The Evolution of the FT/TFL1 Genes in Amaranthaceae and Their Expression Patterns in the Course of Vegetative Growth and Flowering in Chenopodium rubrum

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ABSTRACT

The FT/TFL1 gene family controls important aspects of plant development: MFT-like genes affect germination, TFL1-like genes act as floral inhibitors, and FT-like genes are floral activators. Gene duplications produced paralogs with modified functions required by the specific lifestyles of various angiosperm species. We constructed the transcriptome of the weedy annual plant Chenopodium rubrum and used it for the comprehensive search for the FT/TFL1 genes. We analyzed their phylogenetic relationships across Amaranthaceae and all angiosperms. We discovered a very ancient phylogenetic clade of FT genes represented by the CrFTL3 gene of C. rubrum. Another paralog CrFTL2 showed an unusual structural rearrangement which might have contributed to the functional shift. We examined the transcription patterns of the FT/TFL1 genes during the vegetative growth and floral transition in C. rubrum to get clues about their possible functions. All the genes except for the constitutively expressed CrFTL2 gene, and the CrFTL3 gene, which was transcribed only in seeds, exhibited organ-specific expression influenced by the specific light regime. The CrFTL1 gene was confirmed as a single floral activator from the FT/TFL1 family in C. rubrum. Its floral promoting activity may be counteracted by CrTFL1. C. rubrum emerges as an easily manipulated model for the study of floral induction in weedy fast-cycling plants lacking a juvenile phase.

KEYWORDS

transcriptome FLOWERING LOCUS T/TERMINAL FLOWER1 gene family evolution flowering gene rearrangement Amaranthaceae Chenopodium rubrum

Land plants evolved numerous adaptations to protect against drying, to ensure fertilization, and to cope with Earth’s gravity. The effective control of plant architecture was made possible by an intricate network of regulatory proteins, phytohormones, and growth substances (Vařková et al. 2014). Novel gene families encoding transcription factors and cofactors appeared when plants conquered the land. One of them, the FLOWERING LOCUS T/TERMINAL FLOWER1 (FT/TFL1) gene family, regulates the transition from the vegetative to the reproductive phase and controls plant growth (Wickland and Hanzawa 2015). The family can be divided into three phylogenetic clusters: MOTHER OF FT AND TFL1 (MFT)-like, TFL1-like, and FT-like. The most ancestral clade includes MFT-like genes, found in mosses, lycopods, and all seed plants (Hedman et al. 2009). Their original function is related to growth arrest and dormancy, satisfying the essential need of land plants to control their size and architecture. The TFL1-like clade originated in seed plants in order to independently regulate seed and bud dormancy (Kaligren et al. 2011). The most recent FT-like clade arose with angiosperms. The FT-like proteins constitute the principal
component of florigen, a long sought after substance promoting flowering (Corbesier et al. 2007; Jaeger and Wigge 2007). The evolution of the FTTFL1 genes was driven by extensive gene duplications. They occurred in all lineages of flowering plants and were often associated with functional shifts (Pin et al. 2010; Navarro et al. 2011; Wang et al. 2015).

Six members of the FTTFL1 gene family exist in Arabidopsis thaliana, a model long-day plant (Kardailsky et al. 1999; Kobayashi et al. 1999). The FT and TWIN SISTER OF FT (TSF) genes are floral promoters. In contrast with FT, the TSF gene is activated by cytokinins under nonpermissive short days (D’Alonzo et al. 2011), demonstrating the functional diversification of both flowering activators. Members of the TFL1 subfamily act as floral repressors. TFL1 maintains inflorescence meristem in the shoot apex and delays its differentiation into floral organs (Simon et al. 1996). ARABIDOPSIS THALIANA CENTRORADIALIS HOMOLOG (ATC) functions as a graft transmissible floral repressor under short days (Huang et al. 2012). BROTHER OF FT AND TFL1 (BFIT) inhibits floral initiation under salt stress (Ryu et al. 2011). Finally, MFT is highly expressed in seeds and affects germination by interacting with abscisic acid and gibberellin signaling pathways (Xi et al. 2010).

Functional shifts of FT proteins have occurred in many plant species, e.g., in sunflower (Blackman et al. 2010), tobacco (Harig et al. 2012), sugarcane (Coelho et al. 2014), and soybean (Wang et al. 2015). Novel FT-derived floral repressors carry mutations in the positions proven to be critical for regulatory function by site-specific mutagenesis in A. thaliana (Hanzawa et al. 2005; Ahn et al. 2006; Ho and Weigel 2014). For example, BvFT1 inhibits flowering in sugar beet, whereas its paralog BvFT2 is a floral promoter. This functional shift was associated with the exchange of Tyr-134 for Asn, and Trp-138 for Gln (Pin et al. 2010).

Chenopodium rubrum (red goosefoot) is the only representative of the family Amaranthaceae besides sugar beet, in which FT-like genes have been identified and their functions estimated in transgenic A. thaliana. The CrFT1 gene acted as a floral promoter similarly to its ortholog BvFT2 in sugar beet (Pin et al. 2010). In contrast, the CrFTL2 gene orthologous to the sugar beet repressor BvFT1 was not involved in flowering control (Cháb et al. 2008; Drabešová et al. 2014). C. rubrum is a tetraploid species (Loeve and Loeve 1982), most likely an allotetraploid (Fuentes-Bazán et al. 1999; Navarro et al. 2012). The evolution of FT and TSF genes was driven by extensive gene duplications. They occurred in all lineages of flowering plants and were often associated with functional shifts (Pin et al. 2010; Navarro et al. 2011; Wang et al. 2015).

In the current work, we performed a comprehensive study of the FT/TFL1 gene family in C. rubrum. We constructed a reference transcriptome, identified the members of this family, and generated the phylogenetic tree across angiosperms. The absence of the juvenile phase and the existence of only one floral activator from the FT/TFL1 gene family makes C. rubrum an attractive model to study floral induction and for comparison with other amaranths.

**MATERIALS AND METHODS**

**Plant material and growth conditions**

Seeds of C. rubrum ecotype 374 (Cumming 1967) were germinated in Petri dishes with wet filtration paper. Germinating seeds were planted...
in 96-well flat-bottom ELISA plates (one seedling per well). The wells were filled with perlite (particle size 0.4–0.8 mm) and perforated at the bottom (1 mm-hole) to provide a nutrient solution. The plates were floated in half-strength Hoagland solution which was replaced each second day. After 3 or 5 d, only average sized seedlings with opened cotyledons (75%) were maintained; the remaining plants were discarded. Selected plantlets were exposed to various photoperiodic treatments – permanent light, one or three periods of darkness followed by permanent light, and a diurnal regime with 12 hr light and 12 hr darkness (Supplemental Material, File S1). The modified floral dip method used in attempts to transform C. rubrum is described in File S2.

**RNA isolation**

Leaf, root, stem, or apical tissues from seedlings, young, or mature plants cultivated under various photoperiodic regimes were collected and flash frozen in liquid nitrogen. Sampling in dark was performed under a dim green light (about 520 nm, Green Hornet LED headlight). Total RNA was isolated using a Plant RNeasy Mini kit (Quiagen, Valencia, CA). DNA contamination was removed by DNaseI treatment according to the manufacturer's protocol (DNA-free, Ambion, TX). RNA quality and concentration were checked on a 0.9% agarose gel and by NanoDrop (Thermo Fisher Scientific, Finland).

**RNAseq**

We sequenced and assembled several C. rubrum transcriptomes, utilizing both 454 pyrosequencing and Illumina HiSeq to achieve a reliable reference transcriptome. The mixture of equal amounts of 44 RNA samples extracted from various tissues of seedlings or mature plants cultivated under various photoperiodic treatments in the growth chamber or in the greenhouse (200 μg in total) was dried in GenTegra tubes (GenTegra, Pleasanton, CA) and sent to Evrogen Joint Stock Company (Moscow, Russia) to prepare a normalized cDNA library (10 μg), which was afterward sequenced using Roche 454 GS-FLX platform with Titanium reagents in the DNA Core facility at Brigham Young University (Provo, UT). We obtained 2,285,349 raw reads from which 1,830,810 reads passed quality filtering. Median read length was 463 bp and the average was 412 bp. The total number of bases reached 754,859,592.

In addition, we selected RNAs isolated in two replicates from 9 organs and developmental stages and sent 12 samples to the University of Southern California Epigenome Center (CA) for library preparation and HiSeq Illumina sequencing, which generated paired end reads (50 bp, fragment size about 200 bp).

**Transcriptome assembly**

Raw Illumina reads were processed to eliminate artifacts from library construction and low quality reads with the Trimmomatic v0.32 software (Bolger et al. 2014). We trimmed all edge bases below quality score 20 and discarded reads shorter than 48 bp. Orphan reads were assigned as single reads. Only paired end reads were used for the reference transcriptome assembly.

454 reads were assembled using Newbler (Gs De novo Assembler v2.8, Roche, Germany) with default settings. A file with the list of sequencing adaptors and primers was specified in order to remove sequencing and PCR artifacts.
For Illumina data we used the following four de novo assemblers: Trinity v2013-02-25, v2014-04-13, and v2.0.6 (Grabherr et al. 2011) SOAPdenovo-Trans v1.03 (Xie et al. 2014), Velvet-Oases v0.2.09 (Schulz et al. 2012), and Trans-Abyss v1.5.1 (Robertson et al. 2010). Trinity was used with the default k-mer size 25, SOAPdenovo-Trans was used with k-mer sizes 20–45 and a step size of 5, Velvet-Oases was used with k-mer sizes 21–29 and step size of 2, and Trans-Abyss was used with k-mer sizes 25–45 and a step size of 2. The assemblies calculated with various k-mers by the same assembler were combined to produce a merged assembly. The utilities offered by individual software packages were applied. Raw data were deposited in SRA database under the accession number PRJNA305086.

Transcriptome assemblies were performed with a 12-core Linux workstation with 60 GB memory (Laboratory of Plant Reproduction, IEB) and with computing resources of virtual organization Metacentrum (Czech National Grid Organization). Contigs shorter than 200 bp were discarded from all assemblies. Redundant contigs were further discarded using CD-HIT v4.6 (Li and Godzik 2006) with settings -c 1.0 -n 5. Contigs shorter than 200 bp were excluded from assemblies and the "best" set of assembled transcripts were than selected using the tr2aacsds pipeline from the EvidentialGene package v2013.07.27 (http://arthropods.eugenes.org/about/EvidentialGene/EvidentialGene_trassemble_pipe.html). Only the primary (main) output transcripts were used for follow-up analyses. The coverage of selected genes was quantified using RSEM (Li and Dewey 2011) bundled with the Trinity software package.

Assembly quality metrics

Several tools were adopted to compare the quality of the assemblies. The first method estimated the proportion of completeness of each assembled transcript by the Ortholog Hit Ratio (OHR) (O’Neil et al. 2010), where an OHR close to 1.0 indicates that the particular transcript was assembled to its full length. The transcripts were aligned against two reference databases: 357 ultraconserved ortholog coding sequences from A. thaliana (Kozik et al. 2008), and a list of 959 single copy nuclear genes shared among Arabidopsis, Oryza, Populus, and Vitis (Duarte et al. 2010). Whereas OHR refers to the completeness of the newly assembled transcripts, the following two metrics—contiguity and completeness (Martin and Wang 2011)—consider the coverages of selected reference transcripts. Completeness is defined as the percentage of expressed reference transcripts covered by all the assembled transcripts, contiguity is the percentage of expressed reference transcripts covered by a single, longest-assembled transcript. The threshold value is the proportion of a particular reference transcript that is covered by an assembled transcript. Both metrics were calculated according to Zhang et al. (2013). Open reading frames in assembled transcripts were identified and translated using the protein databases of five species: Citrus demetina, C. sinensis, Vitis vinifera (downloaded from the Phytozome, Goodstein et al. 2012), Beta vulgaris (downloaded from the Beta vulgaris Resource: bvsseq.molgen.mpg.de, Dohn et al. 2014), and Arabidopsis thaliana (downloaded from the TAIR10, www.arabidopsis.org). Protein sequences were then aligned against databases used also for the calculations of OHR as described above (Kozik et al. 2008; Duarte et al. 2010).

RSEM-EVAL package, part of DETONATE (De novo Transcriptome rNase Assembly with or without the Truth Evaluation) toolkit was used to calculate each assembly score (Li et al. 2014). Due to a big number of contigs in the Oases assembly we were not able to calculate the score for this assembly. Chimeric transcripts were identified and cut using the approach described by Yang and Smith (2013). Chimera identification was based on blastx analyses against protein databases derived from five different species as described above.

RT qPCR

One microgram of RNA and oligo dT primers (500 ng) were heated for 5 min at 65°C, chilled on ice, and mixed with Transcriptor buffer (Roche, Mannheim, Germany), 0.5 μl of Protector RNase Inhibitor (Roche, Germany), 2 μl of 10 mM dNTPs, and 10 units of Transcriptor Reverse Transcriptase (Roche, Germany). The first strand of cDNA was synthesized at 55°C for 30 min. RNA samples were reverse transcribed in two independent RT reactions and each cDNA specimen was measured twice.

The first strand of cDNA was diluted 10−20 times and qPCR was performed using the LightCycler 480 SYBR Green I Master (Roche, Germany) in a final volume of 10 μl with 300–500 nM of each of the high performance liquid chromatography (HPLC) purified primers (Table S1), supplied by Metabion (Germany). The LightCycler LC 480 (Roche, Germany) was programmed as follows: 10 min of initial denaturation at 95°C, then 40 cycles for 10 s at 95°C, 10 s at 60°C (CrFTL1, CrBFT, CrMFT1, CrMFT2, CrCAB) or 8 s at 58°C (actin, CrFTL1, CrFTL2), followed by 15 s at 72°C. PCR efficiencies were estimated from calibration curves generated from serial dilution of cDNAs. A calibrator was used to correct for run-to-run variation. The relative ratio of the target and reference gene was calculated as follows:

Figure 2 (A) The genomic structures of the CrFTL genes in C. rubrum: CrFTL1, CrFTL2 with the additional intron and the novel exon 1a, CrFTL2 pseudogene, CrFTL3. (B) The 3D structure of the CrFTL2 protein as predicted by Modeler (left) or I-TASSER using an A. thaliana FT template (right). The CrFTL2 chain is depicted as a ribbon with a blue N-terminus and a red C-terminus. The FT chain is represented by a backbone of the same color. Arrows show Gly-18, the starting point of the sequence homology between FT and CrFTL2.
Identification of FT/TFL1 genes

A local database was made from the reference transcriptome of C. rubrum. It was searched using the tblastn algorithm with A. thaliana FT/TFL1 protein sequences as queries. The first hits were blasted against an A. thaliana protein database using blastx to confirm mutual homology. The coding sequences of the FT/TFL1 genes in C. rubrum were amplified by PCR with primers (Table S1) designed according to sequences from the reference transcriptome and with cDNA as a template. Another set of primers (Figure S1 and Table S1) was developed to amplify the CrFTL genes from genomic DNA. Cleaned PCR products (GeneJET PCR purification kit, Thermo Fisher Scientific, Finland) were sent to Macrogen Europe Laboratory (Netherlands) for Sanger sequencing. All GenBank accession numbers including newly obtained sequences and the list of species are given in Table S2.

Spinach FT/TFL1 genes were identified in the Spinach 1.0.1 genomic draft published on http://bvseq.molgen.mpg.de/blast/ using the tblastn tool with C. rubrum queries and named according to their respective A. thaliana or C. rubrum homologs. The exons recognized in genomic sequences according to their similarity with C. rubrum genes were joined together to provide virtual sequences of the particular transcripts. Two copies of the SoFTL1-2 gene found in close mutual vicinity in the scaffold 8759 were designated SoFTL1-2a and SoFTL1-2b. The SoFTL1 gene was assembled from the sequences found in two scaffolds, 68,707 and 48,765, most likely due to a misassembly of the spinach genomic draft. Sugar beet genes were retrieved from GenBank by blastp with C. rubrum protein queries, except for BvFTL3, which was identified in ReBeet-1.1 (http://bvseq.molgen.mpg.de/blast/). Owing to an inherent incompleteness of transcriptomes, Amaranthaceae transcriptomes published by One Thousand Plants (1KP) Consortium were not used for data mining.

Phylogenetic analyses

Multiple nucleotide sequence alignment of coding regions guided by the protein sequence alignment was conducted using MUSCLE (Edgar 2004) with default parameters, as implemented in Geneious 7.1.5, and extensive manual editing. The alignment was analyzed by the maximum-likelihood (ML) method using RAxML (Stamatakis 2014). A γ model of rate heterogeneity was applied on three distinct data partitions corresponding to three codon positions. Bootstrap support of the majority rule consensus tree was calculated from 1000 pseudo-replicates. Gaps were treated as missing characters. The proportion of synonymous (Ks) and nonsynonymous (Ka) substitutions between two sequences was calculated using DnaSP v.5 (Librado and Rozas 2009).

3D structure model

Amino acid CrFTL2 sequence in FASTA format was uploaded through the I-TASSER web interface (http://zhanglab.ccmb.med.umich.edu/I-TASSER/) together with the template FT (A. thaliana, MMDB ID: 33642) in Program Database (PDB) format. In addition, a 3D model of CrFTL2 was independently computed with Modeller software (Webb and Sali 2014) using multiple templates (pdb codes 1wkp, 3axy, 1qou, 2iqy, 2jyz) in order to avoid biases introduced by single template and prediction algorithm.

Data availability

The authors state that all data necessary for confirming the conclusions presented in the article are represented fully within the article.

RESULTS

Transcriptome assembly

454 pyrosequencing produced 2,285,349 raw reads from which 1,830,810 reads passed quality filtering. We also obtained ~25 million reads...
raw reads from each of 12 RNA samples sequenced by Illumina (altogether 293,391,190 raw read pairs). 253,682,808 read pairs (86.5%) passed quality check and were used for assembly. A single assembly was generated from the 454 data set by Newbler and 22 assemblies were created from all Illumina reads by four distinct assemblers. A combined superassembly was produced by the EvidentialGene pipeline. The assembly characteristics are summarized in Table 1.

Newbler assembled reads derived from the normalized cDNA library. It produced 22,587 contigs (N50 = 1354) with nearly zero redundancy. Trans-Abyss generated fewer transcripts (478,002) than Oases or SOAPdenovo-Trans, N50 = 1041. The newest version of Trinity (2015) produced 22,587 contigs (N50 = 1354) with nearly zero redundancy. Finally, a combined superassembly was compiled by the EvidentialGene pipeline from all the assemblies except of those produced by SOAPdenovo-Trans. The main output comprised 40,487 transcripts with no redundancy, defined as 100% nucleotide sequence identity. Basic assembly characteristics (for example N50) did not allow to decide which assembly should be chosen as a reference transcriptome. We have therefore employed additional quality metrics to evaluate the assemblies.

**Assembly quality metrics**

The highest completeness (93.7%) and contiguity (91.7%) values, estimated using Beta vulgaris reference, were achieved by Trans-Abyss (Table 1). Using A. thaliana as a reference brought consistent results with slightly lower values owing to a large phylogenetic distance between Oenopodium and Arabidopsis. Trans-Abyss was immediately followed by Trinity and Oases. The assembly of the normalized cDNA library performed by Newbler exhibited only moderate completeness (68.7%) and contiguity (65.7%). Newbler used a 454 data set, which contained <1% of reads compared to the Illumina data set, though the reads were much longer. The worst performing program was SOAPdenovo-Trans with the lowest contiguity: 30.6%. This ranking was confirmed by DETONATE metrics.

The EvidentialGene superassembly (main output) showed the second highest contiguity (88.5%), a slightly lower completeness (89.4%) and a much lower number of transcripts (40,487). The reduction in transcript number was achieved owing to decreased redundancy and chimerism (Table 1), which represent a challenge for the assembly of the transcriptomes in polyploid plants (Nakasugi et al. 2014) Thus, we selected this superassembly as a suitable reference transcriptome of C. rubrum for further studies. At the same time, we retained the Newbler, Trans-Abyss, and Trinity assemblies, and the alternative set of contigs from EvidentialGene superassembly as useful resources to search for rare or alternative transcripts.

### Evolution of the FT/TFL1 genes in Amaranthaceae

We identified eight members of the FT/TFL1 gene family in the reference C. rubrum transcriptome, including the previously described CrFTL1 and CrFTL2 genes (Cháb et al. 2008). Most transcripts occurred in two slightly different variants (nucleotide sequence similarity of coding regions >98%) most likely derived from two homeologous copies existing in tetraploid C. rubrum. Owing to a very low divergence of the homeologous pairs, only one representative sequence (confirmed by Sanger sequencing) was included in phylogenetic analyses. Only three short reads transcribed from the CrFTL3 gene were found in all data sets. Thus, the entire CrFTL3 genomic sequence was obtained by Sanger sequencing genomic DNA (Figure S1) and the CrFTL3 coding region was predicted from it.

We aligned the FT/TFL1 homologs from C. rubrum, spinach, and sugar beet together with Amborella trichopoda, Zea mays, Arabidopsis thaliana, and Jatropha curcas genes and constructed a ML phylogenetic tree depicting the evolutionary history of the FT/TFL1 family in angiosperms (Figure 1). The phylogram shows two well-supported clades corresponding to the FT and TFL1 subfamilies. Furthermore, it contains unresolved basal branches representing the members of the MFT subfamily—the single AtrIMFT gene from A. trichopoda, the cluster of Z. mays genes, and two clades with C. rubrum MFT paralogs. The CrMFT1 gene clustered together with spinach SoMFT1 and two BvMFT paralogs. The CrMFT2 gene and its spinach homolog belonged to the same clade as A. thaliana MFT.

The gene duplication in C. rubrum and sugar beet, which generated CrFTL1 and CrFTL2 (Cháb et al. 2008), and BvFT2 and BvFT1 (Pin et al. 2010), was well documented in the FT clade. Moreover, another cluster composed of FT3 genes diverged before this duplication, but after the separation of Amaranthaceae genes from monocots and Vitis vinifera. We found no other FT3 homologs in any public database except for spinach and sugar beet. One homeolog pair of each of the BFT, CEN, and TFL1 genes was identified in C. rubrum. The BFT genes formed the clade at the base of the TFL1 subfamily.

The evolution of the FT/TFL1 genes was accompanied by gene duplications and gene losses. The deepest gene duplication occurred in the MFT lineage in early angiosperm evolution. C. rubrum and spinach, as well as J. curcas retained both paralogs, but MFT2 was lost in sugar beet. Instead, two MFT1 copies evolved in sugar beet. The FT clade exhibited the duplication leading to FTL2 genes, but also a more ancient event creating the FTL3 cluster. Recent duplications of SoCEN and SoFTL1 genes occurred in spinach.

**Figure 4** Phenotypes of C. rubrum plantlets growing under three light regimes. LL: permanent light; 3 LD–LL: three consecutive periods 12 hr light/12 hr dark followed by permanent light; LD: 12 hr light/12 hr dark. The actual size (in cm) is given on the left. The plants were pressed and scanned.
Genomic structure of the CrFTL2 gene and 3D structure of the CrFTL2 protein
To understand the structural evolution of the CrFTL genes, we determined their genomic sequences (Figure S1). We revealed a large intron (3157 bp) inserted in the first exon of the CrFTL2 gene. Unlike the other angiosperm FT/TFL1 genes which contain three introns and four exons, CrFTL2 harbors four introns and five exons. The novel exon 1a replaced part of the former first exon in a mature transcript and coded for a stretch

Figure 5 Relative expression of the CrFTL1, CrTFL1, CrCEN, and CrBFT genes in apical parts, hypocotyls, cotyledons, roots, stems, and leaves of C. rubrum plants under three light regimes. LL: permanent light (yellow); 3 LD–LL: three consecutive periods 12 hr light/12 hr dark followed by permanent light (red); LD: 12 hr light/12 hr dark (black).
of 17 amino acids with no significant sequence similarity to anything. A fragment of a novel intron (about 1100 bp) was highly similar (80%) to the first exon of the CHOLINE TRANSPORTER LIKE gene (CTL) from sugar beet (XM_010692082). However, this intron was spliced out leaving no CTL sequence in the mature CrFTL2 transcript. The substantial rearrangement of the CrFTL2 gene was most likely achieved by recombination which removed the start of the first exon and replaced it with an additional, long intron and a novel exon (Figure 2A).

We constructed 3D models of the CrFTL2 protein using both multitemplate modeling and A. thaliana FT only as a template (Figure 2A). The two 3D predictions were very similar and showed an α helical structure at the N-terminus similar to FT protein and animal phosphatidylethanolamine-binding proteins (Ahn et al. 2006). Thus, the novel exon encoded a very similar 3D structure as the original one despite a completely different primary sequence. The CrFTL2 protein lacked 11 amino acid residues at the C-end, which might have changed its ligand-binding capacity.

We also identified a homeolog CrFTL2 copy carrying the mutation in the splice site (AG>TG) upstream of the fourth exon, which prevented the production of a functional transcript. This copy also lacked exon 1a. Thus, only one of the CrFTL2 homeologs was functional, the other one was a pseudogene. The CrFTL1 and CrFTL3 genes harbored a typical gene structure with variable intron sizes (Table S3).

**Amino acid divergence in the FT subfamily in Amaranthaceae**

We aligned amino acid sequences of the FT subfamily from sugar beet, spinach, and C. rubrum with A. thaliana FT protein (Figure 3). The FT1 proteins of the three amaranths showed identity in almost all conserved positions (marked dark green in Figure 3) and high mutual sequence similarity (83–93%). The FT2 proteins carried mutations in the positions critical for a regulatory function (Ho and Weigel 2014). Gln-140 was exchanged for Pro in SoFTL2, or for Ile in CrFTL2. Trp-138 was replaced by Gln in BvFT1, which turned the floral activator into a repressor in sugar beet (Pin et al. 2010). The CrFTL2 protein diverged very much from its counterparts, exhibiting only 78% similarity with its closest homolog in spinach. In addition to the different N-terminus encoded by the novel exon 1a, it lacked the conserved GGRR motif at the C-terminus owing to a premature stop codon. The Ka/Ks ratio (0.41) calculated from the nt alignment of CrFTL2 and SoFTL2 suggested relaxed selection constraints. This finding together with the constitutive expression of the CrFTL2 gene (Cháb et al. 2008), not compatible with a floral repressor function, indicates subfunctionalization.

The FT3 lineage belonged to the FT subfamily based on the phylogenetic tree and also on the occurrence of critical amino acid residues. Tyr-85, Gln-109, Thr-138, Gln-140, and Asn-152 (Figure 3) were all conserved with Pro-140 in CrFTL3 a notable exception. In contrast, FT3 proteins contained unique amino acid residues in the positions conserved in other FT/TFL1 proteins: Ser-7, Ala-39, Gly-78, Thr-163 (Table S4). Synapomorphic amino acid replacements in the FTL3 lineage indicated possible changes of function.

**Plant growth under various light regimes**

We grew C. rubrum plants till the age of 32 d under three distinct light regimes: (1) constant light (LL), (2) 12 hr D–12 hr L during an entire experiment (LD), and (3) three periods 12 hr D–12 hr L applied to 5-d-old seedlings followed by permanent light (3LD LL) (File S1). The first regime did not induce flowering, whereas the second and third one resulted in flowering in all plants. Constant light used as a control regime suppressing flowering may be considered to be a nonphysiological treatment. However, the C. rubrum ecotype 374 was collected close to the Arctic Circle (Cumming 1967). Constant light represents natural conditions in its native sites in the weeks around the summer solstice. We collected the plants and prepared herbarium specimens to document their habitus (Figure 4). Phenotypes of LL and 3LD LL plants were similar which documented a strong morphogenetic effect of constant light. Seedlings treated with at least three dark periods produced longer hypocotyls and roots that were twice as short as those in LL plants.

Mature (25 d) LD plants were branched with well visible inflorescences. In contrast, LL and 3LD LL plants were shorter and less branched and produced broader leaves. Their root systems were dense, with many adventitious roots, in contrast with the narrow root systems of LD plants (Figure 4).

**Organ-specific expression of the FT/TFL1 genes**

The expression of the TFL1 subfamily in whole aerial parts of seedlings was very low. Only CrTFL1 transcripts were measurable; they displayed a weak diurnal rhythmicity under both short-day and long-day conditions (Figure S2 and File S3). However, when gene expression was estimated in separated organs, prominent transcript patterns were discovered (Figure 5).

We followed transcripts of the FT/TFL1 genes by RT qPCR in roots, hypocotyls, cotyledons, and apical parts of C. rubrum seedlings, as well as in stems, roots, leaves, and apical parts of mature plants cultivated under three light regimes as described above (Figure 5). The first RNA collection occurred in the middle of the third dark period applied on light-grown seedlings 5 d old. The second sample was taken in the middle of the following light period. Seedlings grown under permanent light were sampled at the same time. We continued RNA collection in 10 d-, 15 d-, 20 d-, and 25-d-old plants, always in the middle of a light period. High activation of the floral promoter CrTFL1 was observed in cotyledons treated by the inductive dark period (Figure 5). Increased CrTFL1 expression was recorded in leaves of mature LD plants, albeit at
We concluded that the seedlings often germinated from large seeds produced by young plants. Increased herbicide concentration killed all plants. Naturally resistant of organ speci-
a lower level than in cotyledons, and also in LD apical parts. The CrFTL1 expression profile was complementary to CrFTL1 in terms of organ specificity. High expression was observed in hypocotyl, stems, and roots, but was zero in leaves. The CrFTL1 transcript levels in aerial parts were higher in constant light. It was inhibited at night and also during the day following the dark period. The CrFTL1 transcript remained low in LD plants, but increased when 3LD LL plants were transferred to permanent light. Darkness activated CrFTL1 expression in roots, opposite to the effect in hypocotyls. CrFTL1 expression remained low when root samples were taken at light under any regime.

The CrCEN1 gene was moderately expressed in apical parts with only small differences among the light regimes. Its expression increased in roots of mature plants grown at light. In contrast, the CrBFT gene was highly expressed in roots of seedlings grown under constant light and its transcript levels dropped in mature plants. CrBFT expression in light-grown hypocytols might be an overflow of root expression (Figure 5). In general, the members of the TFL1 subfamily substantially differed in expression patterns and also in their responses to light regimes.

The CrMFT1 gene was transcribed in roots. It seemed to be activated by light in roots and also in stems of 25-d-old plants. CrMFT2 expression was low in all organs except for a single outlier: the roots of 25-d-old plants (Figure S3).

In addition to vegetative tissues, we also examined gene expression in C. rubrum seeds (Figure 6). The two CrMFT paralogs exhibited very high expression in dry and imbibed seeds, with a sharp decrease following germination. Other FT/TFL1 genes, including CrFTL2, showed zero or very low transcript levels in seeds. Interestingly, we measured a very low, but detectable level of CrFTL3 transcripts in dry seeds, the only organ in which CrFTL3 expression was recorded.

Table 2 shows a summary of distinct organ-specific expression of the FT/TFL1 genes. The highest levels were achieved by the TFL1 subfamily genes in roots and by MFT genes in seeds. The distinct organ-specific expression of the CrFTL1, CrFTL2, and CrCEN genes in above-ground parts of the plants is documented. The results obtained by RT qPCR were in good agreement with coverage values (FPKM) estimated from Illumina data (Table S3).

Gene expression profiles provide valuable clues about possible function but more direct evidence is needed to elucidate gene functions with certainty. The functional proof may be achieved by a stable transformation of the plant with particular genes. Thus, we tried to transform C. rubrum by the floral dipping method described by Veit et al. (2006) using the same binary vector pFGC5941 (File S2). However, we failed to confirm DNA transfer by PCR. Moreover, we noticed that some control plants were able to grow on the plate with 5 mg L⁻¹ of herbicide BASTA. Increased herbicide concentration killed all plants. Naturally resistant seedlings often germinated from large seeds produced by young plants. We concluded that the floral dipping method described by Veit et al. (2006) was not a reliable tool to achieve stable transformation of C. rubrum.

DISCUSSION

CrFTL1 is a single floral activator of the FT/TFL1 gene family in C. rubrum

Flowering may be induced by environmental clues only when the plants are ready to bloom. Trees start to flower at the age of several years, sometimes even decades, in contrast with annual plants. Short-day C. rubrum represents an extreme even among annuals owing to its capability to flower at the seedling stage. Very early flowering and fast generation cycling is widespread among weedy plants, but it has been only rarely investigated at molecular level. Ipomoea nil (Japanese morning glory) is another example in which flowering can be induced as a seedling in short days (Hayama et al. 2007; Wada et al. 2010).

We generated a reference transcriptome of C. rubrum based on a superassembly combined from several individual assemblies by EvidentialGene pipeline and used it for a comprehensive survey of the FT/TFL1 genes. Unlike A. thaliana or Japanese morning glory with two floral activators, C. rubrum relies on the single inducer from the FT/TFL1 gene family – CrFTL1. The other two FTL paralogs – CrFTL2 (Cháb et al. 2008) and the newly identified gene CrFTL3 – were not involved in the control of flowering as documented by the constitutive or nearly zero transcription, respectively (Table 2), which was unchanged by floral induction.

The structural evolution of the CrFTL2 gene indicates a functional shift

The CrFTL2 gene has undergone a dramatic structural evolution and shown an accelerated substitution rate since its divergence from the sugar beet floral repressor BvFT1 (Pin et al. 2010). A new exon and a long intron replaced the first 50 bp of the coding sequence. The novel exon encoded an α helix similar to the original chain, preserving the protein 3D structure (Figure 2B), despite a distinct primary sequence. The new intronic sequence was partly derived from the CTL gene, which is interesting in light of the recent finding that A. thaliana FT protein binds phosphatidylcholine in vitro (Nakamura et al. 2014). The novel intron is spliced out and the CTL sequence does not appear in a mature transcript. However, the recombination event, which probably restructured the gene, might have been a part of broader rearrangements affecting the control of both choline metabolism and flowering.

The spinach SoFTL2 gene possesses the standard first exon similar to sugar beet BvFT1. Thus, the rearrangement affecting the CrFTL2 gene (Figure 2A) had to occur relatively recently, after the separation of spinach and C. rubrum ancestors. The second homeolog CrFTL2 copy is not functional which raises the question of whether it was inactivated...
before or after the origin of tetraploid C. rubrum from its so far unknown diploid ancestors.

The function of the CrFTL2 gene remains enigmatic, but it is certainly not related to flowering control. A reliable protocol for gene transfer in C. rubrum has not been developed yet. Our attempt to adopt floral dipping method (Veit et al. 2006) for the stable C. rubrum transformation failed, but other methods like VIGS (virus induced gene silencing) may be successful in the future to provide evidence about the CrFTL2 function.

The loss of floral repressor may allow seedlings to flower immediately after germination, if days are shortening in the fall. It appears to be a useful adaptation to a weedy opportunistic life style of C. rubrum. The loss of function occurs in pseudogenization. However, relatively high and stable expression and the preservation of the 3D structure of the CrFTL2 protein after a complex gene rearrangement indicate a functional shift.

**The CrFTL3 and CrMFT genes diverged early**

We discovered a third FTL paralog in Amaranthaceae. It arose early in the dicot evolution, most likely on the base of Caryophyllales (Figure 1). We cannot decide whether this clade is restricted to Amaranthaceae. We may have found FTL3 homologs only in spinach and sugar beet, because no other Caryophyllales genomic drafts were available. Transcriptomic records are more numerous, but they may miss FTL3 sequences due to very low transcription. We detected CrFTL3 expression in seeds by RT qPCR, albeit at a negligible level. The FTL3 proteins contained several synapomorphic amino acid substitutions (Figure 3) which suggested a substantial functional divergence. We speculate that this gene may be involved in embryo growth control, which is in line with its ancient origin.

The two CrMFT genes were highly expressed in seeds and downregulated after germination (Figure 6), which implicates their role in seed dormancy control, as in A. thaliana (Xi et al. 2010). However, unlike A. thaliana having only one MFT gene, C. rubrum retained two MFT paralogs. Their different expression in roots indicates their function in vegetative growth.

**The genes of the TFL1 subfamily in C. rubrum show diverse expression patterns**

The CrFTL1 gene displayed the most variable expression, highly responding to darkness when applied on 5-d-old seedlings. Whereas CrFTL1 was strongly inhibited by dark in hypocotyls and retained a low activity the following day, it was highly upregulated in roots but only at night (Figure 5). The TFL1 and FT proteins are non-cell-autonomous in A. thaliana; they spread among tissues (Conti and Bradley 2007; Corbesier et al. 2007). It is therefore possible that the CrFTL1 protein migrates at light from hypocotyl to the apex in C. rubrum seedlings. It may maintain apical meristematic activity, support vegetative growth, and counteract the FT protein in a similar way as in A. thaliana (Hanano and Goto 2011). A sudden decrease in CrFTL1 transcripts caused by dark may contribute to floral induction in C. rubrum. The role of TFL1 in roots was little investigated. The most recent evidence based on whole genome-association mapping (Lachovic et al. 2015) suggests that TFL1 acts as a repressor of root growth in A. thaliana seedlings. The coincidence of short roots in dark-treated seedlings (Figure 4) and CrFTL1 upregulation by dark in roots (Figure 5) indicate a similar inhibitory function in C. rubrum.

FT and TFL1 regulate a shoot architecture in various plants. For example, the SFT and SP genes, orthologs of FT and TFL1 in tomato, control branching pattern and leaf shape in an antagonistic way. Their ratio, rather than individual transcript levels, shape tomato compound leaves (Liščitz et al. 2014). We observed CrFTL1 expression in leaves, whereas CrFTL1 was transcribed in stem and roots, not in leaves (Figure 5). Thus, CrFTL1 does not seem to affect leaf shape.

CrBFT was transcribed mostly in seedling roots, less in mature plants. Its expression was downregulated by dark. The opposite effect of darkness on CrBFT and CrFTL1 could reflect their antagonistic roles in root growth regulation. CrCEN expression was little influenced by light regime, being limited to shoot apical parts in seedlings (Figure 5). In general, the three members of the TFL1 subfamily exhibited very distinct patterns of organ-specific expression (Table 2), suggesting their different roles in plant growth and reproduction.

**Future perspectives**

C. rubrum emerges as a very promising model for the studies of flowering owing to the absence of a juvenile phase and the presence of the single FT-like floral activator CrFTL1, which is upregulated 6 hr after lights-on, regardless of photoperiod (Drabešová et al. 2014). A midnight break inhibits both flowering and CrFTL1 transcription (Cháb et al. 2008). The determination of the time period critical for floral induction and the availability of the reference transcriptome make it possible to conduct experiments to identify the genes controlling the induction to flowering in C. rubrum. The comparison of floral regulatory pathways among C. rubrum and other amaranths will improve our understanding of the adaptation of crops and weedy species to the ever changing environment.

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**LITERATURE CITED**


Hedman, H., T. Källman, and U. Lagercrantz, 2009 Early evolution of the

Dohm, J. C., A. E. Minoche, D. Holtgräwe, S. Capella-Gutierrez, F. Zakrzewski et al., 2014 The genome of the recently domesticated crop plant sugar


Veit, J., E. Wagner, and J. T. P. Albrechtova, 2006 Floral dip transformation of Chenopodium rubrum, pp. 49–53 in Floriculture, Ornamental and...


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