Natural variation within a species for traits underpinning C₄ photosynthesis

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One sentence summary: The C₄ species Gynandropsis gynandra exhibits natural variation in traits important for C₄ photosynthesis.

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ABSTRACT

Engineering C₄ photosynthesis into C₃ crops could substantially increase their yield by alleviating photorespiratory losses. This objective is challenging because the C₄ pathway involves complex modifications to the biochemistry, cell biology and anatomy of leaves. Forward genetics has provided limited insight into the mechanistic basis of these properties, and there have been no reports of significant quantitative intra-specific variation of C₄ attributes that would allow trait mapping. Here, we show that accessions of the C₄ species *Gynandropsis gynandra* collected from locations across Africa and Asia exhibit natural variation in key characteristics of C₄ photosynthesis. Variable traits include bundle sheath size and vein density, gas exchange parameters, and carbon-isotope discrimination associated with the C₄ state. Abundance of transcripts encoding core enzymes of the C₄ cycle also showed significant variation. Traits relating to water use showed more quantitative variation than those associated with carbon assimilation. We propose that variation in these traits likely adapted the hydraulic system for increased water use efficiency rather than improving carbon fixation, indicating that selection pressure may drive C₄ diversity in *G. gynandra* by modifying water use rather than photosynthesis. The accessions analyzed can be easily crossed and produce fertile offspring. Our findings therefore indicate that natural variation within this C₄ species is sufficiently large to allow genetic mapping of key C₄ traits and regulators.
INTRODUCTION

Plants that use C₄ photosynthesis can effectively abolish photorespiratory losses that occur when Ribulose 1,5-Bisphosphate Carboxylase/Oxygenase (RuBisCO) fixes oxygen rather than CO₂ (Bowes et al., 1971; Sharkey, 1988). In C₄ plants, RuBisCO is typically sequestered in bundle sheath (BS) cells that are concentrically arranged around the vasculature. Establishment of a molecular CO₂ pump delivers carbon to RuBisCO from Mesophyll (M) cells via C₄ acid intermediates (Garner et al., 2001). C₄ photosynthesis relies more heavily on the BS for photosynthesis, and less on M cells. It also involves more chloroplasts in BS cells, an increased proliferation of plasmodesmata between M and BS cells, and a higher vein density to increase the volume of the leaf occupied by the BS. These morphological alterations to the leaf that facilitate the C₄ cycle are known as Kranz anatomy (Langdale, 2011; Lundgren et al., 2014). Moreover, photosynthesis gene expression is modified such that genes encoding components of the C₄ and Calvin-Benson-Bassham cycles are strongly and preferentially expressed in either M or BS cells (Garner et al., 2001; Marshall et al., 2007; Hibberd and Covshoff, 2010).

Despite the complex modifications associated with C₄ photosynthesis, current estimates are that the C₄ pathway has independently evolved more than sixty times in angiosperms (Sage, 2016), which suggests that a relatively straightforward route may allow the transition from the ancestral C₃ to the derived C₄ state. A number of factors appear to have facilitated this apparently complex transition. First, proteins of the C₄ pathway operate in the ancestral C₃ state (Hibberd and Quick, 2002; Brown et al., 2010; Eastmond et al., 2015). Second, the modifications to gene expression associated with C₄ leaves appear to have been built on partly pre-existing regulatory architecture found in C₃ species (Brown et al., 2011; Kajala et al., 2012; Burgess et al., 2016; Williams et al., 2016; Reyna-Llorens et al., 2018). Moreover, after a binary categorization of phenotypes into either C₃ or C₄, mathematical modelling indicates that there is likely more than one route from which to acquire the C₄ state (Williams et al., 2013), but that subsequent modifications, many of which are associated with rebalancing photorespiration, reinforce these improvements in photosynthesis and fitness (Heckmann et al., 2013; Mallmann et al., 2014; Brautigam and Gowik, 2016).

Genome-wide analysis of transcript abundance in multiple C₃ and C₄ species has provided unbiased insight into processes that likely change in C₄ compared with C₃ leaves (Aubry et al., 2018).
Furthermore, *cis*-elements that control the expression of genes encoding components of the C₄ cycle have been documented (Akyildiz et al., 2007; Williams et al., 2016; Reyna-Llorens et al., 2018). However, the regulators that recognize these motifs have not been isolated (Reeves et al., 2017). Thus, despite the progress in our understanding of C₄ photosynthesis, it is currently not possible to rationally design a C₄ pathway in a C₃ leaf.

When natural variation is present, the development of a mapping population enables molecular marker-trait associations by methods such as Quantitative Trait Loci (QTL) mapping and Genome-Wide Association Studies (GWAS). Molecular marker-trait association studies help delineate genomic regions associated with trait variation. Fine genetic mapping of these genomic regions with major effects allows identification of causal genes underpinning the variation. Such approaches have been used extensively to map loci responsible for numerous complex traits in plants (Mauricio, 2001).

The application of molecular marker-trait associations to study C₄ photosynthesis would expedite the discovery of key regulators to engineer increased photosynthetic efficiency in C₃ plants. However, to our knowledge, there are currently no examples showing that variation in C₄ traits within a single species is sufficient to allow breeding and molecular trait mapping.

Interspecific hybrids have been generated between C₃ and C₄ species of the dicotyledon *Atriplex* (Oakley et al., 2014). Although the progeny possessed variation in C₄ phenotypes, specific traits showed limited penetrance, and there were high rates of sterility (Brown and Bouton, 1993). In the grass family, *Alloteropsis semialata* shows natural variation in C₄ parameters and has been classified into C₃ or C₄ subspecies (Ueno and Sentoku, 2006; Lundgren et al., 2016), but there are currently no reports that these populations have been bred. We, therefore, investigated the extent to which key C₄ traits varied in the C₄ dicotyledon *Gynandropsis gynandra*, which is a leafy green vegetable (Sogbohossou et al., 2018) in a clade sister to the Brassicaceae that contains both C₃ and C₄ species (Brown et al., 2005; Marshall et al., 2007; Feodorova et al., 2010). Here, we show that accessions of *G. gynandra* show significant variation in both anatomical and physiological traits associated with C₄ photosynthesis. These accessions have short generation spans, are sexually compatible, and produce fertile offspring. Our findings indicate that there is sufficient...
natural variation to allow the use of classical genetics to identify loci controlling the complex $C_4$ phenotype.
RESULTS AND DISCUSSION

Accessions of *G. gynandra* were collected from Africa and Asia (Supplemental Table 1). DNA sequencing and phylogenetic reconstruction generated a taxonomy that was consistent with geographical origin, but also indicated that the accession from Benin (West Africa) was more similar to Asian accessions than to those from East Africa (Fig. 1A). These accessions displayed considerable variation in macroscopic characteristics associated with leaf appearance (Fig. 1B, Supplemental Fig. 1A). For example, fully expanded leaflets varied in size and shape, and there was variation in petiole length, presence of trichomes, and anthocyanin pigmentation. As there was considerable macroscopic variation in leaf characteristics, we then evaluated these accessions for variation in features of Kranz anatomy. Interestingly, there were statistically significant differences in vein density (Fig. 1C&D, Supplemental Fig. 1B), cross-sectional area of BS strands (Fig. 1C&E, Supplemental Fig. 1C), size of individual BS cells (Fig. 1F), and stomatal density (Fig. 1C&G).

There was no discernable variation in inter-vein distance or number of BS cells surrounding each vein (Supplemental Fig. 2). However, on average East African accessions showed higher vein density, reduced distance between veins, and a greater stomatal density than Asian accessions (Supplemental Fig. 3A-C). Asian accessions typically had larger BS areas and cell sizes than those from the African continent (Supplemental Fig. 3D&E). Vein density was inversely correlated with BS area and BS cell size, but positively correlated with stomatal density (Supplemental Table 2). The average number of BS cells around each vein showed no statistically significant differences between lines (Supplemental Fig. 3F), but the cross-sectional area of the BS and the size of individual BS cells were positively correlated (\( \rho = 0.8, P < 0.0001 \)). We, therefore, conclude that the area of individual BS cells, rather than the number of these cells per vein bundle, drives the increased BS strand area observed in some accessions. This suggests that genetic determinants of cell size rather than cell proliferation are involved in the variation in BS tissue in *G. gynandra*. Despite the lower phenotypic variation associated with C\(_4\) compared with C\(_3\) leaves (Sage and McKown, 2006), our findings demonstrate that flexibility is still possible within individual species that are fully C\(_4\).

We next investigated whether differences observed in Kranz anatomy affected photosynthetic performance. For all accessions, their CO\(_2\) response curves (assimilation, \(A\), response to the
concentration of CO$_2$ inside the leaf, $C_i$) were typical of C$_4$ plants with high carboxylation efficiencies and low CO$_2$ compensation points ($\Gamma$, Fig. 2A, Supplemental Fig. 4A). Parameters associated with instantaneous gas exchange such as maximum rate of photosynthesis ($A_{\text{max}}$), rate of photosynthesis under the conditions of growth ($A_{400}$), CO$_2$ carboxylation efficiencies, and $\Gamma$ showed little variation between accessions (Fig. 2B-E, Supplemental Fig. 4B-E). As C$_4$ species typically grow under relatively high light intensities, variation in these traits may become apparent at higher light. In fact, modifications to stomatal density in A. thaliana impact assimilation rates at high light, but not at lower light intensities (Schlüter et al., 2003). Thus, it is possible that when grown under different conditions these G. gynandra accessions would demonstrate additional variation in photosynthetic characteristics.

There were statistically significant differences in transpiration (Fig. 2F), stomatal conductance (Fig. 2G), and water use efficiency (WUE, Fig. 2H). Furthermore, there was also significant variation in the carbon isotope discrimination against $\delta^{13}$C ($\delta^{13}$C) in leaf dry matter (Fig. 2I), which is a measure of the efficiency of the C$_4$ carbon pump over the lifetime of the leaf. Accessions from Asia-Benin showed reduced discrimination against $\delta^{13}$C compared with the East African lines (Supplemental Fig. 4I). Therefore, these data indicate that accessions of G. gynandra possess significant variation in parameters linked to the balance between water use and photosynthesis that influenced the efficiency of the C$_4$ cycle over their lifetimes.

We next sought to investigate the extent to which transcript abundance of core genes in the C$_4$ cycle differed between the accessions. Interestingly, there were statistically significant differences in the abundance of transcripts encoding Phosphoenolpyruvate carboxylase (PEPC) which catalyses the first committed step of the C$_4$ cycle, the BS-specific decarboxylase NAD-dependent Malic Enzyme (NAD-ME), the small subunit of RuBisCO (RbcS), and pyruvate,orthophosphate dikinase (PPDK) that regenerates PEP, the primary acceptor of HCO$_3^-$ (Fig. 3A-D). These differences in C$_4$-related transcript abundance were associated with the geographical location and phylogeny of the accessions, with the accessions from Asia-Benin accumulating greater levels of C$_4$-related transcripts than those from East Africa (Supplemental Fig. 5A-D). Understanding how the genes encoding photosynthetic enzymes become strongly expressed and patterned to either M or BS cells of C$_4$ species is a longstanding area of research. Although progress has been made in
identifying the cis-elements responsible for this phenomenon, little is known about the transcription factors involved. Therefore, the intraspecific variation in expression of genes encoding enzymes of the C₄ cycle in *G. gynandra* provides an opportunity to identify trans-factors important for C₄ photosynthesis. Despite accessions functioning with similar photosynthetic efficiencies under ambient CO₂ and light conditions, when assessed by phylogenetic grouping those with more pronounced Kranz traits (e.g., larger BS tissues and lower vein densities) exhibited increased $A_{\text{max}}$, WUE and $\delta^{13}C$ (Supplemental Fig. 4C,H,I) and stronger expression of the core genes of the C₄ cycle (Supplemental Fig. 5). To summarize, there were striking differences between accessions such that some possessed higher WUE, lower density of stomata and veins, larger BS areas and cell sizes, higher $\delta^{13}C$ (indicative of a stronger C₄ cycle), and increased expression of genes encoding C₄ enzymes (Fig. 4).

The considerable variation reported in this study offers a valuable germplasm resource to identify regulators of the C₄ pathway and Kranz anatomy through genetic mapping. All accessions in this study hybridize easily. Emasculation and pollination need only take 15-30 seconds per flower. For example, the most divergent accessions regarding anatomy ‘Malaysia-1’ X ‘Malawi’, ‘Malaysia-2’ X ‘Malawi’, and their reciprocal crosses produce an average 52 ± 11 seeds per silique (n=6), whose offspring are fully fertile. The F₁ hybrids displayed intermediate characteristics, differing in leaflet number, presence of trichomes on the petiole, and leaf size and shape (Supplemental Fig. 6). Therefore, these hybrid populations provide a breeding foundation to delineate regulatory mechanisms. More broadly, the discovery of intraspecific variation in a C₄ grass would be particularly useful in mapping traits relevant to improving photosynthesis in crops, and thus introduce C₄ photosynthesis into C₃ cereals.

While our understanding of the regulatory mechanisms underlying C₄ metabolism is growing, there is still a significant gap in tools to expand our understanding of the regulation behind Kranz anatomy and the C₄ biochemical cycle. Methods such as QTL mapping or GWAS in *G. gynandra* or an equally diverse C₄ species may provide insights into the regulation of Kranz development. In this study, most trait variation in *G. gynandra* was associated with characteristics relating to water use that impact carbon capture. It is noteworthy that modifications to C₃ leaves considered to represent early steps on the path towards the C₄ phenotype are also associated with water use.
rather than CO$_2$ fixation (Sage, 2004; Williams et al., 2013). As natural vegetation is not considered to be under strong selection pressure to optimize photosynthesis (Long et al., 2015; Ort et al., 2015), it seems likely that C$_4$ trait variation continues to be driven at least partially through the optimization of water use rather than photosynthesis \textit{per se}. 
MATERIALS AND METHODS

Plant accessions and growth conditions

A selection of nine diverse accessions of *G. gynandra* were made from a larger germplasm collection based on initial phenotypic and genetic screening. Five accessions were from Africa and four from Asia (Supplemental Table 1, materials available on request from MES). Plants from all *G. gynandra* accessions were grown under identical conditions prior to sampling. After germination, all seeds were planted in 5:1 F2 compost (Levington Advance, UK) to fine vermiculite premixed with 0.17 g/L insecticide (Imidasect 5GR, Fargro, UK) in 5 cm³ cells. Seedlings were kept in a growth chamber at 350 μmol photons m⁻² s⁻¹ photosynthetic photon flux density (PPFD) with a 16 h photoperiod, at 25 °C, 60% relative humidity (RH), ambient [CO₂]. A single dose of 3 mL/L slow release 17N-9P-11K fertilizer (All Purpose Continuous Release Plant Food, Miracle-Gro, UK) was applied after 1.5 weeks. Plants for physiological measurements were grown under identical conditions to those for Kranz measurements for the first three weeks, after which the plants for Kranz measurements were assayed and plants for physiological measurements were re-planted in 13 cm³ pots with 5:1 M3 soil (Levington Advance, UK) to medium vermiculite soil mixture and moved to a growth room set to 23 °C, 60% RH, ambient [CO₂], 350 μmol photons m⁻² s⁻¹ PPFD with a 16 h photoperiod. All plants were watered by an automated system whereby the bottom of the trays containing the 13 cm³ pots was flooded to a depth of 4 cm every 48 h for 10 min, following which the irrigation water was drained.

DNA sequencing and phylogenetic analyses

Genomic DNA was extracted using a cetyltrimethylammonium bromide (CTAB) extraction method. Briefly, leaf samples were ground uniformly in 300 μL of CTAB extraction buffer containing 2% (w/v) polyvinylpyrrolidone-40 and 1.7% (v/v) β-mercaptoethanol. After vortexing, samples were incubated at 65 °C for 30 min and 300 μL of 24:1 chloroform to isoamyl alcohol then added. After vortexing and centrifugation, 300 μL of supernatant was removed and placed in 300 μL isopropanol. DNA was precipitated overnight at -20 °C and then centrifuged at full speed for 15 min. The supernatant was removed, the pellet washed with 200 μL of 96% (v/v) ethanol prior to drying, and the DNA was resuspended in nuclease-free water.
To generate a phylogeny for the accessions, internal transcribed spacer (ITS) regions were sequenced using universal primers ITS 1 and ITS 4, following a protocol published previously (White et al., 1990). In short, ITS regions I, II, and the 5.8 S polycistronic ribosomal RNA precursor transcribed region were amplified by polymerase chain reaction (PCR). These PCR products were purified, and fragments sequenced. Sequences were then aligned using the MAFFT online server (MAFFT version 7, https://mafft.cbrc.jp/alignment/server/) and a best scoring maximum likelihood tree was generated with RAxML v.8.0.0 on the CIPRES science gateway (Miller et al., 2010).

Preparation of leaf tissue sections for Kranz measurements

Three weeks after germination, tissue was harvested from healthy plants from the centre trifoliate leaves of the second pair of fully expanded true leaves. A 3 mm$^2$ rectangle was cut from the leaf adjacent to the midvein with a razor blade for transverse sections. Two slightly larger rectangles were cut from identical regions for paradermal sectioning and RT-qPCR analysis.

For transverse sections, leaf tissue in plastic cuvettes was submerged in a 4% (v/v) paraformaldehyde in PBS solution (Sigma-Aldrich, St. Louis, MO, USA), placed in a vacuum chamber for 1 h, and incubated at 4 °C overnight for fixing. Cuvettes then underwent an ethanol dehydration series from 30% to 90% (v/v) ethanol solutions (Thermo Fisher Scientific, Waltham, MA, USA) in 10% (v/v) increments for 45 minutes each at 4 °C with a final overnight treatment at 4 °C in 95% ethanol with 0.1% (w/v) eosin dye solution (Sigma-Aldrich, St. Louis, MO, USA). The dye solution was washed thrice with 100% (v/v) ethanol at room temperature. The samples were embedded in resin according to the Technovit 7100 (Kulzer GmbH, Wehrheim, Germany) manufacturer’s protocol. Hardened resin blocks were cut with a manual rotary microtome (Thermo Fisher Scientific, Waltham, MA, USA). Sections were placed on microscope slides and stained with 0.1% (w/v) toluidine blue solution (Sigma-Aldrich, St. Louis, MO, USA) prior to imaging on a light microscope.

For paradermal sections, fresh tissue samples were placed in plastic cuvettes and incubated in 3:1 100% (v/v) ethanol to acetic acid solution before treatment with 70% (v/v) ethanol solution (refreshed once) at 37 °C overnight. To clear the samples, cuvettes were submerged in 5% NaOH solution for three hours at 37 °C, rinsed twice with 70% (v/v) ethanol, and stored at 4 °C. After
storage, the samples were stained with a 0.1% (v/v) eosin dye in 95% (v/v) ethanol solution. Samples were stored overnight at 4 °C and washed with 70% (v/v) ethanol thrice before transfer to slides for imaging. To determine stomatal density impressions of the abaxial epidermis of each central leaflet were generated by applying a thin coat of transparent nail varnish (Boots, Nottingham, UK). After drying, the varnish was peeled off and mounted onto a glass slide for imaging.

Measurement of Kranz anatomy traits

Slides of all leaf sections were imaged with an Olympus BX41 light microscope with a mounted Micropublisher 3.3 RTV camera (Q Imaging, Surrey, BC, Canada). Images were captured with Q-Capture Pro 7 software, and measurements were analyzed with the software ImageJ (Schneider et al., 2012). To maximize comparability, strict criteria were applied for all image analyses. Microscopy of transverse leaf sections was used to quantify the BS in terms of average BS tissue area (the total cross-sectional area of all BS cells immediately surrounding a vein) and BS cell size (the average cross-sectional area of individual BS cells around the vein). To quantify BS tissue area, the freehand selection tool was used to subtract the integrated area of each vein from the integrated area of all BS cells in direct contact with the vein on images with 200X total magnification. This value was divided by the number of BS cells in each vein bundle to obtain the average BS cell size. For inter-vein distance (the distance between the centers of adjacent veins in transverse sections), only vein bundles were measured for which the following criteria did not apply: wide (indicates branching) or extremely large veins, veins with distorted BS cells due to contact with adjacent BS tissues (indicates merging), veins with damaged BS cells. The line selection tool was used to measure the linear distance between the centers of adjacent veins on images with 40X total magnification. Vein density (vein length per unit area of leaf) was quantified on paradermal sections on images with 100X total magnification. Slides were imaged with the same microscopy equipment as transverse sections but set to Ph3 (phase contrast). Three images (from three different leaves per plant) were randomly selected for measurement. The freehand line tool was used to trace all veins (both major and minor) along their center. As it was not possible to trace all veins in an image simultaneously, individual vein sections were progressively measured.
without overlap and the individual lengths summed. The total vein length was divided by the image area to obtain the density. Stomatal density (the number of stomata per unit area of leaf) was measured on three subsampled leaves from three random plants on images with 200X total magnification. The total number of stomata were divided by the image area to obtain the density.

**Photosynthetic performance**

A LI-6800 portable photosynthesis infrared gas analyzer (IRGA) system (LI-COR, Lincoln, NE, USA) equipped with a multiphase flash fluorimeter was used to assess physiological differences for photosynthetic parameters between *G. gynandra* accessions. All physiological measurements were performed on the central leaflet of three independent five-week-old plants, grown in separate pots. For stomatal conductance, transpiration (*E*), and assimilation (*A*<sub>400</sub>), measurements were taken during ambient conditions of growth (400 ppm atmospheric [CO<sub>2</sub>], *C<sub>a</sub>*; PPFD 350 µmol m<sup>-2</sup> s<sup>-1</sup>). Water use efficiency (WUE) was defined as *A*<sub>400</sub>/*E*. A combination chlorophyll fluorescence and assimilation / intracellular CO<sub>2</sub> concentration (*A*/*C<sub>i</sub>) curve was measured for three plants from each accession. Atmospheric CO<sub>2</sub> (*C<sub>a</sub>*) reference values were: 400, 400, 300, 200, 100, 50, 25, 400, 400, 400, 600, 800, 1000, 1200, 400 ppm, with a saturating rectangular pulse of 12,000 µmol m<sup>-2</sup> s<sup>-1</sup> at each reference point. Otherwise, measurements were made at a PPFD of 2000 µmol m<sup>-2</sup> s<sup>-1</sup>, 23 °C and 60% RH at each reference point. All leaves covered the full area of the cuvette. Measurements were carried out on consecutive days between one and eight hours post dawn, measuring one plant selected at random from each accession per day. Rates of gas exchange including *A*<sub>max</sub> at 1200 ppm *C<sub>a</sub>* represent the measurements made, but a line of best fit was also plotted to fit the *A*/*C<sub>i</sub> response data to a logarithmic trend using the generalized additive model (gam) feature of the ‘tidyverse’ package in R. CO<sub>2</sub> compensation points (*I*) were calculated using linear regression of *A* and *C<sub>i</sub>* measurements made between *C<sub>a</sub>* 25 to 200 ppm (Sharkey, 1988). Adjusted *R*<sup>2</sup> values for all regression lines ranged between 0.993 and 0.997. Carboxylation efficiency was calculated as the partial derivative \( \frac{\partial A}{\partial C_i} \) at *A* = 0. Stable carbon isotope (*δ<sup>13</sup>C*) analysis was performed according to methods previously described (Royles et al., 2016) on three biological replicates per accession with 500 µg of dried leaf tissue.
Statistical Analysis

For all tests, individual plants were considered experimental units in a complete randomized design. Data were analyzed in SAS (University Version, SAS Institute, Cary, NC, USA) and in R (Version 3.4.2, R Studio, Inc., Boston, MA, USA). R packages: ‘agricolae’, ‘car’, ‘cowplot’, ‘dplyr’, ‘ggplot2’, ‘multcompView’, and ‘tidyverse’ were used for data analysis and downloaded via the Install Packages Tool in RStudio (Version 1.0.143, R Studio, Inc., Boston, MA, USA). A One-Way Analysis of Variance (ANOVA, $\alpha=0.05$) with type III sums of squares, which accounts for unequal replication, compared all means from anatomical and physiological measurements among $G. gynandra$ accessions and a Student’s t-test ($\alpha=0.05$) was used to compare means of accessions by phylogenetic proximity using the PROC GLM and PROC TTEST functions in SAS, respectively. Null hypotheses were rejected for specific ANOVAs or t-tests for any population with $P$ value $\leq 0.05$. Levene’s Test was used to evaluate homoscedasticity and was centered at the median (Levene, 1960) using the ‘car’ package in R. All analyses showed equal variance ($\alpha=0.05$), except for the number of bundle sheath cells (Supplemental Table 3). Duncan’s Multiple Range post-hoc Test was used for mean separation on accessions ($\alpha=0.05$) with statistically significant ANOVAs in the R package ‘agricolae’ (Duncan, 1955). To provide conservative lower Type I experiment error rates, Tukey’s Studentized Range Test (HSD) was also used ($\alpha=0.05$) with statistically significant ANOVAs in SAS and was plotted in R with packages ‘dplyr’ and ‘multcompView’ (Supplemental Fig. 7). Pearson product-moment correlation coefficients were calculated to find associations among features of Kranz traits (Pearson, 1895) using the PROC CORR function in SAS. Linear regression was performed using the PROC REG function in SAS to calculate CO$_2$ $\Gamma$ and carboxylation efficiency. The total number of replicates used in each experiment are summarized in Supplemental Table 4.

Analysis of transcript abundance

Leaf tissue samples for RNA extraction were harvested simultaneously with samples for Kranz trait measurements after three weeks of growth using the opposite paired trifoliate leaf to that harvested for sectioning and imaging. These fresh leaf samples were immediately flash frozen with
liquid nitrogen and stored at -80 °C. Total RNA was extracted from three tissue samples per accession with an RNeasy Mini Kit (QIAGEN, Hilden, DE) according to the manufacturer’s instructions. An On-Column DNase digestion protocol was applied to remove genomic DNA contamination (QIAGEN, Hilden, DE) before cDNA was synthesized with Invitrogen Superscript II RT enzyme according to the manufacturer’s instructions (Thermo Fisher Scientific Inc., Waltham, MA, USA). All cDNA samples were stored at -20 °C before RT-qPCR. Primers were designed for quantitative PCR of C₄ cycle genes PEPC, NAD-ME, RbcS, and PPDK (Supplemental Table 5), and reactions carried out as reported previously (Burgess et al., 2016) on three biological and three technical replicates.

**Accession Numbers**

Sequence data from this article can be found in the GenBank/EMBL data libraries under accession numbers MH188307-MH188315.

**Supplemental Data**

Supplemental Figure 1. Representative images for macroscopic and microscopic variation in leaf anatomy across a panel of *G. gynandra* accessions.

Supplemental Figure 2. Non-variable features of Kranz anatomy among accessions.

Supplemental Figure 3. Natural variation in features of Kranz anatomy between *G. gynandra* accessions from Asia-Benin compared with those from East Africa.

Supplemental Figure 4. Physiological variation for photosynthetic gas exchange parameters between *G. gynandra* accessions from Asia-Benin compared with those from East Africa.

Supplemental Figure 5. Transcript abundance differences for key enzymes in the C₄ cycle between *G. gynandra* phylogenetic clusters.

Supplemental Figure 6. Leaf appearance of F₁ hybrids between *G. gynandra* lines that exhibited the greatest differences in Kranz features.

Supplemental Figure 7. Quantitative natural variation among diverse *G. gynandra* accessions controlling for lower Type I error rates.

Supplemental Table 1. Accessions of *G. gynandra* investigated and their source regions.

Supplemental Table 2. Pearson product-moment correlation coefficients for Kranz anatomy traits.

Supplemental Table 3. Summary statistics for Levene’s Test for homogeneity of variance for individual ANOVAs (α=0.05).

Supplemental Table 4. The number of replicates (n) for anatomical measurements.

Supplemental Table 5. List of primers for RT-qPCR analyses.
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Figure 1. Natural variation in Kranz anatomy among a diverse panel of *G. gynandra* accessions. A, geographic and phylogenetic relationships for nine accessions from seven countries across Africa and Asia. B, variation in fully mature whole leaves of six-week-old plants. C, traces indicate variation in venation, bundle area, bundle sheath cell size, and stomata density of fully mature leaves for two extreme accessions. D, vein density, E, bundle area, F, bundle sheath cell size, and G, stomata density for all accessions. Asterisks indicate significant differences between accessions (one-way ANOVA, *P* < 0.05, **P** < 0.01, ***P*** < 0.001, ****P*** < 0.0001). Letters above individual box-scatter plots indicate significant groupings according to Duncan’s Multiple Range Test (α=0.05). The number of replicates (n) for each accession ranged from 3 to 7. Scale bars represent 5 cm (B) and 100 µm (C).

Figure 2. Physiological variation for photosynthetic gas exchange parameters among a diverse panel of *G. gynandra* accessions. A, assimilation (A) versus internal CO$_2$ (C$_i$) response curve. B, ambient assimilation (A$_{400}$) (400 ppm atmospheric [CO$_2$], C$_a$; PPFD 350 µmol m$^{-2}$s$^{-1}$), C, maximal assimilation (A$_{max}$) (1200ppm C$_a$, PPFD 2000 µmol m$^{-2}$s$^{-1}$), D, CO$_2$ compensation point (I), E, carboxylation efficiency, F, transpiration, G, stomatal conductance, H, water use efficiency (WUE), and I, carbon isotope composition ($\delta^{13}$C), respectively. Asterisks indicate significant differences between accessions (one-way ANOVA, n=3, *P*<0.05, **P**<0.01, ***P***<0.001, ****P***<0.0001). Letters above individual box-scatter plots indicate significant groupings according to Duncan’s Multiple Range Test (α=0.05).

Figure 3. Transcript abundance for key enzymes in the C$_4$ cycle among diverse *G. gynandra* accessions. Gene abbreviations: A, PEPC, PHOSPHOENOLPYRUVATE CARBOXYLASE 2; B, NAD-ME, NAD-DEPENDENT MALIC ENZYME 2; C, RbcS, RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT 1A; PPDK, D, PYRUVATE,ORTHOPHOSPHATE DIKINASE. Differences in transcript abundance were determined by RT-qPCR relative to the ACTIN7 gene. Asterisks indicate significant differences between accessions (one-way ANOVA, n=3, *P*<0.05, **P**<0.01, ***P***<0.001, ****P***<0.0001). Letters above individual bar charts indicate significant groupings among accessions according to Duncan’s Multiple Range Test (α=0.05).

Figure 4. Summary of differences in anatomy, physiology and C$_4$-related transcript abundance exhibited by extreme *G. gynandra* accessions. The accessions ‘Thailand’ and ‘Uganda-1’ had larger BS cells, lower vein and stomatal density, higher WUE, $\delta^{13}$C, and higher transcript abundance of core C$_4$ cycle enzymes. Differential transcript abundance among accessions are indicated by black arrows, and larger font represents higher relative transcript abundance. Gene abbreviations: PEPC, PHOSPHOENOLPYRUVATE CARBOXYLASE 2; NAD-ME, NAD-DEPENDENT MALIC ENZYME 2; RbcS, RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT 1A; PPDK, PYRUVATE,ORTHOPHOSPHATE DIKINASE. Enzymatic steps in white were not investigated.
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Figure 1. Natural variation in Kranz anatomy among a diverse panel of *G. gynandra* accessions. A, geographic and phylogenetic relationships for nine accessions from seven countries across Africa and Asia. B, variation in fully mature whole leaves of six-week old plants. C, traces indicate variation in venation, bundle area, bundle sheath cell size, and stomata density of fully mature leaves for two extreme accessions. D, vein density, E, bundle area, F, bundle sheath cell size, and G, stomata density for all accessions. Asterisks indicate significant differences between accessions (one-way ANOVA, *P*<0.05, **P*<0.01, ***P*<0.001, ****P*<0.0001). Letters above individual box-scatter plots indicate significant groupings according to Duncan’s Multiple Range Test (α=0.05). The number of replicates (n) for each accession ranged from 3 to 7. Scale bars represent 5 cm (B) and 100 µm (C).
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