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Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts

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ABSTRACT

In 2010, when the National Alliance for Advanced Biofuels and Bioproducts (NAABB) consortium began, little was known about the molecular basis of algal biomass or oil production. Very few algal genome sequences were available and efforts to identify the best-producing wild species through bioprospecting approaches had largely stalled after the U.S. Department of Energy's Aquatic Species Program. This lack of knowledge included how reduced carbon was partitioned into storage products like triglycerides or starch and the role played by metabolite remodeling in the accumulation of energy-dense storage products. Furthermore, genetic transformation and metabolic engineering approaches to improve algal biomass and oil yields were in their infancy. Genome sequencing and transcriptional profiling were becoming less expensive, however; and the tools to annotate gene expression profiles under various growth and engineered conditions were just starting to be developed for algae. It was in this context that an integrated algal biology program was introduced in the NAABB to address the greatest constraints limiting algal biomass yield. This review describes the NAABB algal biology program, including hypotheses, research objectives, and strategies to move algal biology research into the twenty-first century and to realize the greatest potential of algae biomass systems to produce biofuels.

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1. Introduction

1.1. Preface

Unlike competing renewable energy production systems (wind, solar, or hydroelectric), biomass has the advantage that it can be

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converted into an energy-dense, liquid fuel feedstock (biocrude) that is compatible with current petroleum refinery technologies. In addition, biological systems provide their own chemical energy storage systems, reducing potential inefficiencies from the conversion and/or storage of electrical energy generated by wind or photovoltaic systems [1]. Recently, there has been substantial interest in the use of microalgae for sustainable production of biofuels, which can be attributed to the ability of algae to produce two- to ten-fold greater annual aerial biomass than that produced by terrestrial crops [2–6]. In addition, algae have the potential to capture inorganic carbon injected into ponds as CO₂ and hydrate it to nongaseous bicarbonate, substantially reducing the potential residence time of CO₂ emitted from point sources in the atmosphere. With respect to fuel conversion technologies, algae are particularly attractive since many are facultatively capable of accumulating between 4% and 60% lipids by dry weight, making them among the most efficient biofuel feedstock production systems [7]. Various estimates indicate that potential oil and biomass yields from algal ponds range from 20,000 to 60,500 L/ha/year and 50,000 to 15,000 kgdw/ha/year, respectively [5]. Emerging developments in genetically modified algae promise to increase production yields by as much as two- to three-fold [8–10].

Before the start of the National Alliance for Advanced Biofuels and Bioproducts (NAABB) consortium, there had been efforts to characterize growth and lipid-generation potential of a variety of algal species. It was known that under nitrogen limitation, many algae stored reduced carbon in the form of triglycerides, terpenoids, or polysaccharides that could be used for high-energy density fuel production. However, little was known about the fundamental physiology involved in partitioning carbon or the role played by metabolite remodeling in the accumulation of energy-dense storage products. At the outset of the NAABB, very few algal genome sequences were available and efforts to identify the best-producing wild species through bioprospecting approaches had largely stalled after the U.S. Department of Energy's Aquatic Species Program. Furthermore, algal genetic transformation required for metabolic engineering approaches was only possible in a few model species. At that same time commercial next-generation DNA sequencers and the computational tools to assemble to annotate complex genomes and expression profiles were becoming widely available, making rapid algal

genome sequencing and transcriptional profiling possible. It was in this context that an integrated algal biology program was introduced in NAABB to address the greatest constraints limiting algal biomass yield. The NAABB final report to the Department of Energy provides details on the consortium and all of the technical and scientific efforts undertaken [11]. In the following sections, we describe the hypotheses, research objectives, and strategies of this program to move algal biology research into the twenty-first century and to realize the greatest potential of algae biomass systems to produce biofuels.

1.2. Approach

At the outset of NAABB, our techno-economic analysis showed that increasing the productivity of algae would have the greatest impact on the economic viability and sustainability of an algal biofuels industry; this observation remains true today. The overall objective of the algal biology teams was to increase the overall productivity of algal biomass accumulation and lipid/hydrocarbon content. The specific targets were to increase by more than 50% the total lipid dry weight and to improve pond cultivation by more than 20 gdw/m²/day. Our approach to characterizing the biological potential of algal biofuels is outlined in Fig. 1 and the Algal Biology Work Breakdown Structure (WBS) (Table 1). Two potentially complementary paths were explored to achieve the program's objectives, including bioprospecting algal diversity, and/or genetic modification of algae to increase both yield and robustness while reducing energy and material inputs. Clearly, given the extensive biological diversity of algae (>100,000 species), tremendous advantages can be achieved by identifying the most robust and productive strains of algae that could be further improved through genetic engineering. Thus, our bioprospecting efforts focused on surveying the natural diversity of wild algal strains for production-relevant traits. Independently, substantial efforts were also focused on targeted transformations and directed engineering of high-performance algae, which required a greater understanding of the molecular basis of the observed traits. Our systems biology and bioinformatics efforts included genome sequencing along with transcriptomic, proteomic, and phenomic analyses. At each step in the process, it was often necessary to develop new technologies or tools to address the unique biology of algae. To develop and

Algal Biology Task Framework

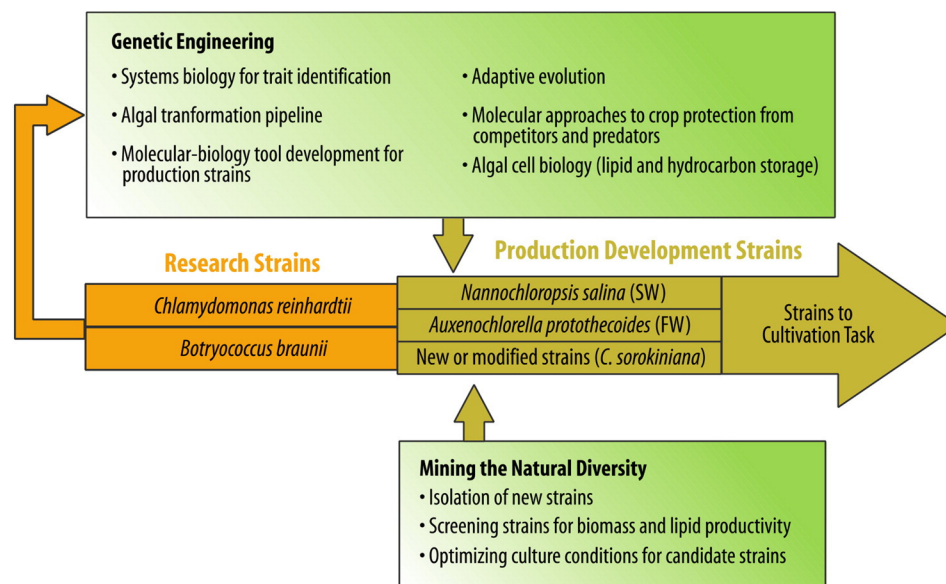


Fig. 1. Algal biology task framework.

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