



RESEARCH PAPER

Key changes in gene expression identified for different stages of C₄ evolution in *Alloteropsis semialata*

Luke T. Dunning^{1,*}, Jose J. Moreno-Villena^{1,*†}, Marjorie R. Lundgren^{1,‡}, Jacqueline Dionora², Paolo Salazar², Claire Adams³, Florence Nyirenda⁴, Jill K. Olofsson¹, Anthony Mapaura⁵, Isla M. Grundy⁶, Canisius J. Kayombo⁷, Lucy A. Dunning⁸, Fabrice Kentatchime⁹, Menaka Ariyaratne¹⁰, Deepthi Yakandawala¹⁰, Guillaume Besnard¹¹, W. Paul Quick^{1,2}, Andrea Bräutigam^{12, ID}, Colin P. Osborne¹ and Pascal-Antoine Christin^{1,§, ID}

¹ Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield S10 2TN, UK

² International Rice Research Institute, DAPO, Metro Manila, Philippines

³ Botany Department, Rhodes University, 6140 Grahamstown, South Africa

⁴ Department of Biological Sciences, University of Zambia, Lusaka, Zambia

⁵ National Herbarium and Botanic Garden, Harare, Zimbabwe

⁶ Institute of Environmental Studies, University of Zimbabwe, Harare, Zimbabwe

⁷ Forestry Training Institute, Olmotonyi, Tanzania

⁸ Department of Social Sciences, University of Sheffield, 219 Portobello, Sheffield S1 4DP, UK

⁹ CABAlliance, PO Box 3055 Messa, Yaoundé, Cameroon

¹⁰ Department of Botany, Faculty of Science, University of Peradeniya, Galaha Road, Peradeiya 20400, Sri Lanka

¹¹ Laboratoire Évolution et Diversité Biologique (EDB UMR5174), Université de Toulouse, CNRS, IRD, UPS, Toulouse, France

¹² Bielefeld University, Universitätsstrasse 35, D-33501 Bielefeld, Germany

†Present address: Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA.

‡Present address: Lancaster Environment Centre, Lancaster University, Lancaster LA1 4YQ, UK.

* These authors contributed equally to this work.

§ Correspondence: p.christin@sheffield.ac.uk

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Abstract

C₄ photosynthesis is a complex trait that boosts productivity in tropical conditions. Compared with C₃ species, the C₄ state seems to require numerous novelties, but species comparisons can be confounded by long divergence times. Here, we exploit the photosynthetic diversity that exists within a single species, the grass *Alloteropsis semialata*, to detect changes in gene expression associated with different photosynthetic phenotypes. Phylogenetically informed comparative transcriptomics show that intermediates with a weak C₄ cycle are separated from the C₃ phenotype by increases in the expression of 58 genes (0.22% of genes expressed in the leaves), including those encoding just three core C₄ enzymes: aspartate aminotransferase, phosphoenolpyruvate carboxykinase, and phosphoenolpyruvate carboxylase. The subsequent transition to full C₄ physiology was accompanied by increases in another 15 genes (0.06%), including only the core C₄ enzyme pyruvate orthophosphate dikinase. These changes probably created a rudimentary C₄ physiology, and isolated populations subsequently improved this emerging C₄ physiology, resulting in a patchwork of expression for some C₄ accessory genes. Our work shows how C₄ assembly in *A. semialata* happened in incremental steps, each requiring few alterations over the previous step. These create short bridges across adaptive landscapes that probably facilitated the recurrent origins of C₄ photosynthesis through a gradual process of evolution.

Keywords: Adaptation, C₄ photosynthesis, complex trait, intermediates, phylogenetics, transcriptomics

Introduction

The origins of traits composed of multiple anatomical and/or biochemical components have always intrigued evolutionary biologists (Darwin, 1859; Meléndez-Hevia *et al.*, 1996; Lenski *et al.*, 2003). If such traits gain their function only through the co-ordinated action of multiple components, their evolution via natural selection must cross a valley in the adaptive landscape. Despite this obstacle, complex traits have evolved repeatedly in diverse groups of organisms. This apparent paradox is solved for most traits by the existence of intermediate stages, which act as evolutionary enablers, creating bridges over the valleys of the adaptive landscape (Jacob, 1977; Dawkins, 1986; Weinreich *et al.*, 2006; Blount *et al.*, 2012; Vopalensky *et al.*, 2012; Werner *et al.*, 2014). The accessibility of new traits probably depends on the length and complexity of such bridges, which are generally unknown. Quantifying the evolutionary gap between phenotypic states is therefore crucial to contextualize the likelihood of a novel trait evolving.

An excellent system to study the evolutionary trajectories of an adaptive trait is C₄ photosynthesis. This metabolic pathway increases CO₂ concentration at the active site of assimilation via the Calvin–Benson cycle (Hatch, 1987; Sage, 2004; Christin and Osborne, 2014). This avoids the energetically costly process of photorespiration, effectively increasing photosynthetic efficiency in warm and arid conditions (Sage *et al.*, 2012, 2018). This CO₂-concentrating mechanism relies on a set of specific leaf anatomical properties and the co-ordinated action of up to 10 enzymes carrying the C₄ reactions (hereafter ‘core C₄ enzymes’) and numerous associated proteins (Supplementary Table S1 at JXB online; Hatch, 1987; Bräutigam *et al.*, 2011; Sage *et al.*, 2012; Külahoglu *et al.*, 2014; Lundgren *et al.*, 2014; Yin and Struik 2018). Despite its apparent complexity, C₄ photosynthesis is a textbook example of convergent evolution, having independently evolved >60 times within flowering plants (Sage *et al.*, 2011). The origins of C₄ photosynthesis were probably facilitated by the presence of anatomical enablers in some groups (Christin *et al.*, 2013b; Sage *et al.*, 2013), but the processes leading to a functioning C₄ biochemical pathway within these anatomical structures are less well understood. All C₄ enzymes studied so far exist in C₃ plants, but are involved in different pathways (Aubry *et al.*, 2011). There is a bias in the recruitment of genes into the C₄ system, with genes ancestrally abundant in the leaves of C₃ plants preferentially co-opted for C₄ (Christin *et al.*, 2013a; John *et al.*, 2014; Emms *et al.*, 2016; Moreno-Villena *et al.*, 2018). Changes to their expression patterns and/or kinetic properties of the encoded enzyme then followed (Bläsing *et al.*, 2000; Hibberd and Covshoff, 2010; Huang *et al.*, 2017; Moreno-Villena *et al.*, 2018), with cell-specific expression realized in some cases through the recruitment of pre-existing regulatory mechanisms (Brown *et al.*, 2011; Kajala *et al.*, 2012; Cao *et al.*, 2016; Reyna-Llorens and Hibberd, 2017; Borba *et al.*, 2018; Reyna-Llorens *et al.*, 2018).

The evolutionary transition between C₃ and C₄ phenotypes involves intermediate stages that only have some of the anatomical and biochemical modifications typical of C₄ plants (Monson and Moore, 1989; Sage *et al.*, 2012, 2018).

In particular, some C₃+C₄ plants perform a weak C₄ cycle that is responsible for only part of their carbon assimilation (these correspond to ‘type II C₃–C₄ intermediates’; Ku *et al.*, 1983; Monson *et al.*, 1986; Schlüter and Weber, 2016). This weak C₄ cycle might have emerged through the up-regulation of C₄-related enzymes to balance nitrogen among cellular compartments in the multiple lineages of plants that use a photorespiratory pump (Sage *et al.*, 2011, 2012; Mallmann *et al.*, 2014; Bräutigam and Gowik, 2016). Metabolic models suggest that any increase in flux of CO₂ fixed through the C₄ cycle in intermediate plants directly translates into biomass gain, selecting for gradual increases in C₄ gene expression (Heckmann *et al.*, 2013; Mallmann *et al.*, 2014). The current model of C₄ evolution therefore assumes gradual, yet abundant, changes in plant transcriptomes and genomes during the transition from C₃ ancestors to physiologically C₄ descendants. Indeed, comparisons of C₃ and C₄ species have typically identified thousands of differentially expressed genes encoding C₄ enzymes, regulators, and accessory metabolite transporters (Bräutigam *et al.*, 2011, 2014; Gowik *et al.*, 2011; Külahoglu *et al.*, 2014; Li *et al.*, 2015; Lauterbach *et al.*, 2017). These large numbers might partially result from the comparison of species typically separated by millions of years of divergence (Christin *et al.*, 2011), which leaves ample time for the accumulation of secondary changes linked to the C₄ trait beyond the minimal requirements, as well as variation in other unrelated traits (Heyduk *et al.*, 2019). Even within a single species where photosynthetic transitions can be induced, the number of differentially expressed genes identified in transcriptome comparisons can be extremely high (Chen *et al.*, 2014). Previous efforts have, however, typically targeted very few individuals per C₄ lineage, such that the initial bout of co-option that generated a C₄ cycle cannot be distinguished from subsequent adaptation via natural selection and diversification caused by genetic drift (Christin and Osborne, 2014; Reeves *et al.*, 2018; Heyduk *et al.*, 2019).

In this study, the transcriptomes of mature leaves are compared among plant populations using a phylogenetic approach. The work aims to quantify the phenotypic differences in gene expression between the C₃ phenotype and plants using a weak C₄ cycle (C₃+C₄ state), independently from those responsible for the transition to the full C₄ type, and finally from those involved in the adaptation of an existing C₄ phenotype. The time elapsed between transitions, and therefore the number of changes unrelated to C₄ emergence, is reduced by focusing on a single species containing a diversity of photosynthetic types, the grass *Alloteropsis semialata*. Congeners of *A. semialata* are C₄, but previous comparative transcriptomics and leaf anatomy have shown that C₄ biochemistry emerged multiple times in the genus, from a common ancestor with some C₄-like characters (Fig. 1; Dunning *et al.*, 2017). Capitalizing on the physiological diversity existing within *A. semialata*, leaf transcriptomes from multiple individuals originating from diverse populations of each photosynthetic type in this species are analysed, together with closely related C₃ and C₄ species, to detect the changes in gene expression linked to (i) the phenotypic difference between C₃ plants and C₃+C₄ intermediates;

(ii) the shift to fixing carbon exclusively via the C₄ pathway in solely C₄ plants; and (iii) the subsequent adaptation of the C₄ cycle in geographically isolated C₄ populations. This deconstruction of the genetic origins of a complex biochemical pathway sheds new light on the number of genetic changes needed to move to another part of the adaptive landscape during different stages of a stepwise physiological transition.

Materials and methods

Species sampling and growth conditions

Three biological replicates from 10 separate populations/species were used for differential gene expression analyses. Seven of these were geographically distinct *Alloteropsis semialata* populations including: two C₃ populations from South Africa (RSA6) and Zimbabwe (ZIM1502) that represent extremes of the C₃ geographic range (Fig. 1B; Lundgren *et al.*, 2015), two geographically distant C₃+C₄ populations from Tanzania (TAN1602) and Zambia (ZAM1503) that are hypothesized to operate a weak C₄ cycle (Lundgren *et al.*, 2016), and three C₄ populations from Cameroon (CMR1601), Tanzania (TAN4), and the Philippines (PHI1601) that sample the two C₄ genetic subgroups (Olofsson *et al.*, 2016; Supplementary Fig. S1). The C₄ populations of *A. semialata* have decreased CO₂ compensation points, increased carboxylation efficiencies, and shifts in carbon isotopes compared with the C₃ populations that confirm their photosynthetic type (Lundgren *et al.*, 2016). The C₄ leaves are characterized by increased vein density, phosphoenolpyruvate carboxylase (PEPC) protein abundance, and transcript abundance of genes encoding some C₄ enzymes compared with the C₃ types (Lundgren *et al.*, 2016, 2019; Dunning *et al.*, 2017). The C₃+C₄ *A. semialata* also show elevated leaf levels of PEPC protein and genes for some C₄ enzymes, and increased concentration of chloroplasts in bundle sheaths in comparison with the C₃ populations, but no increase in vein density (Lundgren *et al.*, 2016; Dunning *et al.*, 2017). However, while slightly shifted compared with their C₃ conspecifics, their carbon isotope ratios are not in the C₄ range, which is common in plants performing a weak C₄ cycle, responsible for only part of their CO₂ uptake (i.e. 'type II intermediates'; Monson *et al.*, 1988; von Caemmerer, 1992; Sage *et al.*, 2012; Lundgren *et al.*, 2016). This results in a reduced CO₂ compensation point and oxygen inhibition (Lundgren *et al.*, 2016), as observed in other species acquiring part of their carbon via a weak C₄ cycle (Ku *et al.*, 1991). In addition to the seven *A. semialata* populations, we included one population of each of the C₄ congeners *A. angusta* (AANG1 from Uganda) and *A. cimicina* (from Madagascar) to enable comparison of convergent C₄-related changes in gene expression (Supplementary Fig. S1). Finally, an *Entolasia marginata* population from Australia was included as a C₃ outgroup. Three distinct genotypes for eight of the 10 populations described above were retrieved from a recent data set (Dunning *et al.*, 2019) or sequenced here. For the two other populations, sufficient biological replicates were not available. For *A. angusta*, we sequenced three clones of a single wild collected plant that were established >1 year before the study, while for *E. marginata* we sequenced two different genotypes and a clone of one of these genotypes, similarly established before the study (see Supplementary Table S2 for detailed sample collection information).

To evaluate the diversity of gene expression across the spectrum of photosynthetic types and the genetic variation within each photosynthetic type, we supplemented the above data with a single biological replicate from a further 15 geographically distinct populations (12 from previously published data; Dunning *et al.*, 2017, 2019; Fig. 1A). The three newly sequenced individuals are two C₄ *A. semialata* from Sri Lanka (SRI1702, lat: 6.81 long: 80.92) and Zambia (ZAM1726, lat: -14.21 long: 28.60), and a C₃ individual from Zimbabwe (ZIM1503, lat: -18.78 long: 32.74). In total, we had 45 RNA sequencing (RNA-Seq) libraries from 25 populations/species, with three biological replicates sampled from 10 populations and a single biological replicate sampled from the remaining 15 populations (Fig. 1A).

All plants were collected from the field as seeds or live cuttings, and subsequently grown under controlled conditions at the University of Sheffield as previously described (Dunning *et al.*, 2017). In brief, plants were potted in John Innes No. 2 compost (John Innes Manufacturers Association, Reading, UK) and maintained under wet, nutrient-rich conditions in controlled-environment chambers (Conviron BDR16; Manitoba, Canada) set to 60% relative humidity, 500 μmol m⁻² s⁻¹ light intensity, 14 h photoperiod, and day/night temperatures of 25/20 °C. After a minimum of 30 d in these growth conditions, young fully expanded leaves were sampled for transcriptome analyses.

RNA extraction, sequencing, and transcriptome assembly

RNA extraction, library preparation, and sequencing were performed as previously described (Dunning *et al.*, 2017). In brief, total RNA was extracted from the distal half of fully expanded fresh leaves, sampled in the middle of the light period, using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany) with an on-column DNA digestion step (RNase-Free DNase Set; Qiagen). Total RNA was used to generate 34 indexed RNA-Seq libraries using the TruSeq RNA Library Preparation Kit v2 (Illumina, San Diego, CA, USA). Each library was subsequently sequenced on 1/24 of a single Illumina HiSeq 2500 flow cell (with other samples from the same or unrelated projects), which ran for 108 cycles in rapid mode at the Sheffield Diagnostic Genetics Service.

The raw RNA-Seq data were cleaned using the Agalma pipeline v.0.5.0 to remove low quality reads (Q<30), and sequences corresponding to rRNA or containing adaptor contamination (Dunn *et al.*, 2013). *De novo* transcriptomes were assembled using Trinity (version trinityrnaseq_r20140413p1; Grabherr *et al.*, 2011). All raw data and transcriptome assemblies have been submitted to the NCBI repository (Bioproject PRJNA401220). Coding sequences (CDS) longer than 500 bp were predicted for each population using OrfPredictor (Min *et al.*, 2005), which uses homology to a user-supplied reference protein database or *ab initio* predictions if no suitable match is found. The protein database used comprised the complete coding sequences of eight model species: *Arabidopsis thaliana*, *Brachypodium distachyon*, *Glycine max*, *Oryza sativa*, *Populus trichocarpa*, *Setaria italica*, *Sorghum bicolor*, and *Zea mays*.

Phylogenetic reconstruction using core orthologs

Single-copy orthologs were extracted from the newly and previously published transcriptome assemblies (Dunning *et al.*, 2017) to infer phylogenetic relationships among individuals. Homologous sequences to 581 single-copy plant core orthologs previously determined in the Inparanoid ortholog database (Sonnhammer and Östlund, 2015) were identified using a Hidden Markov Model-based search tool (HaMSTR v.13.2.3; Ebersberger *et al.*, 2009). Sequences of the single-copy plant core orthologs were subsequently aligned using a previously described stringent alignment and filtering pipeline (Dunning *et al.*, 2017). In brief, the CDS were translationally aligned and filtered using T-COFFEE v. 11.00.8cbe486 (Notredame *et al.*, 2000) before trimming with gblocks v.0.91 (Castresana, 2000). Sequences shorter than 100 bp after trimming, and ortholog alignments with a mean nucleotide identity <95% were discarded, retaining 504 markers. A maximum likelihood tree was inferred using IQ-TREE v.1.6.3 (Nguyen *et al.*, 2014), which determined the most appropriate nucleotide substitution model prior to inferring a phylogeny with 1000 ultrafast bootstrap replicates.

Differential expression analyses

For differential expression analysis, we used the 45 144 cDNA sequences from the *A. semialata* reference genome (Dunning *et al.*, 2019; accession number QPGU00000000) as a reference. Cleaned reads were mapped to the reference using Bowtie2 v.2.3.4.1 (Langmead and Salzberg, 2012) recording all alignments. Counts for each transcript were then calculated using eXpress v.1.5.1 (Roberts and Pachter, 2013) with default parameters, and are reported in reads per kilobase of transcript per million mapped reads (RPKM). A multivariate analysis was

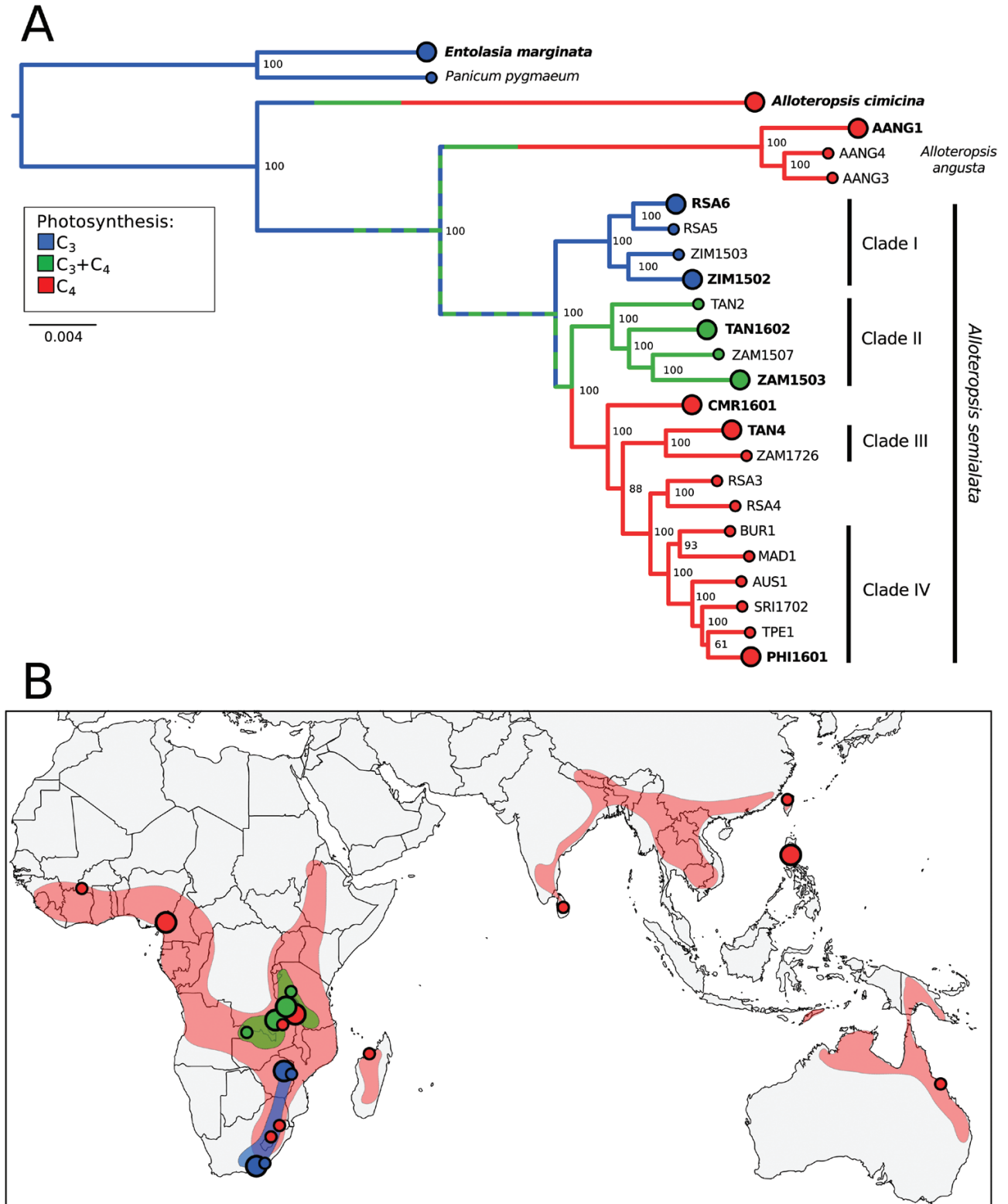


Fig. 1. Phylogenetic tree inferred from multiple nuclear markers and sampling locations. (A) This phylogeny was inferred under maximum likelihood using transcriptome-wide markers. The scale indicates the number of nucleotide substitutions per site, and bootstrap support values are indicated near nodes. AANG=*A. angusta*. For *A. semialata*, population names indicate the country of origin; AUS=Australia, BUR=Burkina Faso, CMR=Cameroon, MAD=Madagascar, PHI=Philippines, RSA=South Africa, TAN=Tanzania, SRI=Sri Lanka, TPE=Chinese Taipei, ZAM=Zambia, ZIM=Zimbabwe. Populations sampled with biological replicates and used for differential expression analysis are indicated by the large circles and bold population names. Nuclear clades from Olofsson et al. (2016) are indicated. Branch colors indicate the ancestral photosynthetic types, based on the transcriptomes and leaf anatomy detailed investigations of Dunning et al. (2017). The hashed green at the base of *A. semialata* indicates uncertainty between C₃ and C₃+C₄ states. (B) Distribution of *A. semialata* photosynthetic types and sampling locations, with color codes as in (A). Shadings indicate the approximate ranges of the three photosynthetic types of *A. semialata*, based on Lundgren et al. (2016).

used to assess similarities and differences in overall transcriptome expression profiles between samples. Clustering of expression profiles based on the biological coefficient of variation (BCV) were identified with multidimensional scaling (MDS) in edgeR v3.4.2 (Robinson *et al.*, 2010).

Differential expression analysis in edgeR was restricted to the 10 populations with three biological replicates. For each pair of populations, differentially expressed genes were identified as those with an associated false discovery rate (FDR) below 0.05. The overlap between pairwise comparisons was used to identify changes associated with specific branches of the phylogenetic tree inferred from core orthologs. Changes were assigned to a branch if significant results were detected for all pairwise tests involving one member of the descending clade and one population outside the clade, and the direction of expression change was consistent. This summary of pairwise tests was done separately for each C_3+C_4/C_4 clade (*A. cimicina*, *A. angusta*, and *A. semialata*) with all C_3 populations so that convergent gene expression shifts could be detected. Overall, by grouping the differential expression results based on the phylogenetic clades, we are able to identify changes in gene expression that coincide with specific physiological transitions, as well as those that precede or follow these transitions.

Results

Transcriptome sequencing

Over 190 million 108 bp paired-end reads were used in this study, including >167 million for the 10 populations sampled in triplicate (Supplementary Table S3). For these 30 samples used in differential expression analyses, the data comprised 36.13 Gb, with a mean of 1.20 Gb per library (SD=0.54 Gb; Supplementary Table S3). Over 95% of reads were retained after cleaning, and a *de novo* transcriptome was assembled for each of the populations using all available reads.

Phylogenetic relationships based on concatenated ortholog alignments

A phylogenetic tree was inferred from a concatenated alignment of 504 ‘core orthologs’ extracted from the predicted coding sequences from 25 transcriptome assemblies (12 assembled here), for a total of 573 762 bp after cleaning. Each population was represented by at least 126 048 bp (mean=468 507 bp; SD 94 782 bp). The concatenated alignment had 21.1% gaps and 6.3% of sites were parsimony informative. The phylogeny was inferred using the GTR+F+R4 substitution model, which was the best fit model according to the Bayesian information criterion (BIC). The phylogenetic relationships were congruent with previous genome-wide nuclear trees (Olofsson *et al.*, 2016; Dunning *et al.*, 2019), and confirmed that all the sampled C_4 populations of *A. semialata* form a monophyletic group, which is sister to the C_3+C_4 populations (Fig. 1). These two are in turn sister to the C_3 populations, so that previously inferred nuclear clades I (C_3), II (C_3+C_4), III and IV (both C_4) are retrieved, with the polyploid populations (RSA3 and RSA4) branching in between and the Cameroonian population at their base (Olofsson *et al.*, 2016; Fig. 1). *Alloteropsis angusta* and *A. cimicina* branched successively outside of *A. semialata* (Fig. 1), again mirroring previous results (Lundgren *et al.*, 2015; Olofsson *et al.*, 2016; Dunning *et al.*, 2019).

Transcriptome-wide patterns

A mean of 57.4% (SD=12.05%) of cleaned reads from the 45 RNA-Seq libraries mapped back to the 45 144 cDNA sequences extracted from the reference *A. semialata* genome (only *A. semialata* samples $n=34$, mean=64.1%, SD=4.3%). In total, 59.8% ($n=26\ 975$) of gene sequences had expression levels of >1 read per million of mapped reads in at least three samples and were retained for differential expression analysis. Based on their expression profiles, samples group strongly by species (Fig. 2A). When focusing on *A. semialata*, the main phylogenetic groups are recovered, which match the photosynthetic types (Figs 1, 2B). There is no apparent effect of the source study, with previous and new transcriptomes of the same species grouping together (Fig. 2). Differential expression analysis was performed for each pair of the 10 populations that had three biological replicates. The 45 pairwise tests performed returned an average of 4880 (SD=2125) significantly (FDR <0.05) differentially expressed genes (Fig. 3; Supplementary Table S4). The number of differentially expressed genes is highest between the most distantly related populations and lowest among close relatives (Fig. 3). Complete expression results are available in Supplementary Tables S4 and S5.

Differences between the C_3 and C_3+C_4 states of *A. semialata*

As expected, the long divergence time between the C_3 outgroup (*Entolasia marginata*) and *A. semialata* results in a large number of significant expression changes (branch A in Fig. 4). A total of 825 genes are down-regulated along this branch (3.1% of those expressed in leaves), including two genes encoding PEPC (*ppc-1P2* and *ppc-2P1*; ASEM_AUS1_43423 and ASEM_AUS1_37421; Supplementary Table S6), which drop to barely detectable levels in all *A. semialata* accessions, and are therefore unlikely to be linked to photosynthetic diversification. A total of 1500 genes (5.6%) are up-regulated in *A. semialata* compared with the C_3 outgroup (branch A in Fig. 4; Supplementary Table S6). This includes genes encoding the C_4 -related enzymes malate dehydrogenase (NAD-MDH; *nadmdh-2P4*; ASEM_AUS1_14800), AMP kinase (AK; *ak-3P3*; ASEM_AUS1_08191 and ASEM_AUS1_08195), glyceraldehyde 3-phosphate dehydrogenase (GAPDH; *gapdh-1P2*; ASEM_AUS1_06811), and phosphoenolpyruvate carboxylase kinase (PEPC-K; *pepck-1P3* and *pepck-3P6*; ASEM_AUS1_38337 and ASEM_AUS1_12272), although their expression levels remain fairly low in all *A. semialata* regardless of the photosynthetic type (mean=42 RPKM; SD=37; Supplementary Table S5). One gene encoding an enzyme linked to the photorespiratory pathway is also up-regulated (*hpr-2P3*; ASEM_AUS1_28984), although levels again remain fairly low within *A. semialata* (mean=19 RPKM; SD=13; Supplementary Table S5). The rest of the numerous genes varying in expression between the whole of *A. semialata* and the outgroup do not have known links to the C_4 pathway. A total of 60 genes (0.22%) are differentially expressed along the branch leading to the C_3 populations of *A. semialata*

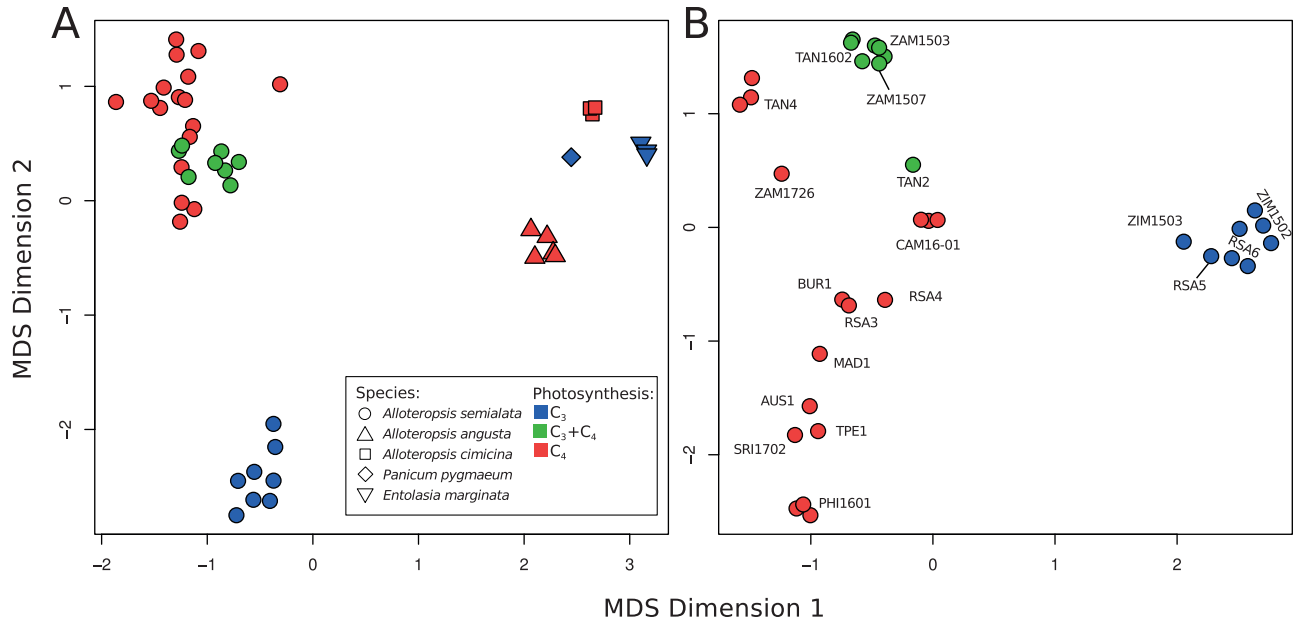


Fig. 2. Expression profile similarity across all samples. Expression profiles are clustered in multidimensional scaling (MDS) plots using (A) all samples and (B) only *A. semialata* samples. Species and photosynthetic types are indicated and population names are as in Fig. 1.

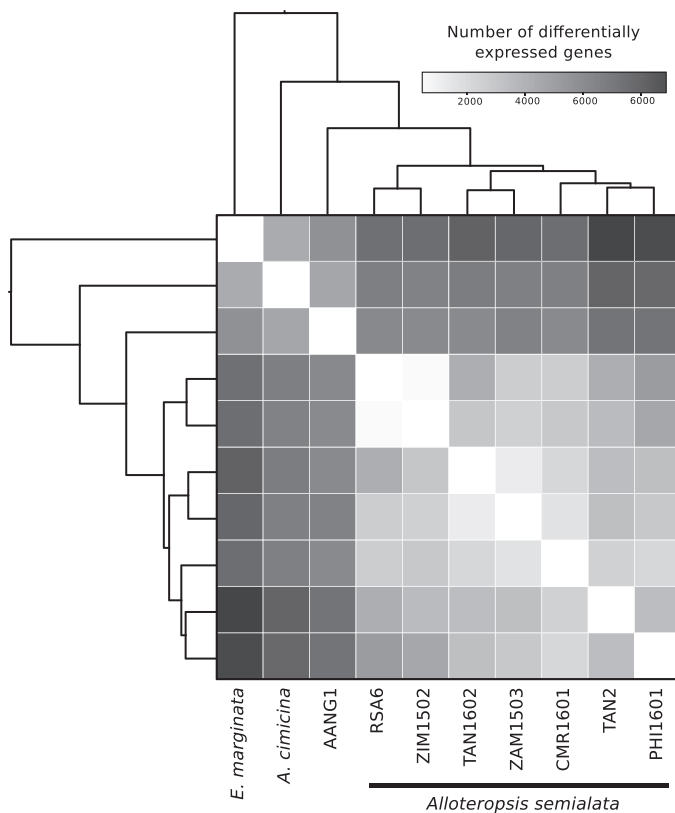


Fig. 3. Number of differentially expressed genes among pairs of populations. The heatmap shows the number of significantly differentially expressed genes detected for each pair of populations. The phylogenetic relationships among populations are indicated on the side, using an ultrametric version of the tree presented in Fig. 1.

(branch B in Fig. 4). None of these 60 genes encodes a protein known to function as part of the C₄ pathway (Table S6).

Within *A. semialata*, a C₄ cycle, weak or strong, characterizes the monophyletic group of C₃+C₄ and C₄ populations,

but not its C₃ sister group. Along the branch leading to C₃+C₄ and C₄ accessions, we detect 67 significantly differentially expressed genes (branch E in Fig. 4; Table 1). Of those, 58 (0.22% of all expressed genes) are consistently up-regulated in the C₃+C₄ and C₄ populations compared with the C₃ samples, including three genes that encode key C₄ enzymes: aspartate aminotransferase (ASP-AT; *aspat-3P4*; ASEM_AUS1_08268), phosphoenolpyruvate carboxykinase (PCK; *pck-1P1*; ASEM_C4_17510), and PEPC (*ppc-1P3*; ASEM_C4_19029; Supplementary Table S6). These three genes reach very high levels in the leaves of all C₃+C₄ and C₄ individuals (mean=1766 RPKM; SD=585; Fig. 5; Supplementary Table S5), including the C₄ congener *A. angusta* (mean=5002 RPKM; SD=2607; Supplementary Table S5). The other genes whose expression changes significantly along the same branch mostly remain at low to moderate levels in all *A. semialata*, but a number of them are also significant in *A. angusta*, and two of them in *A. cimicina* (Table 1; Supplementary Table S6). The significant genes include one for Nudix hydrolase, which was previously identified in a comparison of rice and C₄ grasses (Ding et al., 2015). The remaining genes have not, however, been related to C₄ photosynthesis in previous screens of grasses (Ding et al., 2015; Huang et al., 2017). A gene for a callose synthase is down-regulated in the C₃+C₄/C₄ group as well as in *A. angusta* (Table 1), which might be linked to plasmodesmatal widening to facilitate intercellular fluxes, as suggested for other genes linked to callose synthesis (Brütigam et al., 2011; Huang and Brutnell, 2016). Some of the other differentially expressed genes encode proteins that have been previously suggested as being involved in metabolic/structural differences between photosynthetic types (e.g. acyl transferase and pyruvate dehydrogenase; Huang and Brutnell, 2016) or that might be linked to plasmodesmata (e.g. phosphatidylglycerol/phosphatidylinositol transfer

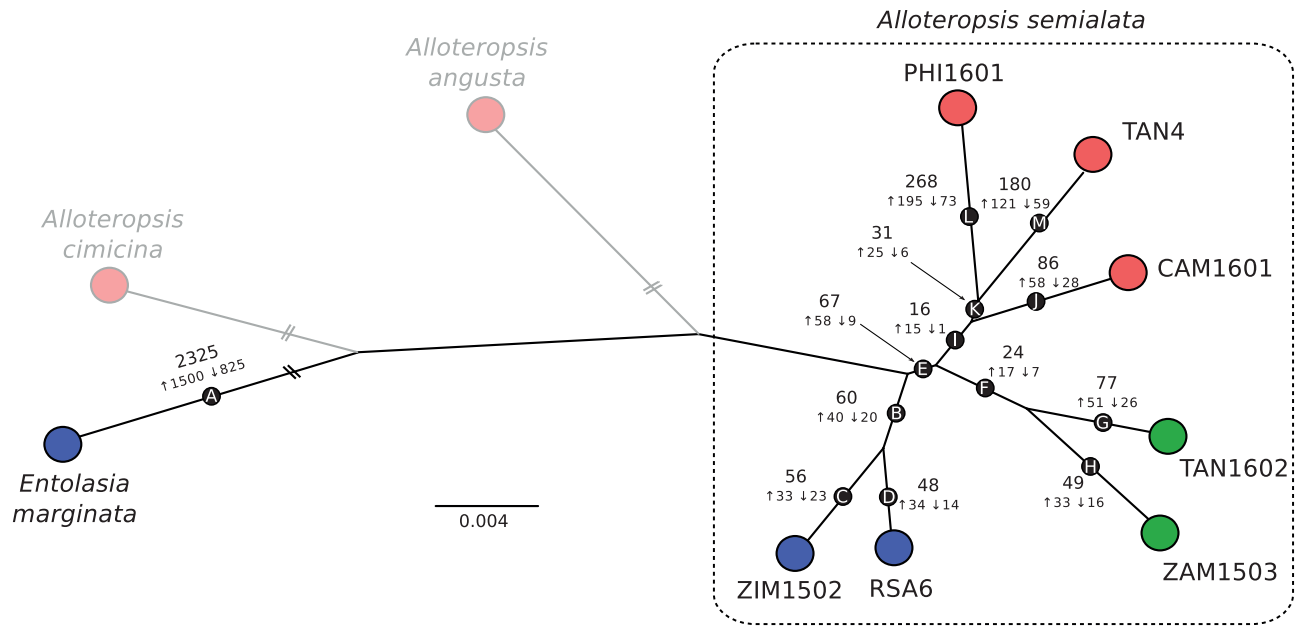


Fig. 4. Phylogenetic patterns of changes in gene expression. The maximum-likelihood phylogeny from Fig. 1 is shown unrooted after pruning the populations not used for expression analyses. For each branch, the number of differentially expressed genes is indicated, with numbers next to arrows indicating those that are consistently up- or down-regulated as one moves along the tree from the outgroup *Entolasia marginata*. Each population has three biological replicates, and colors indicate the photosynthetic type (blue=C₃; green=C₃+C₄; red=C₄). The scale indicates number of nucleotide substitutions per site, with truncated branches highlighted by two bars. The two grayed out C₄ congeners were excluded from these analyses, and results that involve them can be found in Supplementary Fig. S3.

protein), although the functional links with photosynthetic diversification remain to be tested.

Changes during the transition from C₃+C₄ to C₄ in *A. semialata*

Within *A. semialata*, a strong C₄ cycle characterizes a monophyletic group of populations (Fig. 1A), but only 16 genes (0.06% of all expressed genes) were significantly differentially expressed along the branch separating this group from the other populations (branch I in Fig. 4). Of these, 15 were consistently up-regulated in the C₄ populations, including one gene encoding the core C₄ enzyme pyruvate orthophosphate dikinase (PPDK; *ppdk-1P2*; ASEM_AUS1_39556), which reaches very high levels in all C₄ populations (mean=4479 RPKM; SD=2293; Table 1; Fig. 5; Supplementary Table S6), including the congeners *A. cimicina* (mean=1766 RPKM; SD=585; Table S5) and *A. angusta* (mean=1367 RPKM; SD=1100; Supplementary Table S5). The other genes up-regulated in the C₄ accessions, which include transcription factors and some transporters, reach moderate levels in the C₄ accessions, although some are also significantly up-regulated in *A. angusta* (Table 1). Significant changes in the abundance of the genes for the phosphatidylglycerol/phosphatidylinositol transfer protein might be linked to modifications of plasmodesmata to facilitate metabolite exchanges (Grison *et al.*, 2015), while aquaporins might be involved in membrane diffusion of CO₂ (Kaldenhoff *et al.*, 2014). However, whether these genes played a direct role in the photosynthetic diversification of *A. semialata* remains speculative.

Adaptation of C₄ photosynthesis in independent lineages

The three C₄ populations included in the differential expression analyses come from geographically distant locations and diverged more than half a million years ago (Lundgren *et al.*, 2015; Olofsson *et al.*, 2016), explaining the large number of differentially expressed genes among them (Fig. 3). Interestingly, this includes enzymes linked to the C₄ cycle, with genes encoding PEPC (*ppc-1P3*; ASEM_AUS1_12633), NAD-MDH (*nadmdh-1P8*; ASEM_AUS1_25602), PEPC-K (*pepck-1P3*; ASEM_C4_38337), NADP-MDH (*nadpmdh-3P4*; ASEM_AUS1_33376), and a sodium bile acid symporter (SBAS; *sbas-4P4*; ASEM_AUS1_12098) all up-regulated in the C₄ plants from the Philippines (PHI1601; Supplementary Table S6). A comparison of expression levels in the other transcriptomes (including the 15 populations not used for the differential expression) indicates that the gene *sbas-4P4* has qualitatively higher expression in all C₄ individuals from clade IV of *A. semialata* (mean=898 RPKM; SD=483), but not in the other C₄ individuals (mean=27 RPKM; SD=19) or the other *A. semialata* populations as a whole (mean=20 RPKM; SD=13; Fig. 5; Supplementary Table S5). This gene is orthologous to a group of Arabidopsis paralogs including BASS6 (At4g22840), which has the ability to transport glycolate, and appears to be involved in a process decreasing photorespiration (South *et al.*, 2017). The Arabidopsis paralog previously related to C₄ photosynthesis transports pyruvate (BASS2; Furumoto *et al.*, 2011), but its precise function might differ between the *Alloteropsis* and Arabidopsis orthologs. In addition, a gene encoding the photorespiratory enzyme

Table 1. List of genes with SwissProt annotations differentially expressed in key comparisons within *Alloteropsis semialata* from C_3 to C_3+C_4 , and C_3+C_4 to C_4

Gene	SwissProt protein description	Arabidopsis ortholog	Mean RPKM		
			C_3	C_3+C_4	C_4
Genes up-regulated in C_3+C_4 and C_4 <i>A. semialata</i> (branch E in Fig. 4)					
ASEM_AUS1_17510 ^a	Phosphoenolpyruvate carboxykinase (PCK)	AT4G37870	2	1168	3017
ASEM_AUS1_08268 ^a	Aspartate aminotransferase (ASP-AT)	AT5G11520	158	1843	1196
ASEM_AUS1_19029 ^a	Phosphoenolpyruvate carboxylase (PEPC)	AT2G42600	95	828	1118
ASEM_AUS1_30031 ^a	Fruit bromelain	AT1G06260	11	260	497
ASEM_AUS1_08709	Iron-sulfur cluster assembly protein 1	AT4G22220	67	394	473
ASEM_AUS1_11198	Bifunctional TENA2 protein	AT3G16990	10	43	80
ASEM_AUS1_19914	50S ribosomal protein L17	AT5G64650	1	78	58
ASEM_AUS1_02887 ^a	Cysteine proteinase 1	AT2G32230	0	44	54
ASEM_AUS1_16281 ^a	Probable carboxylesterase 15	AT5G06570	1	16	50
ASEM_AUS1_11666	Putative protease Do-like 14	AT5G27660	1	63	39
ASEM_AUS1_18766 ^a	Nudix hydrolase 16	AT3G12600	4	24	38
ASEM_AUS1_21431 ^a	DNA-binding protein MNB1B	AT4G35570	0	94	30
ASEM_AUS1_24040 ^{a,b}	Putative phosphatidylglycerol/phosphatidylinositol transfer protein	AT3G11780	4	32	24
ASEM_AUS1_08934	Putative F-box protein	AT4G38870	0	18	23
ASEM_AUS1_44075	Indole-3-acetaldehyde oxidase	AT5G20960	0	28	22
ASEM_AUS1_24692	Dihydrolipoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex	AT3G52200	0	13	20
ASEM_AUS1_38810	UDP-glycosyltransferase	AT1G05680	0	35	17
ASEM_AUS1_24427	Putative F-box protein	AT1G65770	0	19	16
ASEM_AUS1_43609 ^a	Flavin-containing monooxygenase FMO GS-OX-like 9	AT5G07800	0	7	13
ASEM_AUS1_40960	Cysteine-rich receptor-like protein kinase 26	AT4G23240	1	18	13
ASEM_AUS1_16960 ^a	Valine-tRNA ligase	AT1G14610	0	26	12
ASEM_AUS1_27461 ^b	Aspartic proteinase nepenthesin-2	AT2G03200	0	2	12
ASEM_AUS1_15840	Tyrosine-tRNA ligase	AT2G33840	0	4	10
ASEM_AUS1_22664	Probable nucleolar protein 5-1	AT5G27120	0	19	8
ASEM_AUS1_39034	Putative protease Do-like 14	AT5G27660	0	11	7
ASEM_AUS1_21913	Protein NEN1	AT5G07710	0	5	6
ASEM_AUS1_01903	Disease resistance protein RPM	AT3G07040	0	7	2
Genes down-regulated in C_3+C_4 and C_4 <i>A. semialata</i> (branch E in Fig. 4)					
ASEM_AUS1_21734	60S ribosomal protein L23a	AT3G55280	206	0	72
ASEM_AUS1_01414 ^{a,b}	Acyl transferase 4	AT3G62160	150	18	17
ASEM_AUS1_31537	Pumilio homolog 23	AT1G72320	49	12	9
ASEM_AUS1_00061	40S ribosomal protein SA	AT3G04770	42	7	7
ASEM_AUS1_22162	Tubulin alpha-3 chain	AT4G14960	32	6	3
ASEM_AUS1_22449 ^a	Callose synthase 3	AT5G13000	30	2	1
ASEM_AUS1_04268 ^a	40S ribosomal protein S21	AT5G27700	20	0	0
ASEM_AUS1_06562 ^{a,b}	PT11-like tyrosine-protein kinase 3	AT3G59350	5	1	1
Genes up-regulated in C_4 <i>A. semialata</i> (branch I in Fig.4)					
ASEM_AUS1_39556 ^{a,b}	Pyruvate, phosphate dikinase 1 (PPDK)	AT4G15530	60	133	1149
ASEM_AUS1_24184 ^a	Phosphatidylglycerol/phosphatidylinositol transfer protein	AT3G11780	0	1	104
ASEM_AUS1_29700	Protein SRG1	AT1G17020	2	1	86
ASEM_AUS1_16577 ^a	Lactoylglutathione lyase	AT1G11840	0	0	46
ASEM_AUS1_06220	S-Norcochlorine synthase 1	AT1G17020	1	1	39
ASEM_AUS1_24241	DnaJ homolog subfamily A member 1	AT3G14200	1	1	33
ASEM_AUS1_44200 ^a	Aquaporin TIP1-1	AT2G36830	0	0	17
ASEM_AUS1_13652	Transcription factor TGAL4	AT1G08320	0	0	7
ASEM_AUS1_00246	Nicotinamide adenine dinucleotide transporter 2	AT1G25380	0	0	2
Genes down-regulated in C_4 <i>A. semialata</i> (branch I in Fig.4)					
ASEM_AUS1_43847 ^{a,b}	Short-chain dehydrogenase TIC 32	AT4G23420	18	11	0

SwissProt protein description and Arabidopsis ortholog information are based on top-hit blast matches. Mean RPKM is derived from the seven *A. semialata* populations used for differential expression analysis (full summary of results can be found in Supplementary Table S6).

^a Significant change in the same direction in *A. angusta*.

^b Significant change in the same direction in *A. cimicina*

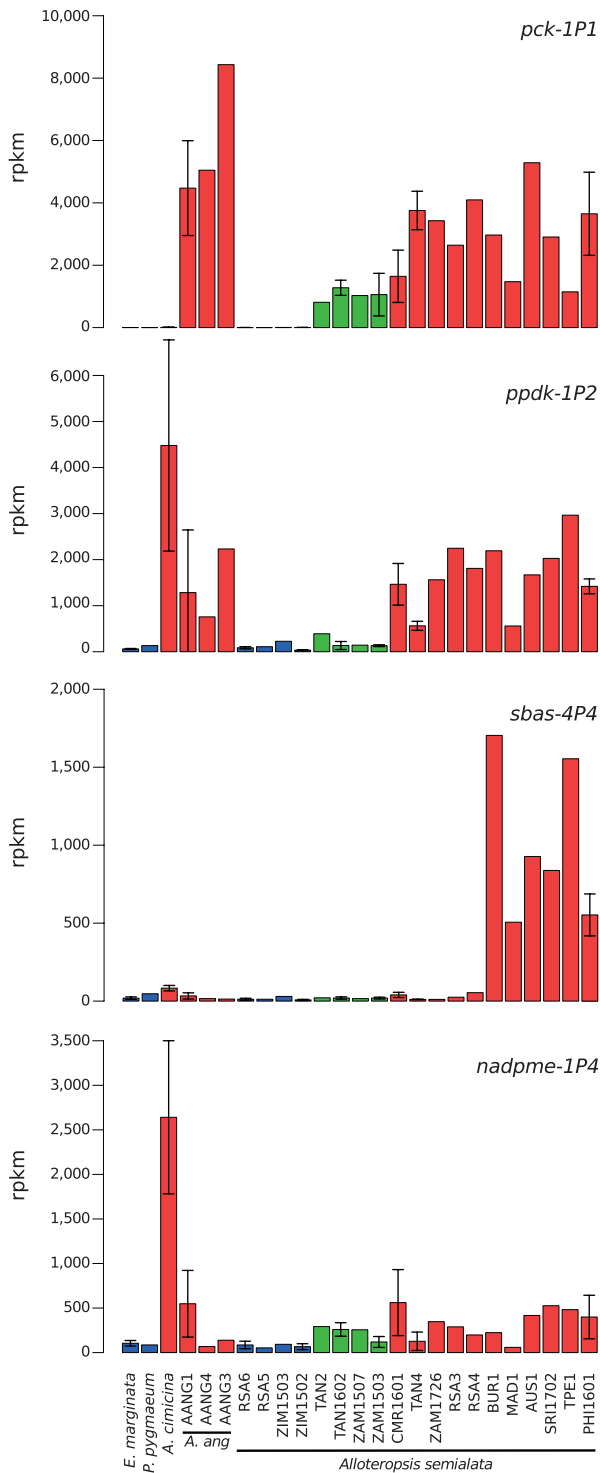


Fig. 5. Expression levels across accessions. Expression levels in reads per kilobase of transcript per million mapped reads are shown for four example genes. The SD for populations with biological replicates is indicated. Colors indicate the photosynthetic types; blue=C₃; green=C₃+C₄; red=C₄.

peroxisomal (S)-2-hydroxy-acid oxidase (GLO; *glo-1P1*; ASEM_AUS1_30871) is down-regulated in only one of the three C₄ populations (CMR1601; Supplementary Table S6).

There is quite a large variation in the expression of individual genes encoding some other C₄ enzymes, with some more abundant in the C₄ than C₃+C₄ *A. semialata* populations on average, yet relatively low in other C₄ individuals. These genes include alanine aminotransferase (ALA-AT; *alaat-1P5*; ASEM_AUS1_25403; C₄ mean=1105 RPKM; SD=812; C₃+C₄ mean=134 RPKM; SD=59; significantly differentially expressed in 13 of the 15 required pair-wise tests), which has low expression in C₄ individuals from Tanzania (TAN4-08; RPKM=135) and Cameroon (CMR1601-07; RPKM=154). Similarly, one of the genes encoding the NADP-malic enzyme (*nadpme-1P4*; NADP-ME, ASEM_AUS1_06611; significantly differentially expressed in seven of the 15 required pair-wise tests) is on average more abundant in the C₄ and C₃+C₄ (mean=300 RPKM; SD=235) than C₃ (mean=75 RPKM; SD=32) *A. semialata* populations, but low within some C₄ individuals (e.g. TAN4-01 RPKM=82; TAN4-08 RPKM=54; ZAM1503-08 RPKM=50; Fig. 5). This gene is also significantly up-regulated in *A. cimicina* and *A. angusta* (Supplementary Table S5). One of the genes for PEPC kinase (*pepck-1P3*) reaches high levels in several C₄ accessions of *A. semialata* (Supplementary Table S5). Similarly, some genes for the small unit of Rubisco reach very low levels in some C₄ accessions. For instance, the gene AUS1_20231 is at low levels in most C₄ *A. semialata*, yet remains very high in others, while the paralog AUS1_26631 reaches extremely low levels, specifically in the Asian group of C₄ *A. semialata* (Supplementary Table S5). A third paralog (AUS1_26630) remains high in all accessions, so that the total abundance of genes for Rubisco is not markedly decreased, which is congruent with the high Rubisco protein abundance in the leaf of the C₄ *A. semialata* (Ueno and Sentoku, 2006).

The number of genes significantly differentially expressed in the C₄ *A. cimicina* and *A. angusta* lineages is much higher, since only one population represents each of these species (Supplementary Fig. S3). As previously reported (Dunning *et al.*, 2017), a high number of genes encoding core C₄ enzymes, regulatory proteins, and transporters are up-regulated in *A. cimicina* (Supplementary Table S7), and to a lesser extent in *A. angusta* (Supplementary Table S8), while some photorespiration and Rubisco genes are down-regulated in both species. Besides the differentially expressed genes, a number of C₄-related genes are abundant in all samples independent of their photosynthetic type. This is especially the case of genes encoding β -carbonic anhydrase (*beta-2P3*; ASEM_AUS1_16750; mean=1682 RPKM, SD=1027, minimum=290) and malate dehydrogenases [*nadpmdh-1P1* (ASEM_AUS1_23802; mean=443 RPKM, SD=501, minimum=117), *nadpmdh-3P4* (ASEM_AUS1_33376; mean=447 RPKM, SD=184, minimum=166), and *nadmdh-3P5* (ASEM_AUS1_22160; mean=157 RPKM, SD=69, minimum=41)]. Transcripts for these genes were also abundant in the leaves of distantly related C₃ grasses, and their up-regulation very probably pre-dates the diversification of the group (Moreno-Villena *et al.*, 2018).

Discussion

Sampling the natural diversity to limit false positives

RNA-Seq is routinely used to identify genes differentially expressed between individuals with distinct phenotypes, leading to lists of candidate genes underpinning these differences (e.g. Shen et al., 2014; Dunning et al., 2016; Fracasso et al., 2016). When comparing distinct species, the risk of false positives is very high, as all changes in gene expression unrelated to the studied phenotypic transitions are detected. Here, 77.1% of genes expressed in the leaves are significantly differentially expressed in at least one pairwise comparison between our 10 populations (49.8% within *A. semialata*), which all belong to a relatively small group of closely related grasses. A powerful strategy to reduce false positives is to consider multiple independent origins of the trait of interest, and retain only those genes differentially expressed in all lineages (Ding et al., 2015; Rao et al., 2016). Such a filter would, however, exclude non-convergent changes in gene expression.

The alternative approach adopted here was to carry out multi-individual comparisons to infer changes along specific branches of the phylogenetic tree. The problem of false positives remains, as changes coinciding with the studied transitions would also be detected. However, working within a species complex decreases the number of false positives, as shorter divergence times are likely to result in fewer unrelated changes in gene expression. Because most changes cluster on terminal branches (Fig. 4), probably representing neutral changes that do not persist over evolutionary time, the inference of changes on short internal branches is less likely to be affected by drift. Indeed, a comparison of a C_3 *A. semialata* with the C_4 sister species *A. angusta* would identify >5000 (18% of genes expressed in the leaves) differentially expressed genes (Fig. 3). This number drops by ~50% when comparing individual C_3 and C_4 populations within *A. semialata*, but still includes all changes that occurred before, during, and after the C_3 to C_4 transition. After incorporating multiple populations of each type, only 67 genes (0.25% of genes expressed in the leaves) are identified that differ in expression between the C_3 and C_3+C_4 phenotypes, and 16 (0.06% of genes expressed in the leaves) between the C_3+C_4 and C_4 states. Changes in some of these genes might not be directly linked to the diversification of photosynthetic types, but several were convergently modified in *A. angusta* and/or *A. cimicina* (Table 1). These genes represent the best candidates for a role in the emergence and subsequent strengthening of a C_4 cycle in the group.

Emergence and reinforcement of the C_4 cycle in *Alloteropsis semialata*

The phylogenetic relationships and genus-wide comparisons of transcriptomes and leaf anatomical traits indicate that the last common ancestor of all *A. semialata* might have possessed a weak C_4 cycle based on the up-regulation of some enzymes (Fig. 1; Dunning et al., 2017). A large number of genes are differentially expressed between all *A. semialata* and the C_3 outgroup, which is not surprising given the evolutionary

distance of at least 15 million years (Christin et al., 2014). However, these include relatively few genes encoding C_4 enzymes (Supplementary Table S6). We conclude that the transcriptome of the C_3 *A. semialata* differs from that of other C_3 grasses by relatively few C_4 -related genes. The C_3 group might represent a reversal from a C_3+C_4 state to a phenotype with expression levels similar to the C_3 outgroup. In such a scenario, C_4 -related changes that happened in the last common ancestor of *A. semialata* and were reversed in the C_3 group would be assigned to the branch leading to the C_3+C_4 and C_4 groups. Because they focus on the phenotypic gaps in gene expression between the C_3 state and those using a weak or strong C_4 cycle, our transcriptome comparisons are therefore not heavily influenced by potential evolutionary reversals or reticulate evolution.

In total, 67 genes are differentially expressed in the group encompassing C_3+C_4 and C_4 phenotypes, and these include only three genes encoding core C_4 enzymes that are up-regulated in all C_3+C_4 and C_4 individuals (genes for ASP-AT, PCK, and PEPC; Table 1; Supplementary Table S5). These three enzymes form an aspartate shuttle based on the PCK decarboxylase (Fig. 6), which theoretically cannot sustain a full C_4 pathway on its own without creating an energetic imbalance among cell types (Wang et al., 2014). However, it might create a weak CO_2 -concentrating mechanism in C_3+C_4 plants that can function without dramatic energetic consequences due to its co-existence with a C_3 type of photosynthesis. While the functional significance of the other changes detected along the same branch is not always known, several might be linked to the control of plasmodesmata and thereby intracellular exchanges (Table 1). Other small adjustments of the cellular metabolism might remain undetected, but none

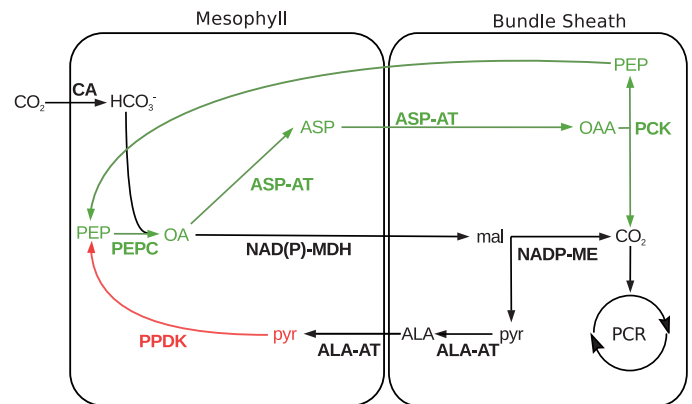


Fig. 6. Putative C_4 pathway in *Alloteropsis semialata*. A C_4 cycle is suggested for *A. semialata* based on the transcript abundance of C_4 -related genes, and the literature (Frean et al., 1983; Ueno and Sentoku, 2006). Pathway components are colored per the differential expression analysis, with those in black being putatively sufficiently abundant in C_3 ancestors, parts of the pathway in green those up-regulated during the transition to C_3+C_4 , and parts in red those up-regulated during the transition from C_3+C_4 to C_4 . ALA-AT=alanine aminotransferase, ASP-AT=aspartate aminotransferase, CA=carbonic anhydrase, NADP-MDH=NADP malate dehydrogenase, NAD(P)-ME=NAD(P) malic enzyme, PCK=phosphoenolpyruvate carboxykinase, PEPC=phosphoenolpyruvate carboxylase, PEPP=phosphoenolpyruvate phosphatase, PPK=pyruvate orthophosphate dikinase, PCR=photosynthetic carbon reduction (Calvin-Benson cycle).

of the other major C₄ enzymes or transporters is significantly up-regulated during the emergence of a weak C₄ cycle (Table 1). The apparently few changes in transcription required to operate a weak C₄ cycle in the C₃+C₄ intermediates may be facilitated by C₄-like anatomical properties and an abundance of genes for some key enzymes in the ancestor, as observed in other C₃ grasses (Christin *et al.*, 2013a, b; Emms *et al.*, 2016; Dunning *et al.*, 2017; Moreno-Villena *et al.*, 2018), and recent evidence suggests that some anatomical traits themselves might emerge via very few genetic changes (Wang *et al.*, 2017). While it is only responsible for part of the plant's CO₂ uptake, the weak C₄ cycle of C₃+C₄ plants reduces photorespiration (Ku *et al.*, 1991; Lundgren *et al.*, 2016), which confers a selective advantage analogous to that of a complete C₄ cycle in tropical conditions (Sage *et al.*, 2012; Christin and Osborne, 2014; Lundgren and Christin, 2017), and allows the evolution of a stronger C₄ cycle under natural selection for faster biomass accumulation (Heckmann *et al.*, 2013; Mallmann *et al.*, 2014; Bräutigam and Gowik, 2016).

The transition from a weak to a strong C₄ cycle in *A. semialata* changes carbon isotope signatures (the method most often used to identify photosynthetic types) from non-C₄ values to values diagnostic of C₄ plants (von Caemmerer, 1992; Lundgren *et al.*, 2015). This shift indicates a strengthened connection between the C₃ and C₄ cycles and a decreased leakiness, so that less atmospheric CO₂ is directly fixed by the Calvin–Benson cycle (Monson *et al.*, 1988; von Caemmerer, 1992). Within *A. semialata*, this might have been mediated by the reduced distance between veins in the C₄ *A. semialata* (Lundgren *et al.*, 2016, 2019; Dunning *et al.*, 2017) and/or biochemical alterations. The up-regulation of relatively few genes (0.06%) coincided with the phenotypic transitions, and only one of these encoded an enzyme with a known C₄ function, namely PPDK. This enzyme is responsible for the regeneration of PEP, the substrate of PEPC (Fig. 6). An increased PPDK activity is also observed between species of *Flaveria* performing a weak and a strong C₄ cycle, and it has been suggested that this provides PEPC with PEP at higher rates, thereby increasing the efficiency of the C₄ pathway (Monson and Moore, 1989; Sage *et al.*, 2012). Based on the literature and our transcriptome data, the C₄ cycle of *A. semialata* relies on a minimum of seven enzymes (Fig. 6; Frean *et al.*, 1983; Ueno and Sentoku, 2006). Genes for some of these enzymes (NAD-MDH and AK) increased in the common ancestor of the whole group, potentially as part of an ancestral weak C₄ cycle (Fig. 1; Dunning *et al.*, 2017). Within *A. semialata*, further increases in transcript abundance are observed in the C₃+C₄ versus C₃ or C₄ versus C₃+C₄ comparisons (Table 1) for genes encoding PEPC and three other enzymes (i.e. ASP-AT, PCK, and PPDK; Fig. 5). The expression of genes encoding carbonic anhydrase and others NAD(P)-MDHs in the C₃ ancestor of the group might have been sufficient to sustain a functioning C₄ cycle (Supplementary Table S5; Moreno-Villena *et al.*, 2018). Genes for the last of these enzymes (NADP-ME) are abundant in some C₄ individuals (Fig. 5; Supplementary Table S5), and might be expressed only in specific conditions, as suggested previously (Frean *et al.*, 1983).

C₄ populations of *A. semialata* are also characterized by a set of specific anatomical modifications and changes in the cellular localization of some enzymes (Ueno and Sentoku, 2006; Lundgren *et al.*, 2016, 2019; Dunning *et al.*, 2017). Gene expression changes responsible for these modifications would not necessarily be captured by our transcriptome analyses of full mature leaves, and the evolution of the C₄ phenotype almost certainly involves more genetic changes than those detected here. While protein abundance is not a direct function of gene expression, the two are correlated (Schwanhäusser *et al.*, 2011; Csárdi *et al.*, 2015; Koussounadis *et al.*, 2015). In the case of *A. semialata*, the three C₄ enzymes with genes differentially expressed in the C₃+C₄/C₄ transcriptomes (PEPC, ASP-AT, and PCK) are also those with large differences in activities between the C₃ and C₄ *A. semialata* in a previous study (Ueno and Sentoku, 2006). Transcriptome comparisons offer a first assessment of the changes underlying adaptive transitions, allowing subsequent investigations of responsible regulatory elements, post-transcriptional processes, changes of the protein kinetics, and verification of gene functions via genetic manipulation (e.g. Wang *et al.*, 2017; Borba *et al.*, 2018). Overall, our comparative transcriptomics show that, once the required enablers are present, the transition between C₃ and C₃+C₄ with some C₄ activity, and between C₃+C₄ and a rudimentary C₄ metabolism might have required fewer changes in gene expression in *A. semialata* than previously suggested based on other comparisons (Bräutigam *et al.*, 2011, 2014; Gowik *et al.*, 2011; Külahoglu *et al.*, 2014; Li *et al.*, 2015). These changes were spread between the C₃/C₃+C₄ and C₃+C₄/C₄ transitions, supporting a stepwise model of evolution (Mallmann *et al.*, 2014), where evolutionarily stable adaptive peaks can be reached with few mutations.

Adaptation continued after the emergence of a rudimentary C₄ pathway

The CO₂ pump generated by the C₄ cycle of *A. semialata* is less efficient than that of other C₄ species (Niklaus and Kelly, 2019), as illustrated by the incomplete segregation of enzymes between different cell types (Ueno and Sentoku, 2006) and slightly elevated CO₂ compensation points lying at the upper limit of those observed in C₄ species (Lundgren *et al.*, 2016). Therefore, *A. semialata* may be considered to exhibit an incipient C₄ cycle, which has not been optimized through protracted evolutionary periods, as suggested in the most recent models (Bräutigam and Gowik, 2016). The analyses conducted here, which compared all C₄ individuals with the C₃+C₄ or C₃ conspecifics, can detect the changes that happened in the early C₄ members of the group, before the diversification of the C₄ genotypes. However, transcriptome comparisons across C₄ individuals of *A. semialata* show evidence of additional alterations of the leaf biochemistry subsequent to the initial emergence of a C₄ cycle, with the abundance of some C₄-related enzymes varying across C₄ populations (e.g. NAD-MDH) and photorespiratory proteins down-regulated in only some of the C₄ populations (Supplementary Tables S5, S6). These changes are likely to represent the adaptation of the C₄ cycle after its initial emergence (Heyduk *et al.*, 2019; Niklaus and Kelly,

2019), previously illustrated for *A. semialata* by variation in the identity of genes responsible for an abundance of the key C₄ enzyme PEPC across C₄ genotypes (Dunning *et al.*, 2017) and leaf anatomy (Lundgren *et al.*, 2019), and recently reported for *Gynandropsis gynandra* (Reeves *et al.*, 2018).

The C₄ pathway proposed for *A. semialata*, based on the up-regulation of four core C₄ enzymes in addition to those present in C₃ ancestors (Fig. 6), might serve as an intermediate stage toward more complex and more efficient C₄ cycles. The congeneric C₄ *A. cimicina* and *A. angusta* have transcriptomes more typical of other C₄ species, with very high levels of numerous C₄-related enzymes, including a number of regulatory proteins and metabolite transporters (Supplementary Table S5), as would be predicted from other study systems, and an abundance of amino acid transitions adapting the proteins for the new catalytic context (Bräutigam *et al.*, 2011, 2014; Gowik *et al.*, 2011; Mallmann *et al.*, 2014; Christin *et al.*, 2015; Dunning *et al.*, 2017). These two species might have undergone more adaptive changes, due to an earlier C₄ origin or faster evolutionary rate. As illustrated by the additional C₄-related genes up-regulated in the C₄ plants from the Philippines, the rudimentary C₄ trait of *A. semialata* is likely to undergo similar secondary adaptations over evolutionary time.

Conclusions

In this study, the transcriptomes of individuals from the grass *A. semialata* are analysed in a phylogenetic context to show that the changes in gene expression required for a physiological innovation can be spread over time. The relatively few changes required for the initial emergence of a metabolic pathway contrasted with the numerous modifications involved in the adaptation of this new pathway. Indeed, the emergence of a weak C₄ cycle in our study system was accompanied by the up-regulation of three enzymes with a known C₄ function and 55 others proteins. The evolution of a stronger C₄ cycle then involved the up-regulation of one other C₄ enzyme and 14 other proteins. However, adaptation of C₄ photosynthesis, illustrated here by population-specific expression of C₄-specific enzymes, continues when the plants are already in a C₄ state. The evolutionary modifications required to generate a rudimentary C₄ pathway can therefore be modest in species possessing C₄ enablers, but even a suboptimal C₄ pathway is important because it changes the environmental responses of the species. This creates an opportunity for natural selection to act on the standing variation, new mutations, and, in some cases, laterally acquired genes, to assemble a trait of increasing complexity, allowing the colonization and gradual dominance in a larger spectrum of ecological conditions.

Data deposition

All raw DNA sequencing data (Illumina reads) and transcriptome assemblies generated as part of this study have been deposited with NCBI under Bioproject PRJNA401220.

Supplementary data

Supplementary data are available at *JXB* online.

Table S1. List of enzymes considered as core C₄ enzymes.

Table S2. Information for populations sampled in triplicate.

Table S3. RNA-Seq data and mapping statistics for 10 populations with triplicates.

Table S4. Pairwise differential expression test results for all genes.

Table S5. Leaf abundance, annotation, and summary of significance for all genes.

Table S6. Summary of differentially expressed genes referred to in Fig. 1.

Table S7. Summary of differentially expressed genes referred to in Supplementary Fig. S1A.

Table S8. Summary of differentially expressed genes referred to in Supplementary Fig. S1B.

Fig. S1. Phylogenetic patterns of changes in gene expression in (A) *Alloteropsis angusta*, and (B) *Alloteropsis cimicina*.

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Author contributions

LTD, JJMV, AB, CPO, and PAC designed the research; LTD, MRL, JD, PS, CA, FN, JKO, AM, IMA, CJK, LAD, FK, MA, DY, GB, WPQ, CPO, and PAC identified and collected plant material; LTD and JJMV generated and analysed the transcriptome data, with the help of AB and PAC; LTD, JJMV, and PAC wrote the paper with the help of all co-authors.

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