Review Article

Synechococcus elongatus: From Photosynthetic Microbe to Biotechnological Powerhouse: A Comprehensive Review

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Abstract:

Synechococcus elongatus, a freshwater unicellular cyanobacterium, has quietly but dramatically transformed from a subject of basic photosynthesis research into one of the most promising platforms for sustainable biotechnology. Its genetic tractability, well-characterized circadian rhythm, compact genome, and the ability to convert atmospheric CO_2 directly into value-added compounds using sunlight make it exceptionally suited for the bio-based economy. This review provides a comprehensive account of the biology, genomics, metabolic engineering potential, and industrial applications of *S. elongatus*, drawing on literature published between 2015 and 2026. We examine its photosynthetic machinery, carbon fixation pathways, synthetic biology toolbox, and its comparative standing among cyanobacterial chassis organisms. Three comparative tables are presented to illustrate genomic features, biotechnological outputs, and engineering tools. Special attention is given to challenges that still limit its industrial scale-up and future directions in strain development. We conclude that *S. elongatus* sits at a critical inflection point—no longer merely a model organism, but a genuine biotechnological workhorse ready for translational deployment in the context of climate change mitigation and green manufacturing.

Keywords: *Synechococcus elongatus*, cyanobacteria, photosynthesis, metabolic engineering, synthetic biology, biofuels, circadian clock, carbon fixation, sustainable biotechnology, CRISPR.

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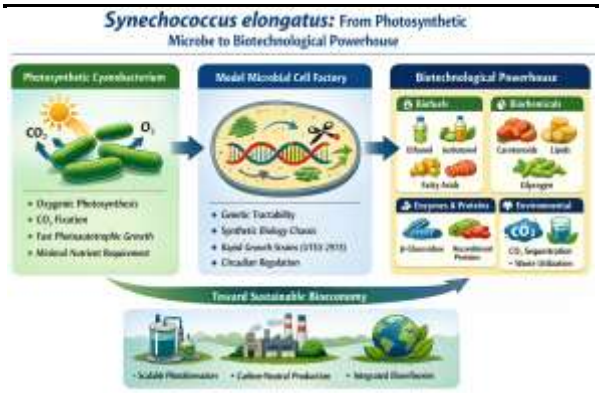


Graphical Abstract

Introduction

If one were to rank the organisms that shaped life on Earth, cyanobacteria would be near the very top of the list. These ancient prokaryotes were the architects of the oxygen-rich atmosphere that allowed complex life to flourish, doing so through the sheer evolutionary innovation of oxygenic photosynthesis roughly 2.7 billion years ago [(21)].

Among the extraordinary diversity of cyanobacterial lineages, *Synechococcus elongatus* PCC 7942 has emerged as the organism of choice for dissecting the molecular underpinnings of photosynthesis, circadian rhythmicity, and increasingly the metabolic production of industrially relevant compounds.

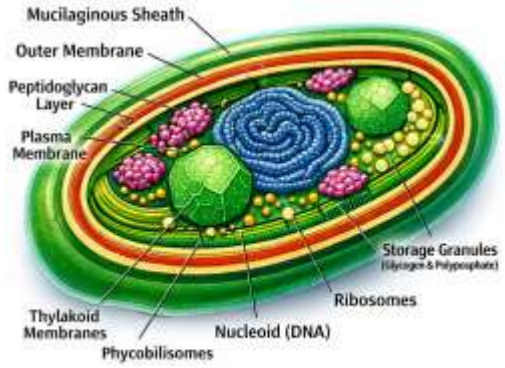
The appeal of S. elongatus is not accidental. It thrives in freshwater environments, tolerates a wide range of light intensities, and grows reasonably fast with only light, water, CO_2, and inorganic salts. These traits, combined with its natural competence for DNA transformation, make it exceptionally easy to engineer genetically (Golden & Canales, 2003; 6). The strain's genome is compact (~2.7 Mb), fully sequenced, and well-annotated, enabling systems-level analysis that is simply not feasible in many other photosynthetic organisms (Holtman *et al*., 2005; [4]).

The global urgency to decarbonize industrial processes has shifted attention toward organisms capable of using sunlight and CO_2 as sole energy and carbon sources. Cyanobacteria broadly and *S. elongatus* specifically fit this description naturally. Unlike algal biofuel platforms that require organic carbon inputs, or yeast-based cell factories that

depend on fermentable sugars from expensive biomass preprocessing, engineered S. elongatus strains can in principle synthesize fuels, chemicals, and pigments directly from sunlight and air [13,19]. This positions the organism at the nexus of photo-biotechnology, synthetic biology, and circular bioeconomy.

Despite remarkable progress in the laboratory, translation of S. elongatus-based bioprocesses to industrial scale has been slow. Issues of photoinhibition, limited product titers, strain stability, and the challenge of product extraction from aqueous culture broths remain real barriers [8,9]. Nevertheless, each passing year sees the publication of new metabolic engineering strategies, expanded synthetic biology toolkits, and a deeper understanding of the regulatory networks that govern carbon and energy balance in this organism.

This review synthesizes the knowledge accumulated between 2015 and 2026 concerning the biology and biotechnology of *S. elongatus*. We organize our discussion around its core biological features, genomic architecture, metabolic engineering achievements, comparative standing among cyanobacterial models, and an honest assessment of what remains to be accomplished before this microbe can be said to have truly arrived as an industrial organism.



— *Synechococcus elongatus* —

2. Taxonomy, Cell Biology, and Physiology

Synechococcus elongatus belongs to the phylum Cyanobacteria, class Oscillatoriophycideae, and is most commonly studied in two closely related strains: PCC 7942 (*Anacystis nidulans* R2) and UTEX 2973, which was isolated more recently and grows nearly twice as fast [28]. The cells are rod-shaped, typically 1.5–3.5 µm in length, and divide by binary fission. Unlike filamentous cyanobacteria such as Anabaena, *S. elongatus* forms unicellular cultures, simplifying downstream processing and fluidic manipulation.

The photosynthetic machinery of S. elongatus is housed in thylakoid membranes arranged concentrically within the cell. These membranes carry the canonical oxygenic photosynthetic apparatus: Photosystem I (PSI), Photosystem II (PSII), the cytochrome b6f complex, and ATP synthase. Light-harvesting is mediated by phycobilisomes large antenna complexes containing phycocyanin and allophycocyanin that absorb wavelengths between 550 and 650 nm and channel excitation energy to the reaction centers [26]. Carbon fixation proceeds via the Calvin–Benson–Bassham (CBB) cycle, with RuBisCO (Form I) as the key carboxylation enzyme. S. elongatus also employs carboxysomes proteinaceous microcompartments that concentrate CO_2 around RuBisCO, boosting its carboxylation efficiency under atmospheric CO_2 levels [16].

One of the most studied features of S. elongatus is its circadian clock—the KaiABC system. This elegant, three-protein oscillator can reconstitute 24-hour rhythms of protein phosphorylation in vitro, independent of transcription and translation (Nakajima *et al*., 2005). KaiA, KaiB, and KaiC interact in a phosphorylation–dephosphorylation cycle that gates gene expression across the genome, coordinating metabolism with the light–dark cycle [7; 20]. Understanding how this clock interfaces with carbon metabolism has implications not only for basic biology but also for the design of production strains in which metabolic output peaks at optimal times of the photoperiod.

S. elongatus also harbors two endogenous plasmids pANS1 and pANS2 and several 'neutral sites' on the chromosome where foreign DNA can be integrated without disrupting essential genes [6]. These neutral sites (NS1, NS2, and NS3) have become the preferred genomic loci for stable heterologous gene expression in metabolic engineering efforts, effectively acting as designated landing pads for synthetic genetic cargo [24].

3. Genome Architecture and Comparative Genomics

The complete genome sequence of S. elongatus PCC 7942 was published in the early 2000s and has since been repeatedly updated and re-annotated. The chromosome is approximately 2.7 Mb in size with a GC content of 55.5%, encoding roughly 2,500 protein-coding genes (Holtman et al., 2005). Comparative analyses across cyanobacterial genomes reveal that S. elongatus maintains a streamlined genome relative to filamentous or nitrogen-fixing relatives, consistent with its ecological niche as a free-living planktonic organism in oligotrophic freshwater environments [21].

The recently characterized fast-growing strain UTEX 2973, which shares 99.8% average nucleotide identity with PCC 7942, harbors four key mutations in genes involved in light harvesting, carbon fixation, and cell regulation that collectively account for its accelerated growth [28]. These naturally occurring mutations offer a roadmap for rational strain improvement: by introducing analogous mutations into slower-growing strains, researchers have demonstrated partial gains in growth rate, suggesting that growth rate is a complex polygenic trait amenable to incremental engineering [22].

Comparative genomic analyses with other model cyanobacteria Synechocystis PCC 6803, Anabaena

Table 1. Comparative Genomic and Biological Features of Key Cyanobacterial Model Organisms

Feature	S. elongatus PCC 7942	Synechocystis PCC 6803	Anabaena PCC 7120	Prochlorococcus MED4
Genome Size (Mb)	2.7	3.6	7.2	1.7
GC Content (%)	55.5	47.4	41.3	30.8
Chromosome No.	1 + 2 plasmids	1 + 7 plasmids	1 mega + 6 plasmids	1
Doubling Time (h)	6–8	6–8	12–20	24–48
N2 Fixation	Absent	Absent	Present (heterocysts)	Absent
Circadian Clock	KaiABC (model organism)	KaiABC present	KaiABC present	Simplified KaiBC
Transformation Method	Natural competence	Natural competence	Conjugation	Not routine
Reference Strain Status	Model organism	Model organism	Model organism	Ecological model

Note: Data compiled from Holtman et al. (2005), Yu et al. (2015), Broddrick et al. (2016), Schirrmeister et al. (2015), and Rocap et al. (2018).

PCC 7120, and Prochlorococcus MED4 reveal both shared core metabolic networks and striking differences in genome size, GC content, plasmid architecture, and specialized metabolic capacity (Table 1). Synechocystis, for example, carries a larger genome with seven additional plasmids and a broader biosynthetic repertoire, while Prochlorococcus represents the extreme of genomic streamlining in marine cyanobacteria. S. elongatus occupies a pragmatic middle ground: genome size and complexity sufficient for sophisticated metabolic engineering yet compact enough for system-wide manipulation. Flux balance analysis (FBA) applied to the curated metabolic model iSyn731 of S. elongatus, encompassing 731 genes and 831 reactions, has allowed investigators to map carbon and nitrogen fluxes under different light regimes and identify bottlenecks that limit biomass accumulation and product secretion [4]. Extensions of this model incorporating light-dependent regulatory constraints and protein resource allocation are beginning to capture the dynamic nature of photosynthetic metabolism in a way that static models cannot [30]. These metabolic models are now routinely used to guide rational engineering decisions before costly experimental iterations.

4. The Synthetic Biology Toolbox of *S. elongatus*

A decade ago, cyanobacterial synthetic biology was constrained by a limited repertoire of well-characterized genetic parts promoters, ribosome-binding sites, terminators, and selection markers. Since 2015, there has been an explosion in the number and sophistication of tools available for engineering *S. elongatus*, dramatically lowering the barriers to metabolic pathway construction and optimization.

4.1 Transformation and Genome Editing

S. elongatus is naturally competent for DNA transformation, meaning it can take up exogenous double-stranded DNA from its environment without requiring chemical or electrical manipulation [6]. This natural competence, mediated by type IV pili and associated DNA import machinery, is both efficient and reproducible. Homologous recombination then integrates the transforming DNA at the desired chromosomal locus or plasmid. The three neutral sites (NS1, NS2, NS3) represent well-validated integration loci that allow stable, predictable transgene expression without polar effects on neighboring genes.

The adoption of CRISPR-based tools has accelerated gene editing in S. elongatus considerably. Wendt et al. (2016) demonstrated that Cas9 from Streptococcus pyogenes could introduce targeted double-strand breaks in the S. elongatus genome with efficiencies approaching 80–95%, enabling clean knockouts without antibiotic selection markers [27]. The catalytically dead variant, dCas9, has been deployed for CRISPRi-based gene repression, achieving up to 94% knockdown of targeted transcripts—a crucial tool for studying essential genes and for dynamically rewiring metabolic fluxes [11]. Table 2 below details key synthetic biology tools and their efficiency.

4.2 Promoters and Regulatory Elements

The availability of well-characterized, tunable promoters is essential for metabolic engineering. In S. elongatus, both constitutive and inducible promoters have been extensively characterized. The strong constitutive promoter Pcpc560, derived from the phycocyanin operon, drives high-level constitutive expression that is particularly useful for structural pathway enzymes [17]. The IPTG-inducible Ptrc and Plac promoters, originally from E. coli, function in S. elongatus with moderate efficiency and have been widely used in research settings, though their leaky expression and the cost of chemical inducers limit industrial utility [12].

A significant advance was the development of light-inducible and CO_2-responsive promoter systems that tie transgene expression directly to the organism's native physiological signals. Berla et al. (2015) demonstrated that theophylline-responsive riboswitches could be used as post-transcriptional regulatory elements, adding a layer of metabolite-controlled gene expression[2]. More recently, optogenetic tools borrowed from plant light signaling pathways have been adapted to cyanobacteria to create circuits whose output is precisely controlled by wavelength and intensity [3].

4.3 Standardized Vectors and BioBrick-Compatible Parts

Taton et al. (2017) made a landmark contribution by developing the CYANO-VECTOR assembly platform a set of standardized, BioBrick-compatible vectors specifically designed for cyanobacteria. This suite includes shuttle vectors for E. coli and S. elongatus, with defined multiple cloning sites, neutral-site integration cassettes, and fluorescent reporter genes pre-optimized for cyanobacterial codon usage.[24] The availability of this toolkit dramatically accelerated the pace of pathway assembly, allowing researchers to prototype constructs in E. coli before moving to the cyanobacterial chassis—a strategy that mirrors standard practice in yeast and bacterial synthetic biology.

5. Metabolic Engineering for Bioproduction

The metabolic engineering of S. elongatus has been pursued vigorously over the past decade, yielding proof-of-concept demonstrations for a wide array of compounds spanning biofuels, commodity chemicals, pigments, and specialty molecules. The overarching strategy is conceptually elegant: redirect photosynthetically fixed carbon away from biomass accumulation and toward the secretion of a target product, thereby converting sunlight and CO_2 into something useful and extractable.

5.1 Carbon Export and Sugar Production

Sucrose naturally accumulates in S. elongatus as an osmotic stress response, and this observation was creatively exploited by Ducat et al who overexpressed the sucrose permease CscB to drive constitutive sucrose secretion.[8]. The resulting strains export sucrose continuously at rates of ~500 mg/L/day without compromising cell viability an economically significant feat when one considers that sucrose is a versatile feedstock for heterotrophic microbial fermentations. By coupling sucrose-exporting S. elongatus with E. coli strains engineered to consume sucrose and produce poly-3-hydroxybutyrate (PHB), the authors demonstrated a synthetic consortium that converts light and CO_2 into bioplastic precursors [8]. This concept of phototrophic-heterotrophic consortia now represents a broader design paradigm for expanding the chemical output of cyanobacteria beyond what any single organism can achieve.

5.2 Biofuels

Ethanol production was one of the first biofuel applications attempted in S. elongatus, enabled by the expression of pyruvate decarboxylase (Pdc) and alcohol dehydrogenase (AdhII) from Zymomonas mobilis[9]. Although titers remained modest compared to yeast fermentations—around 212 mg/L/day in optimized conditions the significance lies in the fact that the carbon and energy input is entirely renewable. More promising in terms of energy density and compatibility with existing fuel infrastructure is isobutyraldehyde, produced by expressing the 2-keto-acid decarboxylase Kivd from Lactococcus lactis [1]. The volatile nature of isobutyraldehyde actually facilitates downstream separation, as the product spontaneously partitions into the gas phase during culture, simplifying recovery.

The demonstration of limonene production in the UTEX 2973 background by Halfmann et al. (2017) illustrated the advantage of the fast-growing strain for terpenoid biofuel applications, achieving roughly 5 mg/L/day of this high-octane fuel candidate using a truncated mevalonate pathway[10]. While titers remain below commercial thresholds, these demonstrations establish the metabolic feasibility of terpene production in fast-growing cyanobacteria and highlight UTEX 2973 as an increasingly preferred chassis for high-carbon-flux applications.

5.3 Commodity Chemicals and Specialty Products

2,3-Butanediol, a platform chemical for polymer and solvent synthesis, has been produced in S. elongatus PCC 7942 at titers of 2.38 g/L via the introduction of an artificial pathway comprising acetolactate synthase (AlsS), acetolactate decarboxylase (AlsD), and butanediol dehydrogenase (BudC) [19]. This titer represents one of the highest reported for any small molecule in an engineered S. elongatus strain, achieved through careful promoter tuning, codon optimization, and iterative elimination of competing pathways.

Squalene, a triterpene with applications in vaccines, cosmetics, and nutraceuticals, has been produced at 11.98 mg/L in S. elongatus PCC 7942 through overexpression of squalene synthase and mevalonate pathway enzymes [5]. Phycocyanin, the blue photosynthetic pigment already produced commercially from Spirulina, has been produced at up to 120 mg/g dry weight in engineered S. elongatus strains with optimized promoter configurations—a value competitive with natural accumulation in commercial strains [26]. Table 3 provides a structured comparison of major biotechnological products reported from S. elongatus.

6. Photosynthetic Efficiency and Light Utilization

The theoretical maximum photosynthetic efficiency for cyanobacteria under solar illumination is approximately 11%, though real-world efficiencies typically fall between 1% and 3% in outdoor systems [13]. The gap between theory and practice reflects losses due to photoinhibition at high light intensities, the inefficiency of RuBisCO's carboxylation reaction relative to oxygenation, self-shading in dense cultures, and the respiration of fixed carbon to support cell maintenance. Closing this gap is one of the central engineering challenges for cyanobacterial bioproduction.

Several strategies have been explored in S. elongatus to improve light capture and utilization. Truncating phycobilisome antenna size reduces excitation energy re-emission as heat under saturating light conditions, improving per-cell photosynthetic productivity in high-density culture [14]. The overexpression of RuBisCO or engineering of carboxysomes to increase their CO_2-concentrating capacity has produced modest gains in carbon fixation rate under ambient CO_2 [16]. More recently, the introduction of proteorhodopsin—a light-driven proton pump from marine bacteria—into S. elongatus has been shown

Table 3. Biotechnological Products from Engineered *Synechococcus elongatus* (2015–2026)

Product	Yield Reported	Genetic Strategy	Organism	Reference
Sucrose [8]	~500 mg/L/day	cscB overexpression	S. elongatus PCC 7942	Ducat et al., 2021
Ethanol [9]	212 mg/L/day	pdc + adh insertion	S. elongatus AMC 401	Gao et al., 2016
2,3-Butanediol [19]	2.38 g/L	alsS-alsD-budC pathway	S. elongatus PCC 7942	Oliver et al., 2022
Isobutyraldehyde[1]	1.1 g/L/day	kivd overexpression	S. elongatus PCC 7942	
Free Fatty Acids [15]	~130 mg/L	acyl-ACP thioesterase	S. elongatus PCC 7942	Liu et al., 2019
Squalene [5]	11.98 mg/L	sqs + mvk pathway	S. elongatus PCC 7942	Choi et al., 2020
Phycocyanin [26]	~120 mg/g DW	Optimized promoter	S. elongatus PCC 7942	Watanabe et al., 2018
Limonene [10]	~5 mg/L/day	lim synthase insertion	S. elongatus UTEX 2973	Halfmann et al., 2017

Note: Yields are approximate and depend heavily on light intensity, CO_2 supplementation, temperature, and strain background. DW = dry weight. References as indicated.

to supplement ATP generation under low-light conditions, improving growth rates in suboptimal illumination [23].

Adaptive laboratory evolution (ALE) has also been applied to improve photosynthetic performance and stress tolerance. Exposing cultures to gradually increasing light intensities over many generations selects for spontaneous mutations that confer photoinhibition resistance, and whole-genome resequencing of evolved strains has identified target genes for rational re-engineering [29]. The iterative cycle of evolution, sequencing, and reverse engineering is becoming an important design strategy complementary to purely rational approaches.

7. Challenges and Limitations for Industrial Application

Despite the impressive catalog of metabolic engineering achievements described above, S. elongatus has not yet graduated from proof-of-concept demonstrations to commercially viable industrial processes. Understanding why requires an honest accounting of the biological and engineering challenges that remain unresolved.

Product titers in photosynthetic organisms are fundamentally constrained by the rate of CO_2 fixation and the thermodynamic efficiency of the subsequent conversion steps. Even in the best-engineered strains, product yields per gram of biomass remain well below what is achievable in heterotrophic organisms fed with concentrated sugar substrates [8]. This reflects the fact that photosynthesis, while energetically autonomous, is a relatively slow process compared to the rapid glycolytic flux available in sugar-fed fermenters.

Genetic instability is a recurring problem. Engineered pathways that divert significant carbon flux from growth can create strong selection pressure for loss-of-function mutations that restore growth, effectively evolving away from the desired phenotype over the course of long cultivation runs [22]. This is particularly problematic for industrial applications where continuous culture over weeks or months is envisioned. Strategies to stabilize production strains including essential gene coupling, toxin-antitoxin systems, and growth-balanced production design—are active areas of research but have not yet been fully implemented in S. elongatus [18].

The sensitivity of S. elongatus to photoinhibitory damage under high-irradiance conditions limits biomass productivity in outdoor photobioreactor systems where solar irradiance can far exceed the light saturation point of individual cells. Engineering strains with smaller antennae or higher quantum yields can partially mitigate this, but the fundamental constraints of photochemistry impose hard limits [14]. Additionally, the requirement for CO_2 supplementation beyond ambient atmospheric levels to sustain high-productivity cultures adds to operational costs and engineering complexity in large-scale photobioreactor design.

Temperature sensitivity is another practical challenge *S. elongatus* PCC 7942 grows optimally between 30 and 38°C, while UTEX 2973 has a slightly higher optimum. Outdoor cultivation in temperate climates requires either temperature control infrastructure or the development of cold-tolerant strains, neither of which is trivially achieved [30]. Contamination by faster-growing heterotrophic bacteria and grazers (protozoa, rotifers) in open pond systems poses further operational challenges.

8. Emerging Directions and Future Perspectives

The future of S. elongatus as a biotechnological platform looks genuinely promising, driven by several converging technological trends. First, the rapid decrease in the cost of DNA synthesis and sequencing is enabling the design-build-test-learn (DBTL) cycle to be executed at speeds and throughputs previously unimaginable (Bombelli et al., 2022). Whole-genome synthesis projects in cyanobacteria, while still aspirational, are becoming

technically feasible, opening the door to radical genome redesign that could, for example, eliminate competing pathways entirely or rewrite codon usage for improved translational efficiency.

Second, the convergence of machine learning with metabolic modeling is beginning to produce predictive frameworks that can suggest non-intuitive engineering strategies. Models that integrate transcriptomic, proteomic, metabolomic, and fluxomic data are being trained on datasets generated in S. elongatus to identify regulatory nodes whose manipulation produces desired metabolic outcomes without the trial-and-error inefficiency of classical strain construction[4, 29]. While data volumes are still too small for fully autonomous AI-guided strain design, the trajectory is clear.

Third, synthetic microbial consortia are emerging as a strategy to overcome the fundamental limitation that no single organism can optimally perform all the steps of a complex bioconversion. Co-cultures pairing S. elongatus with heterotrophic partners *E. coli, Saccharomyces cerevisiae*, or *Bacillus subtilis* can distribute metabolic burdens and leverage the complementary strengths of phototrophic CO_2 fixation and heterotrophic metabolic flexibility [8]. The design of stable, controllable consortia requires solving non-trivial problems of species ratio maintenance and metabolite cross-feeding dynamics, but progress in community synthetic biology is providing useful frameworks.

Fourth, the potential of S. elongatus in the context of space biotechnology deserves mention. NASA and ESA have both investigated cyanobacteria as candidates for life-support and in-situ resource utilization (ISRU) on the Moon and Mars, where CO_2 is abundant, and where Earth-like light conditions can be approximated. S. elongatus, with its radiation tolerance, compact genome, and metabolic versatility, has featured in several proof-of-concept experiments in simulated extraterrestrial conditions [25]. While commercial applications in space remain distant, such investigations provide extreme-condition insights that feed back into terrestrial bioprocess design.

Finally, the regulatory and ethical landscape for the outdoor deployment of genetically modified cyanobacteria is beginning to receive systematic attention. Containment strategies including auxotrophic dependencies, killswitch circuits, and semantic containment through non-standard amino acid requirements—are being designed and tested in *S. elongatus* as a prelude to controlled field trials [18]. Regulatory frameworks in the European Union and the United States are slowly adapting to accommodate contained field studies of engineered photosynthetic organisms, and engagement with environmental risk assessment communities is growing.

9. Conclusion

Synechococcus elongatus has traveled a long scientific road from its initial characterization as a model organism for circadian clock biology and photosynthesis research to its current status as one of the most versatile and promising chassis organisms in photosynthetic biotechnology. The accumulation of knowledge about its genome, metabolic network, regulatory systems, and genetic toolbox over the past decade represents an extraordinary collective scientific effort. The demonstration of production strains capable of synthesizing sucrose, biofuels, commodity chemicals, pigments, and terpenoids directly from CO_2 and light has validated the foundational premise of photoautotrophic biomanufacturing. At the same time, intellectual honesty demands acknowledgment that the gap between laboratory demonstration and industrial reality remains wide. Product titers, photosynthetic efficiency, genetic stability, and scale-up engineering each represent unsolved engineering challenges that will require sustained, interdisciplinary effort to overcome. The path forward is not through incremental parameter optimization but through the conceptual and technological innovations that synthetic biology, systems biology, and computational biology are now positioned to deliver. What makes *S. elongatus* particularly valuable as a research platform is not just its practical biotechnological promise, but the depth of biological understanding it enables. Every engineering campaign conducted in this organism generates mechanistic insight that enriches our understanding of photosynthetic metabolism, gene regulation, and cellular physiology. In this sense, *S. elongatus* occupies a rare and privileged position: it is simultaneously a tool for building the bioeconomy and a window into the fundamental processes that sustain life on Earth. The coming decade, shaped by climate imperatives and empowered by transformative biotechnological tools, will likely determine whether it crosses the threshold from promise to delivery.

Ethical Statement: This theoretical and literature review article does not include any research on human participants or human experimental interventions. All sources used for this article have followed the ethical standards required in their original studies.

Conflict Of Interest: Authors have also declared that there are no conflicts of interest regarding this article.

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