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REVIEW PAPER

The possible evolution₂ and future₂ of ~~CO₂-concentrating~~ mechanisms

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Running head: The possible evolution and future of ~~CO₂-concentrating mechanisms~~

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Running head: Raven *et al.*

Highlight

The probable timing of the origin of CCMs in cyanobacteria and eukaryotic algae is
computed from Rubisco kinetics and CO₂ changes over geological time. An analysis of
factors determining the role of CCMs with global environmental change is presented.

Abstract

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CO₂-concentrating mechanisms (CCMs), based either on active transport of inorganic carbon (biophysical CCMs) or on biochemistry involving supplementary carbon fixation into C₄ acids (C₄ and CAM), play a major role in global primary productivity. However, the ubiquitous CO₂-fixing enzyme in autotrophs, Rubisco, evolved at a time when atmospheric CO₂ levels were very much higher than today and O₂ was very low and, as CO₂ and O₂ approached (by no means monotonically), today's levels, at some time subsequently many organisms evolved a CCM that increased the supply of CO₂ and decreased Rubisco oxygenase activity. Given that CO₂ levels and other environmental factors have altered considerably between when autotrophs evolved and the present day, and are predicted to continue to change into the future, we here examine the drivers for, and possible timing of, evolution of CCMs. CCMs probably evolved when CO₂ fell to 2–16 times the present atmospheric level, depending on Rubisco kinetics. We also assess the effects of other key environmental factors such as temperature and nutrient levels on CCM activity and examine the evidence for evolutionary changes in CCM activity and related cellular processes as well as limitations on continuity of CCMs through environmental variations.

Key words: Algae, cyanobacteria, CO₂-concentrating mechanisms, CO₂ diffusion, evolution, Rubisco.

Introduction

All cyanobacteria, eukaryotic algae, and embryophytes ('plants') rely on the enzyme ribulose-1,5-bisphosphate carboxylase oxygenase (Rubisco) and the photosynthetic carbon reduction cycle (PCRC; otherwise known as the Calvin-Benson-Bassham cycle) for the net assimilation of inorganic carbon to organic matter. Less than 1% of the

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primary production on the planet is carried out by processes that do not involve Rubisco (Raven 2009; Beardall and Raven 2016)

There is a broad range of Rubisco forms with differing kinetic properties (Beardall and Raven 2016). However, even the Rubiscos with the highest CO₂ affinity are not saturated by dissolved CO₂ in equilibrium with present atmospheric CO₂ concentrations at the temperatures at which the organisms from which the Rubiscos were derived normally grow (Uemura *et al.* 1997; Galmés *et al.* 2016). All Rubiscos also have a competing oxygenase reaction that uses a photorespiratory carbon oxidation cycle (PCOC) or its equivalent to deal with the 2-phosphoglycolate produced by the oxygenase reaction. This increases the energy and other resource costs of photosynthesis in today's atmosphere with diffusive CO₂ entry into cells, relative to when Rubisco is operating at CO₂ saturation. Even organisms with relatively high CO₂ affinity Rubiscos sometimes have CCMs involving biophysical processes based on active transport of inorganic carbon species (cyanobacteria and eukaryotic algae) or biochemical pathways based on additional, high affinity, carboxylases [C₄ and CAM (Crassulacean acid metabolism) plants] (see Beardall and Raven 2016 and references therein). These CCMs have their own energy and other resource costs, and the factors determining the relative selective advantages of diffusive CO₂ entry and of CCMs are incompletely understood, except that organisms possessing Rubiscos with very low CO₂ affinity (cyanobacteria and basal dinoflagellates) always have CCMs (e.g. Raven and Beardall 2014, 2016a, b).

There are few exceptions (Raven *et al.* 2005, 2012; Maberly *et al.* 2009) to the rule that algae and cyanobacteria possess CCMs (Beardall and Raven 2016), so CCMs support at least 39 Pg C (80%) of annual marine net primary production (Field *et al.*

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1998; Raven and Beardall, 2014). CCMs also contribute at least 14 Pg C annually, mainly by C₄ flowering plants, to terrestrial net primary production (Field *et al.*, 1998; Still *et al.*, 2003). This means that at least 53 Pg C year⁻¹ of the global net primary productivity of 105 Pg C year⁻¹ involves CCMs rather than diffusive CO₂ entry (Field *et al.*, 1998; Raven *et al.*, 2012; Raven and Beardall, 2014).

In this review we discuss how CCMs respond to changes in environmental conditions and explore through this how CCMs may have evolved and persisted through major climatic shifts such as 'Snowball Earth' and how they may fare under predicted changes in our future climate.

Response of extant cyanobacteria, eukaryotic algae, and embryophytes to environmental changes in relation to the evolution and possible future of CCMs

The objective here is to determine how changes in inorganic carbon, combined nitrogen, phosphorus, and iron concentrations, photosynthetically active radiation (PAR), and temperature alter expression of CCMs by acclimation and, in a few cases, adaptation in experimental evolution. For inorganic carbon, a major consideration for organisms with CCMs in the context of past and future high CO₂ episodes is the external concentration of CO₂ at which diffusive CO₂ influx gives the same photosynthetic rate as is produced by the present atmospheric CO₂ concentration using a CCM, assuming no change in the kinetics or content of Rubisco. The real world is more complex, and account is taken of changes in Rubisco kinetics through evolution (Young *et al.*, 2012, 2016) and of Rubisco content by changes over hours in the rates of transcription and of translation resulting in

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the large observed differences in the fraction of the proteome occupied by Rubisco among extant oxygenic photosynthetic organisms (Losh *et al.*, 2013; Raven, 2013; Flynn and Raven, 2017).

Using the kinetics of whole-cell CO₂ assimilation in the absence of CCMs, and of Rubisco, in extant cyanobacteria to predict the level to which CO₂ would have to have fallen to make a CCM essential

Dealing first with cyanobacteria, a CCM appears to be constitutive (i.e. occurs in all photosynthetically competent species under all of the conditions so far tested), although the occurrence of the various plasmalemma and thylakoid membrane components varies phylogenetically. The minimal requirements for the cyanobacterial CCM are one energized transporter accumulating HCO₃⁻ in the cytosol, the absence of carbonic anhydrase from the cytosol, and anion-permeable carboxysomes containing the entire intracellular carbonic anhydrase activity as well as all the Rubisco (Price and Badger 1989a; Hopkinson *et al.*, 2014). Badger *et al.* (2002, 2006), Badger and Price (2003), and Price *et al.* (2008) pointed out that all cyanobacteria examined at the time have

carboxysomes and associated mechanisms, and subsequent work has shown that 125 of the 126 cyanobacterial genomes sequenced contained coding for carboxysomal components (Abdul-Rahman *et al.*, 2013; Gonzalez-Esquer *et al.*, 2016). The exception is the genome of UCYN-A, a diazotrophic symbiont of marine prymnesiophycean phytoplankton that also lacks PSII and autotrophic CO₂ fixation by the PCRC (Zehr *et al.*, 2008; Abdul-Rahman *et al.*, 2013; Bombar *et al.*, 2014; Cornejo-Castillo *et al.*, 2016).

Other cyanobacteria lacking carboxysomes are the non-photosynthetic diazotrophic endosymbionts of freshwater diatoms of the family Rhopalodiaceae; these cyanobionts

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lack all photosynthetic genes (Nakayama *et al.*, 2014). All the sequenced genomes of photosynthetically competent cyanobacteria also have one or more energized transporters for HCO_3^- , and many have catalysed, downhill, CO_2 entry and unidirectional conversion of cytosolic CO_2 to HCO_3^- energized by the NAD(P)H-PQ oxidoreductase in the thylakoid membrane; or in the plasma membrane in the thylakoid-less *Gloeobacter*. The default assumption is that all photosynthetically competent cyanobacteria grown in present atmospheric CO_2 express CCMs. This agrees with the low CO_2 affinity and CO_2/O_2 selectivity of the Form IB Rubisco of the ancestral (Badger *et al.*, 2002; Badger and Price, 2003) β -Cyanobacteria ($K_{0.5}$ for CO_2 , i.e. the CO_2 concentration at which the enzyme achieves half of its CO_2 -saturated rate) of 105–290 mmol m^{-3} ; CO_2/O_2 selectivity 38–56; and CO_2 -saturated specific reaction rate 2.6–11.4 $\text{site}^{-1} \text{s}^{-1}$ (Jordan and Ogren, 1981; Tcherkez *et al.*, 2006; Badger and Bek, 2008; Shih *et al.*, 2016). The Form IA Rubisco of the (derived SynPro clade; Badger *et al.*, 2002; Badger and Price, 2003) α -cyanobacterium *Prochlorococcus* MIT9313 has the highest known $K_{0.5}$ for CO_2 of a Form I Rubisco of 750 mmol m^{-3} , combined with a moderate CO_2 -saturated specific reaction rate of 4.7 $\text{site}^{-1} \text{s}^{-1}$ (Scott *et al.*, 2007; see also Tcherkez *et al.*, 2006). However, Shih *et al.* (2016) found a K_m of only 309 mmol m^{-3} for the same strain of *Prochlorococcus* as was used by Scott *et al.* (2007), although the Rubisco was expressed in *Escherichia coli* in the work of Shih *et al.* (2016).

The low (but essential) C flux through P-glycolate and its subsequent metabolism reveals the presence of Rubisco oxygenase activity in wild-type cyanobacteria (Eisenhut *et al.*, 2008; Raven *et al.*, 2012) although the steady-state CO_2 concentration in the carboxysome is close to saturating for Rubisco carboxylase (assumed to be four times the

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$K_{0.5}$ for Michaelis-Menten kinetics), namely 420–1160 mmol m⁻³ for β -Cyanobacteria with Form IB Rubiscos and 1240–3000 mmol m⁻³ for an α -cyanobacterium with Form IA Rubisco. These calculations assume that the Rubisco content is just sufficient to account for the *in vivo* inorganic C-saturated rate of photosynthesis. These values correspond to 52–116 and 124–300 times the present atmospheric concentration of CO₂ (dissolved in water of a temperature and salinity to give an equilibrium concentration of 10 mmol m⁻³), corresponding to $K_{0.5}$ values 10.5–29 and 31–75 times the present atmospheric level respectively. Lower atmospheric CO₂ values consistent with diffusive CO₂ entry are possible if a larger relative flux through P-glycolate is assumed, or if there are higher contents of Rubisco per cell, for example in the type II mutants or the carboxysome-less mutants of *Synechococcus* PCC7942 (Price and Badger, 1989b; Harano *et al.*, 2003). That one or both of these effects occur is because the high CO₂ values used in mutant studies of the CCM in β -Cyanobacteria can be only 25-fold the present atmospheric level (Price and Badger 1989a, b), so the half-saturated value is $\sim 25/4$ or ~ 6 times the present atmospheric level. Badger *et al.* (2002) and Riding (2006) suggest that a value of ≤ 10 times the present atmospheric level of CO₂ favours cyanobacterial CCMs over diffusive CO₂ entry. Changed Rubisco kinetics (increased CO₂ affinity and CO₂/O₂ selectivity, preferably with an unchanged specific reaction rate, if this is possible; Tcherkez *et al.*, 2006) might occur over evolutionary time of 100–1000 or more generations. While Kapralov and Filatov (2007) found no evidence for positive selection in cyanobacterial Form IB Rubiscos, their small sample size means positive selection could have been missed, as seen above, there is a significant range of kinetic properties of cyanobacterial Form IB Rubiscos.

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Using the kinetics of whole-cell CO₂ assimilation in the absence of CCMs, and of Rubisco, in extant eukaryotic algae to predict the level to which CO₂ would have to have fallen to make a CCM essential

Eukaryotic algal CCMs are very probably homoplastic, having originated independently in different clades of algae. Homoplasy can be inferred from an earlier origin of a clade than of eukaryotic CCMs, although the timing of both cladogenesis and the origin of CCMs is poorly constrained (Raven 1997; Badger *et al.* 2002; Raven *et al.* 2012).

Additional evidence for a homoplastic origin is the diversity of inorganic C transporters and of carbonic anhydrases among eukaryotic algae, with horizontal as well as vertical gene transfer, and the lack of a strict correlation between occurrence of a CCM and the presence of a pyrenoid (Kevekordes *et al.* 2006; Meyer and Griffiths 2013; Raven and Giordano 2017).

For eukaryotic algae with CCMs, the approach taken is similar to that used above for cyanobacteria. In the eukaryotic algae there is no indicator of occurrence of a CCM like the carboxysome of cyanobacteria. For example, while the presence of pyrenoids is often associated with the occurrence of a CCM, there are a substantial number of exceptions (Badger *et al.* 1998; Kevekordes *et al.* 2006; Raven and Giordano 2017).

Many, or perhaps all, of the eukaryotic algal CCMs are subject to down-regulation when grown at high CO₂, but to avoid incomplete down-regulation of the CCM, deletion of one or more components of the CCM is needed. There are very few such measurements, and those that have been carried out are mainly on *Chlamydomonas reinhardtii*. Wang *et al.*

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(2014) isolated a mutant (H82) of *C. reinhardtii* that lacked expression of two CCM-related proteins (HLA3 and LCIA, operating in series in inorganic C movement from the extracellular medium to the stroma) but retained the same inorganic C-saturated photosynthetic rate as the wild type when grown at either high (50 mmol mol⁻¹ total gas) or low CO₂ (0.4 mmol mol⁻¹ total gas). Assuming an experimental temperature of 25 °C and allowing for the ionic strength of the experimental buffer to give a pK_{a1} for inorganic C of 6.30, the K_{0.5} for CO₂ of H82 was 14.3 mmol m⁻³ and 16.6 mmol m⁻³, respectively, for high and low CO₂-grown cells; the corresponding values for wild-type cells were 9.44 mmol m⁻³ and 1.51 mmol m⁻³, respectively. Assuming, as for cyanobacteria, that inorganic C-saturated photosynthesis requires four times the K_{0.5} CO₂, this would be, respectively, 57.2 mmol m⁻³ and 66.4 mmol m⁻³ for high and low CO₂-grown cells of H82 (i.e. 5.72–6.64 times the present atmospheric CO₂). The external CO₂ concentration must be higher than the steady-state concentration of CO₂ at the active site of Rubisco when CO₂ entry is by diffusion, given the diffusive limitation to the CO₂ flux from the bulk medium to Rubisco imposed by membranes and path tortuosity in the aqueous phase. This has been analysed by, for example, Raven *et al.* (2005), Raven and Beardall (2016b) and Barbour *et al.* (2016). Supplementary Information S1 at JXB online, including Supplementary Table S1, provides a more detailed analysis specific to eukaryotic algal cells in the size range considered here. Such data are not available for cyanobacteria, apart from the CO₂ concentration needed to saturate *in vivo* photosynthesis by diffusive CO₂ entry, but the constraint on CO₂ assimilation by resistance to CO₂ diffusion through membranes (Raven and Beardall, 2016b) would be smaller in

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cyanobacteria (~~Gram~~-negative outer membrane and plasmalemma) than in green algae (plasmalemma and two chloroplast envelope membranes).

Similar Rubisco kinetic data to ~~those~~ used in the discussion of the CO₂ concentration needed to saturate photosynthesis with diffusive CO₂ entry in cyanobacteria are also available for *C. reinhardtii*, with *K*_{0.5} for CO₂ of 29–31 mmol m⁻³ and CO₂/O₂ selectivity of 61 (Jordan and Ogren, 1981; Genkov *et al.* 2010). To achieve half of the CO₂-saturated rate of photosynthesis by diffusive CO₂ entry would thus require at least 30 mmol m⁻³ CO₂ in the bulk phase, allowing for the necessary decrease in CO₂ concentration along the diffusion pathway from the bulk medium to Rubisco (i.e. equivalent to almost ~~three~~ times the present atmospheric concentration at sea level).

Importantly, Sharkey and Berry (1985) showed that shifting *C. reinhardtii* cultures from aeration with 3300 μmol CO₂ mol⁻¹ to 200 μmol CO₂ mol⁻¹, total gas induced the CCM, meaning that the diffusive CO₂ entry is adequate with dissolved CO₂ in equilibrium with not more than 8.25 the present atmospheric level. Making the same assumption as for the cyanobacteria (i.e. CO₂-saturated photosynthesis needs ~~four~~ times the *K*_{0.5} concentration of CO₂), CO₂ saturation of photosynthesis using a diffusive supply of CO₂ requires at least (allowing for the necessary decrease in CO₂ concentration along the diffusion pathway from the bulk medium to Rubisco, Raven *et al.* 2005) 120 mmol m⁻³ dissolved CO₂, equivalent to almost 10 times the present atmospheric concentration at sea level.

The measurements and modelling of Yokota *et al.* (1987) suggest a larger flux through Rubisco oxygenase relative to Rubisco carboxylase in *C. reinhardtii* than occurs in cyanobacteria when CCMs are functioning, and photosynthesis using diffusive CO₂ entry would need about twice the present atmospheric concentration of CO₂ to achieve half the

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maximum rate of photosynthesis. This is a lower value than the factor of 4.5 based on the CO₂ dependence of CCM-less mutants of *C. reinhardtii* described in the previous paragraph. Kapralov and Filatov (2007) did not include the Chlorophyceae, the Class to which *C. reinhardtii* belongs, in their search for positive selection in Rubiscos; such a search, with a large sample size, would be useful.

For comparison, the freshwater Synurophyceae (and the closely related Chrysophyceae) lack CCMs (Saxby-Rouen *et al.*, 1997, 1998; Bhatti and Colman 2005, 2008, 2011; Raven *et al.*, 2005; Maberly *et al.*, 2009). These algae have Form ID Rubiscos which are reported to have $K_{0.5}$ values (mmol m⁻³) *in vitro* of 18.2 (*Mallomonas papulosa*), 28.4 (*Synura petersenii*), and 41.8 (*Synura uvella*) (Bhatti and Colman 2008). The $K_{0.5}$ values for CO₂ for *in vivo* photosynthesis for the three synurophyceans are 92.0–440.5 mmol m⁻³ for *M. papulosa* (varying with the buffer used to maintain the pH at 7.0), 40.4–43.7 mmol m⁻³ (varying with pH 6–7) for *S. petersenii*, and 44.9–209 mmol m⁻³ for *S. uvella* (varying with pH 6–7) (Bhatti and Colman 2008). These *in vivo* values can be accommodated by diffusive CO₂ entry with a Rubisco content giving a V_{max} for Rubisco equal to the V_{max} for *in vivo* photosynthesis, granted the necessary decrease in CO₂ concentration along the diffusion pathway from the bulk medium to Rubisco (Raven *et al.*, 2005; Raven and Beardall, 2016b; see Supplementary Information S1) which involves passage through five membranes (plasmalemma, two chloroplast endoplasmic reticulum membranes, and two chloroplast envelope membranes) in these algae resulting from secondary plastid endosymbiosis rather than three in green algae and two in cyanobacteria (see discussion above). The Rubisco assays cited above involved unpurified cell extracts (Bhatti and Colman, 2008) so the CO₂-saturated Rubisco-specific

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reaction rate cannot be calculated. The half-saturation values for CO₂ fixation *in vivo* correspond to at least 2.5 times the present atmospheric concentration. Analyses by [Young et al. \(2012\)](#) show no positive selection on Rubisco from the Chrysophyceae or Synurophyceae; however, the analytical method was very conservative. There is evidence for positive selection of the Rubisco of diatoms that, like synurophyceans, are members of the Heterokontophyta (=Ochrophyta=Ochrista), but have CCMs ([Young et al. 2012](#)). The Rubiscos of diatoms show a range of kinetic properties, possibly related to trade-offs between Rubisco kinetics and the properties of the CCM in individual diatom species ([Young et al. 2016](#)).

In summary then, for cyanobacteria, the external CO₂ concentration needed to give half the CO₂-saturated rate when CO₂ is supplied to Rubisco by diffusion *in vivo* is estimated at 6–25 (β-Cyanobacteria) or 35–75 (α-Cyanobacteria) times the present atmospheric level. For eukaryotic algae, estimated half-saturated rate values *in vivo* are 2–2.5 times the present atmospheric level. For CO₂-saturated rates, the values are ~4 times higher.

Effects of temperature on the CO₂ affinity (1/K_{0.5}) and CO₂/O₂ selectivity of Rubisco and its relationship to geographic distribution of photosynthetic organisms with and without CCMs

Here we consider terrestrial C₄ photosynthesis in terrestrial flowering plants as well as aquatic organisms with CCMs, since temperature as a possible factor in the evolution of CCMs was first mooted for C₄ plants on land. Furthermore, [Raven and Beardall \(2014\)](#) noted that some aquatic organisms with CCMs occur in colder habitats than do terrestrial C₄ plants, and their analysis is extended here.

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The starting point for considering the temperature dependence of the natural occurrence of oxygenic photosynthetic organisms with CCMs and those relying on diffusive CO₂ entry is the temperature dependence of the kinetic properties of Rubisco and also of the solubility of CO₂ and O₂ and the kinetics, and equilibrium constants, of the dissolved CO₂-HCO₃⁻-CO₃²⁻-H⁺-OH⁻ system. Regardless of the absolute values of the K_{0.5} for CO₂, the CO₂/O₂ selectivity factor, and the specific reaction rate at CO₂ saturation (mol CO₂ mol site⁻¹ s⁻¹) for a particular Rubisco, the CO₂ affinity (1/K_{0.5} CO₂) and CO₂/O₂ selectivity factor both increase with decreasing temperature, while the specific reaction rate decreases (Ehleringer *et al.*, 1991; Tcherkez *et al.*, 2006; Edwards and Still, 2008; Galmés *et al.*, 2016). The temperature effect on K_{0.5} for CO₂ and CO₂/O₂ selectivity, and also the greater rate of increase of CO₂ solubility than of O₂ solubility with decreasing temperature (Ku and Edwards 1977), has been related to the occurrence of C₄ terrestrial flowering plants in higher temperature environments where higher K_{0.5} for CO₂, lower CO₂/O₂ selectivity factor, and the lower CO₂:O₂ solubility ratio at higher temperatures increases the relative rate of Rubisco oxygenase and hence photorespiration in C₃ plants, and hence favours the occurrence of C₄ (a biochemical form of CCM) (Ehleringer *et al.*, 1991; Edwards and Still 2008). For low temperatures, the prediction is a lower selective value of CCMs (Ehleringer *et al.*, 1991; Raven *et al.*, 2002a, b; Edwards and Still, 2008), though the evidence discussed below suggests that CCMs of cyanobacteria and algae can occur in cold habitats. We note that there is some evidence of down-regulation of CCMs in Antarctic marine diatoms (Kranz *et al.*, 2015), and also that there is no evidence of adaptive changes to the Rubisco-specific reaction rate in Antarctic diatoms (Young *et al.*, 2015b) despite the known variability of Rubisco kinetics

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among diatoms (Young *et al.*, 2016) and the sea close to the Antarctic having had its present low temperatures for at least 15 million years (Raven *et al.*, 2002b).

Expanding on Raven and Beardall (2014), Table 1 shows that terrestrial C₄ (and CAM plants, also using a biochemical CCM) do not extend to such high latitudes and altitudes (i.e. lower temperatures, among other differences) as do C₃ flowering plants and other C₃ terrestrial embryophytes. Table 1 also shows that marine, freshwater and terrestrial cyanobacteria and algae (free-living and lichenized) with CCMs are much more significantly represented in high latitudes and (for freshwater and terrestrial organisms) high altitudes than is the case for terrestrial C₄ and CAM plants. Certainly some Antarctic microalgae (Mitchell and Beardall, 1996) and macroalgae (Beardall and Roberts, 1999) express CCMs despite the low temperatures and higher dissolved CO₂ levels in their high latitude environments; see also Johnston and Kennedy (1998), Raven *et al.* (2002a, b), Marconi *et al.* (2011), Kranz *et al.* (2015), Stepien (2015), Young *et al.* (2015a, b) and Stepien *et al.* (2016), noting that the ¹³C:¹²C cut-off for assignment to 'CO₂ diffusion only' may need revision for some algae with Form ID Rubiscos (Boller *et al.* (2011, 2015). This current distribution is relevant to consideration of what might have happened in the past and might happen in the future, granted the mechanistic positive relationship (other things being equal) between increased atmospheric CO₂ and increased temperature.

Effects of incident PAR and the concentration of combined nitrogen, phosphorus, and iron on the expression of CCMs in organisms in which the CCM expression is not constitutive

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We regard CCMs as constitutive if they are always expressed under the conditions that the organisms encounter in their natural environment, as well as at larger CO₂ concentrations than are found in those environments. By this definition, all photosynthetically competent cyanobacteria, some terrestrial CAM plants, and almost all terrestrial C₄ plants have a constitutive CCM. The exception for the C₄ plants is the sedge *Eleocharis*, where submergence causes some C₄ species to switch to C₃ or C₃-C₄ intermediate metabolism (Ueno *et al.*, 1988; Murphy *et al.*, 2007). Ontogenetic changes from C₃ cotyledons to C₄ in the leaves and/or stems in some members of the Chenopodiaceae are not environmentally determined (Pyankov *et al.*, 1990, 2000).

Organisms in which the extent of expression of CCMs varies with the supply of resources are algae with biophysical CCMs, some CAM plants, and some submerged and amphibious tracheophytes with CCMs. Here we deal with algae, based on the literature analysis in Raven and Beardall (2014) and the earlier reviews of Beardall and Giordano (2002) and Raven *et al.* (2000).

Decreased PAR decreases the CO₂ accumulation in cells of the cyanobacterium *Anabaena variabilis* (with a constitutive CCM) (Beardall, 1991; Raven and Beardall, 2014). In this cyanobacterium and in two marine red macroalgae and the green marine (to hypersaline) alga *Dunaliella tertiolecta*, there is a smaller increment of photosynthetic rate per unit increment in inorganic C concentration, (i.e., a lower affinity for inorganic C) at low PAR relative to high PAR for growth, although the reverse is true for a seagrass that may have a CCM (Kübler and Raven, 1995; Young and Beardall, 2005; Raven and Beardall, 2014). In most cases, the natural abundance ¹³C:¹²C ratio of organic C of algae with CCMs is higher at low PAR, consistent with, among other possibilities, increased

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CO₂ leakage as a fraction of inorganic C entering at low PAR, thus decreasing the energetic effectiveness of the CCM (Raven *et al.*, 2000; Beardall and Giordano, 2002; Raven and Beardall, 2014, 2016b). Overall, the data support a less effective CCM at low PAR for the cyanobacterium and the algae examined.

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Stepien (2015) performed a meta-analysis of data on the natural abundance ¹³C:¹²C ratio of organic C of marine macroalgae collected from their natural habitats and showed that at greater depths (low PAR) a greater proportion of algae showed very low ¹³C:¹²C ratios, indicative of diffusive CO₂ transport from bulk seawater to Rubisco. It is not clear whether the very deep-growing marine macroalgae have CCMs; the deepest growing red coralline alga at 268 m is only exposed to PAR of ~2 nmol photon m⁻² s⁻¹ (Raven *et al.*, 2000; Runcie *et al.*, 2008), with full sunlight at the ocean surface of up to 10⁶-fold higher at 2 mmol m⁻² s⁻¹ PAR. It is very unlikely that the algae are supplementing photosynthesis with phagotrophy of organic C, though use of dissolved organic C has not been ruled out (Raven *et al.*, 2000). For cyanobacteria, with their constitutive CCMs, the planktonic *Prochlorococcus* is a, and usually the, predominant photosynthetic organism in the Deep Chlorophyll Maximum peaks in the tropical and subtropical ocean at 80–100 m with incident PAR of ~10 μmol photons m⁻² s⁻¹, although outliers at greater depths may decrease that value to not less than 1 μmol photons m⁻² s⁻¹ (Campbell and Vault, 1988; Smith *et al.*, 1989; Letelier *et al.*, 2004; Casey *et al.*, 2007). Cyanobacteria may grow at lower PAR in cryptoendolithic environments with a PAR range imposed by self-shading of 150–0.1 μmol photons m⁻² s⁻¹ since the stratification of the organisms is not known (Nienow *et al.*, 1988).

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Data on nutrient supply effects on CCMs from Raven and Beardall (2014) are summarized in Table 2. For combined N limitation, there is variability in the data for the influence of N concentration both on the CCM and on the N use efficiency of growth, the latter generally being higher in C₄ than in C₃ flowering plants. P limitation usually (three out of five instances, including the most detailed data set) decreases CCM expression. Finally, the only data set for the effects of Fe deficiency shows an increased CCM expression under Fe limitation (Table 2; Young and Beardall, 2005). Overall, the data show a decreased CCM expression when PAR or P are limiting, an increased CCM expression when Fe is limiting, and variable effects of combined N deficiency or decreased UV. These short-term, acclimatory, effects have relevance to altered surface ocean stratification with global warming, as is occurring at the moment, but not necessarily to long-term evolutionary effects in the more distant future or in the past.

Evolution of CCMs and the possibility of their continuation through both 'Snowball Earth' and high CO₂ 'hothouse' episodes in Earth history

The focus here is on oxygenic photolithotrophic organisms, although a core part of the cyanobacterial CCM, the carboxysome, also occurs in autotrophic proteobacteria (anoxygenic photosynthesizers and chemolithotrophs) that use Rubisco and the PCRC (Raven *et al.* 2012). Mechanisms in oxygenic photosynthetic organisms that metabolize the unique product, phosphoglycolate, formed from the oxygenase activity of Rubisco, that go beyond the excretable (in aquatic organisms) immediate product of phosphoglycolate metabolism, glycolate, are ubiquitous in oxygenic organisms and are

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essential even in organisms using CCMs (Raven *et al.*, 2012). This is consistent with a pre-CCM occurrence of phosphoglycolate production that in turn requires the occurrence of oxygen in the organism's environment. The predominant source of O₂ on Earth is oxygenic photosynthesis, and the earliest oxygenic organisms were what in extant organisms are cyanobacteria, so the temporal sequence was (Raven *et al.*, 2012):

oxygenic photosynthesis in cyanobacteria or their ancestors,



production of phosphoglycolate and its metabolism beyond glycolate



CCMs

While the timing of origin for the crown group of extant cyanobacteria is still debated (Shih *et al.*, 2016), evolutionary studies agree that oxygenic photosynthesis must have evolved before the Global Oxygenation Event (GOE) some 2.3 Ga (Blank and Sánchez-Baracaldo, 2010; Sánchez-Baracaldo, 2015; Schirmer *et al.*, 2016). Other lines of evidence are consistent with oxygenic photosynthetic organisms appearing at least 2.7 Ga (e.g. Buick, 1992, 2008; Schirmer *et al.*, 2015, 2016). It is unclear whether Proterozoic cyanobacteria resemble extant taxa; however, the oldest reliable cyanobacteria microfossils appeared in carbonate strata ~1.9 Ga in the Belcher Islands, Canada (Hofmann, 1976). Based on phylogenetic analyses, we now know that the sister clade of the cyanobacteria is the non-photosynthetic Melainabacteria, many of which are purely fermentative, while some have anaerobic and, possibly, aerobic respiration (Di Rienzi *et al.*, 2013; Soo *et al.*, 2014). There are views explaining how PSII and PSI of oxygenic photolithotrophy reached the ancestral cyanobacterium. One hypothesis

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involves lateral gene transfer of, respectively, a Type II reaction centre from a proteobacterium, and a Type I reaction centre from a member of the Chloroflexi, together with their associated peptides, as well as those of the (bacterio)chlorophyll synthesis pathway and of the PCRC (Soo *et al.*, 2014). A second hypothesis proposes that both PSII and PSI evolved in an ancestral phototroph as a result of gene duplication.

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Consequently anoxygenic phototrophs selectively lost one of the photosystems, while cyanobacteria retained both (Cardona, 2015). Here, it is implied that phototrophy is mostly vertically inherited and that non-phototrophs (e.g. Melainabacteria; Soo *et al.*, 2014) that evolved from a phototroph lost both photosystems.

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The basal extant cyanobacterium is the β -cyanobacterium (Badger *et al.*, 2002; Badger and Price, 2003) *Gloeobacter*, possessing Form IB Rubisco, β -carboxysomes and associated inorganic C transporters, which grows in low-salinity water films on limestone and dolomite (*G. violacea*; Nakamura *et al.*, 2003; Horath and Bachofen, 2009; Mareš *et al.*, 2013) or igneous rocks (*G. kiluaeensis*; Saw *et al.*, 2013). Independent phylogenomic studies, including both protein and nucleotide data and implementing a relaxed Bayesian molecular clock approach, suggest that *Gloeobacter* could have evolved before the GOE (Blank and Sánchez-Baracaldo, 2010; Sánchez-Baracaldo *et al.*, 2014; Sánchez-Baracaldo, 2015; Schirmeister *et al.*, 2015, 2016; see also Dillon and Castenholz, 1999; Olsson-Francis *et al.*, 2010). An opposite view from Butterfield (2015; see also Lyons *et al.*, 2014) is that extant cyanobacteria evolved later as crown group Cyanobacteria with no basal or stem group Cyanobacteria extant. According to this view, the environment in the late Archaean and Proterozoic may be irrelevant to the origin and perpetuation of the cyanobacterial CCM.

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Assuming that phylogenomics and Bayesian molecular clock analyses are correct, and that *Gloeobacter* has retained features present in the basal cyanobacterium, it is possible that cyanobacteria at the time of the GOE had CCMs. This seems contrary to the need for greenhouse gases at greater than present, and recent (10 Ma), partial pressures if a Snowball Earth is to be avoided given the lower than present luminosity of the Faint Young Sun (Claire *et al.*, 2012; see also Som *et al.*, 2016). One such gas is CO₂, and another, CH₄, was probably at low partial pressures after the GOE even with low atmospheric O₂ as an oxidant for CH₄ (Olson *et al.*, 2016). This would argue for relatively high CO₂ concentrations through most of the Proterozoic, with the exception of the Palaeoproterozoic (Huronian) and Neoproterozoic (Sturtian, Marinoan, and Gaskiers) glaciations of the Snowball/Slushball Earth episodes (Hoffman, 2016; Figs 1, 2. Riding (2006) suggests that CO₂ was 25 times the present atmospheric level at 1.4–1.3 Ga, based on the geochemistry of CaCO₃ precipitation; Kah and Riding (2007) suggest that CO₂ could be as low as 6–10 times the present atmospheric level, assuming 100–200 ppm CH₄ in the atmosphere (but see Olson *et al.*, 2016 who suggest CH₄ <10 ppm) (Fig. 2). [A further consideration for the evolution of marine CCMs is the variation in ocean pH over the last 4 Ga \(Halevy and Bachan 2017\).](#)

Accepting the timings of cyanobacterial evolution in Sánchez-Baracaldo *et al.* (2014; see also Lyons *et al.*, 2014; Butterfield, 2015), *Gloeobacter*-like organisms could have had CCMs during all of the Neoproterozoic glacial periods and this could have included, for the three Neoproterozoic glaciations, open ocean planktonic cyanobacteria. Eukaryotic photosynthetic organisms [are first known from marine deposits from ~1.6 Ga \(Bengtson *et al.* 2017\) and the bangiophycean red alga *Bangiomorpha pubescens* from](#)

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~1.2 Ga (Butterfield, 2000), and freshwater and terrestrial eukaryotes, some of them probably photosynthetic, from 1.2 Ga to 1.0 Ga (Strother *et al.*, 2011; Wacey *et al.*, 2016). Oehler (1977) interprets structures in 740–950 Ma cells as pyrenoids, although there are alternative explanations of the nature of the structures, and the correlation of pyrenoids with CCMs is not exact (Kevekordes *et al.*, 2006; Meyer and Griffiths, 2013; Raven and Giordano, 2017). If at least some of the Proterozoic glaciations were at the more extreme end of the glaciological possibilities for global ice cover, it is very difficult to see how marine photosynthetic organisms could have survived. For cyanobacteria, the lower limit for growth may be not less than 1 $\mu\text{mol photon m}^{-2} \text{s}^{-1}$ of PAR as discussed above (Campbell and Vault, 1988; Smith *et al.*, 1989; Letelier *et al.*, 2004; Casey *et al.*, 2007). This would be achieved under a few metres of ice containing dust and gas bubbles rather than a kilometre of ice. In contrast, freshwater and, perhaps, terrestrial organisms could have survived on the glacial surface in freshwater-filled ‘cryoconite holes’ produced by dust (cryoconite) from vulcanism and (to a small extent) meteorites, decreasing the albedo and allowing warming (Vincent *et al.*, 2000; Hoffman, 2016). Phylogenomic and trait evolution analyses have recovered clades common to Arctic, Antarctic, and alpine regions; these clades of cyanobacteria from terrestrial/freshwater clades probably evolved the ability to cope with such extreme cold environments independently (Christmas *et al.*, 2015, 2016). Bayesian statistical analyses have identified at least 20 clades with high probability of having a cold-adapted ancestor (Christmas *et al.*, 2015). While molecular clock analyses are yet to provide any dates of when these groups evolved, it is likely that some of these ‘cold-adapted’ clades date as far back to the Neoproterozoic glaciations. Furthermore, geological evidence and models shows habitat

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availability for atmosphere-exposed marine and terrestrial habitats (Campbell *et al.* 2014; Fairchild *et al.* 2015; Retallack *et al.* 2015) and there is biomarker evidence of green sulphur bacteria, cyanobacteria and probable eukaryotes in organic-rich shales (Olcott *et al.* 2005) as well as palaeontological evidence of marine macroalgae (Ye *et al.* 2015) occurring in the glacial episodes in the Cryogenian. These lines of evidence showing the occurrence of cyanobacteria and of eukaryotic algae as photosynthetic primary producers in the glacial episodes of the Cryogenian are consistent with the geologically (not depending on biological evidence) recognized possibility of a Slushball Earth, with ice-free low latitude marine and coastal habitats, rather than more extreme Snowball Earth conditions (Hoffman and Schrag 2002).

The previous section suggests that a CCM is needed to give half the rate of CO₂-saturated photosynthesis in a cyanobacterium with the highest extant cyanobacterial Form IB Rubisco CO₂ affinity when the atmospheric CO₂ is ≤ 12 times the present atmospheric level. If the requirement is for the rate of CO₂-saturated photosynthesis, the necessary CO₂ concentration is 48 times the present atmospheric CO₂ level. For eukaryotes with Form IB Rubisco, only involved in the Cryogenian, the equivalent values are as low as two and eight times the present atmospheric level. The presumed low atmospheric CO₂ during the glacial episodes has not been adequately modelled. The atmospheric greenhouse gases would have been higher than would be needed today for the same extent of glaciation as a result of the lower luminosity of the weak young sun, especially in the Paleoproterozoic Huronian (Claire *et al.* 2012). While extreme glaciations in the Proterozoic might give CO₂ concentrations consistent with the evolution of CCMs, it is less clear what would happen during the warmer time between the Huronian and

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Cryogenian, especially in view of the low modelled levels of the more powerful greenhouse gas, CH₄ (Olson *et al.*, 2016). As noted above, Riding (2006) suggests 25 times the present atmospheric level for CO₂ at 1.4–1.3 Ga, with the Kah and Riding (2007) value of 6–10 times the present level assuming 100–200 ppm CH₄ in the atmosphere rendered unlikely by the arguments of Olson *et al.* (2016) for CH₄ < 10 ppm when O₂ (oxidant of CH₄) was relatively low (Figs 2, 3).

There are more proxies for CO₂ for the Phanerozoic, and especially after tracheophytes became significant components of the terrestrial flora, and even earlier with non-tracheophyte flora (Berner 2004; Breecker *et al.*, 2010; Lenton *et al.*, 2012; Franks *et al.*, 2014; Royer, 2014; Wellman and Strother, 2015; McElwain *et al.*, 2016; Lenton and Daines, 2017). Breecker *et al.* (2010) suggest that the mean of estimates of the CO₂ concentration in the warmest episode of the Mesozoic were only 2.5 times the present atmospheric value, and McElwain *et al.* (2016) consider a similar value (1000 μmol CO₂ mol⁻¹ total gas, as compared with 400 μmol CO₂ mol⁻¹ total gas today) as a possible cap on CO₂ over the last 300 million years (i.e. since the late Palaeozoic glaciation; Figs 1–3). This would permit not only cyanobacterial CCMs, but possibly also eukaryotic CCMs, to survive had the cyanobacterial and eukaryotic CCMs evolved in the low CO₂ episode (CO₂ at about the present level) of the Carboniferous–Permian (fig. 5.21 of Berner 2004; Breecker *et al.*, 2012), or earlier (e.g. the Cryogenian). However, there is very considerable variance in the estimates. (Berner 2004; Breecker *et al.*, 2010), and Berner (2004) estimates five times the present CO₂ level in the Mesozoic. Lenton *et al.* (2012) modelled atmospheric CO₂ at the time of the Ordovician glaciations as 6–8 times

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the present value, and before the glaciations at 16 times the present, similar to values in [fig. 5.21 of Berner \(2004\) \(Figs 2, 3\)](#).

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A possible refuge for organisms with CCMs during episodes of globally high CO₂ is produced by the organisms themselves. The relatively slow exchange of CO₂ between water bodies and the atmosphere, and between parcels of water within the water bodies, means that CO₂ can be drawn down to values less than a third of the air-equilibrium values at times of high ecosystem primary productivity. Freshwater phytoplankton ([Maberly, 1996](#)) can decrease CO₂ to air-equilibrium equivalent values of <20 μmol mol⁻¹ and marine phytoplankton ([Codispoti et al., 1982, 1986](#)) to 125 μmol mol⁻¹, and marine macrophyte beds ([Delille et al., 2000](#)) can decrease CO₂ to air-equilibrium equivalent values of 20 μmol mol⁻¹. The presence of a CCM could be of importance at these times of high productivity even with high global CO₂ concentrations; the largest drawdowns observed today would yield the present atmospheric equilibrium values with five times the present CO₂ content, although this would be partly offset by the higher total inorganic C concentration under higher atmospheric CO₂ so that more inorganic C would have to be assimilated to get down to the present air-equilibrium CO₂. This effect is much less marked, with a maximum drawdown to 86% of the tropospheric CO₂ within a *Zea mays* canopy ([Buchman and Ehleringer, 1998](#)) as a result of greater mixing with the bulk atmosphere than in aquatic habitats.

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Comparison of the estimates of CO₂ over the last 2 Ga with the estimates of the CO₂ required for diffusive CO₂ entry to support the CO₂-saturated growth rate, and the $K_{0.5}$ (CO₂) for growth, of cyanobacteria and chlorophytes that currently operate CCMs allows the following conclusions about retention of CCMs. The ancestral β-

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Cyanobacteria (Form IB Rubisco and β -carboxysomes; Badger and Price 2003) might, and the derived α -Cyanobacteria (Form IA Rubisco and α -carboxysomes: the SynPro clade; Badger and Price 2003) could have retained CCMs throughout the Phanerozoic, and possibly from the late Mesoproterozoic, had the CCMs evolved before the Cryogenian. For the chlorophytes, had they evolved that early, the possibilities of retention of CCMs through the mid-Palaeoproterozoic are minimal, although the post-Carboniferous may not pose an insuperable problem for CCM retention.

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An origin of the biophysical CCMs later than diversification of the clades in which they occur would involve further horizontal gene transfer. For cyanobacteria, an origin in the Cryogenian or later would, on any of the suggested timings of cyanobacterial diversification, involve significant horizontal gene transfer in addition to that replacing β -carboxysomes with Form IB Rubisco with α -carboxysomes with Form IA Rubisco (Badger *et al.* 2002, 2006; Badger and Price 2003; Price *et al.* 2008; Sánchez-Baracaldo *et al.* 2014; Butterfield 2015). The biophysical CCMs of eukaryotic algae are more diverse than those of cyanobacteria (Badger *et al.* 1998; Meyer and Griffiths 2013; Clement *et al.* 2016), but there is probably significant horizontal gene transfer involved in an origin as late as the Carboniferous low CO₂ and high O₂ period (Raven 1997; Badger *et al.* 1998, 2002; Badger and Price 2003; see Fig. 1a and b), granted the timing of diversification of algae (Butterfield 2010; Baurain *et al.* 2010; Brown and Sorhanus 2010; Strother *et al.* 2011; Yang *et al.* 2012). An even later origin (Palaeogene) is possible for the biophysical CCM of the hornworts (Villareal and Renner 2012). C₄ flowering plants also originated in the Palaeogene; this biochemical CCM may have involved limited horizontal gene transfer to account for the ≥ 60 independent origins

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of flowering plant C₄, at least as far as the enzymes involved in variants on the C₃-C₄ cycle are concerned (Still *et al.* 2003; Aubry *et al.* 2011; Chi *et al.* 2014). Limited horizontal gene transfer would also be the case for the possible occurrence of C₄ photosynthesis in algae (Koch *et al.* 2013; Clement *et al.* 2016; Raven and Giordano 2017).

Possible future of CCMs

For marine organisms, the immediate (until 2100) effects of global environmental change in the surface ocean influence the availability of many resources. The increased atmospheric CO₂ means an increase in the concentration of CO₂, a smaller relative increase in the concentration of HCO₃⁻ and a decrease in the concentration of CO₃²⁻ and in the pH. The increased ocean temperature results initially in an increased surface (upper mixed layer) ocean temperature relative to the deeper ocean, with a larger temperature difference across, and a shoaling of, the thermocline, with a decreased flux of NO₃⁻, HPO₄²⁻ and other nutrients from the deeper ocean to the upper mixed layer (Doney *et al.* 2012; Gao *et al.* 2012; Reusch and Boyd 2013; Raven and Beardall 2014). In addition, the decreased thickness of the upper mixed layer means that phytoplankton are exposed to a higher mean flux of PAR and of UV radiation (Doney *et al.* 2012; Gao *et al.* 2012; Reusch and Boyd 2013; Raven and Beardall 2014), with higher UVB and lower nutrient levels potentially causing a shift in the size structure of phytoplankton populations favouring smaller organisms such as the cyanobacteria *Prochlorococcus* and *Synechococcus* (Finkel *et al.* 2010). In the longer term (1000–100 000 years), usable fossil fuel reserves will all have been consumed, and shoaling of the lysoclines for calcite and aragonite will weaken as CO₂-enriched water circulates deep into the ocean and

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dissolves sedimented CaCO₃, thereby increasing the carbonate alkalinity of the seawater that, when it is upwelled to the surface, will absorb some or much of the anthropogenic atmospheric CO₂ released from fossil fuel burning and land use change (Archer *et al.*, 2009). Furthermore, the downwelled heat from the surface ocean will eventually increase the temperature of the deep ocean and decrease the temperature difference across the thermocline, allowing an increase in the thickness of the upper mixed layer. This combination of changes will thus, in time, produce an oceanic state similar to the pre-industrial ocean.

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The multiplicity of changing and interacting environmental influences makes it difficult to carry out short-term studies of the acclimation of phytoplankton to these factors: what has been accomplished is summarized by Gao *et al.* (2012), Beardall *et al.* (2014), and Raven and Beardall (2014). A subsequent experiment with eight drivers, including increased CO₂, on *C. reinhardtii* had the final sample at 120 h (Brennan and Collins 2015).

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The complications of multifactorial experimentation are even more of a problem with longer term experimental evolution studies of genetic change. It is therefore not surprising that most work on experimental evolution has involved only a single variable of increased CO₂. As a simplifying factor, cultures were initiated with clonal algal inocula; even so, epigenetic changes as well as genetic changes can occur, potentially complicating interpretation (Kronholm and Collins 2016). Following the pioneering work of Collins and Bell (2004), what has been achieved subsequently is summarized by Low-Décarie *et al.* (2013), Reusch and Boyd (2013), Schlüter *et al.* (2014), Li *et al.* (2016), and Schlüter *et al.* (2016). The longest experiment (4 years, 2100 generations;

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Schlüter *et al.* (2016) examined the response of an 'adapted' population of *Emiliania huxleyi* by testing how they responded to being returned to the original CO₂ conditions and hence the occurrence of genetic changes, either by strain selection or mutation or, for clonal cultures, genetic mutation alone. In the work reported by Schlüter *et al.* (2016) some traits that showed selective changes under high CO₂ reverted when cells were placed back in present day CO₂ levels, but others, such as the PIC/POC ratio, overcompensated under such conditions, showing that adaptive (genetic) changes had occurred. Particularly interesting is the work on N₂ fixation by the marine cyanobacterium *Trichodesmium* exposed to elevated CO₂ for 4.5 years (~850 generations) (Hutchins *et al.* 2015). Consistent with the results of short-term (2 week) incubations, the 4.5 year exposure cultures showed significantly higher N₂ fixation rates and specific growth rates under P-limited conditions, as well as shifts in the diel occurrence of peak N₂ fixation; this occurred for all six biological replicate cultures. These three effects continued when the cultures were returned to present CO₂ levels for 2 years. Analysis of the proteome and enzyme activities did not, however, reveal the basis of these changes (Hutchins *et al.* 2015; Wallworth *et al.* 2016).

Schaum and Collins (2014) examined 16 strains of *Ostreococcus* and showed that strains with a greater acclimatory response to increased CO₂ also showed a greater adaptive (genetic change) response to increased CO₂. Padfield *et al.* (2016) investigated the changes to metabolism of the freshwater *Chlorella vulgaris* over 100 generations of exposure to a higher temperature, but without demonstrating that the effects are due to adaptation rather than acclimation. Schlüter *et al.* (2014) examined increased temperature and increased CO₂, separately and together, on *E. huxleyi* and showed that there was no

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interaction of CO₂ and temperature. Bermúdez *et al.* (2015) used a fully factorial design (three CO₂ concentrations, two temperatures) to study the amino and fatty acid composition of *Cylindrotheca fusiformis* over 250 generations and showed significant changes in polyunsaturated fatty acid content with both CO₂ and temperature, although again the authors were not able to distinguish between acclimatory and adaptive changes.

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Whereas transcriptomic data are available for some of the acclimation and adaptation studies (e.g. Lohbeck *et al.*, 2014), there are no genomic data for the adaptation experiments and the mutations involved are not documented at the molecular genetic level. In addition to the need for these data, additional environmental factors should be investigated by experimental evolution experiments. Interesting possibilities for predicting the adaptation of phytoplankton strains comes from the work of Schaum and Collins (2014) and Schaum *et al.* (2016). Schaum and Collins (2014) examined 16 strains of *Ostreococcus* and showed that strains with a greater acclimatory response to increased CO₂ also showed a greater adaptive (genetic change) response to increased CO₂. Schaum *et al.* (2016) used the same strains of *Ostreococcus* to show that exposure to temporally varying increased CO₂ showed a more rapid response to further increases in CO₂ than for treatments with constant high CO₂ (see also Doblin and van Sebille, 2016).

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Determination of whether these responses occur for other microalgae, and for other aspects of global environmental change, is required. The interactive effects of the various aspects of global change also need to be taken into account (see, for example, Boyd *et al.*, 2016a, b). Finally, all of these sources of laboratory data must eventually be related to natural ecosystems (Brodie *et al.*, 2014; Mock *et al.*, 2016).

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A beginning has been made by Scheinin *et al.* (2015), who deployed the centric diatom *Skeletonema costatum* in control and CO₂-enriched mesocosms in the natural environment of a fjord on the west coast of Sweden for 107 d; there was a 1.3-fold increased growth in high CO₂-evolved mesocosms. This contrasts with the findings for the pennate diatom *Phaeodactylum tricoratum* grown for ~1860 generations (Li *et al.* 2016) where the cultures supplied with increased CO₂ had lower growth, photosynthesis and respiration rates than did the controls.

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Perhaps the ultimate in long-term high CO₂ treatments for comparison with growth in present day CO₂ is freshwater springs (Collins and Bell, 2006) and marine shallow water vents emitting mainly, or solely, CO₂ as the gas dissolved in the emerging water (Porzio *et al.*, 2011, 2013; Johnson *et al.*, 2012). There are a number of issues with such systems in comparison with laboratory work. One is the problem of finding comparative ecosystems for the planktonic and benthic algal communities of freshwater springs. This problem seems smaller for benthic macroalgae close to marine vents where the surrounding habitats differ (mainly) in CO₂ input, but there can be exchange of genotypes between the vents and the surroundings, as well as differential effects on epiphyte settlement and on motile macroalgal genotypes (Porzio *et al.*, 2011, 2013; Johnson *et al.*, 2012).

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Conclusions

CCMs, based on active transport of inorganic carbon or, in vascular plants, on C₄ and CAM biochemistry, support over half of the planet's primary productivity. In algae and cyanobacteria there is considerable diversity in the kinetic properties of Rubisco, but data based on the CO₂ level needed to support half-saturated rates of C₃ fixation suggest that

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evolution of CCMs would have been favoured when atmospheric CO₂ levels were <16 times (cyanobacteria) or as low as <2 times present day values. CCM activity in extant photoautotrophs is regulated by a range of environmental factors, including temperature, light, and nutrient availability. This information allows us to make some predictions about CCM activity and evolutionary changes in a future climate, though the complexity of interactions between environmental factors will necessitate more complex experimental approaches than have been employed in the past if we are to obtain an accurate picture of how CCMs and primary productivity will respond in the next century and beyond.

Supplementary data

Supplementary data are available at *JXB* online.

Table S1. Comparison of *K*_{0.5} values (mmol m⁻³) for CO₂ assimilation by whole cells with *K*_{0.5} values (mmol m⁻³) for CO₂ transformation into 3-phosphoglycerate by extracted Rubisco for three species of the Synurophyceae and one of Trebouxiophyceae lacking CCMs.

Information S1. Diffusion limitations on photosynthesis by algae lacking CCMs

Acknowledgements

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Table 1. Effects of altitude and latitude as general proxies for low temperature, for oxygenic photosynthetic organisms with and without CCMs

Organisms	Altitude	Latitude	References
C ₃ terrestrial flowering plants	6400 m	83°N	Körner (1999); Crawford (2014)
C ₄ terrestrial flowering plants	3300 m	60°N	Pitterman and Sage (2001); Kubien and Sage (2003); Still <i>et al.</i> (2003)
CAM terrestrial flowering plants	4700 m	50°N	Keeley and Keeley (1989); Lüttge (2004)
CAM freshwater tracheophytes	4750 m	61°N	Keeley (1998)
Marine planktonic algae	Not applicable	Increasing contribution of algae lacking CCMs at high southern latitudes	Johnston and Kennedy (1998); Henley <i>et al.</i> (2012); Trimbom <i>et al.</i> (2015); Young <i>et al.</i> (2015)
Marine macroalgae	Not applicable	Increasing fraction of algae lacking CCMs at higher latitudes for Phaeophyceae and	Stepien (2015)

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Inland water and terrestrial cyanobacteria (CCMs constitutive in photosynthetically competent cyanobacteria)	5997 m (volcanic area; possibly higher temperatures than other tropical sites at this altitude)	87°S (Antarctic dry valleys)	Fleming <i>et al.</i> (2010); Namsernaev <i>et al.</i> (2010)

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Table 2. Effects of limitation of growth by the availability of N (NH₄⁺), N (NO₃⁻), P, Fe, and S on CCMs as indicated by the half-saturation value for CO₂ (K_{0.5}), inorganic carbon concentration factor (CCF), and natural abundance ¹³C: ¹²C stable isotope of organic matter relative to source CO₂ (Δ¹³C)

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Organism	Limiting nutrient	Effect of limitation on CCM activity	Basis of CCM determination	References
<i>Chlorella emersonii</i> (Trebouxiophyceae)	N (NH ₄ ⁺)	Increase	CCF, K _{0.5} , Δ ¹³ C	Beardall <i>et al.</i> (1982)
<i>Chlorella emersonii</i> (Trebouxiophyceae)	N (NO ₃ ⁻)	Increase (only when μ < 10% μ _{max})	K _{0.5}	Beardall <i>et al.</i> (1991)
<i>Chlamydomonas reinhardtii</i> (Chlorophyceae)	N (NH ₄ ⁺)	Decrease	K _{0.5}	Giordano <i>et al.</i> (2003)
<i>Dunaliella tertiolecta</i> (Chlorophyceae)	N (NO ₃ ⁻)	Increase	K _{0.5}	Young and Beardall (2005)
<i>Nannochloropsis</i> sp. (Eustigmatophyceae)	N (NO ₃ ⁻)	Increase at moderate limitation, but no difference compared, with an N-replete control at greater limitation	K _{0.5}	Hu and Zhou (2010)
<i>Phaeodactylum tricoratum</i> (Bacillariophyceae)	N (NO ₃ ⁻)	Decrease under N _v limitation in cells grown in air-equilibrium CO ₂ ; similarly decreased values in both replete and limited	K _{0.5}	Li <i>et al.</i> (2012)

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		cells at elevated (1000 $\mu\text{mol mol}^{-1}$) CO_2		
<i>Synechococcus</i> sp. UTEX LB2380	N (NH_4^+ , NO_3^-)	CCF higher in NH_4^+ -grown than NO_3^- -grown cells under light limitation and repletion. Lower CO_2 affinity for NO_3^- -cells only at low light	CCF, $K_{0.5}$	Ruan <i>et al.</i> (2017)
<i>Chlorella vulgaris</i> (Trebouxiophyceae)	P	Increase	$K_{0.5}$	Kozłowska-Szerenos <i>et al.</i> (2004)
<i>Chlorella emersonii</i> (Trebouxiophyceae)	P	Decrease	$K_{0.5}$, $\Delta^{13}\text{C}$, CCF	Beardall <i>et al.</i> (2005)
<i>Chlamydomonas acidophila</i> (Chlorophyceae)	P	Increase	$K_{0.5}$, CCF	Spijkerman <i>et al.</i> 2014
<i>Cylindrospermopsis raciborskii</i> (Cyanobacterium)	P	Increase	$K_{0.5}$	Wu <i>et al.</i> (2012)
<i>Gracilaria lemaneiformis</i> (Floridiophyceae)	P	Decrease	$K_{0.5}$	Xu and Gao (2009), Xu <i>et al.</i> (2010)
<i>Nannochloopsis</i> sp. (Eustigmatophyceae)	P	Decrease	$K_{0.5}$	Hu and Zhou (2010)
<i>Dunaliella tertiolecta</i> (Chlorophyceae)	Fe	Increase	$K_{0.5}$, CCF	Young and Beardall 2005
<i>Dunaliella salina</i> (Chlorophyceae)	S	Decrease	$K_{0.5}$	Giordano <i>et al.</i> , 2000

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Fig. 1. Time line of major geological eras, showing glaciation events referred to in the

text. Within the Phanerozoic, eras are: Cen. Cenozoic; Mes. Mesozoic; Pal. Paleozoic.

For the Archean and Proterozoic, Paleo, Meso and Neo prefixes for the eras.

Fig. 2. Estimates of past CO_2 in $\mu\text{mol mol}^{-1}$ total gas. Data were abstracted from

Breecker *et al.* (2010), Kah and Riding (2007), and Royer (2014).

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Fig. 3. Estimates of past O₂ in kPa partial pressure. Data were abstracted from Berner

(2009), Kump (2008), and Royer (2014).

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