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Journal of Experimental



REVIEW PAPER

The C₄ plant lineages of planet Earth

Rowan F. Sage^{1,*}, Pascal-Antoine Christin² and Erika J. Edwards²

¹ Department of Ecology and Evolutionary Biology, The University of Toronto, 25 Willcocks Street, Toronto, Ontario M5S3B2 Canada
² Department of Ecology and Evolutionary Biology, Brown University, 80 Waterman St., Providence, RI 02912, USA

* To whom correspondence should be addressed. E-mail: R.Sage@utoronto.ca

Received 30 November 2010; Revised 1 February 2011; Accepted 2 February 2011

Abstract

Using isotopic screens, phylogenetic assessments, and 45 years of physiological data, it is now possible to identify most of the evolutionary lineages expressing the C₄ photosynthetic pathway. Here, 62 recognizable lineages of C₄ photosynthesis are listed. Thirty-six lineages (60%) occur in the eudicots. Monocots account for 26 lineages, with a minimum of 18 lineages being present in the grass family and six in the sedge family. Species exhibiting the C₃–C₄ intermediate type of photosynthesis correspond to 21 lineages. Of these, 9 are not immediately associated with any C₄ lineage, indicating that they did not share common C₃–C₄ ancestors with C₄ species and are instead an independent line. The geographic centre of origin for 47 of the lineages could be estimated. These centres tend to cluster in areas corresponding to what are now arid to semi-arid regions of southwestern North America, southcentral South America, central Asia, northeastern and southern Africa, and inland Australia. With 62 independent lineages, C₄ photosynthesis has to be considered one of the most convergent of the complex evolutionary phenomena on planet Earth, and is thus an outstanding system to study the mechanisms of evolutionary adaptation.

Key words: Angiosperms, C₃–C₄ photosynthesis, CO₂-concentrating mechanism, convergent evolution, photorespiration, phylogeny.

Introduction

The metabolic pathway of C₄ photosynthesis was first described in the mid-1960s (Hatch and Slack, 1966, 1967; Osmond, 1967; Hatch, 1999), although many of the traits associated with C₄ photosynthesis, such as Kranz anatomy, low CO₂ compensation points of photosynthesis, and dimorphic chloroplasts were described years earlier (Haberlandt, 1914; Rhoades and Carvalho, 1944; Hodge et al., 1955; Moss, 1962). Once the C₄ pathway was identified in \sim 1966– 1967 (Hatch and Slack, 1966, 1967; Osmond, 1967), the integrated picture of C₄ photosynthesis was quickly formulated from the distinct patterns of physiology, structure, and ecology that were associated with the group of plants known to have Kranz anatomy (Downton and Tregunna, 1968; Black et al., 1969; Downton et al., 1969; Hatch et al., 1971). With this comprehensive understanding, plant biologists were able to survey the plant kingdom rapidly and by the mid-1970s identified most of the genera containing C_4 species (Smith and Epstein, 1971; Downton, 1975; Smith and Turner, 1975; Webster et al., 1975; Sankhla et al., 1975). Detailed surveys of individual families followed, providing comprehensive understanding of the distribution of the C₄ pathway in grasses (Brown, 1977; Raghavendra and Das, 1978; Hattersley and Watson, 1992; Watson and Dallwitz, 1992), sedges (Ueno and Koyama, 1987; Soros and Bruhl, 2000; Bruhl and Wilson, 2007), and various eudicot groups (Raghavendra and Das, 1978; Winter, 1981; Ziegler et al., 1981; Pyankov and Vakrusheva, 1989; Batanouny et al., 1991; Akhani et al., 1997). In the edited volume C_4 plant biology (Sage and Monson, 1999), Sage et al. (1999) assembled this information into comprehensive lists of genera containing C_4 species, and Kellogg (1999) mapped many of the C₄ genera onto the phylogenetic trees available at the time. While these treatments synthesized understanding as of the late 1990s, they also identified significant gaps in the knowledge of the taxonomic distribution of C₄ photosynthesis in higher plants. For example, phylogenetic information was often sparse, and isotopic surveys were incomplete for most taxonomic groups. As a

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result, the treatments in C_4 plant biology stimulated new research that has filled in many of these gaps. Of major significance since the publication of C_4 plant biology has been the generation of increasingly detailed phylogenies that resolve the relationships between C₃ and C₄ species within an evolutionary group (e.g. McKown et al., 2005 for Flaveria; Giussani et al., 2001, Aliscioni et al., 2003, Christin et al., 2008; Vicentini et al., 2009 for grasses; Besnard et al., 2009; Roalson et al., 2010 for sedges; and Pyankov et al., 2001; Kapralov et al., 2006, Kadereit et al., 2003, 2010; Kadereit and Freitag, 2011 for Chenopods). In addition, intensive isotopic surveys of both C3 and C4 species have been undertaken in families known to contain C4 species, and the result has been detailed accounting of C₃ and C₄ species in a phylogenetic context in the Amaranthaceae (Sage et al., 2007), Cleomeaceae (Marshall et al., 2007; Voznesenskaya et al., 2007; Feodorova et al., 2010), Cyperaceae (Roalson et al., 2010), Molluginaceae (Christin et al., 2011b), and Portulacineae (Ocampo and Columbus, 2010; Vosnesenskava et al., 2010). This accumulation of phylogenetic information coupled with a better understanding of the taxonomic distribution of the C₄ pathway facilitates the formulation of evolutionary hypotheses regarding the number of C₄ origins and their ecological and geographic context. Here, this phylogenetic and biogeographic information is synthesized to present the most comprehensive listing of C_4 plant lineages known to date.

Methodology

The literature was screened for taxonomic surveys of photosynthetic types as well as phylogenetic information, and then the occurrence of C₄ photosynthesis was mapped onto recent phylogenies following the approach of Kellogg (1999) and Sage (2004). Where C_4 groups were separated in the phylogeny by nodes branching to C₃ taxa, they were inferred to be independent C₄ lineages, unless a scenario of fewer C₄ origins followed by reversal to the C₃ ancestral state was more parsimonious. The exception to this approach occurs in the Chenopodiaceae, where the biochemical and anatomical differences between the different clusters of C4 taxa were also taken into account. If a C₄ group appeared to have arisen following a C₄ to C₃ reversion, it was only accepted as a distinct lineage if there were multiple intervening C₃ lineages suggesting that the C_4 line evolved from C_3 species. However, the direction of past photosynthetic transitions is still unknown for several groups, and the possibility of C₄ to C₃ reversion is an open question that is difficult to address based solely on species relationships (Christin et al., 2010).

In some taxonomic groups (e.g. *Polycarpea* in the Caryophyllaceae), taxa that are known to contain C_4 species have not yet been included in any molecular phylogenetic study. Because they are the only known C_4 representatives of broader and presumably monophyletic taxonomic groups whose phylogenetic positions have been determined (APG III, 2009), they are reported as distinct C_4 lineages. This approach provides only a minimum estimate, as it cannot discern whether C₄ species form more than one lineage within a genus unless there is a detailed, species level phylogeny and the photosynthetic pathways of the species are clearly known. Higher resolution phylogenies and surveys of photosynthetic pathways have been forthcoming in the past decade for many C₄-containing groups such as Aizoaceae (Hassan et al., 2005), Amaranthaceae (Sage et al., 2007), Cyperaceae (Bruhl and Wilson, 2007; Besnard et al., 2009; Roalson et al., 2010), Flaveria (Asteraceae; McKown et al., 2005), Nyctaginaceae (Douglas and Manos, 2007), Chenopodiaceae (Pyankov et al., 2001; Kadereit et al., 2003, 2010; Kapralov et al., 2006; Akhani et al., 2007; Wen et al., 2010; Kadereit and Freitag, 2011), Euphorbiaceae (Steinmann and Porter, 2002), Molluginaceae (Christin et al., 2011b), and Poaceae (Giussani et al., 2001; Aliscioni et al., 2003; Duvall et al., 2003; Christin et al., 2008; Vicentini et al., 2008; Edwards and Smith, 2010). In most cases, these detailed phylogenies have revealed more complex evolutionary patterns than originally anticipated. In Amaranthaceae sensu stricto (ss) (excluding Chenopodiaceae),

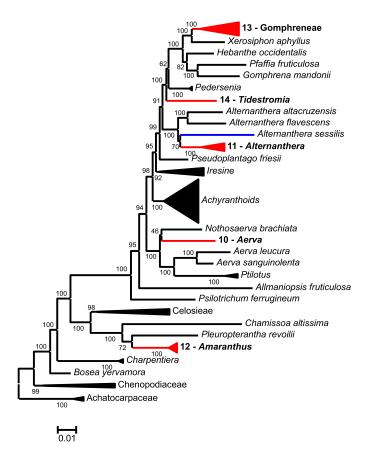


Fig. 1. The distribution of C_4 photosynthesis in the Amaranthaceae *sensu stricto*. The phylogeny was obtained through Bayesian inference on the *trnK–matK* data set of Sage *et al.* (2007). It is rooted on the Achatocarpaceae. Bayesian support values are indicated near branches. Clades that contain a single photosynthetic type for which names are available are compressed and coloured in red for C_4 , blue for C_3 – C_4 , and black for C_3 . Names of C_4 clades are in bold and numbers beside C_4 groups correspond to lineage number (Table 1). Photosynthetic types were determined previously by $\delta^{13}C$ assay (Sage *et al.*, 2007).

for example, two lineages were hypothesized by Kellogg (1999) based on poorly resolved phylogenies. Three lineages were suggested by Kadereit et al. (2003), although there was uncertainty in the relationship between C₄ species in the Gomphrenoids, Alternanthera and Tidestromia. Sage et al. (2007) provided detailed sampling of the isotopic ratios of most Amaranthaceae ss species, and with the inclusion of additional species in the region of the phylogeny containing the Gomphrenoids, Alternanthera and Tidestromia, they were able to resolve five distinct clades of C₄ photosynthesis (Fig. 1). A more problematic situation is present in the Chenopodiaceae ss. While recent phylogenetic work has clarified relationships within this family, patterns of C₄ evolution remain uncertain because the C₃ and C₄ pathways have not been clearly identified in some parts of the phylogeny. To clarify matters, the photosynthetic types were mapped on a phylogenetic tree for the Chenopodiaceae inferred from data accumulated in recent studies (Fig. 2). This approach indicates that 10 C₄ lineages are present in the Chenopodiaceae ss. More lineages may be present, as there is a possibility that the Salsola kali and Halothamnus groups may represent two independent C₄ lines. The situation is also unclear in Camphorosmeae, where anatomical variations could be interpreted as the fingerprint of two different C_4 origins (Kadereit and Freitag, 2011). The distribution of photosynthetic types also indicates a C_4 to C_3 reversion and reacquisition of the C_4 pathway in the branches between the *S. kali* group and the *Haloxylon/Anabis* group (Fig. 2). Because *Haloxylon/Anabis* presumably acquired C_4 photosynthesis from ancestors with a fully expressed C_3 pathway, as indicated by the *Sympegma* and *Oreosalsola* nodes, it is treated as an independent lineage, regardless of whether there may have been ancestral C_4 species at deeper nodes in the phylogeny.

Species level resolution has also facilitated the identification of the centres of origin for many of the listed C_4 lineages. This can be accomplished by identifying closely related C_3 and C_4 species within a phylogeny, and any related C_3 - C_4 intermediate species. By mapping the geographic distribution of the sister groups and intermediate forms, the region where the C_4 lineage arose can in many cases be identified with a good degree of confidence, thereby facilitating evaluation of the environmental conditions that promoted the emergence of C_4 photosynthesis.

To visualize broadly the phylogenetic distribution of C_4 taxa, as many C_4 groups as possible were mapped onto a recently published phylogeny of 9412 angiosperms (Smith

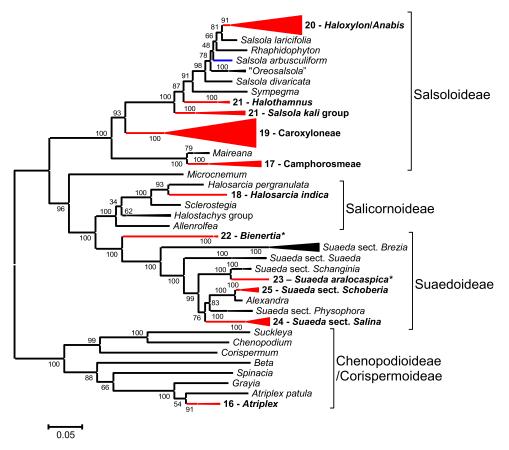


Fig. 2. The distribution of C_4 photosynthesis in the Chenopodiaceae sensu stricto. The phylogeny was obtained through Bayesian inferences on the nuclear internal transcribed spacer (ITS) and plastid *psbB–psbH* markers generated in previous studies (Kapralov *et al.*, 2006; Akhani *et al.*, 2007; Wen *et al.*, 2010; see Christin *et al.*, 2011*a* for details) and is rooted on the Chenopodioideae/ Corispermoideae. Bayesian support values are indicated near branches. Clades that contain a single photosynthetic type are compressed and coloured in red for C_4 , blue for C_3 – C_4 , and black for C_3 . Names of C_4 clades are in bold and numbers beside C_4 groups correspond to lineage number (Table 1). Asterisks indicate single-celled C_4 taxa. Subfamilies are circumscribed on the right.

et al., 2009; Fig. 3). Because the phylogeny was built for other purposes and taxon sampling was therefore agnostic with respect to the photosynthetic pathway, it was felt that this presents a valid means to evaluate broad phylogenetic patterns of C_4 evolution across angiosperms. It was possible to place 47 C_4 lineages on the tree. In several cases (e.g. *Mollugo, Flaveria*, and *Cleome*), the phylogeny included only closely related C_3 congeners, which were used as 'placeholders'. Futhermore, to place *Blepharis* (Acanthaceae), the close relative *Acanthus* (McDade *et al.*, 2005) was highlighted, and *Aptosimum* and *Peliostomum* (Scrophulariaceae) were used to represent *Anticharis* (Oxelman *et al.*, 2005).

Results

The lineages of C_4 photosynthesis

Table 1 lists 62 distinct groups of C_4 taxa in terrestrial and aquatic vascular plants. Some diatoms can also operate C_4

metabolic cycles but are not discussed here (Reinfelder *et al.*, 2004). These 62 groups are treated as distinct evolutionary lineages, on the assumption that each lineage arose from ancestors that were fully functional C_3 species. It is recognized that the evolutionary independence of some C_4 lines could be debated if their common ancestors share well-developed traits associated with the C_4 syndrome, notably Kranz anatomy. This could be the case in *Flaveria, Mollugo*, and Camphorosmeae, where multiple C_4 species may derive from well-developed C_3 – C_4 intermediates expressing Kranz-like anatomy (McKown *et al.*, 2005; Christin *et al.*, 2011b; Kadereit and Freitag, 2011). None of these potential lineages are included in Table 1 because of phylogenetic ambiguity and uncertainty regarding evolutionary independence.

Thirty-six of the 62 lineages occur in the eudicots, six in the sedges, and 18 in the grasses (Table 1). The aquatic monocot family Hydrocharitaceae has two C_4 lineages, in the genera *Hydrilla* and *Egeria*. C_4 photosynthesis in these two groups is distinct from that of the other 60 lineages

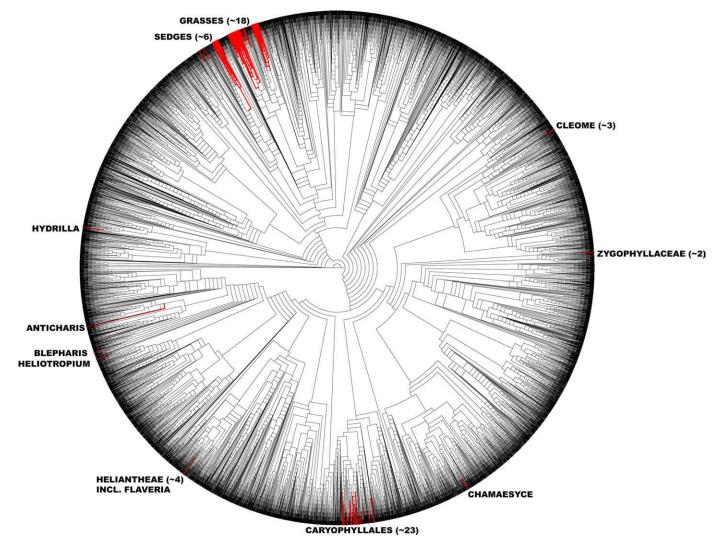


Fig. 3. The phylogenetic distribution of C_4 lineages in the angiosperms, depicted on a phylogeny of 9412 angiosperms species that was pruned from the viridiplantae phylogeny of Smith et al. (2009). C_4 lineages are indicated by red branches. Numbers beside named lineages refer to the estimate of the number of independent origins of C_4 in that clade. Forty-seven of the 62 C_4 lineages could be placed on the phylogeny; in several cases, C_3 taxa were highlighted to represent the position of closely related C_4 species (see text).

Table 1. The postulated lineages of C_4 taxa in higher plants

Centre of origin codes are AA, northeastern Africa and Arabia; Aus, Australia; CeA, central Asia; SA, southern Africa; SAM, South America; NAM, North America. Kranz types and biochemical types are from Muhaidat *et al.* (2007), Edwards and Vosnesenskya (2011), and the references noted in the last column. Grass lineage names follow those of Roalson (2011) and Christin *et al.* (2009). Centres of origin are estimated from the references indicated, and unpublished results from RFS and EJE.

No.	Order	Family	Lineage	Kranz type	Biochemical type	Centre of origin	Reference
Eudicots							
1	Unplaced	Boraginaceae	Heliotropium section Orthostachys (= Euploca)	Atriplicoid	NADP-ME	NAM	Frohlich (1978)
2	Asterales	Asteraceae/ Heliantheae	Chrysanthellum/Isostigma	Simplicifolioid, Isostigmoid, Glossocardioid	NADP-ME, NAD-ME	Unknown	Kellogg (1999)
3	Asterales	Asteraceae/ Heliantheae	Flaveria clade A	Atriplicoid	NADP-ME	NAM	Powell (1978); McKown <i>et al.</i> (2005)
4	Asterales	Asteraceae/ Heliantheae	<i>Flaveria brownii^a (Flaveria</i> clade B)	Atriplicoid	NADP-ME	NAM	Powell (1978); McKown <i>et al.</i> (2005)
5	Asterales	Asteraceae/ Heliantheae	Pectis	Atriplicoid	NADP-ME	NAM	Kellogg (1999)
6	Brassicales	Cleomeaceae	Cleome angustifolia	Angustifolioid	NAD-ME	AA	Feodorova <i>et al.</i> (2010)
7	Brassicales	Cleomeaceae	Cleome gynandra	Atriplicoid	NAD-ME	SA	Feodorova <i>et al.</i> (2010)
8	Brassicales	Cleomeaceae	Cleome oxalidea	Unknown	Unknown	AUS	Feodorova <i>et al.</i> (2010)
9	Caryophyllales		Sesuvium/ Trianthema/	Atriplicoid	NADP-ME	AA, SA	Hassan <i>et al.</i> (2005)
5	Caryophynaics	Sesuvioideae	Zaleya	Anpicola		AA, OA	11assairtet al. (2003)
10	Concorbullaloo	Amaranthaceae	Aerva	Atriplicoid	NADP-ME	AA	Space at al. (2007)
11					NADP-ME	SAM	Sage <i>et al.</i> (2007)
12	, , ,	Amaranthaceae	Alternanthera	Atriplicoid			Sage <i>et al.</i> (2007)
		Amaranthaceae	Amaranthus	Atriplicoid	NAD-ME	New World	Sage <i>et al.</i> (2007)
13		Amaranthaceae	Gomphreneae	Atriplicoid	NADP-ME	SAM	Sage <i>et al.</i> (2007)
14	, , ,	Amaranthaceae	Tidestromia	Atriplicoid	NADP-ME	NAM	Sage <i>et al.</i> (2007)
15	Caryophyllales	Caryophyllaceae	Polycarpaea	Atriplicoid	NADP-ME	Old World	Kellogg (1999)
16	Caryophyllales	Chenopodiaceae	Atriplex	Atriplicoid	NAD-ME	CeA	Kadereit <i>et al.</i> (2010)
17	Caryophyllales	Chenopodiaceae	Camphorosmeae	Kochioid	NADP-ME	CeA	Kadereit <i>et al.</i> (2003); Kadereit and Freitag (2011)
18	Caryophyllales	Chenopodiaceae	Halosarcia indica	Tecticornoid	NAD-ME	CeA	Kadereit <i>et al.</i> (2003); Kapralov <i>et al.</i> (2006)
19	Caryophyllales	Chenopodiaceae/ Salsoloideae	Caroxyloneae	Salsoloid	NAD-ME	CeA	Kadereit <i>et al.</i> (2003); Kapralov <i>et al.</i> (2006)
20	Caryophyllales	Chenopodiaceae/ Salsoloideae	Haloxylon/Anabasis (includes Noaea)	Salsaloid	NADP-ME	CeA	Kapralov <i>et al.</i> (2006); Wen <i>et al.</i> (2010)
21	Caryophyllales	Chenopodiaceae/ Salsoloideae	Salsola kali group (includes Halothamnus)	Salsaloid	NADP-ME	CeA	Kadereit <i>et al.</i> (2003)
22	Caryophyllales	Chenopodiaceae/ Suaedoideae	,	Single-celled (Bienertioid)	NAD-ME	CeA	Kapralov <i>et al.</i> (2006)
23	Caryophyllales	Chenopodiaceae/ Suaedoideae	Suaeda aralocaspica (=Borszczowia)	Single-celled (Borszczowioid)	NAD-ME	CeA	Kapralov <i>et al.</i> (2006)
24	Caryophyllales	Chenopodiaceae/ Suaedoideae	Suaeda sect. Salsina	Salsinoid	NAD-ME	CeA	Kapralov <i>et al.</i> (2006)
25	Caryophyllales	Chenopodiaceae/ Suaedoideae	Suaeda sect. Schoberia	Schoberioid	NAD-ME	CeA	Kapralov <i>et al.</i> (2006)
26	Caryophyllales	Gisekiaceae	Gisekia	Unknown	Unknown	Old World	APG III (2009)
27	, , ,	Molluginaceae	Mollugo cerviana/ M. fragilis	Atriplicoid	NADP-ME	SA	Christin <i>et al.</i> (2011 <i>b</i>)
28	Caryophyllales	Nyctaginaceae	Allionia	Atriplicoid	NADP-ME	NAM	Douglas and Manos (2007)
29	Caryophyllales	Nyctaginaceae	Boerhavia	Atriplicoid	NADP-ME	NAM	Douglas and Manos (2007)
30	, , ,	Polygonaceae	Calligonum	Salsaloid	NAD-ME	CeA	Kellogg (1999)
31		Portulacaceae	Portulaca	Pilosioid,	NADP-ME,	SAM	Ocampo and Columbus (2010);
01			, o, tuluou	Portulacenoid	NAD-ME	0/ 101	Voznesenskaya <i>et al.</i> (2010)
32	Lamiales	Acanthaceae	Blepharis	Atriplicoid	NADP-ME,	SA	Vollesen (2000);
00	Levelal	O anna ha chuidh a'			NAD-ME	0.4	Akhani <i>et al.</i> (2008)
33	Lamiales	Scrophulariaceae	Anticharis	Atriplicoid	NAD-ME	SA	Kellogg (1999)

Table 1. Continued

No.	Order	Family	Lineage	Kranz type	Biochemical type	Centre of origin	Reference
34	Malpighiales	Euphorbiaceae	Euphorbia subgenus Chamaesyce	Atriplicoid	NADP-ME	NAM	Steinmann and Porter (2002); Sage <i>et al.</i> (2011)
35	Zygophyllales	Zygophyllaceae	Tribulus/Kallstroemia	Atriplicoid	NADP-ME	AA	Sheahan and Chase (1996)
36	Zygophyllales	Zygophyllaceae	Zygophyllum simplex	Kochiod	NAD-ME	AA	Sheahan and Chase (1996)
Monoc	ots						
37	Alismatales	Hydrocharitaceae	Hydrilla	Single cell, non-Kranz	NADP-ME	Unknown	Bowes (2011); Roalson (2011)
38	Alismatales	Hydrocharitaceae	Egeria	Single cell, non-Kranz	NADP-ME	Unknown	Bowes (2011); Roalson (2011)
39	Poales	Cyperaceae	Bulbostylis	Fimbrystyloid	NADP-ME	Unknown	Besnard <i>et al.</i> (2009)
40	Poales	Cyperaceae	Cypereae	Chlorocyperoid	NADP-ME	Unknown	Besnard <i>et al.</i> (2009)
41	Poales	Cyperaceae	Eleocharis section	Eleocharoid	NAD-ME	Unknown	Roalson <i>et al.</i> (2010);
		-)	Tenuissimae ss				Roalson (2011)
42	Poales	Cyperaceae	Eleocharis vivipara	Fimbrystyloid	NAD-ME	NAM	Besnard <i>et al.</i> (2009);
	1 Galloo	ojpolaoodo	Lioconano impara	i inibi jetijiela			Roalson <i>et al.</i> (2010)
43	Poales	Cyperaceae	Fimbrystylis	Fimbrystyloid	NADP-ME	Unknown	Besnard <i>et al.</i> (2009)
44	Poales	Cyperaceae	Rynchospora	Rynchosporoid	NADP-ME	Unknown	Besnard <i>et al.</i> (2009)
45	Poales	Poaceae/	Alloteropsis	Neurachneoid	PCK	Africa	Christin <i>et al.</i> (2009)
		PACMAD clade	·				
46	Poales	Poaceae/	Altoparidisum/	Classical	NADP-ME	SAM	Christin <i>et al.</i> (2009)
		PACMAD clade	Arthropogon/ Mesosetum/Tatianyx				
47	Poales	Poaceae/ PACMAD clade	Andropogoneae	Classical	NADP-ME	Unknown	Christin <i>et al.</i> (2009)
48	Poales	Poaceae/ PACMAD clade	Anthaenantia lanata (=Leptocoryphium)	Classical	NADP-ME	SAM	Christin et al. (2009)
49	Poales	Poaceae/ PACMAD clade	Aristida	Aristidoid	NADP-ME	Unknown	Christin <i>et al.</i> (2009)
50	Poales	Poaceae/	Axonopus/Ophiochloa	Classical	NADP-ME	SAM	Christin et al. (2009)
51	Poales	PACMAD clade Poaceae/	Centropodia	Classical	NADP-ME	Africa	Christin <i>et al.</i> (2009)
52	Poales	PACMAD clade Poaceae/	Core Chloridoideae	Classical	NAD-ME, PCK	Old World	Christin <i>et al.</i> (2009)
53	Poales	PACMAD clade Poaceae/	Danthoniopsis/	Arundinelloid	NADP-ME	Unknown	Christin <i>et al.</i> (2009)
54	Poales	PACMAD clade Poaceae/	Loudetia Digitaria	Classical	NADP-ME	Unknown	Christin <i>et al.</i> (2009)
		PACMAD clade					
55	Poales	Poaceae/ PACMAD clade	Echinochloa	Classical	NADP-ME	Unknown	Christin <i>et al.</i> (2009)
56	Poales	Poaceae/ PACMAD clade	Eriachne/ Pheidochloa	Eriachnoid	NADP-ME	Unknown	Christin <i>et al.</i> (2009); Roalson (2011)
57	Poales	Poaceae/ PACMAD clade	Neurachne	Neurachneoid	NADP-ME, PCK	AUS	Christin <i>et al.</i> (2009)
58	Poales	Poaceae/	Panicum/Pennisetum/	Classical	NADP-ME, NAD-	Unknown	Christin <i>et al.</i> (2009)
59	Poales	PACMAD clade Poaceae/	Urochloa/Setaria Paspalum	Classical	ME, PCK NADP-ME	SAM	Christin <i>et al.</i> (2009)
60	Poales	PACMAD clade Poaceae/	Sorengia (ex Panicum	Neurachneoid	NADP-ME	SAM	Christin <i>et al.</i> (2009)
01	Declar	PACMAD clade	prionitis)	Olean's st		0414	Obviation at -1 (0000)
61	Poales	Poaceae/ PACMAD clade	Streptostachys	Classical	NADP-ME	SAM	Christin <i>et al.</i> (2009)
62	Poales	Poaceae/ PACMAD clade	Stipagrostis	Stipagrostoid	NADP-ME	Old World	Christin <i>et al.</i> (2009)

^a Flaveria brownii is physiologically a C₄-like intermediate, in that it expresses Rubisco in the mesophyll (Cheng *et al.*, 1988). It is treated here as an independent C₄ clade as it has a fully functional C₄ cycle, and photosynthetic gas exchange properties and resource use efficiencies that are equivalent to those of many C₄ species.

where plants have aerial photosynthetic structures. In Hydrilla and Egeria, the C₄ pathway operates in submersed leaves and concentrates CO_2 from the cytosol into an adjacent chloroplast of a single cell (Bowes, 2011). In all other known C_4 plants, the C_4 pathway concentrates CO_2 from a mesophyll-like compartment into a distinct inner tissue region (58 lineages) or concentrates CO_2 from an outer to an inner region of the same cell (in two Chenopodiaceae lineages, Bienertia and Suaeda aralocaspica; Edwards and Voznesenskaya, 2011). Clustering is evident in the distribution of the lineages in the angiosperm phylogeny (Fig. 3), with large numbers of lineages in the Poales (grass and sedge families) and Caryophyllales (which includes Aizoaceae, Amaranthaceae, Caryophyllaceae, Chenopodiaceae, Gisekiaceae, Molluginaceae, Nyctaginaceae, Polygonaceae, and Portulacaceae).

In the eudicots, there are $\sim 1600 \text{ C}_4$ species (Sage et al., 1999). The Amaranthaceae sensu lato (= Chenopodiaceae ss and Amaranthaceae ss; APG III, 2009) is the most prolific family, with 15 distinct lineages of C₄ taxa and \sim 750 C₄ species (Figs 1, 2; Sage et al., 1999). Of these 15 lineages, the largest is Atriplex, with 200-300 C₄ species (Kadereit et al., 2010). Two of the C_4 clades in the Salsoloideae (Caroxyloneae and Haloxylon/Anabis) have 100-140 species each, while the S. kali lineage contains a minimum of 23 species (Sage et al., 1999; Akhani et al., 2007). In the Amaranthaceae ss, the Gomphreneae have $\sim 125 \text{ C}_4$ species and Amaranthus \sim 70 C₄ species (Sage *et al.*, 2007). The most species-rich C₄ eudicot lineage other than Atriplex is Euphorbia section Chamaesyce with about 250 species. Other large C₄ lineages include Heliotropium section Orthostachys (=Euploca) with ~ 120 C₄ species (Frohlich, 1978), and the *Calligonum*, Pectis, and Portulaca lineages with 80-100 C₄ species each (Sage *et al.*, 1999). Fourteen eudicot C_4 lineages contain <10 C₄ species: Aerva, Allionia, Bienertia, and Mollugo have two C₄ species each, while Suaeda aralocaspica (=Borszczowia aralocaspica), the three C_4 lineages in the Cleomeaceae, Flaveria clade B, Halosarcia, and Zygophyllum have one C_4 species each. Anticharis, Flaveria clade A, and Gisekia have 5-10 C₄ species each (Sage et al., 1999; McKown et al., 2005 for Flaveria).

In the sedges, there are ~1300 species (Bruhl and Wilson, 2007; Roalson, 2011). The largest C₄ sedge lineages are the Cypereae (eight genera with ~750 species), *Fimbrystylis* (300 species), and *Bulbostylis* (205 species). Fifteen C₄ species are known in the *Eleocharis* section *Tenuissimae ss*, while 21 C₄ species are known from *Rhynchospora*. In both *Eleocharis* and *Rhynchospora*, >90% of the species are C₃ plants (Bruhl and Wilson, 2007). The smallest C₄ sedge lineage is *Eleocharis vivipara* with a single C₄ species (Bruhl and Wilson, 2007; Roalson *et al.*, 2010; Roalson, 2011).

There are ~4600 C₄ grasses, all occurring in the PACMAD clade (Sage *et al.*, 1999). The largest C₄ lineage is the core Chloridoideae with 160–170 genera and 1500 species, followed by the Andropogoneae lineage with ~1100 species and then the *Panicum/Pennisetum/Urochloa/Setaria* clade with >500 species (Christen *et al.*, 2009; Roalson, 2011). Thirty-five to 350 species are in each of the lineages repre-

sented by Altoparadisium, Aristida, Axonopus, Danthoniopsis, Digitaria, Echinochloa, Eriachne, Paspalum, and Stipagrostis. C₄ grass lineages with a small (<10) number of species are Alloteropsis (5 species), Anthaenantia (2 species), Centropodia (4 species), Neurachne (2 species in two genera), Sorengia (>5 species), and Streptostachys (1 species). The estimates of C₄ grass numbers within numerous lineages will change, as many grass genera and species cannot be accurately placed in a lineage yet, due to limited phylogenetic information. This is especially true for Panicum, which contains several hundred C₄ taxa, but is highly polyphyletic (Aliscioni *et al.*, 2003). Summing the C₄ eudicot and monocot estimates, the total number of C₄ species on planet Earth is ~7500, which is the same as estimated by Sage *et al.* (1999).

About 43 of the 62 lineages contain species using the NADP-malic enzyme (NADP-ME) as their primary decarboxylase (Table 1; Gutierrez et al., 1974; Edwards and Walker, 1983; Hattersley and Watson, 1992; Sage et al., 1999; Muhaidat et al., 2007; R Khoshravesh, H Akhani, and RF Sage, unpublished data). NAD-malic enzyme (ME) is used by species from 20 lineages. Most of the lineages with NAD-ME species are eudicots, as only two grass and two sedge lineages include species that are classified into this biochemical subtype. Only grasses appear to utilize PEP carboxykinase (PCK) as the primary decarboxylating enzyme; however, this enzyme may also be active as a secondary decarboxylase in the C_4 cycle of eudicots in the Sesuvioideae (Muhaidat et al., 2007). In the grasses, four C₄ lineages include species that use PCK as the primary decarboxylating enzyme. Of these, two have species that are primarily PCK or NAD-ME, one has species that are PCK or NADP-ME, and one lineage (the Panicum/Pennisetum/Urochloa/Setaria clade) has species that are NADP-ME, NAD-ME, or PCK. In the eudicots, three lineages (Blepharis, Chrysanthellum/Isostigma, and Portulaca) contain species reported to utilize primarily more than one of the C_4 decarboxylating enzymes (Table 1).

Anatomical types are far more varied than biochemical subtypes. Some 22 Kranz anatomy types have been described, and numerous variations within a number of these subtypes are noted (Brown, 1977; Dengler and Nelson, 1999; Kadereit et al., 2003; Edwards and Voznesenskaya, 2011). In the eudicots, the most common anatomical type is the Atriplicoid, which occurs in at least 20 of the 36 eudicot lineages (Table 1). The next most common Kranz type is the Salsaloid, occurring in three lineages in the Chenopodiaceae and one in Calligonum (Polygonaceae). In sedges and grasses, the variation in Kranz type is greater, with most lineages having evolved a unique version of C₄ anatomy. The classical type of Kranz anatomy is described for seven grass lineages; however, there can be important variations in the anatomies that are associated with biochemical subtypes (Dengler and Nelson, 1999). Among these variations, classical NADP-ME species have bundle sheath cells (BSCs) with centrifugally placed chloroplasts that are depleted in photosystem II (PSII) and grana stacks; in contrast, classical NAD-ME species have

Table 2. The postulated lineages of C_3 - C_4 intermediate photosynthesis in higher plants

 C_3 - C_4 as defined here refers to photosynthetic modifications that include refixation of photorespiratory CO_2 in bundle sheath cells, and the engagement of a C_4 metabolic cycle. Compiled from Sage *et al.* (1999), Bauwe (2011), and the references listed below. The list does not include species which show C_3 and C_4 expression in different regions of the same plant (termed C_3/C_4 in Sage *et al.*, 1999) or C_3 and C_4 plants in different subspecies (termed $C_3 \times C_4$ in Sage *et al.*, 1999).

No.	Family	Lineage	Representative species	Species number	Ancestry of a C ₄ lineage?	References
Eudico	ts					
1	Amaranthaceae	Alternanthera	Alternanthera ficoides, A. tenella	2	Yes	Rajendrudu <i>et al.</i> (1986)
2	Asteraceae I	Flaveria sonorensis	Flaveria sonorensis	1	No	McKown <i>et al.</i> (2005)
3	Asteraceae II	Flaveria clade A	Flaveria ramossissima	1	Yes	Monson <i>et al.</i> (1984); McKown <i>et al.</i> (2005)
4	Asteraceae III	Flaveria clade B	<i>Flaveria angustifolia</i> and 6 other species	7	Yes	Monson <i>et al.</i> (1984); McKown <i>et al.</i> (2005)
5	Asteraceae IV	Parthenium	Parthenium hysterophorus	1	No	Hedge and Patil (1981); Kellogg (1999)
6	Boraginaceae	Heliotropium section Orthostachys I	Heliotropium convolvulaceum, H. racemosum	2	Yes	Vogan <i>et al.</i> (2007); Muhaidat (2007)
7	Boraginaceae	Heliotropium section Orthostachys II	Heliotopium greggii, H. lagoense	2	Yes	Vogan <i>et al.</i> (2007); Frohlich, 1978
8	Brassicaceae	Moricandia	Moricandia arvense	5	No	Apel <i>et al.</i> (1978); Holaday <i>et al.</i> (1981); Kellogg (1999)
9	Brassicaceae	Diplotaxis	Diplotaxis tenuifolia	1	No	Apel <i>et al.</i> (1980); Kellogg (1999)
10	Chenopodiaceae	Camphorosmae	Bassia sedoides (=Sedobassia)	1	Yes	Kadereit and Freitag (2011)
11	Chenopodiaceae	Salsoleae ss	Salsola arbusculiformis	1	No	Voznesenskaya <i>et al.</i> (2001); Fig. 3
12	Cleomeaceae	Cleome	Cleome paradoxa	1	Yes	Feodorova et al. (2010)
13	Euphorbiaceae	Chamaesyce	Chamaesyce acuta, C. johnstonii	2	Yes	Sage <i>et al.</i> (2011)
14	Molluginaceae I	Mollugo I	Mollugo nudicaulis	2	Yes	Christin et al. (2011b)
15	Molluginaceae II	Mollugo II	Mollugo verticillata	1	No	Christin et al. (2011b)
16	Nyctaginaceae	Bougainvillia	Bougainvillia cv. Mary Palmer	1	No	Sabale and Bhosale (1984)
17	Portulaceae	Portulaca	Portulaca cryptopetala	1	Uncertain	Ocampo and Columbus (2010); Voznesenskaya <i>et al.</i> (2010)
Monoc						
18	Cyperaceae subgenus Scirpidium	Eleocharis	Eleocharis acicularis, E. pusilla, E. reverchonii	3	No	Bruhl and Perry (1995); Roalson <i>et al.</i> (2010); Keeley 1999); Sage <i>et al.</i> (1999)
19	Hydrocharitaceae	Vallisneria	Vallisneria spirilis	1	Unknown	Bowes (2011)
20	Poaceae 12	Neurachne	Neurachne minor	1	Yes	Hattersley <i>et al.</i> (1982, 1986); Christin <i>et al.</i> (2009)
21	Poaceae 13	Paniceae	Steinchisma	6	No	Duvall <i>et al.</i> (2003); Christin <i>et al.</i> (2009)

centripedal chloroplasts and an abundance of PSII and grana stacks (Dengler and Nelson, 1999; Edwards and Voznesenskaya, 2011).

Lineages of C_3 – C_4 intermediacy

Twenty-one distinct clades have been identified that contain species with photosynthetic characteristics that are intermediate between C_3 and C_4 species (Table 2). Ten of the C_3-C_4 groups branch immediately sister to C_4 lineages, which is consistent with models proposing that C_3-C_4 intermediacy originated before C_4 photosynthesis and served as an ancestral stage (Monson *et al.*, 1984; Monson, 1999; Sage, 2004; Bauwe, 2011). Most C_3-C_4 intermediates cluster in genera known to contain C₄ plants (Table 2), as is best demonstrated by *Flaveria* which has ~9 C₃–C₄ species (McKown *et al.*, 2005). Some of these intermediates, however, do not appear at sister nodes. Where C₃ species branch between the C₃–C₄ intermediate and a C₄ node, as occurs with the C₃–C₄ intermediate *Mollugo verticillata*, it appears that the C₃–C₄ line has independently arisen from different C₃ ancestors than the C₄ line (Christin *et al.*, 2011*b*). Where a C₃–C₄ species branches between two C₄ nodes, as occurs with the C₃–C₄ intermediate *Portulaca cryptopetala* (Ocampo and Columbus, 2010), a reversion from the C₄ condition is possible. Notably, about a quarter of the identified C₃–C₄ species occur in taxa that are not closely related to any C_4 lineage. There are no C_4 species in the Brassicaceae, where two C_3 - C_4 clades occur (*Moricandia* and *Diplotaxis*; Sage *et al.*, 1999), and three C_3 - C_4 *Eleocharis* species occur in the *Eleocharis* subgenus *Scirpidium*, which lacks any C_4 species (Keeley, 1999; Roalson *et al.*, 2010). These patterns highlight the need to consider the C_3 - C_4 condition as a distinct photosynthetic adaptation in its own right, and not just a transitional stage leading to the C_4 condition.

Geographic centres of origins

Geographic centres of origins for C₄ photosynthesis can be estimated for most eudicot lineages, and some of the sedge and grass lineages (Table 1). In the eudicots, lineages occur in one of six centres of origin, corresponding to regions of the Earth that are now warm, semi-arid, and arid (Fig. 4). Central Asia, North America, and a region corresponding to northeast Africa and southern Arabia produced the most C₄ eudicot lineages, with 4–11 each. Two centres corresponding to semi-arid regions of South Africa and South America each produced 4–5 C₄ eudicot lineages, while the driest continent, Australia, produced only one C₄ lineage in the eudicots that can be confirmed at this time.

Identifying the geographic origins of the C₄ monocots is more problematic due to their wide geographical distribution and greater uncertainty regarding the phylogenetic placement of the C₄ lineages. Nevertheless, South America appears to be a major hotspot for C₄ grass origins, including many of the transitions in the x=10 Paniceae clade (Table 1; Fig. 4). Two C₄ grass origins in Africa are apparent, in *Centropodia* and *Alloteropsis*. Only one C₄ grass clade (*Neurachne*) is known to have originated in Australia. *Eleocharis vivipara* is the only sedge lineage where a centre of origin (in Florida, USA) can be postulated at this time.

Discussion

The present survey identified 62 distinct lineages of C₄ taxa, containing \sim 7500 species in 19 families of angiosperms. This compares with 45 lineages listed by Sage (2004) and 31 listed by Kellogg (1999). The increase in the number of lineages is largely due to improved phylogenetic coverage of clades that include C₄ plants, and a more complete accounting of C₃ and C₄ occurrence in the species within these clades. As an example, where only three clades were resolved in the Amaranthaceae ss in 2003 (Kadereit et al., 2003), five lineages were observed by Sage et al. (2007) following a thorough isotope analysis of the family and additional sampling for the phylogeny. Similarly, early molecular phylogenies suggested a minimum of four C₄ grass lineages (Kellogg, 1999), a number that has now increased to 18. The current list of C₄ groups is most probably incomplete, as relationships in some clades are still unresolved. Additional lineages are suspected in *Blepharis* (Aizoaceae), *Flaveria* and Isostigma (Asteraceae), Heliotropium section Orthostachys (Boraginaceae), Eleocharis viridans (Cyperaceae), Sesuvioideae (Aizoaceae), Camphorosmae (Chenopodiaceae), and Salsoloideae (Chenopodiaceae) (Hassan et al., 2005; McKown et al., 2005; Roalson et al., 2010; Kadereit and Freitag, 2011; RFS, unpublished results).

C_3 – C_4 intermediacy

C₃-C₄ intermediacy is a term originally used to describe plants with traits intermediate between C₃ and C₄ species, on the assumption that they might represent an evolutionary transition (Kennedy and Laetsch, 1974; Monson *et al.*, 1984). Currently, C₃-C₄ intermediacy mainly refers to plants with a photorespiratory CO₂-concentrating mechanism, where expression of the photorespiratory enzyme

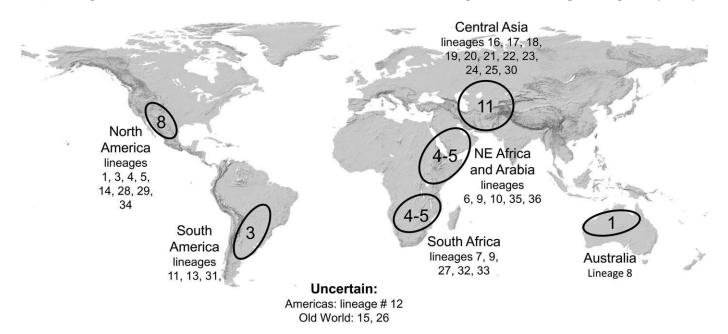


Fig. 4. Locations for the centres of origin for 35 of the 36 C₄ eudicot lineages listed in Table 1. Numbers shown correspond to lineages listed in Table 1. Unlisted lineages have an unknown centre of origin.

glycine decarboxylase (GDC) is localized to BSCs (Monson, 1999; Duvall et al., 2003; Bauwe, 2011; Sage et al., 2011). Localization of GDC to the bundle sheath forces all the glycine produced by photorespiration to move into the BSCs to complete the photorespiratory cycle. A product of the GDC reaction is CO_2 , which accumulates in the BSCs, enhancing the efficiency of BSC Rubisco. Following the mutation leading to GDC localization, C3-C4 species evolve many C₄-like traits such as close vein spacing and enlarged BSCs to optimize the efficiency of photorespiratory CO_2 concentration (Sage, 2004). While these developments may facilitate C₄ evolution (Bauwe, 2011), they also confer fitness in their own right, as reflected by numerous C3-C4 lineages that are distinct from C₄ clades, and the ecological success of numerous C₃-C₄ species in warm to hot environments (Monson, 1999; Christin et al., 2011b; Sage et al., 2011).

Twenty-one distinct lineages of C₃–C₄ intermediate plants have been identified. The first C₃-C₄ intermediate described was M. verticillata, a widespread weedy species (Kennedy and Laetsch, 1974), followed in the late 1970s to mid-1980s by the identification of intermediate species in *Alternanthera*, Bougainvillea, Diplotaxis, Flaveria, Moricandia, Neurachne, Panicum sensu lato (=Steinchisma), and Parthenium (Brown and Brown, 1975; Morgan and Brown, 1979; Apel et al., 1978, 1980; Apel and Maas, 1981; Hedge and Patil, 1981; Holaday et al., 1981; Hattersley et al., 1982, 1986; Ku et al., 1983; Monson et al., 1984; Sabale and Bhosale, 1984; Rajendrudu et al., 1986). After this initial phase of discovery 25-35 years ago, the identification of new intermediates trailed off until recently, when phylogenies and isotopic screens helped identify additional intermediates. For example, the Euphorbiaceae phylogeny of Steinmann and Porter (2002) identified two species of Chamaesyce that are basal in this large C_4 group. One of these, C. acuta, is a C₃-C₄ intermediate (Sage et al., 2011). Intermediates have also been found recently in Cleome and Portulaca (Voznesenskaya et al., 2007, 2010).

Most of the known C_3 - C_4 intermediates are in eudicots, while only two intermediate lineages are described in the grasses, and one each in the Hydrocharitaceae and sedges. This discrepancy may reflect greater species turnover in grasses and sedges, which led to a greater rate of extinction of C₃-C₄ taxa. Alternatively, the greater number of eudicot intermediates may reflect sampling bias. Most known C_3-C_4 intermediates are associated with C4 eudicots, because investigators often focused on eudicot genera having both C₃ and C4 species (Monson, 1999; Vogan et al., 2007; Voznesenskaya et al., 2007, 2010; Sage et al., 2011). With a wider sampling and improved phylogenetic resolution of poorly studied groups, the tally of C_3 - C_4 lineages should grow in the near future. Isotopic screens will pick up some intermediates with less negative δ^{13} C than typical C₃ plants (see, for example, Feodorova et al., 2010 for Cleome); however, most C3-C4 intermediates have δ^{13} C values that cannot be differentiated from those of C₃ species, so such screens will be of limited value. To have a less negative $\delta^{13}C$ value than C₃ species, there must be significant engagement of a C₄ cycle (von Caemmerer, 1992). In order to detect potential C_3 - C_4 intermediates lacking a C_4 cycle, anatomical screens are a useful first step, but detailed physiological studies with live material will still be needed for confirmation.

The biogeography of C_4 evolution

For the eudicots, and the handful of monocots where the centre of C_4 origin can be estimated with confidence, there appear to be six geographic regions where the C_4 pathway evolved. All of these correspond to areas that are now semiarid to arid, with summer precipitation from monsoon weather systems. By identifying the putative centres of origin for many of the C₄ lineages, we hope to facilitate follow-up studies that will evaluate the environmental selection factors responsible for the evolution of specific C_4 lineages. Such studies could examine the ecophysiology of the close C_3 and C_3 - C_4 relatives of the C_4 lines currently present in the centres of origins. Alternatively, paleontology studies could correlate past environmental events with the appearance of a C₄ lineage in a given area. To date, the leading environmental hypothesis for C4 evolution is that reduction in atmospheric CO_2 in the late Oligocene increased photorespiration in warm climates, thereby facilitating selection for CO₂-concentrating mechanisms such as C₄ photosynthesis (Sage, 2001, 2004; Christin et al., 2008; Vicentini et al., 2009; Edwards et al., 2010; Osborne, 2011). However, C_4 photosynthesis repeatedly arose in the 25–30 million years since the late-Oligocene CO₂ reduction (Christin et al., 2011a). In light of this, it is better to think of low CO₂ as a pre-condition, or environmental facilitator, which acted in concert with multiple selection factors. Other proposed drivers of C₄ evolution include increasing aridity, creation of high light habitats, increasing seasonality, fire, and large animal disturbance (Sage, 2001; Osborne and Freckleton, 2009; Edwards and Smith, 2010; Osborne, 2011). While a careful paleo-evaluation is beyond the scope of this study, it should be noted that global climates became cooler and drier in the past 40 million years, promoting the rise of arid-adapted vegetation types (Sage, 2001; Willis and McElwain, 2002). By the late Miocene (11-5 million years ago), warm, semi-arid, summer-wet climate zones were present in south-central North America, central Asia and Arabia, and northeastern Africa (Willis and McElwain, 2002). The mid-to-late Miocene corresponds to the midrange of estimates for the divergence of many eudicot lines (Christin et al., 2011a). The continent with the fewest and youngest C₄ lineages, Australia, developed the warm, dry conditions postulated to support C₄ evolution relatively late, only in the past 4–5 million years (Archer *et al.*, 1995).

If the current environments in the C_4 centres of origin are similar to those at the time when the C_4 lineages appeared, then the climate similarities between the centres of origin suggest the following environmental model for C_4 evolution. Each of the centres of origin experiences hot summers with peak air temperatures >40°C (Walter *et al.*, 1975). Summer humidity is often low, which in combination with the summer heat leads to low humidity and high transpiration potential. Solar radiation is intense, causing high surface temperatures and substantial heating of plants near the ground. Due to the monsoon activity, however, soil moisture is episodically present, allowing for substantial photosynthetic activity during the summer. Because of the high temperature, and reduced stomatal conductance caused by low humidity, photorespiration must have been high in C₃ species, particularly in the low CO₂ conditions of the recent past. This could have favoured the rise of CO₂ scavenging systems such as C₃–C₄ intermediate types of photosynthesis, leading in turn to the more elaborate C₄ carbon-concentrating mechanisms.

Convergence in C₄ evolution

C₄ photosynthesis involves the coordinated changes to genes that affect leaf and stem anatomy, ultrastructure, energetics, metabolite transport, and the location, content, and regulation of many metabolic enzymes, leaving no doubt that it is a complex trait (Hibberd and Covshoff, 2010). Despite this complexity, it has evolved repeatedly in diverse groups of flowering plants and thus can be considered genuinely convergent, in the sense that it has independently emerged from deep within many of the major angiosperm clades (e.g. Asterids, Rosids, Caryophyllales, and Monocots; though not Eumagnoliads). At the same time, however, most origins are clearly clustered in two particular areas of the angiosperm tree. The Poales (~18000 C_3 and C_4 species) harbour fully one-third of C_4 lineages, and Caryophyllales (~11000 C₃ and C₄ species) roughly another third. Within both of these groups, there is additional clustering of C₄ clades. C₄ taxa are absent from most Poales families and the large BEP clade of grasses; however, it has evolved 18 or more times within the PACMAD clade (mostly in the Panicoideae subfamily). Similarly, the Amaranthaceae/Chenopodiaceae alliance encompasses most of the C₄ lineages in Caryophyllales, with 15 postulated origins. This extreme clustering of C₄ lineages, in conjunction with the lack of C₄ taxa across large regions of the angiosperm phylogeny, indicates that there are a limited number of C_3 plant lineages that possess an appropriate suite of characteristics that can facilitate the evolution of C_4 photosynthesis (Sage, 2001). These characteristics could be inherent within the anatomical structure and physiology of the species within a lineage, or may be related to a specific ecological setting. Anatomical characters in C₃ ancestors could include close vein spacing, enlarged BSCs, or low mesophyll to bundle sheath ratios (Sage, 2004; McKown et al., 2005; Sage et al., 2011). These anatomical traits could facilitate C₄ evolution by enabling the establishment of a two-tissue mechanism to refix photorespiratory CO_2 , which is considered a major step in C_4 evolution (Monson, 1999). Physiological facilitators include increased organelle number in BSCs of C3 ancestors, allowing for more photosynthetic activity (Brown and Hattersley, 1989). Cryptic enhancers promoting the evolvability of C₄ photosynthesis may be found in the genomes of shared ancestors of clustered C₄ groups. For example, a

large reservoir of duplicated genes has been suggested as a genetic pre-condition for C_4 evolution (Monson, 2003; Bauwe, 2011). In addition, regulatory elements conferring tissue specificity may be common in C_3 groups from which the C_4 pathway arose. Ecologically, specialization for hot, dry, or saline landscapes could select for carbon conservation mechanisms such as refixation of photorespired CO_2 . Thus, groups such as the C_3 Chenopodiaceae may be prone to evolve C_4 photosynthesis because they tend to occur in extreme habitats where photorespiration would be high and there would be strong and consistent selection pressure favouring carbon-concentrating mechanisms.

With 62 or more distinct origins, the C_4 pathway must be considered one of the most convergent of complex evolutionary phenomena in the living world. On the one hand, such frequent convergence suggests C₄ evolution is relatively easy, a point that has encouraged efforts to engineer the C₄ pathway into C₃ crops (Hibberd *et al.*, 2008). Alternatively, this statement might be overly simplistic, as it implies that all C_4 origins had a similar starting point within a C₃ physiological setting, and evolution converged on a uniform C_4 pathway. As shown by the variation in decarboxylation types, leaf anatomy, and cellular ultrastructure, CO_2 concentration by C_4 photosynthesis can be accomplished in a variety of different ways. Uniformity between the different C_4 types is largely observed in the role of PEP carboxylase and the functional significance of the C₄ pathway (Kellogg, 1999). In this light, convergence on a common function has occurred 62 times, but less so in terms of the specific mechanisms by which CO₂ concentration is achieved.

In addition, there are differing degrees of convergence in terms of the magnitude of modifications to the ancestral C₃ state within the 62 C₄ lineages. Complete transitions from the full C_3 condition to the full C_4 condition unequivocally occurred independently in several clades. Examples include the C₄ clades in Acanthaceae (Blepharis), Boraginaceae, Euphorbiaceae, Scrophulariaceae, Zygophyllaceae, and Asteraceae. At the other extreme are situations where multiple C_4 lineages arose from common C_3 - C_4 ancestors, such as two C_4 clades in *Mollugo* (Christin *et al.*, 2011b). In these instances, the evolutionary transition from C₃-C₄ to C₄ would be relatively small, involving fewer changes than the complete C₃ to C₄ transition. Such cases might better be thought of as a parallel realization of the C₄ condition. The more ambiguous situation involves the independent evolution of C₄ lineages from C₃ ancestors expressing traits which might facilitate C4 evolution, such as high vein density and gene duplication. An example of this occurs in Flaveria, where C₄ photosynthesis in clades A and B appears to have independently arisen from C₃ ancestors with high vein density (McKown and Dengler 2007). In such cases, it is difficult to pinpoint the true 'origin' of the pathway, as multiple lineages have independently built upon a shared ancestral set of key facilitating traits.

Regardless of the categorizations, it is clear that the many lineages of C_4 plants demonstrate the power of evolution repeatedly to resolve the critical environmental challenges

imposed by declining levels of atmospheric CO_2 and increasing aridity that occurred in recent geological time. By comparing the many C_4 groups, it will be possible to better understand how evolution was able to co-opt varying features present in C_3 ancestors to arrive at the C_4 solution to the photorespiratory challenge. In doing so, researchers should be able to identify many of the genetic elements responsible for the recurrent emergence of the C_4 pathway in higher plants.

Acknowledgements

This work was supported by a Discovery grant from the National Science and Engineering Research Council of Canada to RFS, and funds to RFS from the International Rice Research Institute programme for the Engineering of C_4 Rice, which is funded by the Bill and Melinda Gates foundation. Additional support was provided by the Swiss National Science Foundation grant PBLAP3-129423 to PAC, and the National Science Foundation grants DEB-1026611 and IOS 0843231 to EJE.

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