression patterns and expression levels across different taxonomic classes using composite plants and conventional transgenic approaches. Subsequently monocot and dicot "universal" promoter libraries of the detected genes alongside those previously reported will be generated using a semi-high-throughput promoter cloning approach and yeast homologous recombination assembly method and ultimately used for tissue specific metabolic pathway engineering to improve nitrogen use efficiency in bioenergy crops.

We expect that the results of this research will generate a diversity of building blocks for plant engineering and will directly contribute to advance the DOE's mission for the sustainable production of bioenergy.

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## 133. Genetic Parts Screening and Artificial N-glycosylation Motif Engineering for