RESEARCH PAPER

Multiple photosynthetic transitions, polyploidy, and lateral gene transfer in the grass subtribe Neurachninae

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Abstract

The Neurachninae is the only grass lineage known to contain C3, C4, and C3–C4 intermediate species, and as such has been suggested as a model system for studies of photosynthetic pathway evolution in the Poaceae; however, a lack of a robust phylogenetic framework has hindered this possibility. In this study, plastid and nuclear markers were used to reconstruct evolutionary relationships among Neurachninae species. In addition, photosynthetic types were determined with carbon isotope ratios, and genome sizes with flow cytometry. A high frequency of autoploidy was found in the Neurachninae, including in Neurachne munroi F.Muell. and Paraneurachne muelleri S.T.Blake, which independently evolved C4 photosynthesis. Phylogenetic analyses also showed that following their separate C4 origins, these two taxa exchanged a gene encoding the C4 form of phosphoenolpyruvate carboxylase. The C3–C4 intermediate Neurachne minor S.T.Blake is phylogenetically distinct from the two C4 lineages, indicating that intermediacy in this species evolved separately from transitional stages preceding C4 origins. The Neurachninae shows a substantial capacity to evolve new photosynthetic pathways repeatedly. Enablers of these transitions might include anatomical pre-conditions in the C3 ancestor, and frequent autopolyploidization. Transfer of key C4 genetic elements between independently evolved C4 taxa may have also facilitated a rapid adaptation of photosynthesis in these grasses that had to survive in the harsh climate appearing during the late Pliocene in Australia.

Keywords: C3 grass evolution, C4 photosynthesis, C3–C4 intermediate, grass phylogeny, lateral gene transfer, Neurachne, Paraneurachne, polyploidy

Introduction

Despite its complexity, the C4 photosynthetic pathway has evolved independently >62 times in flowering plants (Sage et al., 2011), thus constituting a striking example of convergent evolution. It is especially prevalent in grasses, where 22–24 distinct C4 lineages have been postulated in the PACMAD clade (Grass Phylogeny Working Group II, 2012). Such a clustering of C4 origins is also observed in other groups, with six independent lineages in the sedges (Cyperaceae) and 23 in the Caryophyllales...
Roksandic, 1983; indicating high potential for this group to serve as a model for C₄ grass evolution. However, to make evolutionary inferences, it is necessary to have a well-resolved, species-level phylogeny. Such a phylogeny was not available for the Neurachninae, as only some members of the group have been analysed with a small number of molecular markers (Hudson et al., 1990; Christin et al., 2008; Grass Phylogeny Working Group II, 2012).

The objective of the present study was a reconstruction of the evolutionary history of the Neurachninae, with an emphasis on photosynthetic pathway evolution. Multiple accessions per species were sampled, and phylogenetic analyses of plastid as well as nuclear markers, photosynthetic pathway identification, and measures of genome size were included. This comparative approach established the phylogenetic relationships between Neurachninae species, and revealed the genome dynamics of the group. The outcomes also highlight the diversity of photosynthetic transitions in the Neurachninae, and provide a solid foundation for future studies aimed at elucidating the anatomical and molecular mechanisms underlying these transitions.

Materials and methods

Plant material

Live, field-collected individuals of Neurachninae species were sampled for genome size analyses using flow cytometry (Supplementary Table S1 available at JXB online), while carbon isotope ratios were determined using multiple herbarium samples of each species (Supplementary Appendix S1). Multiple individuals of each Neurachninae species were also sampled for phylogenetic analyses; these were herbarium specimens or plants collected from the field (Supplementary Tables S1, S2).

Carbon isotope ratios ($\delta^{13}C$)

Carbon isotope values were determined for all described Neurachne, Paraneurachne, and Thyridolepis species (Supplementary Appendix S1 at JXB online) by the University of California, Davis Stable Isotope Facility (http://stableisotopefacility.ucdavis.edu). Some of the samples were previously assayed for $\delta^{13}C$ (Hattersley and Roksandic, 1983; Hattersley et al., 1986).

Determination of genome size

Nuclei were simultaneously released from fresh leaf material from a Neurachninae species and a calibration standard [Raphanus sativus cv. Saxa (2C DNA content = 1.11 pg; Doležel et al., 1992) or Lepidoperorna gibsonii (2C DNA content = 0.56 pg; M. Wallace, unpublished results)] by chopping with a razor blade in cold buffer (Roberts, 2007). Samples were filtered, and the nuclei were stained with propidium iodide (Roberts, 2007) and analysed using a BD FACSCanto II flow cytometer (Becton Dickinson, Franklin Lakes, NJ, USA) with 488 nm excitation and 585/424 band pass filter detection. Data were collected with BD FACS DIVA software (v. 5.0.2) and analysed using FlowJo v.7.6.3 software (Tree Star Inc., Ashland, OR, USA). At least 5000 nuclei per day were analysed from each individual on three separate days. The genome size of any individual was then calculated as the average of these three estimates. Genome size and standard deviation (SD) of conspecific homologs (Supplementary Table S1 at JXB online) were calculated using the average genome sizes of the individual homologs. Estimates were only included if the peak heights of the sample and standard were similar, and the coefficient of variation was <5%. Conversion of pg DNA to Mbp DNA followed Doležel et al. (2003).

Amplification of plastid markers and ITS

Five plastid markers (ndhF, trnK/matK, rpoC2, rpl16, and rnlF) that have been used previously to investigate relationships among grasses...
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Amplification of low-copy nuclear markers
As the gDNA extracted from herbarium specimens was too degraded to amplify low-copy nuclear markers, gDNA was isolated (DNeasy Plant Mini Kit, QIAGEN, Hilden, Germany) from selected accessions for which fresh material was available (Supplementary Table S4 at JXB online). Fragments of the genes encoding waxy and arrode were amplified with previously designed primers (Christin et al., 2012b). The ppe-B2 lineage of phosphoenolpyruvate carboxylase (PEPC), which contains most C4-specific forms in grasses as well as non-C4 orthodoxes (Christin et al., 2007), was isolated in one fragment or two overlapping segments, using previously published primers (Christin et al., 2007, 2012b). These three markers were isolated as described previously (Christin et al., 2012b), but with an annealing temperature of 51 °C and an extension time of 2 min. All sequences have been submitted to GenBank (Supplementary Table S4).

Phylogenetic analyses
The veracity of the sequence data was monitored throughout the analyses. The congruence between accessions of the same species and the lack of identical sequences for any of the plastid or nuclear markers, including the ppe-B2 genes, from different Neurachninae species indicated no cross-contamination or misidentification of the samples.

Sequences were aligned with MUSCLE (Edgar, 2004), and the alignments were manually refined. Outgroups were included based on previous work (Christin et al., 2012b; Grass Phylogeny Working Group II, 2012). Best substitution models were determined by hierarchical likelihood ratio tests. In all cases, the general time reversible substitution model with a gamma shape parameter (GTR+G) was selected. Phylogenetic trees were obtained by Bayesian inference with MrBayes (Ronquist and Huelsenbeck, 2003). Two analyses, each consisting of 1 000 000 generations after a burn-in period of 3 000 000, sampling a tree every 1000 generations. A consensus tree was computed on the 14 000 sampled trees. Phylogenetic trees were also inferred under a maximum likelihood (ML) criterion with the software PhyML (Guindon and Gascuel, 2003). Branch support of the ML trees was evaluated with 100 bootstrap pseudo-replications.

Phylogenetic trees were inferred for concatenated plastid data and ITS separately, and a further estimate of phylogeny was carried out by concatenating these two data sets. The three low-copy nuclear markers were analyzed separately. For waxy, parts of the sequences that consisted of simple sequence repeats or short tandem repeats were difficult to align and were removed from the data set, resulting in the elimination of 52 aligned base pairs. To decrease the possibility of a bias due to convergent evolution (Christin et al., 2007, 2012a), ppe-B2 phylogeny was also inferred from introns only. The significance of topological incongruence between the different markers was evaluated by Shimodaira–Hasegawa (S-H) tests with multiple-comparison correction (Shimodaira and Hasegawa, 1999), as implemented in baseml software (Yang, 2007).

Molecular dating
The divergence times of species within the Neurachninae were estimated with a molecular dating approach, which allows for rate variation among branches, following the recommendations from Rutschmann (2006), as described in Christin et al. (2008). Molecular dating requires time constraints set a priori on some nodes of the phylogeny as minimum or maximum ages. In the absence of a reliable fossil record for this group, the root of the Neurachninae was fixed to 11 Million years ago (Ma), a preliminary estimate obtained with a larger phylogeny, and without taking phytolith fossils into account (P.-A. Christin et al., unpublished). If phytoliths are taken into account, this node would probably be moved to ~20 Ma (P.-A. Christin et al., unpublished); however, as the same constraint was set for all markers, the relative ages can be compared among the different markers.

The topology inferred from combined plastid markers and ITS was used for molecular dating as it was better resolved and more complete than those of individual markers. However, the estimate of ages was based only on plastid markers to avoid strong variation in evolutionary rates due to differences between plastid and nuclear markers. Additional molecular dating analyses were carried out from the ITS, as well as each of the low-copy nuclear genes, with topologies compatible with the inferred species relationships. For these markers, an outgroup from outside the Neurachninae was added to the data set and used to estimate the first divergence time of the Neurachninae, but was removed during the molecular dating analyses.

Results
Photosynthetic pathway variation in the Neurachninae
Leaf δ13C assays confirmed previous photosynthetic pathway determinations in the Neurachninae (Hattersley and Rokasandic, 1983; Hattersley et al., 1986; Macfarlane, 2007). Mean δ13C values near –13% in N. munroi and P. muelleri demonstrate that these species are C4 (Table 1). All other Neurachninae members, including the C3-C4 intermediate N. minor, showed δ13C values between –24‰ and –29‰, which are typical of C3 plants (Table 1).

Neurachninae genome size analyses
The 2C DNA estimates varied 4-fold from 0.98 ± 0.01 pg DNA for the diploid N. lanigera S.T.Blake to 3.97 ± 0.04 pg DNA for the tetraploid P. muelleri (Table 1). These values are well within the range observed in the Poaceae (Bennett and Leitch, 2010, Plant DNA C-values database, http://data.kew.org/cvalues/), and agree with previous estimates from the Neurachninae based on 2C values or chromosome counts (Prendergast and Hattersley, 1985; Morgan and Westoby, 2005; Macfarlane, 2007).

Intraspecific ploidy variation was found in N. alopecuroidea R.Br. (4x, 5x, 6x, and 7x), and although multiple ploidy levels have been observed previously for N. lanigera and N. munroi (Prendergast and Hattersley, 1985), only diploid and tetraploid forms of these species, respectively, were detected in this study.

Phylogenetic relationships among the Neurachninae
All plastid and nuclear markers showed that Neurachne and Paraneurachne species formed a strongly supported monophylet
clade, which was sister to *Thyridolepis* ssp., and the monospecific *Paraneurachne* was nested inside *Neurachne* (Supplementary Figs S1–S4 at *JXB* online). The original name of this species, *Neurachne muelleri* Hack. (Hackel, 1895), should thus be resurrected.

Based on plastid markers, each species of the *Neurachne/Paraneurachne* group was strongly supported as monophyletic, with the exception of *N. lanigera*, which was poorly resolved with respect to *N. alopecuroidea* (Supplementary Fig. S1 at *JXB* online). The two C₄ taxa (*N. munroi* and *P. muelleri*) were not closely related, and the C₃–C₄ intermediate *N. minor* was not sister to either of the C₄ taxa (Supplementary Fig. S1).

The topology of the phylogeny inferred from ITS (Supplementary Fig. S2 at *JXB* online) was almost identical to that from plastid markers. The only exception was *N. queenslandica* S.T.Blake, which was positioned as sister to *N. alopecuroidea* and not *P. muelleri*. Forcing *N. queenslandica* to be sister to *N. alopecuroidea* in the phylogeny inferred from plastid markers led to a significant decrease of likelihood (S-H test, difference of log-likelihoods=−2.786, *P*=0.257 and 0.269, respectively). This incongruence between the plastid and ITS inferred phylogenies thus appears real and is symptomatic of incomplete lineage sorting or reticulate evolution. Since *N. queenslandica* is hexaploid (Prendergast and Hattersley, 1985), an allopolyploid origin is likely, with the female parent related to the *P. muelleri* lineage and the male parent to the *N. alopecuroidea/N. lanigera* lineage (assuming maternal chloroplast inheritance). *Neurachne queenslandica*, therefore, may be a natural hybrid between C₃ and C₄ parents, although further support for this hypothesis is required as C₄ photosynthesis may have evolved in *P. muelleri* after the hybridization event.

The phylogeny inferred from combined plastid and ITS markers (plastid+ITS) was strongly resolved (Fig. 1), and was thus considered representative of the species relationships. In this phylogeny, the monophyly of all species was strongly supported, with the exception of *Thyridolepis* taxa.

The relationships between species inferred from *aroadeh* (Supplementary Fig. S3 at *JXB* online) and *waxy* (Supplementary Fig. S4) were poorly supported, but nevertheless compatible with the plastid+ITS phylogeny. Forcing the topologies to that deduced from plastid+ITS did not significantly decrease the likelihood (S-H test, difference of log-likelihoods=−2.786 and −0.822, respectively, *P*=0.257 and 0.269, respectively). All *aroadeh* and *waxy* sequences isolated from the same species were monophyletic, with the exception of the sequences encoding these markers isolated from *T. multiculmis* S.T.Blake. Two sequences encoding both *waxy* and *aroadeh* were isolated from this species, and in both cases one sequence was more similar to that from *T. michelliana* S.T.Blake than it was to the other sequence isolated from *T. multiculmis*.

### Evolutionary history of ppc-B2 in the Neurachninae

The coding sequences encompassing exons 5–10 (1786 bp; 270 parsimoniously informative sites within the Neurachninae) of the Neurachninae *ppc-B2* genes were placed in a larger data set
encompassing many Panicoideae ppc-B2 sequences (Christin et al., 2012b). In this inferred phylogeny, the Neurachninae sequences were positioned near those of affiliated C₃ Paniceae, and were monophyletic, with the exception of one Ancistrachne sequence, which was positioned outside the Neurachninae and was therefore excluded from further analyses.

Inside the Neurachninae, despite a lack of resolution of the deeper nodes, the phylogenetic relationships deduced from ppc-B2 sequences were almost identical to those deduced from other markers (Supplementary Fig. S5 at JXB online). The only exceptions were the sequences from P. muelleri and N. munroi. Three groups of highly divergent ppc-B2 sequences were retrieved from P. muelleri. One of these groups was supported as sister to N. alopecuroidea/N. lanigera ppc-B2 sequences, as expected based on other markers (Fig. 1). The close relationship between N. munroi ppc-B2 sequences and some ppc-B2 sequences from P. muelleri was strongly supported even when a phylogeny was inferred from the five introns only (774 aligned base pairs, including 129 parsimoniously informative sites within the Neurachninae; Supplementary Fig. S6, subclade highlighted in red).

Different hypotheses reconciling ppc-B2 phylogeny with those inferred from other markers were evaluated using the sequence data (Fig. 2). Forcing the monophyly of all P. muelleri ppc-B2 sequences and placing them as expected for the species, and placing the N. munroi sequences in the predicted species position—the hypothesis of gene transmission that followed species genealogy—very strongly decreased the likelihood of the data (S-H test, difference of log-likelihoods= –246.516, P < 0.0001). Thus the close relationship between some of the P. muelleri ppc-B2 sequences and the N. munroi ppc-B2 sequences is unambiguous. A scenario in which a gene transfer occurred from N. munroi to P. muelleri involved placing the closely related N. munroi and P. muelleri sequences as expected for N. munroi, and the other P. muelleri sequences as expected for this species (Fig. 2A). This treatment of the data did not significantly affect the likelihood (S-H test, difference of log-likelihoods= –5.542, P=0.621). The alternative hypothesis, a gene transfer from P. muelleri to N. munroi, was also examined, and involved moving all N. munroi and P. muelleri ppc-B2 sequences to the position expected for P. muelleri (Fig. 2B). Again, no significant effect on the likelihood was seen (S-H test, difference of log-likelihoods= –6.799, P=0.588). The hypothesis that the data set might encompass different paralogues that appeared through gene duplication before the diversification of Neurachne/Paraneurachne was also tested. This implied placing P. muelleri sequences as sister to all other Paraneurachne/Neurachne sequences (Fig. 2C), which did not significantly decrease the likelihood (S-H test, difference of log-likelihoods= –9.391, P=0.485). This hypothesis, however, is not supported by the molecular dating analyses, which indicate that
the divergence of the closely related *N. munroi* and *P. muelleri* ppc-B2 genes occurred long after the initial diversification of Neurachne/Paraneurachne (Fig. 2C). Finally, it was considered whether the phylogenetic analyses might be biased by convergent amino acid changes in these two C₄ species (Christin et al., 2007, 2012a). However, topological tests based only on introns yielded identical results, ruling out such a scenario. The data, therefore, show that at least some Neurachninae ppc-B2 genes were not transmitted following the species genealogy, but the direction of transmission, *N. munroi* to *P. muelleri* or vice versa, cannot be determined with confidence from the current data.

Residues at positions putatively selected for C₄-specific function (Christin et al., 2007) were compared among the predicted amino acid sequences of the Neurachninae ppc-B2 sequences (Fig. 3). Of the 12 positions with the highest probability of having been positively selected in grasses (Christin et al., 2007), four were conserved in all members of the Neurachninae, with amino acid residues characteristic of non-C₄ ppc-B2 proteins (positions 577, 637, 761, and 807). At the other positions, the predicted amino acid sequences encoded by the closely related *N. munroi* and *P. muelleri* ppc-B2 genes presented residues that characterize independently evolved C₄ ppc-B2 genes (Fig. 3), with a serine at position 780 that was shown to be a major determinant of C₄-specific PEPC activity (Bläsing et al., 2000; Svensson et al., 2003). The other *P. muelleri* ppc-B2 sequences were predicted to encode some C₄-characteristic residues (Fig. 3), but also contained several stop codons and deletions altering the reading frame, and are very probably non-functional pseudogenes.

**Fig. 2.** Different evolutionary scenarios for ppc-B2, and divergence times within the Neurachninae. The inferred chronograms are represented for the different statistically plausible hypotheses: (A) gene transfer from *N. munroi* to *P. muelleri*; (B) gene transfer from *P. muelleri* to *N. munroi*; and (C) ancient duplication resulting in different paralogues being compared. Branch lengths are proportional to divergence times, in million years ago (Ma). Sequences with low divergence and belonging to the same species are compressed. Putative C₄-specific forms are highlighted in red. Confidence intervals of age estimates are represented by boxes for interspecific nodes. Purple boxes represent putative lateral gene transfer events. The blue arrow points to the ancient gene duplication postulated for hypothesis C.
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Molecular dating of the Neurachninae

The confidence intervals of estimated species divergence times based on plastid and nuclear markers overlapped (Fig. 4). Within most species, the divergence time between nuclear sequences overlaps with the crown age of the species. However, N. munroi arodeh sequences are estimated to have diverged long before the different N. munroi accessions. The occurrence of this pattern on a single gene can be explained by gene duplication or polyploidy followed by the loss of some gene copies. In addition, with multiple nuclear markers, the divergence of the different T. multiculmis sequences is estimated before the divergence of the different Thyridolepis species. This pattern, restricted to the tetraploid T. multiculmis, suggests an allopolyploid origin, with parents inside Thyridolepis, one of which was either not sampled or is extinct. The different hypotheses for the evolutionary history of ppc-B2 described above yielded similar age estimates (Fig. 2).

Discussion

Evolutionary origins of C4 biochemistry in the Neurachninae

The C4 and C3-C4 members of the Neurachninae are not sister species, but are separated in both plastid- and nuclear marker-based phylogenies by C3 taxa (Fig. 1; Supplementary Figs S1–S4 at JXB online). In other groups containing species demonstrating different photosynthetic types, and for which robust phylogenies exist, some C3-C4 species are directly sister to C4 taxa as in Flaveria (McKown et al., 2005), Cleome (Feodorova et al., 2010), Heliotropium (Hilger and Diane, 2003), and the Molluginaceae (Christin et al., 2011). This pattern suggests that the photosynthetic variation observed in extant taxa reflects a gradual transition from C3 to C3-C4 and finally to C4 photosynthesis. However, several C3-C4 taxa are not closely related to any C4 species (Sage et al., 2011), and many groups encompass a mixture of C3, C3-C4, and C4 taxa, including the Neurachninae, but also other Flaveria (McKown et al., 2005) and Molluginaceae (Christin et al., 2011) lineages, sedges (Roalson et al., 2010), and the Chenopodiaceae (Sage et al., 2011).

The clustering of taxa using different photosynthetic pathways that is observed in the phylogenetic trees of the Neurachninae and other groups suggests a complex evolutionary history, with either multiple transitions from C3 to C3-C4 or C4 photosynthesis, multiple losses of an ancestral C4 or C3-C4 type, or a combination of both (Christin et al., 2010). A simple scenario of a single C4 origin followed by reversals to the C3 (or C3-C4) state can be ruled out for the Neurachninae by the analyses of genes encoding PEPC. During the evolution of this key C4 pathway enzyme, mutations occurred in the genes that resulted in modifications to the catalytic and regulatory properties of the encoded proteins, allowing them to function optimally in C4 photosynthesis (Dong et al., 1998; Blässing et al., 2000). These mutations often occur at identical positions in the PEPC coding sequences of distantly related species (Christin et al., 2007; Besnard et al., 2009). Several amino acid changes characteristic of C4-specific PEPC were predicted from the ppc-B2 genes of C4...
Neurachninae, including the key C₄ determinant alanine to serine mutation at position 780 (Fig. 3). If the C₄-specific properties of PEPC appeared before the diversification of the Neurachninae, the ppc-B2 genes of non-C₄ taxa most probably would have maintained codons for some C₂-characteristic amino acids. However, the ppc-B2 genes of the C₃ and C₂–C₄ Neurachninae do not encode C₂-specific amino acids, and are indistinguishable at these positions from species known never to have been in a C₄ state (Fig. 3), strongly suggesting that the ppc-B2 genes of these non-C₄ taxa did not descend from genes encoding enzymes that were C₄ optimized.

The C₄-specific properties of the PEPC used by N. munroii and P. muelleri evolved after the divergence from non-C₄ Neurachninae, but the C₄ PEPC genes of these two species strongly grouped together in the phylogeny, even when only introns were considered, arguing against genetic convergence as a phylogenetic bias (Supplementary Figs S5, S6 at JXB online). The divergence of these genes occurred long after the split of
N. munroi and the lineage leading to P. muelleri (Fig. 2), excluding paralogy as an explanation for this grouping. Therefore, the transmission of these C₄-optimized genes did not follow the species genealogy. A lateral transfer might have occurred via allopolyploidization, but this is unlikely given that none of the other nuclear markers isolated from P. muelleri showed affinities with those of N. munroi. It is more likely that the transmission occurred via hybridization, followed by backcrossing and introgression into the population, or alternatively through a lateral gene transfer event, as shown for the grass Allotropis (Christin et al., 2012b), and suggested for the sedge Eleocharis (Besnard et al., 2009). Although the direction of the ppc-B2 gene transfer is not known yet, a transfer from N. munroi to P. muelleri is more consistent with the present data. In some regions of Australia, N. munroi and P. muelleri co-occur (Prendergast and Hattersley, 1985; Supplementary Fig. S7), providing opportunities for a gene transfer that might have been favored by natural selection. Some of the native P. muelleri ppc-B2 copies encode residues at positions 466 and 531 that generally characterize C₄-specific PEPC (Besnard et al., 2009), which suggests that these genes previously fulfilled the C₄ function in P. muelleri and underwent a few changes toward C₃ optimization of the encoded enzyme. The acquisition of ppc-B2 genes from N. munroi that were more C₃ optimized would have been advantageous, leading to a replacement of the vertically acquired P. muelleri genes, and their subsequent pseudogenization (Fig. 3).

**Anatomical enablers of photosynthetic transitions in the Neurachninae**

The optimization of C₄ biochemistry is hypothesized to be one of the final steps in the evolution of C₄ plants (Sage et al., 2012), with the initial steps involving the reduction of the mesophyll cell to bundle sheath cell ratio, the enhancement of bundle sheath organelles, and the appearance of a photosynthetic CO₂ pump, which characterizes nearly all known C₃–C₄ intermediates (Hylton et al., 1988; Griffiths, 1989; Hattersley and Watson, 1992; Sage et al., 2012). The C₃ P. muelleri and N. munroi and the C₃–C₄ N. minor have very similar foliar anatomies, with short interveinal distances, low mesophyll to bundle sheath tissue volume, and high numbers of bundle sheath organelles, typical of C₄ taxa (Hattersley et al., 1982, 1986; Brown and Hattersley, 1989). The C₄ taxa that separate them in the phylogeny have a comparatively larger interveinal distance and smaller bundle sheath cells (Hattersley et al., 1982, 1986; Macfarlane, 2007), although the interveinal distance tends to be shorter than that of typical C₃ taxa in N. queenslandica and N. annularis Macfarlane, and especially in N. tenuifolia S.T.Blake, where additional minor bundles reduce the average interveinal distance (Hattersley et al., 1982; Macfarlane, 2007). C₃ species in the Neurachne/Thrydolepis clade have conspicuous mestome sheaths, the tissue that has been recruited for carbon reduction in C₃–C₄ and C₄ Neurachninae species (Dengler et al., 1985). Indeed, while this tissue is usually devoid of organelles in C₃ taxa, it contains some chloroplasts and a high number of mitochondria in these C₃ Neurachninae (Hattersley et al., 1982, 1986; Hattersley and Roksandic, 1983). The presence of these organelles in the mestome sheath may have facilitated the evolution of a photosynthetic CO₂ pump in the Neurachninae, enabling the subsequent transition to a complete C₄ pathway (Sage et al., 2012). As has been hypothesized for other anatomical characters in some eudicot lineages with multiple C₄ origins (Marshall et al., 2007; McKown and Dengler, 2007; Christin et al., 2011), the high organelle content of C₄ Neurachninae mestome sheaths may have contributed to the multiple origins of biochemical carbon-concentrating mechanisms in this grass group.

**Recurrent polyploidizations in the Neurachninae as diversification facilitators?**

The distribution of ploidy levels in the species phylogeny (Fig. 1) suggests either multiple polyploidization events or a few followed by a return to a diploid state (diploidization). The latter suggestion can be disregarded because it would have led to a high chromosome number in the newly formed diploids, which is not observed in the Neurachninae (Table 1). In addition, multiple polyploidizations are supported by the existence of intraspecific ploidy variation in several taxa (Table 1; Prendergast and Hattersley, 1985). The data therefore suggest that seven independent polyploidization events have occurred in the Neurachne/Thrydolepis clade, one per polyploid species (Fig. 1).

The analyses of markers from multiple genomes identified T. multicalmis and N. queenslandica as probable allotetraploids, the latter possibly representing a hybrid from a C₃ and a C₄ parent. In contrast, the tetraploid C₃–C₄ intermediate N. minor does not appear to be the result of an allotetraploidization between C₃ and C₄ Neurachninae species, or at least not between known members, as the sequences from N. minor clustered together in the phylogenies at the same position for all plastid and nuclear markers (Fig. 1; Supplementary Figs S1–S4 at JXB online). With leaf anatomy similar to that of the C₃ N. munroi (Hattersley et al., 1982), and a typically C₃ isotopic value (Table 1; Hattersley and Roksandic, 1983; Hattersley et al., 1986), consistent with minimal or limited C₄ cycle activity (Hattersley and Stone, 1986; Hattersley et al., 1986; von Caemmerer, 1992), N. minor may represent a transitional stage toward an additional origin of full C₄ photosynthesis in the Neurachninae. As for N. minor, all the plastid and nuclear marker sequences belonging to the polyploid N. alopecuroidea, N. lanigera, and N. munroi clustered together in the phylogenies (Fig. 1; Supplementary Figs S1–S6), suggesting that the dominant mechanism for increased chromosome numbers in this grass group was autopolyploidization.

The two C₃ taxa and the C₃–C₄ intermediate species of the Neurachninae are all polyploids of putatively recent origin (Fig. 1), and autopolyploidization might have allowed photosynthetic diversification by providing additional copies of genes encoding enzymes that fulfilled housekeeping functions in the C₃ ancestors. A relaxation of selection due to genetic redundancy has indeed been hypothesized to facilitate the recruitment of enzymes into novel photosynthetic functions (Monson, 2003; Wang et al., 2009); however, as yet no empirical evidence exists to support this hypothesis, and comparison of distantly related grass genomes questioned the importance of gene duplication in the evolution of the C₄ syndrome (Williams et al., 2012). The apparent correlation of autopolyploidy and derived photosynthetic types in the Neurachninae offers an opportunity to test the
link between genetic redundancy and photosynthetic diversification within a sound phylogenetic framework.

Conclusion
The Neurachninae have long been viewed as a potential model for understanding the evolution of C₄ photosynthesis in the grasses due to natural photosynthetic variation in the group; however, evolutionary inferences were hampered by the lack of a phylogenetic framework. Using multiple markers from the chloroplast region, due to natural photosynthetic variation in the group; however, molecular dating indicates that these events most probably occurred during the late Pliocene, an epoch of relatively low atmospheric CO₂ (Gerhart and Ward, 2010), when the Australian continent became drier (Bowler, 1976). The present-day distribution of extant Neurachninae (Prendergast and Hattersley, 1985) indicates that the group appeared in the red sand soils and stony rises of semi-arid west-central Australia. These observations are consistent with recent models of C₄ evolution that hypothesize that climate deterioration in the past 5 million years selected for a series of traits that predisposed taxa to evolve novel photosynthetic mechanisms to deal with the combined effects of severe stress and low atmospheric CO₂ (Sage et al., 2012).

Supplementary data
Supplementary data are available at JXB online.
Figure S1. Neurachninae phylogeny inferred from plastid markers.
Figure S2. Neurachninae phylogeny inferred from the ITS region.
Figure S3. Phylogenetic relationships among *aroideh* sequences.
Figure S4. Phylogenetic relationships among *waxy* sequences.
Figure S5. Phylogenetic relationships among *ppc-B2* sequences.
Figure S6. Phylogenetic relationships among *ppc-B2* sequences deduced from intron sequences.
Figure S7. Distribution of *Neurachne* spp. and *Paraneurachne muelleri* in Australia.
Table S1. *Neurachne*, *Paraneurachne*, and *Thyridolepis* samples used for genome size analyses.
Table S2. Plastid and ITS sequences from *Neurachne*, *Paraneurachne*, and *Thyridolepis* species used in phylogenetic analyses.
Table S3. Primers used in this study.
Table S4. Neurachninae sampled for low-copy number nuclear markers.
Appendix S1. Herbarium vouchers for specimens of *Neurachne*, *Paraneurachne*, and *Thyridolepis* sampled for carbon isotope assays.

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References


