The Metabolic Network of *Synechocystis* sp. PCC 6803: Systemic Properties of Autotrophic Growth

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Unicellular cyanobacteria have attracted growing attention as potential host organisms for the production of valuable organic products and provide an ideal model to understand oxygenic photosynthesis and phototrophic metabolism. To obtain insight into the functional properties of phototrophic growth, we present a detailed reconstruction of the primary metabolic network of the autotrophic prokaryote *Synechocystis* sp. PCC 6803. The reconstruction is based on multiple data sources and extensive manual curation and significantly extends currently available repositories of cyanobacterial metabolism. A systematic functional analysis, utilizing the framework of flux-balance analysis, allows the prediction of essential metabolic pathways and reactions and allows the identification of inconsistencies in the current annotation. As a counterintuitive result, our computational model indicates that photorespiration is beneficial to achieve optimal growth rates. The reconstruction process highlights several obstacles currently encountered in the context of large-scale reconstructions of metabolic networks.

Cyanobacteria are among the evolutionarily oldest organisms and are the only known prokaryotes capable of plant-like oxygenic photosynthesis. As primary producers in aquatic environments, they play an important role in global CO₂ assimilation and oxygen recycling. Recently, cyanobacteria have also attracted growing attention for economic purposes, including drug discovery and as prolific producers of natural products (Sielaff et al., 2006; Tan, 2007). In particular their ability to directly convert atmospheric CO₂ into biomass and organic compounds, driven by sunlight, offers considerable potential as a novel and renewable resource for bioenergy (Deng and Coleman, 1999; Atsumi et al., 2009; Mascarelli, 2009; Lindberg et al., 2010).

Among the diverse cyanobacterial strains, *Synechocystis* sp. PCC 6803 is one of the most extensively studied model organisms for the analysis of photosynthetic processes. With a rich compendium of genomic, biochemical, and physiological data available, *Synechocystis* sp. PCC 6803, therefore, offers an ideal starting point to obtain insights into the systemic properties of phototrophic metabolism. The prerequisite for such a systemic description is a detailed reconstruction of the metabolic network of the organism: that is, a reconstruction of the comprehensive set of enzyme-catalyzed reactions required to support cellular growth and maintenance. Once a metabolic reconstruction is available, the vast array of methods developed by computational systems biology over the past decades allows us to dissect the functioning and interplay of possible metabolic routes and biochemical interconversions. In this respect, constraint-based modeling, most notably flux-balance analysis (FBA), has become a quasi-standard in the field. FBA is increasingly utilized to elucidate and characterize large-scale network properties, to direct the discovery of novel or alternative pathways, to guide metabolic engineering, as well as for the conceptualization of high-throughput data (Oberhardt et al., 2009; Steuer and Junker, 2009). As one of its prime advantages, constraint-based modeling does not require knowledge of the kinetic parameters of individual metabolic reactions, making it applicable to large-scale, up to genome-scale, metabolic networks. Specifically, FBA allows the prediction of optimal steady-state fluxes that maximize a given objective function, usually the synthesis of biomass or biomass precursors required for growth. Although certainly not without pitfalls, the predictions of FBA have proven to reasonably reflect the modes of cellular operation, with manifold applications ranging from microorganisms to algae and plant metabolism (Varma and Palsson, 1994; Shastri and Morgan 2005; Boyle and Morgan, 2009, Feist et al., 2009; Grafahrend-Belau et al., 2009; Oberhardt et al., 2009; Poolman et al., 2009).

The aim of our contribution is to provide a high-quality stoichiometric reconstruction of the primary site for such a systemic description is a detailed reconstruction of the metabolic network of the organism: that is, a reconstruction of the comprehensive set of enzyme-catalyzed reactions required to support cellular growth and maintenance. Once a metabolic reconstruction is available, the vast array of methods developed by computational systems biology over the past decades allows us to dissect the functioning and interplay of possible metabolic routes and biochemical interconversions. In this respect, constraint-based modeling, most notably flux-balance analysis (FBA), has become a quasi-standard in the field. FBA is increasingly utilized to elucidate and characterize large-scale network properties, to direct the discovery of novel or alternative pathways, to guide metabolic engineering, as well as for the conceptualization of high-throughput data (Oberhardt et al., 2009; Steuer and Junker, 2009). As one of its prime advantages, constraint-based modeling does not require knowledge of the kinetic parameters of individual metabolic reactions, making it applicable to large-scale, up to genome-scale, metabolic networks. Specifically, FBA allows the prediction of optimal steady-state fluxes that maximize a given objective function, usually the synthesis of biomass or biomass precursors required for growth. Although certainly not without pitfalls, the predictions of FBA have proven to reasonably reflect the modes of cellular operation, with manifold applications ranging from microorganisms to algae and plant metabolism (Varma and Palsson, 1994; Shastri and Morgan 2005; Boyle and Morgan, 2009, Feist et al., 2009; Grafahrend-Belau et al., 2009; Oberhardt et al., 2009; Poolman et al., 2009).

The aim of our contribution is to provide a high-quality stoichiometric reconstruction of the primary
metabolic network of *Synechocystis* sp. PCC 6803 and a characterization of its functional properties during phototrophic growth. We identify inconsistencies in the current gene annotation and suggest several genes with putative novel or different enzymatic activity for further experimental validation. Our work significantly improves upon earlier reconstructions, which were either restricted to the primary carbon metabolism (Shastri and Morgan, 2005; Hong and Lee, 2007; Navarro et al., 2009) or incomplete with respect to several metabolic routes (Fu, 2008; Kun et al., 2008). During the reconstruction process, we identified various obstacles that currently hamper the large-scale construction of metabolic models. First, despite the rather detailed annotation of the genome sequence of *Synechocystis* sp. PCC 6803, reflecting the high level of curation for this model organism, our analysis reveals a number of glaring gaps even within primary metabolic pathways. For several essential metabolic precursors, no feasible and validated synthesis routes are known. Second, automated reconstruction and comparison of different resources is significantly compromised by heterogeneous naming conventions used in different databases, making a cross-database comparison a laborious and predominantly manual process. To facilitate model exchange and reuse, as well as to provide a resource for further studies, we therefore place specific emphasis on a consistent and standardized nomenclature. Our reconstruction complies with the minimal information requested for the annotation of biochemical models (MIRIAM) and is represented using the systems biology markup language (SBML), allowing researchers to uniquely identify network components and enabling automated reasoning and model comparison (Hucka et al., 2003; Le Novère et al., 2005).

The computational model is subsequently utilized to explore and characterize possible flux states of *Synechocystis* sp. PCC 6803. Making use of the framework of FBA, we identify essential reaction sets and optimal synthesis routes for growth and maintenance as well as the necessary reorganization of metabolic fluxes in the transition from storage-utilizing night metabolism to phototrophic growth. Remarkably, our results indicate that the seemingly wasteful oxygenation of ribulose-1,5-bisphosphate (RuBP) is required to achieve an optimal flux state. This unintuitive result is discussed in the light of ongoing work to elucidate and achieve an optimal flux state. This unintuitive result is discussed in the light of ongoing work to elucidate and achieve an optimal flux state.

**RESULTS**

**A Metabolic Model of *Synechocystis* sp. PCC 6803**

We aim at a comprehensive reconstruction of the primary metabolic pathways of *Synechocystis* sp. PCC 6803. The scope of our reconstruction encompasses the main metabolic pathways, including photosynthetic light reactions, the Calvin cycle, glycolysis, the (incomplete) TCA cycle, the pentose-phosphate pathway, oxidative phosphorylation, photorespiration, amino acid synthesis, as well as supply of nucleotides, lipid precursors, and cofactors. Our starting point is the annotated genome sequence of *Synechocystis* sp. PCC 6803 as obtained from the CyanoBase Web site (Nakamura et al., 1998; Nakao et al., 2010).

Following earlier strategies (Feist et al., 2009; Oberhardt et al., 2009), the reconstruction process comprises four steps. First, the annotated genome, together with pathway repositories such as the Kyoto Encyclopedia of Genes and Genomes (KEGG; http://www.kegg.com/), provide an initial draft network of the organism. Second, gaps and inconsistencies within the draft network are identified, and the network is manually curated based on the available biochemical literature. Third, the set of reactions is converted into a mathematical model, using consistent annotations as well as established exchange formats, such as SBML. The conversion into a computational model entails the addition of several pseudoreactions, such as ATP utilization for cellular maintenance or biomass formation, which do not correspond to genuine enzymatic reactions but reflect overall cellular processes. Finally, the model is evaluated using constraint-based analysis and other methods of computational systems biology. In particular, predictions about optimal flux states are validated using available phenotypic data. Details of the reconstruction process are given in “Materials and Methods.”

Our reconstruction results in a metabolic network of 380 reactions and 291 metabolic compounds. The set of reactions consists of 360 enzymatic reactions, including about 38 isoreactions, four spontaneous uncatalyzed reactions, five diffusion and transport reactions, as well as 11 auxiliary reactions to account for light absorption, photophosphorylation, biomass formation, and cellular maintenance. All processes are assumed to take place in a single compartment, with the exception of transport reactions. The reconstruction is focused on a functional description of phototrophic growth and utilization of storage compounds in the absence of light. Uptake and utilization of organic molecules is not considered. All enzymatic reactions annotated for *Synechocystis* sp. PCC 6803 in KEGG and other repositories but not included in the core reconstruction are provided as a separate file. An overview of the model is shown in Figure 1.

**Objectives for Growth and Maintenance**

During the reconstruction process, the initial draft model obtained from the annotated genome sequence was iteratively refined using extensive manual curation. Our primary objective was to create a metabolically functional model capable of supporting cellular maintenance and growth: that is, a model that is capable of generating all relevant biomass components. In general, the biomass objective function (BOF), an
An equation that specifies all relevant biomass precursors in their appropriate molar ratios, is difficult to obtain experimentally. An estimation of the macromolecular biomass composition for *Synechocystis* sp. PCC 6803 under different growth conditions was given by Shastri and Morgan (2005) and afterward utilized in several studies. However, as the size of our reconstruction is considerably larger, the inclusion of additional components was necessary. To this end, we modified and extended the BOF given by Shastri and Morgan (2005) based on information on the macromolecular composition reported for the cyanobacterium *Arthrospira* (*Spirulina*) platensis (Cogne et al., 2003). The BOF is given in Table I and detailed in “Materials and Methods.”

Knowledge of the BOF allows us to systematically check for available synthesis routes of biomass components. We performed iterative gap filling based on multiple pathway repositories, such as KEGG (http://www.kegg.com/), BioCyc (http://www.biocyc.com/), and BRENDA (http://www.brenda-enzymes.org/), as well as curation of primary biochemical literature and identification of putative enzymes via BLAST search. As expected, the initial draft network did not support the synthesis of all required intermediates. In particular, no complete synthesis routes for the amino acids Gly, Ser, Cys, Met, Asn, and His were annotated. In these cases, we proceeded according to the following scheme. First, we aimed to identify the missing steps to complete the synthesis pathways utilizing information from other cyanobacteria. For example, the enzyme for a methylenetetrahydrofolate reductase (EC 1.5.1.20) was not annotated for *Synechocystis* sp. PCC 6803 but is annotated for *Cyanothece* sp. PCC 8801, which enables the identification of a candidate gene (slr2141) for this enzyme in *Synechocystis* sp. PCC 6803. Second, if no satisfactory results could be obtained by direct comparison, we searched the primary literature for a...
description of the respective pathways, starting with cyanobacterial metabolism and then broadening the search to plants (mainly Arabidopsis [Arabidopsis thaliana]) and finally across all kingdoms. Our strategy resulted in complete synthesis routes for all amino acids except Asn and Met. For the latter, the synthesis steps from Microcystis aeruginosa (EC 2.3.1.31, EC 2.5.1.49) were adopted to allow for a metabolically functional network.

Similarly, the scheme described above was applied to test and complete the pathways for de novo synthesis of cofactors, including CoA, NADs (NAD/ NADH), NADPs (NADP/NADPH), FADs (FAD/ FADH), and tetrahydrofolate. Again, the initial draft network had to be supplemented with additional reactions. A complete list is provided in “Materials and Methods” and as Supplemental File S3. For three reactions, UDP-Glc phosphorylase (EC 2.7.7.9), aminodeoxyschorismate synthase (EC 2.6.1.85), and hydrodrolase of 5-amino-6-(5'-phosphoribitylamino)uracil (EC 3.1.3.-), no reasonable candidate genes could be identified, although each step is necessary to allow for the synthesis of biomass precursors. Finally, it was verified that the model is able to replenish each intracellular metabolite upon dilution by growth.

Main resources during the reconstruction process were the Cyanobase Web site (Nakamura et al., 1998), KEGG (Kanehisa and Goto, 2000), MetaCyc and BioCyc (Caspi et al., 2010), BRENDA (Chang et al., 2009), the Cyanomutants Web site (Nakamura et al., 1999), and to a lesser extent UniProt (UniProt Consortium, 2010). The final network is provided as a MIRIAM-compliant SBML file (Supplemental File S1) and spreadsheet (Supplemental File S2).

Functional Properties of Phototrophic Growth

Based on the reconstructed network, the functional properties of phototrophic growth are evaluated using FBA. Specifically, the rate of change of the vector of metabolite concentrations \( S \) can be described by a differential mass-balance equation of the form

\[
\frac{dS}{dt} = N \cdot v
\]

where \( N \) denotes the stoichiometric matrix and \( v \) indicates the vector of reaction fluxes. Using the steady-state hypothesis for the vector of metabolite concentrations, any stationary flux distribution \( v^0 \) has to satisfy the steady-state constraint \( N \cdot v^0 = 0 \). In addition to the constraint imposed by the mass-balance equation, FBA postulates that the distribution of fluxes is organized such that a given objective function, usually the synthesis of precursors required for cellular growth, is maximized. Mathematically, this assumption translates into a linear optimization problem for the stationary flux vector \( v^0 \), such that:

\[
\text{BOF}[v^0] \rightarrow \text{maximal}
\]

under the conditions:

\[
N \cdot v^0 = 0
\]

and:

\[
v^0_{\text{min}} \leq v^0 \leq v^0_{\text{max}}
\]

for all metabolic fluxes \( v^0_i (i = 1,...,m) \), where \( v^0_{\text{min}} \) and \( v^0_{\text{max}} \) denote optional upper and lower bounds for each stationary flux value. The constraint-optimization problem can be solved using standard techniques of linear programming (Becker et al., 2007; Klamt et al., 2007). The solution to the optimization problem results in a particular flux distribution that achieves a maximal growth yield, given predefined external conditions and exchange fluxes. We note that, owing to redundancy and flexibility within the network, the optimal solution is usually not unique.

Once the constraint-optimization problem is specified, FBA allows for a functional interrogation of the metabolic network with respect to (1) its ability to synthesize all metabolic precursors at their observed molar ratios, (2) essential reactions and prediction of gene deletion studies, (3) optimal routes for maximal growth, (4) flux variability analysis, as well as (5) qualitative reorganization of metabolic routes under different growth conditions.

In the following, we are mainly interested in phototrophic growth under conditions of either limiting light or limiting \( \text{CO}_2 \) availability. Within the network,
inorganic carbon is taken up from the environment as bicarbonate $\text{HCO}_3^-$ by an active (ATP-binding cassette) transport (Ömata et al., 1999). The intensity of light input is represented by flux of absorbed photons and translocation of $\text{H}^+$ through the membrane, partially coupled to regeneration of NADPH. Photophosphorylation and the equations for the respiratory chain are adopted from Shastri and Morgan (2005). Figure 2 shows the predicted maximal growth rate as a function of light intensity and total $\text{CO}_2$ uptake. [See online article for color version of this figure.]

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The predicted maximal growth rate as a function of light intensity and total $\text{CO}_2$ uptake. [See online article for color version of this figure.]

<table>
<thead>
<tr>
<th>Light [mmol photons GDW$^{-1}$ h$^{-1}$]</th>
<th>$\text{CO}_2$ Uptake [mmol GDW$^{-1}$ h$^{-1}$]</th>
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Gene Deletion Studies and Metabolic Robustness

The validity of any computational model can be examined using phenotypic data and information on
metabolic knockouts. In particular, one of the prime accomplishments of FBA is its ability to predict the viability or the expected (relative) decrease in maximal growth rate upon deletion of one or more genes. In this respect, we can assess the essentiality of each gene based on two criteria. The first requirement is the persistent ability of the network to produce all precursors required for biomass formation, as specified by the BOF, even in the absence of a specific gene. Second is the requirement to regenerate all metabolites and cofactors at a specified rate in the absence of the respective gene. Although usually only the first requirement is considered in the literature, both criteria are essential for viability and persistent growth. From an algorithmic point of view, the essentiality of each gene is evaluated by removing its corresponding reactions from the network and reevaluating the constraint-optimization problem for maximal biomass production. Genes are classified as essential if removal of the respective reactions prohibits the formation of biomass. Nonessential genes are further classified according to whether the maximal growth rate is reduced or remains unaltered. Within our network, 126 (of 337) genes are classified as essential for biomass formation, the removal of 26 genes results in a decreased maximal growth yield, whereas the removal of the remaining 185 genes has no effect on the maximal growth yield. The latter set includes a set of 38 isoenzymes. Replacing biomass formation by the ability to regenerate all metabolites results in 177 essential genes, whereas 160 genes are classified as nonessential, including 31 genes that result in a less efficient regeneration of metabolites and cofactors. A comprehensive list of essential genes is provided as Supplementary File S5.

In total, 51 entries in CyanoMutants corresponding to mutational inactivation of distinct genes are directly related to our network reconstruction. Of these, 39 genes encode nonessential genes within the network, of which 35 can be confirmed by a successful knockout reported in CyanoMutants. The discrepant four genes correspond to Cys desulfurase (slr0077), the NADH dehydrogenase type I subunit 4L (sll0522), a polyphosphate kinase (sll0290), and a pyrophosphatase (slr1622). The latter two reactions are easily compensated in silico by pairs of reactions acting together in a cycle, a solution that might not be feasible in vivo under the conditions tested. Essential genes are more difficult to reconcile, as our network does not account for possible roles in regulatory processes or toxicity and other adverse effects upon possible accumulation of metabolites. Of the 51 entries from CyanoMutants, 12 genes are classified as essential within our model, but only for eight of those the construction of a fully segregated mutant failed. The inactivation of the remaining four genes each resulted in a viable geno-

Figure 3. A predicted flux distribution to achieve maximal phototrophic growth yield (BOF). All flux values are given relative to the synthesis of RuBP (100%). The simulation was performed for a given light intensity, while carbon uptake was allowed to adjust as necessary to achieve optimal yield. Intervals indicate variability in possible flux values with equivalent yield. CO2 released by internal reactions was re-fixed by Rubisco. For abbreviations and nomenclature, see “Materials and Methods.”
type. A more detailed comparison, including a summary of discrepant findings, is given in "Materials and Methods."

From Storage Utilization to Phototrophic Growth

In the absence of light, *Synechocystis* is able to temporarily utilize various storage compounds, such as glycogen and to a lesser extent cyanophycin and poly-β-hydroxybutyrate, to provide energy and precursors for cellular maintenance. In this respect, our in silico model allows one to simulate the necessary reorganization of metabolism during the transition from glycogen-utilizing night metabolism to phototrophic growth. Figure 4 shows the metabolic transitions on a two-dimensional plane with the flux of selected reactions color coded as a function of absorbed photons (x axis) and glycogen utilization (y axis). Within each subplot, the transition from night metabolism (glycogen utilization) to phototrophic growth corresponds to a path from the upper left to the lower right corner. Along such a path, we observe several characteristic transitions in the reorganization of metabolic flux.

Under conditions of storage-utilization, corresponding to a point on the y axis in Figure 4, we assume glycogen as the only resource for cellular maintenance. In this case, the flux distribution is characterized by oxygen uptake and the absence of Rubisco-dependent carboxylation or oxygenation. Instead, we observe flux through the TCA cycle utilizing a bypass via the succinate-semialdehyde dehydrogenase (slr0370; EC 1.2.1.16) to circumvent the 2-oxoglutarate dehydrogenase not present in *Synechocystis* sp. PCC 6803. With increasing light intensity and concomitant decrease in glycogen mobilization, flux through the TCA cycle decreases. Instead, the photosynthetic light reactions start to generate the energy (ATP) requirements for cellular maintenance (fixed in the simulation at 0.27 mmol g⁻¹ dry weight h⁻¹), but no CO₂ fixation takes place yet. We note that the observed in silico flux distribution during mixotrophic growth agrees with experimental results from Howitt and Vermaas (1998), who did not observe any effect on mixotrophic and phototrophic growth by the deletion of two oxidases.

Only for a light intensity above a certain threshold, flux through the Calvin-Benson cycle is initiated, resulting in an increasing rate of Rubisco-dependent carboxylation and oxygenation. Remarkably, oxygenation of RuBP occurs slightly before the start of CO₂ fixation, even though within the in silico optimization a complete suppression of photorespiration is possible, if favorable for maximal ATP production or biomass formation. The occurrence of a nonzero photorespiration in the constraint-optimization problem points to a beneficial role of the seemingly wasteful side reaction as a supply of precursors for Gly formation. In particular, during heterotrophic growth, Gly is formed as a result of Pro degradation, which ceases in the presence of photorespiration. Consequently,
the in silico model points to an ambivalent interpretation of the role of photorespiration during phototrophic growth, which is discussed in more detail below. We note that all results are contingent on the reconstructed network structure and the specified exchange (glycogen and light) fluxes imposed on the constraint-optimization problem and therefore may not necessarily replicate the in vivo reality. Nonetheless, the in silico simulation highlights the potential of cellular metabolism to adapt to changes in environmental conditions in complex, surprisingly subtle, and sometimes nonintuitive ways.

Photorespiration Revisited

One of the striking results of the in silico simulation is the occurrence of a nonzero rate of photorespiration during photoautotrophic growth. In *Synechocystis* sp. PCC 6803, as in most other photosynthetic organisms, the fixation of inorganic carbon is catalyzed by the bifunctional enzyme Rubisco, with the carboxylation of RuBP yielding two molecules of PG3. However, carboxylation competes with RuBP oxygenation, a process that generates one molecule of PG3 and one molecule of the two-carbon compound 2-phosphoglycolate (2PG; see Fig. 5). Photorespiration, the photosynthetic oxygenation of RuBP, is often described as one of the most wasteful processes on Earth and is widely considered to be mainly an evolutionary relic, tracing back to the evolution of the enzyme in a low-oxygen atmosphere.

In cyanobacteria, the role and relevance of photorespiration is still only partially understood. Cyanobacteria have evolved dedicated CO2-concentration mechanisms that significantly repress the oxygenase activity of Rubisco and vastly improve photosynthetic performance (Badger and Price, 2003). However, the presence of CO2-concentration mechanisms does not fully eradicate RuBP oxygenation, and Eisenhut et al. (2008) were recently able to show that an active photorespiratory 2PG metabolism is essential for cyanobacterial growth in the present oxygen-containing atmosphere. In particular, a nonnegligible rate of photorespiratory 2PG generation necessitates quick conversion to glyoxylate to avoid toxification and inhibition of the Calvin-Benson cycle.

In this respect, our metabolic reconstruction allows us to augment the current discussion on photorespiration from a network perspective. As shown above, the constraint-optimization problem assigns a nonzero flux to the oxygenation of RuBP under conditions of photosynthetic growth, suggesting a nontrivial role of photorespiration to achieve a maximal rate of biomass formation. Indeed, an intermediate of photorespiration, glyoxylate, plays an important role in cyanobacterial metabolism and can serve as a precursor for Gly synthesis. More specifically, within our reconstruction, the biosynthesis of the amino acids Gly, Ser, and Cys exclusively depends on the allocation of glyoxylate. Although it was suggested that cyanobacteria are capable of synthesizing Ser directly from 3-phosphoglycerate via 3-phosphohydroxy pyruvate and phosphoserine (Colman and Norman, 1997), no candidate genes for such a conversion are currently known for *Synechocystis*. The assumption that glyoxylate is an essential precursor for Ser synthesis is further supported by the fact that Eisenhut et al. (2006) were unable to obtain a completely segregated mutant with an inactivated Ser hydroxymethyltransferase (sll1931). The Ser hydroxymethyltransferase catalyzes interconversion of Ser and Gly and would be dispensable if an alternative synthesis pathway for Ser exists. Correspondingly, our simulations suggest that during phototrophic growth, the photorespiratory 2PG metabolism provides the required flux toward glyoxylate to allow for the formation of metabolic precursors and biomass. The computationally allocated rate of photorespiration is approximately 4.2% of the total Rubisco activity, a value that is in good agreement with the 4% to 5% photorespiration assumed for *Synechocystis* (M. Hagemann, personal communication). Prohibiting photorespiratory activity in silico results in a slightly decreased predicted maximal growth rate of 94% of the original value.

Consequently, in the context of our network reconstruction, photorespiration turns out to be the most efficient way to allocate glyoxylate during phototrophic growth. However, this superior efficiency does not hold for nonphototrophic (dark) metabolism, as already observed in Figure 4. In this case, the (rather low) demand for glyoxylate is met by degradation of Pro, in a series of five enzymatic steps. Despite its
slightly lower carbon efficiency, the synthesis of Pro and subsequent conversion to glyoxylate yields additional units of NADH and ATP, as compared with photorespiration, making the pathway preferable in heterotrophic conditions when optimizing for total biomass formation. We emphasize that this difference highlights the fact that a criterion like metabolic efficiency is usually not a property of individual pathways, but it must be interpreted in the context of the metabolic status and the demands of the remaining network.

Our computational results allow us to formulate two different scenarios. First, the beneficial role of photorespiration may be merely an artifact of an incomplete network topology. In particular, our results depend on the absence of alternative pathways for the formation of Gly and Ser, most importantly the direct conversion of 3-phosphoglycerate to Ser, via 3-phosphohydroxy pyruvate and phosphoserine. Although no candidate genes are currently known, the pathway may be active in *Synechocystis* sp. PCC 6803. In this case, photorespiration would be completely suppressed in both phototrophic and heterotrophic conditions when optimizing for maximal growth yield (data not shown).

Alternatively, the second scenario implies that the current annotation of the *Synechocystis* genome, augmented by our network reconstruction, does provide a correct picture of Gly metabolism. In this case, the metabolism of *Synechocystis* is adapted to make use of the inevitable supply of the side product 2PG under photoautotrophic conditions. In particular, there is no requirement for the organism to establish or maintain alternative and possibly more efficient pathways for Gly and Ser formation. We note that this view does not contradict earlier findings on gene essentiality and growth in a high-CO₂ atmosphere. Within our simulation, photorespiration is not essential, and in the absence of photorespiration, all essential precursors can still be synthesized, albeit with slightly lower efficiency. In the context of our study, it is not possible to conclusively resolve which of the two scenarios mirrors the in vivo reality. Nonetheless, we emphasize that only a thorough reconstruction of cyanobacterial metabolism, to the best of one’s current knowledge, allows us to formulate and probe alternative hypotheses on the efficiency and optimality of reactions.

**DISCUSSION AND PERSPECTIVES**

Elucidation of the structure and function of metabolic networks is increasingly assisted by computational approaches that allow for a systemic view of possible interconversion routes. A prerequisite for such an analysis is the comprehensive reconstruction of the set of enzymatic reactions taking place in a single cell or organism. Here, we have presented a manually curated reconstruction of the metabolic network of *Synechocystis* sp. PCC 6803, an important unicellular model organism for phototrophic metabolism.

Network reconstruction is usually based on the annotated genome sequence, in combination with various reaction and pathway repositories. However, most databases and repositories primarily focus on the “parts lists” of enzymatic reactions: that is, they do not consider the resulting network as a functional entity. Conversely, network reconstruction specifically aims to take into account the multiple requirements that distinguish a list of reactions from a functioning network. Such requirements include the ability of the network to synthesize all essential intermediates and precursors for biomass production, to allow for energy (ATP) generation for cellular maintenance, to maintain the redox balance, as well as to be capable of regenerating metabolites and cofactors upon dilution by growth. Failure to fulfill one or more of these requirements usually points to errors or gaps in the network stoichiometry and necessitates revision of the reconstructed network accordingly. In this sense, network reconstruction is a privilege to metabolic modeling and recognizes that cellular metabolism operates as a highly integrated network.

Despite the great achievements over the last decade, resulting in more than a dozen reconstructions for several organisms, the systematic reconstruction of genome-scale metabolic networks is still in its infancy. While already considerable literature exists on algorithms for automated gap filling, these algorithms are usually exemplified only on highly domesticated examples, such as recovery of a previously known complete network upon artificial deletion of individual reactions. Therefore, as yet, high-quality reconstructions are predominantly based on extensive manual curation utilizing information from primary biochemical literature. A persistent problem is the diverse naming conventions used in different databases and existing reconstructions as well as the sometimes inconsistent or erroneous annotation of enzymes, often based only on sequence comparison. As pointed out previously (Stitt et al., 2010), a great challenge for the future is the development and enforcement of publishing standards and naming conventions. Other problems are rooted in interspecific and intraspecific variations and are less straightforward to overcome. For example, only recently it was shown that even within such a basic and exhaustively analyzed pathway as central carbon catabolism in *Escherichia coli*, previously unreported reactions occur (Nakahigashi et al., 2009). In this respect, we do not expect our reconstruction to be a faultless replica of the in vivo reality; rather, the purpose is to start and foster a discussion about possible inconsistencies and shortcomings of our current understanding of cyanobacterial metabolism. In particular, a high-quality network reconstruction, even if erroneous or incomplete in parts, offers tremendous possibilities to probe and understand the functioning of metabolism.

Most current reconstructions are evaluated using FBA, a constraint-based method that allows one to predict and evaluate optimal flux patterns with re-
spect to a given objective function. In our case, the application of FBA led to several conclusions about (1) the typical optimal reaction routes during phototrophic growth, (2) essential genes and synthesis pathways of photosynthetic metabolism, as well as (3) the necessary reorganization of metabolic flux during a transition from heterotrophic (glycogen-based) to phototrophic growth. The latter highlights the interconnection of cellular pathways as a system of supply and demand. We observe several characteristic switches that emphasize that the efficiency of cellular reaction pathways is not an intrinsic property of the respective pathways but depends on the current status and metabolic demand of the entire metabolism. The most prominent example for such a complex interdependency is the allocation of nonzero flux to the oxygenation reaction of RuBP. While for low light intensities the demand for Gly is met by alternative pathways, such as utilization of Pro, the Rubisco oxygenase reaction becomes more efficient with increasing light intensity and finally provides all glyoxylate required for cellular growth. This transition is not an effect of the efficiency of the pathway per se but rather reflects differences in the “sales value” of cellular commodities under different growth conditions. We note that the fact that the seemingly wasteful side reaction of Rubisco might be used in a constructive way is in good agreement with the known tradeoff between specificity and overall turnover rate of Rubisco (Tcherkez et al., 2006). The hypothesis resulting from our analysis might also explain the remarkably low specificity and high turnover rates observed in some cyanobacteria (Witzel et al., 2010).

Similar consideration with respect to the beneficial role of seemingly wasteful side reactions might also hold for other organisms and tissues. For example, in a recent computational study, Poolman et al. (2009) reported a nonzero Rubisco oxygenase reaction as a result of a constraint-optimization problem in heterotrophic Arabidopsis cells. While the scenario discussed therein is probably unlikely to occur in vivo, as also acknowledged by the authors (Poolman et al., 2009; Stitt et al., 2010), the prediction of flux through previously unrecognized reactions as a result of network optimization is not unusual (Schwender et al., 2004). In this sense, a thorough network reconstruction allows researchers to evaluate the inevitable functional consequences, given the current annotation and knowledge of enzymatic interconversions, and thus opens the possibility of specifically designing experiments to distinguish between alternative hypotheses.

MATERIALS AND METHODS

Abbreviations and Nomenclature

The following terms are used in the figures and supporting materials: 2PG (2-phosphoglycerate), ABC (ATP-binding cassette), AcCoA (acetyl-coenzyme A), BOF (biomass objective function), Cytb6 (cytochrome b/f complex), DHAP (dihydroxyacetone phosphate), DW (dry weight), E4P (D-erythrose 4-phosphate), F6P (D-fructose 6-phosphate), FBP (D-fructose 1,6-bisphosphate), FNR (ferredoxin-NADP+ reductase), G1P (D-glucose 1-phosphate), PG (D-glycerate 2-phosphate), PG5 (D-glycerate 3-phosphate), G6P (D-glucose 6-phosphate), GAP (D-glyceraldehyde 3-phosphate), MTHF (5,10-methylene tetrahydrofolate), PEP (phosphoenolpyruvate), PHB (poly-3-hydroxybutyrate), PR (pyruvate), R5P (D-ribose 5-phosphate), Ru5P (D-ribulose-5-phosphate), RuBP (ribulose-1,5-bisphosphate), S7P (sedoheptulose-7-phosphate), SBP (sedoheptulose-1,7-bisphosphate), THF (tetrahydrofolate), X5P (D-xylulose 5-phosphate).
wardly allow inclusion of quantitative differences in enzyme specificity but is primarily focused on stoichiometric information.

The reconstructed network is provided as Supplemental File S1 (SBML) and Supplemental File S2 (Excel). A complete list of reactions added during the reconstruction process is provided as Supplemental File S3. Supplemental File S6 provides a list of additional enzymes associated with *Synechocystis* sp. PCC 6803 metabolism available from KEGG but not included in our model. The final network model is compliant with MIRIAM standards (Le Novere et al., 2005) and contains links to CHEBI nomenclature (Degtyarenko et al., 2008), a standard endorsed in recent publications (Herrgard et al., 2008). For appropriate tools to visualize and interrogate the network, see the software guide at www.sbml.org.

**BOF**

FBA requires the definition of a BOF that specifies all cellular components in their appropriate molar ratios. A first BOF was provided by Shastri and Morgan (2005) and also used by Fu (2008). However, these BOFs were restricted mainly to precursors for amino acid compositions as constituents of the biomass. A considerably more elaborate function was given by Cognie et al. (2003) for a metabolic model of *Arthrospira platensis*, a blue-green photo-lithoautotrophic cyanobacterium. The function is composed of five classes of macromolecules, namely carbohydrates, proteins, lipids, RNA and DNA, and the pigment chlorophyll. We utilized a modified version of the BOF of Cognie et al. (2003). Specifically, we neglected the flux to chlorophyll, corresponding to only 0.16% of total biomass. Additionally, the lipid demands were simplified to lipid precursors only, and the formation of carbohydrates was slightly simplified. The resulting BOF is given in Table 1.

**Reconciling Existing Models**

Several previous reconstructions of *Synechocystis* sp. PCC 6803 are available. To our knowledge, the first reconstruction was provided by Shastri and Morgan (2005) and subsequently extended by Hong and Lee (2007). Both reconstructions are restricted to the primary metabolism, including glycolysis, the TCA cycle, and the Calvin-Benson cycle. The model of Shastri and Morgan (2005) encompasses 93 metabolic reactions (with reversible reactions counted twice), including 23 lumped reactions for the formation of amino acids and nucleotides.

A considerably larger genome-scale model was recently published by Fu (2008), encompassing about 831 metabolic reactions. However, the BOF was taken over from Shastri and Morgan (2005); therefore, the additional reactions cannot assume any functional role. Rather surprisingly, all previous reconstructions include a bacteria-like glyoxylate shunt, which was apparently suggested by Yang et al. (2002). We find no evidence for this assertion and assume that the inclusion of the glyoxylate shunt in previous reconstructions was mainly motivated by the omission of a C2 cycle.

**FBA**

FBA was based on available software tools and algorithms. All optimization studies were computed using the COBRA toolbox version 1.3.1 (Becker et al., 2007; available at http://gcrg.ucsd.edu/Downloads/Cobra_Toolbox) as well CellNetAnalyzer version 9.2 (Klamt et al., 2007; available at http://www.mpi-magdeburg.mpg.de/projects/cna/cna.html). The toolboxes were run under the MATLB 7.6.0 environment, including the MATLB optimization toolbox as a Linear Program Solver. For the COBRA toolbox, a custom SBML file had to be generated (provided as Supplemental File S7). See also Oberhardt et al. (2009) and refs. therein for introductory tutorials on FBA.

For the constraint-optimization exchange fluxes, only the light input was pre-specified, whereas nitrate, sulfate, and carbon (as hydrogen carbonate) uptake was allowed to adopt as necessary. In this way, we avoided the two-step optimization problem employed by Shastri and Morgan (2005), who first optimized for biomass formation using a fixed carbon uptake and free light flux, followed by a second optimization for minimal light flux, given the previously obtained biomass formation as an additional constraint. During our simulations, the uptake of hydrogen carbonate during phototrophic growth was constrained between 0 and 0.45 mmol HCO3 - g-1 dry weight h-1, which is related to a maximum growth rate of 0.09 h-1. Limitation of growth by sulfate or nitrate was not considered. In addition to the BOF, we assumed a basal ATP demand (maintenance) for each FBA solution. As no reliable experimental data were available, the value was arbitrarily set to 10% of the maximal photosynthetic ATP generation used in Figure 2, corresponding to a value of 0.27 mmol g-1 dry weight h-1. We note that the basal ATP demand, contrary to the situation in heterotrophic organisms, has no influence on the FBA solution. Likewise, the FBA optimization problem does not take dilution of metabolites, including cofactors, into account.

**Comparison of in Silico Knockout Mutants and in Vivo Measurements**

A crucial test for network reconstruction and FBA is the ability to correctly predict lethal gene knockouts. In our case, as described in the main text, we observed a significant overlap between in silico mutants and in vivo experiments. Several of the in silico-predicted lethal genotypes can be confirmed by published data and information from the Cyanobacterial Mutants (Zhong et al., 1999), indicates that there is only one possible pathway for folate biosynthesis. Correspondingly, the in silico gene deletion (fold) results in an inability of the model to produce the essential cofactor tetrahydrofolate.

Other examples include Quintero et al. (2000), who generated mutants showing an impaired Arg synthesis as a result of a knockout of gene slr0802, coding for an Om carbamoyltransferase (ArgF). Also, an insertion in the gene (slr2480) encoding a pyruvate-carboxylate reductase (ProC) resulted in impaired Pro synthesis. Both mutants had to be exogenously supplied by supplementation of the growth medium with either Arg or Pro, respectively. Autotrophic growth of either mutant could not be achieved. The phenotype of both mutants can be confirmed in silico. Under conditions of photautotrophic growth, the coding genes for ArgF and ProC are classified as essential in the model but are dispensable if Arg and Pro are supplied in silico, respectively. Nevertheless, discrepant findings were observed for four genes for which fully segregated mutants were reported, despite being essential in the model. On closer examination, two of these four genes correspond to the hydrogen carbonate transporter Cmp (slr0409, slr0404). In silico essentiality is due to Cmp being the only carbon transport mechanism present in our reconstruction. However, in *Synechocystis* sp. PCC 6803, more than one carbon uptake mechanism exists. A further gene (slr0847) encodes CoaD, a phosphopante-theine adenyllytransferase (EC 2.7.7.3) located in biosynthesis pathway of CoA. In our model, the enzyme catalyzes an essential step, the conversion from pantetheine 4’-phosphate to 3’-diphospho-CoA. Consequently, a mutant lacking this gene would be unable to synthesize CoA. The fact that it was possible to construct a viable mutant implies that the mutant was either not fully segregated or there exists an unknown alternative pathway for the synthesis of CoA in *Synechocystis*. The last discrepant gene (slr0934) is annotated as CcmA, a carboxysome formation protein, as well as a 3-deoxy-7-phosphobehpulonate synthase, which catalyzes the initial step of the aromatic amino acid synthesis. The latter is essential in our model. A fully segregated mutant, therefore, suggests the existence of alternative steps within the formation of aromatic amino acids (Ogawa et al., 1994).

**Supplemental Data**

The following materials are available in the online version of this article.

**Supplemental File S1.** *Synechocystis* network file, including identifiers for metabolites to the CHEBI and KEGG database and UniProt identifiers for genes (SBML format).

**Supplemental File S2.** List of reactions, associated enzymes, and genes implemented in the network with reference to literature (Excel file).

**Supplemental File S3.** Newly annotated genes for *Synechocystis* (Excel file).

**Supplemental File S4.** Comparison of gene knockout predictions in the model with in vivo data available from the Cyanobacterial Mutants database (Excel file).

**Supplemental File S5.** Results of gene deletion study of all genes in the *Synechocystis* network (Excel file).

**Supplemental File S6.** List of additional enzymes associated with the *Synechocystis* metabolism available from the KEGG database (Excel file).

**Supplemental File S7.** *Synechocystis* network compatible for usage with COBRA toolbox version 1.3.1 (SBML format).
Supplemental File S8. Instruction and parameter settings to reanalyze the results in Figures 2 to 4 using the COBRA toolbox version 1.3.1 (PDF file).

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LITERATURE CITED


The Metabolic Network of Synechocystis sp. PCC 6803.