Water lily (*Nymphaea thermarum*) genome reveals variable genomic signatures of ancient vascular cambium losses

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Edited by Peter H. Raven, Missouri Botanical Garden, St. Louis, MO, and approved March 2, 2020 (received for review December 30, 2019)

For more than 225 million y, all seed plants were woody trees, shrubs, or vines. Shortly after the origin of angiosperms ∼140 million y ago (MYA), the Nymphaeales (water lilies) became one of the first lineages to deviate from their ancestral, woody habit by losing the vascular cambium, the meristematic population of cells that produces secondary xylem (wood) and phloem. Many of the genes and gene families that regulate differentiation of secondary tissues also regulate the differentiation of primary xylem and phloem, which are produced by apical meristems and retained in nearly all seed plants. Here, we sequenced and assembled a draft genome of the water lily *Nymphaea thermarum*, an emerging system for the study of early flowering plant evolution, and compared it to genomes from other cambium-bearing and cambium-less lineages (e.g., monocots and *Nelumbo*). This revealed lineage-specific patterns of gene loss and divergence. *Nymphaea* is characterized by a significant contraction of the HD-ZIP III transcription factors, specifically loss of *REVOLUTA*, which influences cambial activity in other angiosperms. We also found the *Nymphaea* and monocot copies of cambium-associated CLE signaling peptides display unique substitutions at otherwise highly conserved amino acids. *Nelumbo* displays no obvious divergence in cambium-associated genes. The divergent genomic signatures of convergent loss of vascular cambium reveals that even pleiotropic genes can exhibit unique divergence patterns in association with independent events of trait loss. Our results shed light on the evolution of herbaceousness—one of the key biological innovations associated with the earliest phases of angiosperm evolution.

Nymphaea | vascular cambium | angiosperm evolution | genome | trait loss

In all seed plants, vascular tissue (xylem and phloem) initially develops in distinct bundles near apical meristems as part of primary growth and differentiation. In stems of most seed plants, the subsequent activation of a population of meristematic cells within and between the bundles forms a continuous layer of vascular cambium, which then produces rings of secondary xylem and phloem responsible for increases in stem or root girth (Fig. 1) (1). Secondary growth provides the additional fluid transport capacity and mechanical support necessary for large, photosynthetic canopies to operate. A vascular cambium and production of secondary xylem and phloem are plesiomorphic for angiosperms. Loss of a vascular cambium is rare (2–5)—even most herbaceous taxa (including *Arabidopsis*) form a vascular cambium at some point in their ontogenies. Although additional losses may have occurred, only five losses of vascular cambium have been well-documented across angiosperms (6) (Nymphaeales, *Ceratophyllum*, monocots, *Nelumbo*, and Podostemaceae), which span ∼140 million y (7) and a diverse array of morphological adaptations and growth habits (Fig. 1*A*).

Although primary and secondary vascular tissues in seed plants are derived from different meristematic cell populations, both are produced by precise patterning of the same suite of cell types. Accordingly, some of the same gene families or genetic modules function in both developmental contexts (1, 6, 8–11): the *CLAVATA* (*CLE*)–*WUSCHEL* (*WOX*) regulatory loop promotes meristem identity at the cost of xylem formation (10–13) while multiple HD-ZIP III family members promote xylem differentiation and bipolar patterning of daughter cell types (14–18) (*SI*

Significance

For ∼225 million y, all seed plants were woody trees, shrubs, or vines. Shortly after the origin of flowering plants ∼140 million y ago, Nymphaeales (water lilies) became one of the first seed plant lineages to become herbaceous through loss of the meristematic cell population known as the vascular cambium. We sequenced and assembled the draft genome of the water lily *Nymphaea thermarum* and compared it to genomes of other plants that have retained or lost the vascular cambium. By using both genome-wide and candidate-gene analysis, we found lineage-specific patterns of gene loss and divergence associated with cambium loss. Our results reveal divergent genomic signatures of convergent trait loss in a system characterized by complex gene-trait relationships.

Author contributions: M.G., C.C.D., and W.E.F. designed research; R.A.P., J.M.D., C.G., M.M., and J.J. performed research; C.C.D. supervised genome sequencing and genome analysis; R.A.P., J.M.D., C.G., M.M., J.J., Z.X., S.M., and C.C.D. contributed new reagents/analytic tools; R.A.P., J.M.D., C.G., P.R.V.S., and Z.X. analyzed data; and R.A.P. wrote the paper with input from S.M., M.G., C.C.D., and W.E.F.

The authors declare no competing interest.

This article is a PNAS Direct Submission.

Data deposition: Raw sequence data, whole-genome assembly, and transcriptomes of *Nymphaea thermarum* are available in to the National Center for Biotechnology Information (NCBI) database, https://www.ncbi.nlm.nih.gov/, under BioProject PRJNA508901.

See online for related content such as Commentaries.

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This article contains supporting information online at https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.1922873117/-/DCSupplemental.

First published March 31, 2020.

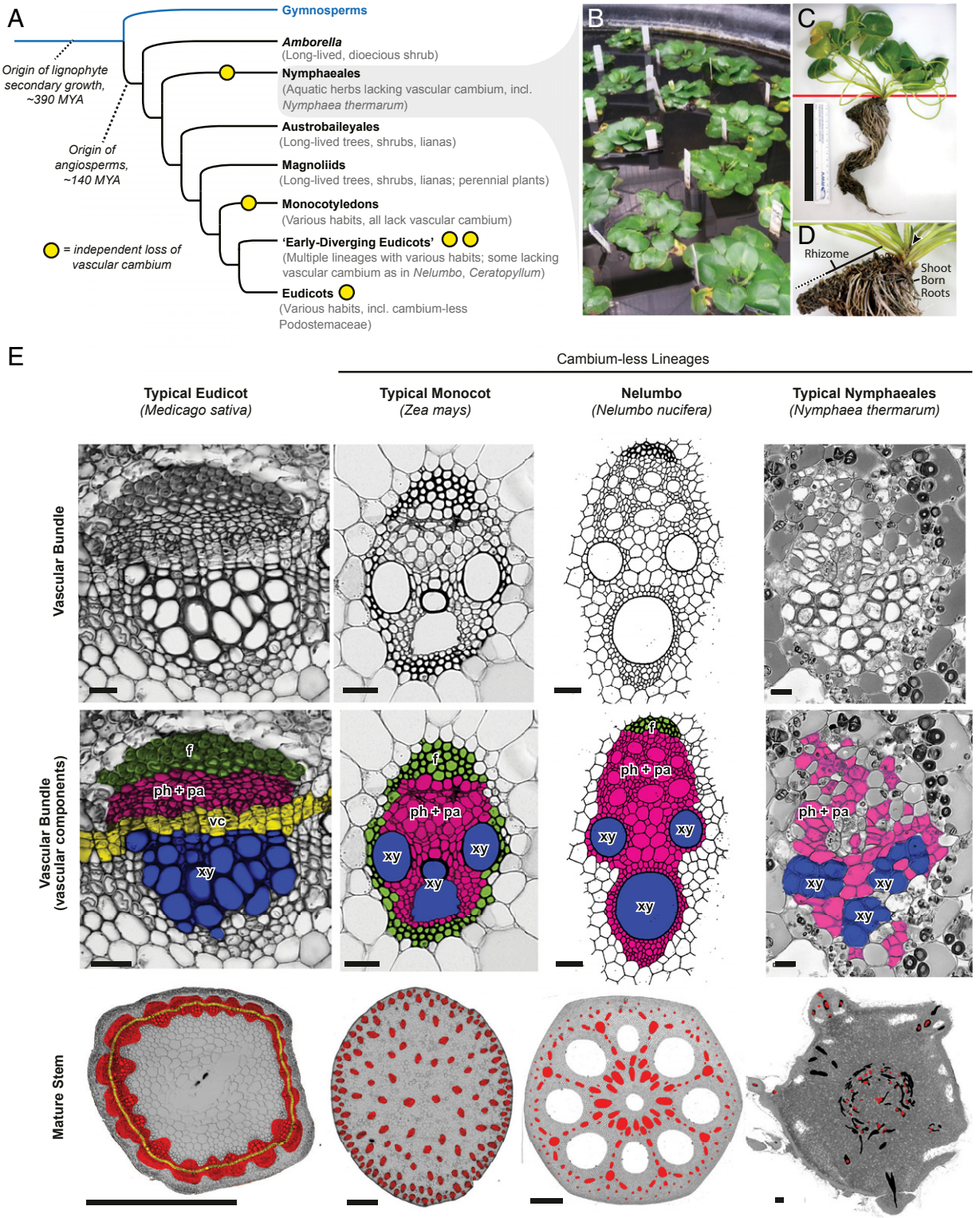

Fig. 1. Vascular cambium evolution and stem vascular anatomy in flowering plants. (*A*) Abbreviated phylogenetic relationships of major clades of seed plants, with notes on diversity of growth habits found in each group. MYA, million years ago. (*B*) Growth habit of *Nymphaea thermarum*. (*C*) One individual of *N. thermarum*. Red line indicates in situ soil level. (Scale bar, 15 cm.) (*D*) Close-up of rhizome from *C*. Arrowhead, apical meristem; black line, living rhizome section; dashed line, dead rhizome section. (*E*) Stem vascular anatomy in clades of flowering plants. Cross-sections were taken from maturing (*Medicago*) or mature (*Zea*, *Nelumbo*, *Nymphaea*) stems. (*Top Row*) Micrographs (*Medicago*, *Zea*, *Nymphaea*) or drawings based on prepared slides (*Nelumbo*) of vascular bundles. (Scale bars, 20 μm.) (*Middle Row*) Vascular components labeled and color-coded. f (green), fibers; ph + pa (pink), phloem and vascular parenchyma; vc (yellow), vascular cambium; xy (blue), xylem. (*Bottom Row*) Whole stem sections. red, vascular bundles and tissue in cross-section; yellow, vascular cambium; black, vascular bundles that are part of a leaf or flower trace; gray, nonvascular tissue. (Scale bars, 0.5 mm.) *Nelumbo* panels adapted with permission from ref. 27.

Appendix, Fig. S1). The functions of HD-ZIP III members and *CLE–WOX* modules have been documented during primary and secondary vascular differentiation in distantly related eudicots, including *Arabidopsis thaliana*, *Populus trichocarpa*, and *Zinnia elegans*, using loss-of-function and/or overexpression studies (1, 8, 19, 20). Whereas at least partial expression or functional redundancy between gene family members is common (15, 18), subfamilies of HD-ZIP III and *CLE* genes display ontogenic specialization.

The complexity of vascular differentiation and its regulation therefore raises the question of how relevant regulatory genes might evolve (21, 22) in association with the loss of the vascular cambium and secondary tissues. Convergent loss or divergence of relevant genes has been documented in cases of convergent trait loss (23–25), suggesting a consistent, predictable association between trait loss and evolution of relevant genetic components. We use the repeated loss of the vascular cambium in angiosperms to test this association in a system characterized by pleiotropy and genetic redundancy.

Results

The loss of vascular cambium during the early evolution of the water lily lineage (Nymphaeales) likely represents one of the oldest vascular cambium losses among seed plants. Stem vascular structure is sparsely documented within the Nymphaeales (26) and undescribed in *Nymphaea thermarum*. We investigated rhizome (underground stem) anatomy in *N. thermarum* and found no evidence of a vascular cambium or secondary vascular tissues (Fig. 1*D*). Additionally, *N. thermarum* vascular bundles contained no fibers, which differs from other cambium-less lineages (27) (Fig. 1*E*). Thus, all vascular tissues in *N. thermarum* are primary tissues derived from apical meristems.

Genomes for representatives of two of the five seed plant lineages that have independently lost the vascular cambium (monocots and *Nelumbo*) are already available. To create a genomic resource for *N. thermarum*, we combined data generated from short insert libraries (~40× coverage) and mate-pair libraries (~20× coverage) to create a draft genome assembly (Dataset S1). The total length of the assembled genome size was 368,014,730 base pairs (bp) after discarding scaffolds <1 kilobase (kb), and a *k*-mer analysis of short insert reads estimated the genome size at 497,339,103 bp. These values are ~74% and ~100%, respectively, of the 1C size estimate of 0.51 pg as evaluated by flow cytometry (28) (roughly 498,780,000 bp). For comparison, the 1C (the total amount of DNA contained within a single [haploid] set of chromosomes) genome sizes of some popular systems for plant genetics are 0.16 pg (*A. thaliana*), 0.50 pg (*Oryza sativa*), and 2.70 pg (*Zea mays*); known 1C values of other members of the ANA-grade lineages (Amborellales, Nymphaeales, and Austrobaileyales), which diverge from the rest of angiosperms at basal nodes, range from 0.46 pg to 14.92 pg (mean = 3.29, median = 1.98, n= 47) (29). We also generated and assembled transcriptomes from leaves, roots, and reproductive material. When combined with available plant protein data, we annotated 25,760 protein-coding genes that overlapped input transcript or protein evidence, a Pfam domain, and/or a hit to the UniProt database (*SI Appendix*, Fig. S2). By comparison, the genome of *Amborella* (30) is annotated with 26,846 protein-coding genes (*SI Appendix*, Fig. S2). The *N. thermarum* assembly contained 865 of 956 (90%) of conserved plant proteins (31), suggesting that its genic regions were well-represented. Whereas changes in noncoding regions likely are important for morphological evolution (25), we limited our analyses to coding regions due to higher confidence in their recovery and annotation across multiple genomes.

To detect significant contraction of gene families in cambium-less lineages, we first identified ortholog clusters from 28 genomes of seed plants, including three of five lineages that have independently lost the vascular cambium (i.e., *Nymphaea*, stem monocot, and *Nelumbo*) (Dataset S2). We estimated gene trees for 1,439 clusters that passed stringent filtering criteria (32) and then used them to estimate species trees with both concatenation and coalescent methods, including different subsets of the data (i.e., fast-evolving sites, slow-evolving sites, or all sites). All method and dataset combinations produced species trees with similar, strongly supported topologies for relationships of interest, including support for *Amborella* as sister to all other extant angiosperm lineages (*SI Appendix*, Fig. S3). We used CAFE (33) to detect significant ortholog cluster contraction and expansion across all branches of our species phylogeny on a fossil-calibrated species tree (ASTRAL-II, all rate classes dataset) and the set of gene cluster sizes (Fig. 2*A* and *SI Appendix*, Fig. S4). Among a total of 8,147 ortholog clusters included in the analysis, we found that 28 clusters underwent significant expansion within the Nymphaeales while 30 significantly contracted (Dataset S3 and *SI Appendix*, Fig. S4). Few clusters were contracted in more than one cambium-less lineage (Fig. 2*B*). Clusters expanded in *N. thermarum* were enriched for Gene Ontology (GO) terms related to secondary metabolism (including carbohydrate and polysaccharide metabolism), biosynthesis, and response to stimuli. Contracted clusters in *Nymphaea* were most strongly enriched for nucleosome assembly, fatty acid biosynthetic process, response to auxin stimulus, and meristem initiation (Fig. 2*B* and *SI Appendix*, Fig. S5 and Dataset S4).

The contracted cluster associated with the meristem initiation GO term comprises class III HD-ZIP genes, a gene family known to regulate differentiation of both primary and secondary vascular tissues (34, 35). Specifically, *N. thermarum* lacks a copy that belongs to the *REVOLUTA* (*REV*) subgroup (Fig. 2*C* and *SI Appendix*, Fig. S6). We further determined that no *REV* homolog was present in the transcriptomes of several *N. thermarum* tissues or in an expressed sequence tag (EST) database of *Nuphar advena* (36), another member of the Nymphaeales (Fig. 2*C* and *SI Appendix*, Fig. S6). The presence of a *REV* gene in *Amborella* and many other angiosperms (Fig. 2*C* and *SI Appendix*, Fig. S6) suggests that the lack of *REV* in *Nymphaea* and *Nuphar* represents a loss within the Nymphaeales. While some *REV* functions overlap with those of other HD-ZIP III members in embryogenesis and primary growth, *REV* misexpression is known to impact both cambial initiation and xylary fiber differentiation during secondary growth in stems of *A. thaliana* and *P. trichocarpa* (14, 15, 18, 37). The combined absence of xylary fibers, vascular cambium initiation, and *REV* in *N. thermarum* (Fig. 1*D* and 2*C* and *SI Appendix*, Fig. S6) is consistent with the hypothesis that *REV* is a key regulator of vascular cambium activity and differentiation of secondary tissues throughout angiosperms.

We further found that significant contraction of the HD-ZIP III family occurred along only two other branches (Fig. 2*A* and Dataset S3): the terminal branches leading to *Zostera* (sea grass) and *Beta* (beet). These species are characterized by either the absence of secondary tissues (*Zostera*) or by a highly anomalous pattern of vascular cambium activity that does not produce continuous rings of secondary xylem and phloem (*Beta*) (38–40). In contrast, some cambium-less lineages (some monocots and *Nelumbo*) retain homologs from all HD-ZIP III subfamilies (Fig. 2*C* and *SI Appendix*, Fig. S6). Therefore, while all lineages with a significant contraction of the HD-ZIP III gene family display a loss of normal vascular cambium development, complete loss of HD-ZIP III genes is not consistently associated with loss of vascular cambium. This result demonstrates variability in the patterns of gene loss associated with independent, homoplasious evolutionary events.

In addition to corroborating the importance of HD-ZIP III genes in vascular development, the ortholog clusters that are contracted in cambium-less lineages can be used to identify candidate genes for vascular cambium regulation. The set of

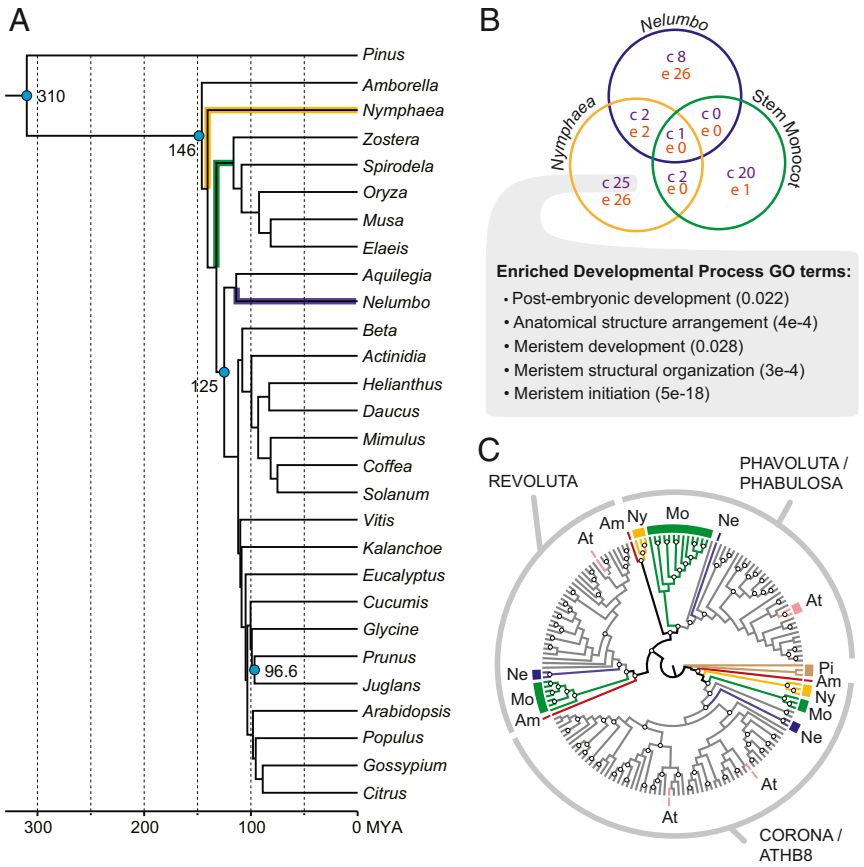

Fig. 2. Gene family contraction in cambium-less lineages. (*A*) Fossil-calibrated phylogenomic analysis, including representatives that have independently lost the vascular cambium: *Nymphaea* (yellow), monocots (stem lineage, green), and *Nelumbo* (indigo). Blue dots indicate age and placement of fossils or other estimates used for calibration; fossils and molecular-based estimates are detailed in *SI Appendix, Supplementary Materials and Methods*. (*B*) Venn diagram showing number of significantly contracted gene families in each cambium-less lineage (c, number of significantly contracted gene families; e, number of significantly expanded gene families). The set of gene families uniquely contracted in *Nymphaea* is enriched for "developmental process" GO terms related to meristem development and function (enrichment test *P* value in parentheses). (*C*) Phylogeny of HD-ZIP III genes, with branches colored to reflect identity of genes from major lineages of seed plants (complete tree in *SI Appendix*, Fig. S6). White dots denote branches with >70% bootstrap support. Am, *Amborella trichopoda*; At, *Arabidopsis thaliana*; Mo, monocots; Ne, *Nelumbo nucifera*; Ny, Nymphaeaceae; Pi, *Pinus taeda*.

clusters contracted in *N. thermarum* include genes that code for the auxin-responsive SAUR proteins (41) and the BIM family of BES1-interacting proteins. Intriguingly, BIM and BES1 proteins regulate *SAUR* gene expression in other developmental contexts (42), and BES1 is known to regulate secondary growth (1) (*SI Appendix*, Fig. S1). Together with the contraction of the *BIM* and *SAUR* gene families in a species that lacks a vascular cambium, this suggests that *BIM* and *SAUR* genes may constitute a novel component of vascular cambium regulation. This remains to be experimentally tested.

The analysis of ortholog cluster expansion and contraction, however, did not include all gene families of interest. The CLE (CLAVATA3/EMBRYO SURROUNDING REGION-RELATED) family of short (~21 amino acids) signaling peptides are known to regulate both primary and secondary tissue differentiation in flowering plants (43), but low sequence conservation among members of this gene family precludes many types of analysis. We therefore used CLANS clustering to assess patterns of relatedness between all putative CLE homologs (10) from Phytozome v12 (44) genomes, genomes of *N. thermarum* and *Nelumbo nucifera* (45), available angiosperm transcriptomes from the OneKP initiative (46), and *N. thermarum* transcriptomes (Fig. 3*A* and *SI Appendix*, Fig. S7). We recovered major groups similar to results from previous studies, including a distinct CLE 41/42/44 group, called group 2 (10, 47). Group 2 is associated with vascular differentiation and patterning (48) while the other groups are associated with root nodulation (group 3) or a wide range of developmental processes, including the activity of shoot and root apical meristems (group 1) (47). After adjusting for evolutionary distance of comparisons (*SI Appendix*, Fig. S8) to calculate APAV (adjusted pairwise attraction values) (scaled from 0 to 1, with 1 indicating the highest sequence similarity), group 2 amino acid sequences from species without a vascular cambium (NVC) and species with a vascular cambium (VC) were overall less similar than sequences from any two species that retain the vascular cambium (VC–VC) (Fig. 3*B*). This relationship was only present and significant (*t* test, P value < 0.05 and a >1% difference) for comparisons within group 2 (*SI Appendix*, Table S1). Therefore, divergence of CLE sequences from cambium-less taxa has occurred within group 2, but not within the other CLE groups that are associated with primary root and shoot development.

The low similarity of group 2 NVC–VC comparisons was largely driven by the divergence of monocot sequences (Fig. 3*C*). However, comparison of the C-terminal residues (Fig. 3*D*) revealed that both monocot and *N. thermarum* sequences show lineage-specific divergences of the five amino acids that precede the signaling peptide. These residues are immediately adjacent to a cleavage site. Changes to residues surrounding the cleavage site may impact cleavage, and therefore mobility, of the peptide (47). Furthermore, in the *N. thermarum* sequence, a proline (P7) that is conserved across almost all angiosperm CLE peptides (47)

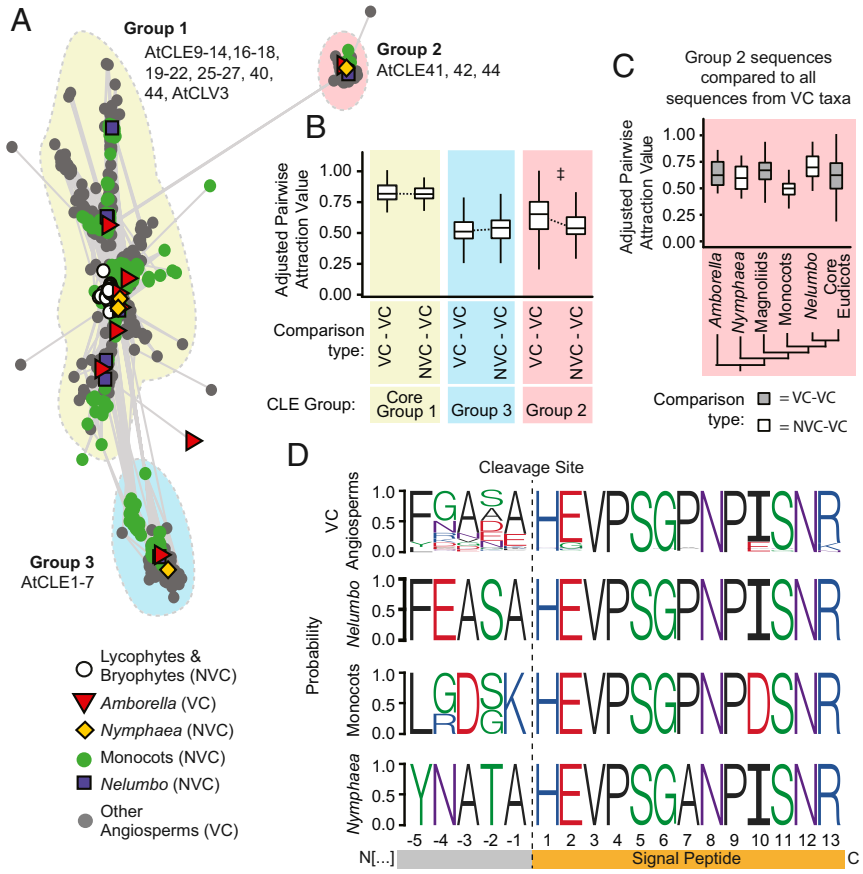

Fig. 3. Evolution of vascular development-associated CLE peptides. (*A*) Two-dimensional CLANS clustering of conserved amino acid sequences of CLE peptides in land plants. Dots/shapes represent individual sequences, coded to indicate whether they are from species within clades that have vascular cambium (VC) or do not have vascular cambium (NVC). Lines indicate PAV < 1e−5. (*B*) APAV for all pairwise comparisons of CLE sequences between two VC taxa (VC–VC) or between one NVC and one VC taxa (NVC–VC), for each group of CLE peptides. Higher APAV indicate higher sequence similarity. ‡ indicates *t* test adjusted *P* value < 0.05 and median APAV difference >1% (Dataset S1). (*C*) APAV values for all sequences within group 2 CLE peptides, for comparisons between all VC taxa and taxa within particular clades of flowering plants. (*D*) Conserved peptide region of group 2, including the 13-amino acid signal peptide at the C terminus and five amino acids upstream of the peptide cleavage site. For box plots: center line, median; box limits, upper and lower quartiles; whiskers, 1.5× interquartile range; outliers removed from plots for clarity, but not from analysis.

is substituted with an alanine. Hydroxylation of this proline (as well as P4) is required for maturation of active group 2 CLE peptides in *Arabidopsis* (49, 50). Additionally, prolines are necessary for certain types of kink formation (51); a substitution with alanine could negatively impact the ability of the peptide to conform to a receptor binding pocket (50, 52). In monocot sequences, a nonpolar C-terminal binding anchor site (I9) is replaced with a negatively charged residue (D9). Intriguingly, cooption of group 1 CLE peptides, but not group 2, has been associated with secondarily derived vascular cambia within monocots (53). This supports our conclusion that the observed divergence of group 2 CLE peptides within some cambium-less taxa might render them nonfunctional during vascular cambium development and activity.

Discussion

Studies of convergent trait loss often document convergent patterns of sequence loss/divergence (23–25, 54). However, many clear examples of gene loss in association with trait loss involve genes with one or few functions (55–57), and highly interconnected genes are less likely to be lost or modified (58). We find, however, that *N. thermarum* is characterized by both divergence of a highly conserved CLE amino acid position and a significant contraction of the HD-ZIP III gene family of transcription factors—specifically loss of *REVOLUTA*, the HD-ZIP III member most closely associated with cambial activity and xylary fiber production in other angiosperms. In contrast, other lineages display unique signatures of cambium loss: All monocot taxa displayed a shared divergence of cambium-associated CLE signaling peptides, supporting a single loss of the cambium early in monocot evolution. Meanwhile, *Nelumbo* displays little obvious evidence of gene loss or divergence of key vascular cambium regulators. Our results confirm that not only can modification of pleiotropic genes occur in systems characterized by complex gene-trait relationships involving pleiotropy and genetic redundancy, but that genomic signatures of trait loss vary between lineages that represent homoplasious loss events.

Loss of the vascular cambium is highly correlated to transitioning from a terrestrial to an aquatic habit: Nymphaeales, *Nelumbo*, *Ceratophyllum*, and Podostemaceae are all aquatic lineages (59). Even in the case of monocots, the last common ancestor of the lineage has been proposed to have been semi-aquatic (60). Although there are many types of aquatic habits, submersion in or proximity to water means that aquatic plants typically do not require extensive mechanical reinforcement or high fluid transport capacity. Thus, the loss of selection for the functions performed by the vascular cambium appears to lead readily to the loss of vascular cambium formation. While the conditions that lead to cambium loss may be consistent across independent evolutionary events, our results suggest that the

associated changes to genetic components of cambium regulation are not.

The exploration of new growth habits, such as nonwoody aquatic herbaceousness in Nymphaeales, is a hallmark of early angiosperm evolution (3). Yet, the genetic basis for the evolutionary diversification of early angiosperms has remained largely inaccessible due to the lack of a tractable system for genetic analyses outside of monocots or eudicots. Publication of the *Amborella* genome (30) represented a significant advance for understanding the genetic basis of flowering plant origins. However, extant members of the ANA-grade lineages, which diverge from the rest of angiosperms at basal nodes, commonly exhibit habits ill-suited to maintaining large populations in controlled laboratory environments, long generation times (Fig. 1*A*), and large genomes (>1 gigabase [Gb]) (29, 61). *N. thermarum*, the smallest member of the Nymphaeaceae, has a short generation time of 4 to 5 mo, has one of the smallest genomes described for any member of the Nymphaeales, and can both self-fertilize and outcross (28, 62, 63). A draft genome of *N. thermarum* represents a critical step in developing a system for functional genetics from within the ANA-grade lineages—a tool that holds great promise for addressing Darwin's "abominable mystery" regarding the early radiation of the most species-rich clade of plants on earth (64, 65).

Methods

Extended methods are available in *SI Appendix, Supplementary Materials and Methods*.

Genome Sample and Sequence Collection. Whole genome sequence data were collected from a live specimen of *N. thermarum* at the Arnold Arboretum at Harvard University. Genomic DNA was extracted using a modified cetyltrimethylammonium bromide extraction protocol (66). Short insert and mate-pair libraries were prepared for sequencing using 1 μg of DNA each with the Illumina TruSeq Library Kit and the Illumina Nextera Mate Pair Library Kit. Size selection was conducted using a Sage Science Pippin Prep machine with a target insert size of 3 kb. Both libraries were sequenced on an Illumina HiSeq 2500 sequencer with v4 chemistry (2× 250-bp reads for the short insert library and 2× 125-bp reads for the mate-pair library).

Transcriptome Sequence Collection, Assembly, and Annotation. RNA was extracted from various tissues (leaves, roots, floral buds, and ovules) of multiple *N. thermarum* individuals grown at the Arnold Arboretum of Harvard University using a hot acid–phenol protocol (67). Libraries for RNA-Seq analysis were prepared by the Whitehead Institute Genome Technology Core, from total RNA (200 to 500 ng) with the Apollo 324 system from WaferGen Biosystems using the WaferGen Prep-X Directional RNA-Seq kit according to the manufacturer's protocols to produce strand-specific complementary DNA (cDNA) libraries. Adapter-ligated cDNA fragments were enriched and amplified with 15 cycles of PCR using the HiFi NGS Library Amplification kit from KAPA Biosystems. Libraries were multiplexed at equimolar concentration and sequenced on the Illumina HiSeq 2500 for 1× 40 bases. Ribosomal RNA (rRNA) reads were filtered out with Bowtie (68) by alignment to rRNA sequences from multiple *Nymphaeales*. Remaining reads were assembled using the Trinity pipeline (69, 70). TransDecoder was applied to contigs with the unstranded option to identify open reading frames (ORFs) (70). BLASTN, querying against the TAIR10 *Arabidopsis* cDNA database at an E-value of 0.05, was used to assign identities to the ORF encoded by the mRNA.

Genome Assembly and Annotation. Reads from the short insert library were assembled into contigs using DISCOVAR de novo v52488 (71). We next used the mate-pair data and SSPACE v3.0 (72) to join contigs into scaffolds, which resulted in a draft de novo assembly of 368,014,730 bp in 6,225 scaffolds with an N50 (the minimum contig length needed to cover 50% of the genome) of 275,242 bp (scaffolds <1 kb were discarded). Repeats were masked with RepeatMasker v4.0.5 (73). The quality of the draft genome was assessed with BUSCO v1.1 (31) for conserved plant genes.

This assembly was then annotated using MAKER v2.31.8 (74) using protein evidence (protein sequences from select angiosperm reference genomes) and transcript evidence (transcripts of *N. thermarum*). Four iterations of MAKER were completed, each with annotations limited to >20 amino acids on scaffolds >5 kb in length. In the first run, we initialized gene models for the ab initio software SNAP (75), and, in subsequent runs, the gene models were refined using the best ~2,500 genes, and the ab initio program AUGUSTUS (76) was also added. MAKER generated 60,427 annotations, of which 25,760 had an annotation edit distance <1, a Pfam domain (searched with InterProScan), or a blastp hit to the UniProt database. We used Proteinortho v5.11 (77), with default settings, to identify shared and unique orthogroups between *N. thermarum*, *A. thaliana*, and *Amborella trichopoda*.

Phylogenomic Analysis. We clustered homologs via an all-vs.-all pairwise search with BLASTP v2.2.25 (78) with an E-value of 1e−20, followed by grouping with MCL v09-308 with an inflation value of 5.0 (79). We clustered in-paralogs at 98.5% identity using CD-HIT v4.6 (80) and retained the longest amino acid, or chose one randomly in case of ties. We required clusters to 1) include at least four species with 2) at least one sequence from *Pinus* (for outgroup rooting), *Amborella*, and *Nymphaea* each, 3) include at least 100 amino acids for each sequence (81), 4) have a mean of less than five homologous sequences per species, and 5) have a median of less than two sequences per species (32). We aligned retained genes with MUSCLE v3.8.31 (82). We removed high-entropy regions of the alignment with TrimAl v1.2rev59 (83) and back-translated the amino acid alignment to codons using PAL2NAL v14 (84). We calculated homolog trees on the back-translated codons using the GTRGAMMA model in RAxML v8.2.8 (85) with *Pinus* designated as the outgroup, running 100 rapid bootstraps, and selecting the best-scoring maximum likelihood tree. We inferred orthologs following the "Maximal Occupancy" methods of Yang and Smith (86). Using only the inferred ortholog sequences, we then made multiple alignments, filtered high-entropy regions, back-translated to codons, and calculated gene trees.

We concatenated the alignments into a supermatrix and identified parsimony informative sites using FASconCAT v1.02 (87). We calculated observed variability for every alignment position in the supermatrix as described by Goremykin et al. (88): For a given alignment position, the sum of all pairwise differences is divided by the total number of characters. We created two synthetic alignments for each gene cluster by partitioning parsimony-informative alignment positions into those evolving faster and slower than the median. We concatenated the fast and slow synthetic alignments into respective supermatrices. We calculated species trees on all three supermatrices and gene trees for the fast and slow evolving synthetic alignments using RAxML as described above. We built species trees from gene trees for all three rate categories using ASTRAL-II v4.10.6 (89) and MP-EST v1.4 (90).

Phylogenomic Dating, Estimation of Gene Family Expansion/Contraction, and GO Enrichment Analysis. We used the ASTRAL II all-rate classes tree for phlyogenomic dating with r8s v1.5 (91). Four nodes were fixed or constrained, based on fossil evidence (7). Clusters used for phylogenomic analysis were filtered for a mean cluster size variance per taxa of less than or equal to 140, with a median size greater than or equal to one, leaving a set of 8,147 clusters included for further analysis with CAFE v3.1 (33).

For nodes of interest within the species tree, clusters for which cluster size changed significantly were identified (*P* value of change from previous node <0.05). Within a cluster of interest, the gene IDs of all *A. thaliana* sequences were then used as the input for AgriGO Singular Enrichment Analysis (92) (against TAIR9 reference, Fischer test with Yekutieli multiple testing correction).

Evolution of HD-ZIP III Gene Family. The cluster that contained HD-ZIP III members was defined by the presence of *A. thaliana* copies of *REVOLUTA*, *PHAVOLUTA*, *PHABULOSA*, *CORONA*, and *ATHB8*. This cluster was comprised of two clearly delineated subclades. One of these distinct subclades contained the HD-ZIP III genes, and only this subclade was used in further gene family analysis. *Nuphar* putative homologs were identified using HMMR v3.1b1 (93) with aligned nucleic acid sequences of all *Nymphaea* and *Arabidopsis* homologs [aligned with MUSCLE v3.8.31 (82) and then manually trimmed to exclude poorly aligned regions] against the *Nuphar* EST database (36) from the Ancestral Angiosperm Genome Project. ORFs were identified within the *Nuphar* sequences using TransDecoder v2.0.1 (70), and tBLASTx was used to identify *Nuphar* ORFs with a sequence similarity to *A. thaliana* HD-ZIP III genes. *Nuphar* sequences were added to the HD-ZIP III nucleotide alignment, which was then used to estimate the gene family phylogeny with RAxML v8.2.8 (85) (GTRGAMMA model, 100 bootstrap replicates). Trees were viewed in FigTree v1.3.1 (94).

Evolution of CLE Peptides. Putative CLE peptide sequences were collected using a HMMR v3.1b1 (93) search of aligned nucleic acid sequences of all *Arabidopsis* homologs (aligned with MUSCLE and then manually trimmed to exclude the most poorly aligned regions) queried against a broad selection of plant genomes and transcriptomes. Amino acid sequences were aligned using MUSCLE and then trimmed to exclude the most poorly aligned regions. The resulting alignment of ∼100 amino acids was used for CLANS (95) cluster analysis.

In order to normalize for different evolutionary distances represented by comparisons, the effect of evolutionary distance on cross-genera pairwise attraction values (PAV) was modeled in R v3.5.1, using the lm function and divergence times collected from TimeTree (96). The model was then used to remove the effect of evolutionary distance on PAV, to give APAV (*SI Appendix*, Fig. S8). Taxa were classified by whether (VC) or not (NVC) they have a vascular cambium. For sequences for each CLE groups of interest, APAV were sorted into VC–VC and NVC–VC categories depending on the taxa they originate from. Two-sample *t* tests in R v3.5.1 were used to assess differences between APAV of the VC–VC and NVC–VC categories within each CLE subgroup. APAV were also compared between the sets of all sequences from taxa or clades of interest and the set of all sequences from VC taxa.

Microscopy. *N. thermarum* rhizomes older than 1 y were collected from specimens at the Arnold Arboretum of Harvard University, embedded in JB4 resin (Electron Microscopy Sciences), and processed for microscopy (97). Sections were stained with periodic acid–Schiff reagent and toluidine blue (98). Prepared slides of *Medicago truncatula* and *Z. mays* stems were purchased from Triarch Incorporated (Ripon, WI). Bright-field and differential interference contrast images were recorded with a Zeiss Axio Imager Z2 microscope equipped with a Zeiss HR Axiocam digital camera (Zeiss, Oberkochen, Germany).

Data Availability. Raw sequence data, whole-genome assembly, and transcriptomes of *N. thermarum* are available in the National Center for Biotechnology Information (NCBI) database under BioProject PRJNA508901. Biological material and all other data are available in Datasets S1–S4 or *SI Appendix*, or from the corresponding authors upon request.

ACKNOWLEDGMENTS. We acknowledge support from National Science Foundation Grants IOS-0919986 (to W.E.F.), DEB-1120243 (to C.C.D.), MCB-1453459 (to M.G.), IOS-1416825 (to S.M.), and IOS-1812116 (to R.A.P.). Botanische Gärten der Universität Bonn provided original plant material for propagation. We thank S. Conway for assistance with archival research. We thank Schweizerbart Scientific Publishing (http://www.schweizerbart.de/144001100) for granting permission to reproduce and adapt original drawings from ref. 27.

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