Terminal-Repeat Retrotransposons with GAG Domain in Plant Genomes: A New Testimony on the Complex World of Transposable Elements

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Abstract

A novel structure of nonautonomous long terminal repeat (LTR) retrotransposons called terminal repeat with GAG domain (TR-GAG) has been described in plants, both in monocotyledonous, dicotyledonous and basal angiosperm genomes. TR-GAGs are relatively short elements in length (<4 kb) showing the typical features of LTR-retrotransposons. However, they carry only one open reading frame coding for the GAG precursor protein involved for instance in transposition, the assembly, and the packaging of the element into the virus-like particle. GAG precursors show similarities with both Copia and Gypsy GAG proteins, suggesting evolutionary relationships of TR-GAG elements with both families. Despite the lack of the enzymatic machinery required for their mobility, strong evidences suggest that TR-GAGs are still active. TR-GAGs represent ubiquitous nonautonomous structures that could be involved in the molecular diversities of plant genomes.

Key words: nonautonomous elements, LTR-retrotransposons, GAG, conservation in plant genomes.

Introduction

Repeated sequences are the main component of plant genomes, especially those with large C-value. In bread wheat, barley, and maize, more than 80% of the sequenced DNA is classified into mobile elements, so called transposable elements (TEs) ( Schnable et al. 2009; Wicker et al. 2009). TEs were traditionally classified into two main classes according to their lifestyle cycle: Class I, or retrotransposons, for TEs moving through an RNA intermediate, which use a so called “copy and paste” mechanism, and Class II, or transposons, for TEs moving through a DNA intermediate, which use a so called “Cut and Paste” mechanisms (Wicker et al. 2007). Long terminal repeat (LTR)-retrotransposons, that pertain to Class I, are the most abundant TEs identified in plant genomes. The activity of TEs has a deep influence on the evolution and function of plant genes and genomes and so contributes to the implementation of molecular diversification and genetic diversity. Their activity is controlled at the transcriptional and posttranscriptional levels by the host. However, the high activity of LTR-retrotransposons overtakes occasionally these mechanisms that control TE proliferation leading to sudden accumulation of LTR-retrotransposon copies (so called
“burst”) and, consequently to a rapid genome size increase (Piegu et al. 2006). With the advent of large-scale plant genome sequencing and the advances in TE bioinformatics analysis (Flutre et al. 2011), it became clear that most of the TEs identified so far were not able to synthesize the full enzymatic machinery and all the molecules involved in their own mobility and to accomplish their multiplication cycle, disabling their coding capacities, that lead to their inactivation and so counteract their impact on genome size increase (Devos et al. 2002; Ma et al. 2004; Vitte and Bennetzen 2006). In some cases, homologous recombination mechanisms occurring between LTR sequences in the same LTR-retrotransposon element lead to solo LTR formation implicating the removal of a large internal portion of elements. These altered elements are usually considered as dead elements, which are no longer capable of transcription and mobility.

However, there are reports where elements carrying a defective transposition machinery can get “back to life” and meet again the ability to move and to multiply their copy numbers in the host genome (Witte et al. 2001; Kalendar et al. 2004; Vitte and Bennetzen 2006). In some cases, homologous recombination mechanisms occurring between LTR sequences in the same LTR-retrotransposon element lead to solo LTR formation implicating the removal of a large internal portion of elements. These altered elements are usually considered as dead elements, which are no longer capable of transcription and mobility.

However, there are reports where elements carrying a defective transposition machinery can get “back to life” and meet again the ability to move and to multiply their copy numbers in the host genome (Witte et al. 2001; Kalendar et al. 2004; Tanskanem et al. 2007). Such elements, often called nonautonomous elements, are supposed to mobilize through a cross activation (in trans) with autonomous and functional partners. This interaction requires that nonautonomous elements still carry recognition domains for proteins encoded by autonomous partners (Wicker et al. 2007; Schulman 2012). Two groups of Class I nonautonomous LTR-retrotransposons were identified in numerous plant genomes: TRIM (terminal-repeat retrotransposons) and LARD (large retrotransposon derivative) (Kalendar et al. 2004) (fig. 1). TRIMs and LARDs are, respectively, short (<2 kb) and long (>4 kb) elements that, although they have lost their internal coding regions, they are involved in restructuring plant genomes (Witte et al. 2001; Kalendar et al. 2008). BARE-2 is another type of active nonautonomous elements found in barley (Tanskanem et al. 2007). BARE-2, which lacks the GAG domain, involved in the packaging of the element into the virus-like particle, remains mobile using the functional GAG capsid protein encoded by the BARE-1 autonomous elements (Tanskanem et al. 2007). BARE-2 elements represent the unique described case of cis-parasitism of an LTR-retrotransposons in plants. However, the BARE-2 nonautonomous structure was investigated only in Triticeae genomes (Vicient et al. 2005). The profusion of LTR-retrotransposons within plant genomes, the abundance of structural variation of defective elements, and the recent discovery of nonautonomous elements raise the question to know whether the whole structural variety of nonautonomous LTR-retrotransposons has been really identified or whether novel structures remain to be characterized.

In an attempt to characterize the whole set of mobile elements within the Coffea genomes, especially in Coffea canephora (Denoeud et al. 2014), we report here a new group of nonautonomous LTR-retrotransposons, called TR-GAG (terminal-repeat retrotransposons with GAG domain) in plants. TR-GAG elements are short LTR-retrotransposons (<4 kb) carrying a unique open reading frame (ORF) coding for a GAG capsid protein. In C. canephora genome, five families of TR-GAG elements were described.
These elements are expressed and their evolutionary dynamics in the Coffea genus indicated different pathways in the copy number variations. Similar structures were found in numerous available sequenced eudicotyledonous, monocotyledonous, and algae genomes, indicating that TR-GAG elements could be ubiquitous TEs in plants.

Materials and Methods

Plant Material, DNA, and RNA Preparation

Three coffee species were used in our analyses: Coffea arabica (accessions AR52 and ET39), Coffea eugenioides (accession DA71), and C. canephora (accessions BA58, BB60, BD69, and DH 200-94). All plants were growing in the greenhouses at the IRD center, Montpellier (France). Leaves were harvested and stored at −80 °C prior to DNA extraction, using Qiagen DNeasy Plant Mini extraction kits. Quantity and quality of DNA were measured using a Nanodrop (ND-1000). RNA preparations were obtained from leaves of C. arabica (accession ET39), C. eugenioides (accession DA71), and C. canephora (accession DH 200-94), using the SV Total RNA Isolation System (Promega).

Identification, Classification, and Annotation of LTR-Retrotransposons

A manual annotation procedure was undertaken on 17 publicly available C. canephora and C. arabica artificial chromosome sequences (accounting for 3,023,472 bp) and from the ten largest C. canephora scaffolds (accounting for 65,698,623 bp, from the C. canephora draft genome generated by the Coffee Genome Consortium) to build an initial database. A total of 948 elements were finally annotated as follows and classified according to the universal classification database. A total of 948 elements were finally annotated as follows and classified according to the universal classification database. A total of 948 elements were finally annotated as follows and classified according to the universal classification database. A total of 948 elements were finally annotated as follows and classified according to the universal classification database. A total of 948 elements were finally annotated as follows and classified according to the universal classification database.
protocol. The library construction and NGS sequencing were performed at Nestlé R&D laboratory according to the Roche/454 Life Sciences Sequencing protocol. In total, 1,624,178 sequences were generated accounting for 678 Mb. Data were submitted to GenBank, BioProject PRJNA242989.

BLASTN searches were carried out with the five TR-GAG families found previously in the C. canephora genome. Reads with more than 80% of nucleotide identity with the reference sequence over a minimum 80% of the read lengths were considered as potential fragments of the element. Cumulative lengths of aligned reads were used to extrapolate the contribution of the element to each genome size investigated. For each element family, the potential number of full-length copies is estimated by the division of the estimated size of total members of the element in the genome by the reference sequence length.

Characterization of TR-GAG Families in 33 Plant Genomes

LTR_STRUC (McCarthy and McDonald 2003) was used to predict LTR-retrotransposons in 33 available plant genomes retrieved from specific sites and the Phytozome website (http://www.phytozome.net; supplementary data S2, Supplementary Material online) as follows: 24 dicotyledonous genomes—Nicotiana sylvestris, Solanum lycopersicum (tomato), Solanum tuberosum (potato), Mimulus guttatus, Urticaria gibba (bladderwort), Vitis vinifera (grape), Cucumis sativus, Citrullus lanatus (watermelon), Fragaria vesca (strawberry), Prunus persica (peach), Malus domestica (apple), Medicago truncatula, Cicer arietinum (chickpea), Lotus japonicus, Glycine max (soybean), Phaseolus vulgaris (common bean), Populus trichocarpa (poplar), Manihot esculenta (casava), Ricinus communis, Theobroma cacao (cacao), Carica papaya (papaya), Arabidopsis thaliana, Brassica rapa (rapeseed), and Citrus clementina (clementine); seven monocotyledonous genomes—Oryza sativa (rice), and two other genomes—Amborella trichopoda (angiosperm) and Selaginella moellendorfii (nonangiosperm). A total of 18.9 Gb of sequence over a minimum 80% of the read lengths was calculated. Differential expression among RNA-seq sequences using bowtie 2 (Langmead and Salzberg 2012).

Search for TR-GAG Pattern in Genomes

We developed an algorithm to automatically detect TR-GAG elements in genomes. The algorithm consists in translating the six frames for every “pseudomolecule” present in the target genome, followed by a search for HMM (Hidden Markov Models) motifs using the hmmer package (http://hmmer.org). The Retrotrans_gag, UBN2, UBN2_2, and UBN2_3 motifs were used to detect GAG protein signatures. Flanking regions of 5 kb are extracted for all hits with e value < 1e-5 and direct repeats greater than 200 bases are searched by dividing the sequence in two and using BLASTN alignment. The region including the direct repeats and the GAG motif is extracted, translated, and searched for reverse transcriptase motifs and only the candidates that present no Copia or Gypsy reverse transcriptase motifs are retained. These candidates are further filtered by size, keeping those sequences between 1 and 6 kb, whereas redundant candidates are eliminated.

Transcriptional Analysis of the TRIM-1-S and TR-GAG1 Elements by Reverse Transcription Polymerase Chain Reaction

RNA sequencing (RNA-seq) data generated under the C. canephora genome project (coffee-genome.org) from leaves, roots (C. canephora accession T3518), stamen, and pistil (C. canephora accession BP961) were used to identify the transcriptional pattern of reference sequences (http://coffee-genome.org; Denoeud et al. 2014). Nearly 130 million of Illumina reads (2 × 100 bp) were cleaned using prinseq (Schmieder and Edwards 2011) and mapped against reference TR-GAG sequences using bowtie 2 (Langmead and Salzberg 2012). Number of mapped reads per reference sequence was processed and RPKM (reads per kilo base per million) was calculated. Differential expression among RNA-seq

Table 1

<table>
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<tr>
<th>Primers</th>
<th>Sequences (5′–3′)</th>
<th>Product Size (bp)</th>
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<tr>
<td>TRIM-1-S-R</td>
<td>ATGTGAGTGGCCCGAGCT</td>
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</tr>
<tr>
<td>TR-GAG1-F</td>
<td>GCAGCAGACCTCTGGAAAAA</td>
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</tr>
<tr>
<td>TR-GAG1-R</td>
<td>TGGTTCTGCTTCTGGTTT</td>
<td>361</td>
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<tr>
<td>G3-F</td>
<td>ACGATGCTTCTGGAGGAG</td>
<td>361</td>
</tr>
<tr>
<td>G3-R</td>
<td>TGGGCTCTGGAGAATCTACC</td>
<td>361</td>
</tr>
</tbody>
</table>

*Control primers used as in Guyot et al. (2009).
libraries was detected from variation of mapped reads and all sequenced reads using Winflat (Audic and Claverie 1997).

Phylogenetic Analyses and TR-GAG Insertion Times

The classification of GAG domains from TR-GAG elements found in the Coffee genome was confirmed by phylogenetic analyses. GAG domains were first identified by similarity against the GAG domains from the Gypsy Database 2.0 (290 domains as in August 2014), extracted from the nucleotide sequence of TR-GAG, and translated into amino acids. Amino acid sequences (with a minimum of 200 residues) were aligned (ClustalW) to construct a bootstrapped neighbor-joining tree, edited with FigTree (http://tree.bio.ed.ac.uk/software/figtree/).

The insertion times of full-length copies, as defined by a minimum of 80% of nucleotide identity over 100% of the reference element length, were dated. Timing of insertion was based on the divergence of the 5′- and 3′-LTR sequences of each copy. The two LTRs were aligned using stretcher (EMBOSS), and the divergence was calculated using the Kimura 2-parameter method implemented in distmat (EMBOSS). The insertion dates were estimated using an average base substitution rate of 1.3 E-8 (Ma and Bennetzen 2004).

Results

Annotation and Identification of the Nonautonomous LTR-Retrotransposons TRIM-1 Family in the C. canephora Genome

We used the draft genome sequence of the C. canephora accession DH 200-94 to annotate TEs (Denoeud et al. 2014; http://coffee-genome.org). We first performed a manual annotation of TEs using the ten largest scaffolds from C. canephora genome sequencing project (accounting for 65,698,623 bp, scaffold1–10), and an initial database of 948 TEs was produced (Guyot R, unpublished data). Among the 948 elements, 11 conserved short elements (<3 kb) harboring a typical LTR-retrotransposon structure (two duplicated regions starting by TG, and finishing by CA, flanked by a target site duplication [TSD] of 5 bp, and a purine tract [PPT] located upstream the 3′-duplicated region) were identified using similarity searches (BLASTN).

After initial analyses, we found two sequence groups with different lengths. Short sequences (~1,700 bp) were called TRIM-1-S have the typical structure of TRIM (Witte et al. 2001), whereas long sequences (~2,500 bp) were called TR-GAG1 (terminal repeat with GAG domain). They are similar to the TRIM but carry an internal region similar to LTR-retrotransposons GAG capsid domain (fig. 2A and B). The last structure was not previously described in plant genomes. The two groups of sequences are conserved except for the presence of the GAG domain in TR-GAG1 (fig. 2C and supplementary data S3, Supplementary Material online). Multiple alignment of the LTR sequences from the TRIM-1-S and TR-GAG1 elements shows an overall strong conservation between the two groups as well the presence of a putative TATA box that could intervene in the initiation of the elements’ transcriptions (supplementary data S3, Supplementary Material online). An exhaustive search against the C. canephora draft genome (568 Mb) indicated the presence of 71 and 60 complete copies of TRIM-1-S and TR-GAG1, respectively. All complete dispersed copies within the chromosomes with conserved LTR extremities, showed different insertion sites (supplementary data S4, Supplementary Material online). The complete elements are flanked by 5-bp direct repeats usually generated during the LTR-retrotransposon insertions, suggesting that they are originated from different replication events. Using BLASTN algorithm, we searched in the C. canephora genome for autonomous elements sharing high nucleotide conservation with TRIM-1-S and TR-GAG1, but we did not find any autonomous full-length elements in the available genomic sequences.

Detailed Analysis of the TR-GAG1 Elements

We detailed the structure of the TR_GAG1 elements (Copy found in C. canephora draft genome located on “Chr 0,” positions 113020990–113023502, accession KM360147), as such conserved structure of nonautonomous LTR-retrotransposon was not described yet. TR-GAG1 elements have LTR lengths of approximately 485 bp. The 5′-LTR is flanked downstream by a primer binding site (PBS) complementary to the Leucine transfer RNA and the 3′-LTR is flanked upstream by a PPT 5′-AAAAGGCAAATGGAG-3′ (fig. 3). Beside LTR regions, no internal duplicated region was found in the TR-GAG1 sequence. The inner region is composed of an ORF of 433 amino acids with strong similarities with GAG (group-specific antigens) and more particularly with the UBN2 family domain from Pfam (gag-polypeptide of LTR Copia superfamily). The small structural motif of Zinc finger (Zf-C2HC) is also found at the amino-acid residue 275 the ORF (position 1245–1286 along the full-length TR-GAG nucleotide sequence). At the C terminal part, few similarities were observed with aspartic proteases from the GydB but no motif was conserved in Pfam database (Punta et al. 2012). The UBN2 Pfam domain (PF14223) from TR-GAG1 is described as associated with Copia Superfamily of complete LTR-retrotransposons (http://pfam.xfam.org). No significant RNA secondary structure was found with the putative leader sequence of TR-GAG1, suggesting either absent or labile PSI (Packaging Signal) and DIS (Dimerization Signal) motifs. These motifs were identified in Retroviruses and are involved in the packaging and RNA dimerization (Tanskanen et al. 2007).
Transcriptional Responses of the TRIM1/TR-GAG Family

We analyzed the transcriptional pattern of TRIM-1-S and TR-GAG1 elements in three coffee species. Specific primers were selected in TRIM-1-S and TR-GAG1 to amplify the inner regions. For TR-GAG1, primers amplify a 328-bp product from the GAG precursor. RT-PCR analyses indicate the presence of transcripts for TRIM-1-S and TR-GAG1 originating from mRNA leaves, suggesting that elements are expressed in *C. canephora*, *C. eugenioides*, and *C. arabica* (supplementary data S4A and B, Supplementary Material online).

RNA-seq analysis using 130 million of Illumina reads shows that 38 complete copies of TR-GAG1 are expressed at low level in vegetative tissues (leaves and roots) whereas no or few expression was detected in reproductive tissues (pistil and stamen) (supplementary data S5, Supplementary Material online).

Characterization of TR-GAG Families in *C. canephora*

We searched the presence of other TR-GAG families in the draft genome of *C. canephora*. We used first the results of
LTR_STRUC prediction of LTR-retrotransposons. The 1,799 putative LTR-retrotransposons predicted by LTR_STRUC were filtered out according to the features identified for TR-GAG1. Beside an overall structure of elements, such as presence of LTR, PBS, and PPT regions, sequences with a maximum length of 4 kb, a minimum redundancy of two copies, and with similarities for GAG Capsid proteins but not with aspartic protease, integrase, reverse transcriptase, and RNase H domains were selected for further analysis. On 1,799 predicted elements, 130 were retained. Sequences were compared against themselves using dot-plot alignments (fig. 4A). Sequences were clustered into five groups of sequences according to their similarities and classified into five different families (called TR-GAG1 to TR-GAG5). One family called TR-GAG2, which exhibited a large number of conserved predicted structures (110 elements) as observed in dot-plot and alignment analysis (supplementary data S6, Supplementary Material online), was analyzed further (fig. 4A and B). Among the 110 conserved predicted elements, we selected one copy for detailed analysis (located on pseudochromosome 4 21003142–21006851). This element presented an overall similar structure to TR-GAG1 (fig. 4C). TR-GAG3, TR-GAG4, and TR-GAG5 families were analyzed and also shown a typical structure of TR-GAG nonautonomous elements (supplementary data S8, Supplementary Material online). Although TR-GAG2 shares similarities with the same Copia GAG Pfam domain family (UBN2) with TR-GAG1, TR-GAG3 and TR-GAG4 contain the RetroTrans_gag motif (Pfam PF03732) that appears associated with annotated Copia and Gypsy polyproteins in Uniprot database (http://www.uniprot.org). Phylogenetic analysis with reference GAG domains from GyDB confirmed the similarity of TR-GAG1 and TR-GAG2 GAG domains with Copia and TR-GAG4 with Gypsy subfamily GAG domains (supplementary data S7, Supplementary Material online). All five TR-GAG families were analyzed using RNA-seq. We observed different pattern of expression
Distribution and Copy Number Estimation of TR-GAG Elements in the Coffea Genus

We first investigate the copy number of the five identified TR-GAG families in the Coffea canephora sequenced genome (supplementary data S9, Supplementary Material online). Complete copies of TR-GAG1 and TR-GAG2, as defined by 80% of nucleotide identity over 100% of the reference element length, were used to estimate their insertion times (supplementary data S10, Supplementary Material online). Our analysis indicates a relatively recent increase of TR-GAG element length, were used to estimate their insertion times (supplementary data S10, Supplementary Material online). We could estimate the copy number of TR-GAG elements in several genomes. Using these conserved reads, TR-GAG was estimated to range from 0 to 696.7 copies in diploid species and from 10.2 to 1,168.7 copies in Coffea arabica. However, in almost all cases (at the exception of Craterispermum and C. tetragona), the highest copy numbers were obtained for TR-GAG-2. Only few copies (respectively, 5 and 7 copies) of TR-GAG-2 and TR-GAG-1 were detected for the Craterispermum outgroup (Rubiaceae) (supplementary data S11, Supplementary Material online). The TR-GAG-2 family contributes to the genome size of diploid species, but with a relatively weak intensity (supplementary data S12, Supplementary Material online). However the genome size contribution of TR-GAG-2 appears to decrease in species going from West to East in species belonging to Eucoffea (C. canephora, C. heterocalyx, C. eugenioides, and C. arabica), Mozambicoffla (C. pseudoazanguebariae and C. racemosa), and Mascarooffea (C. humblotiana, Coffea millotii ex-dolichophylla, and C. tetragona). The Indonesian C. hirsfieldiana appears intermediate between Eucoffea and Mozambicoflaxa or Mascarooffea botanical groups. Only traces of TR-GAG2 and TR-GAG1 were detected in Craterispermum (Rubiaceae).

Characterization of TR-GAG Families in Genomes Using LTR_STRUC Algorithm

We searched TR-GAG element structures in 33 available plant genomes. In total, more than 18 Gb of genomic sequences were processed with LTR_STRUC and a total.

### Table 2

<table>
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<tr>
<th>Species</th>
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<th>Estimated Genome Size (Mb)</th>
<th>#454 Sequences</th>
<th>Produced Bases (Mb)</th>
<th>Genome Coverage (%)</th>
<th>TR-GAG1 Copies</th>
<th>TR-GAG2 Copies</th>
<th>TR-GAG3 Copies</th>
<th>TR-GAG4 Copies</th>
<th>TR-GAG5 Copies</th>
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Note.—Only 454 reads with a minimum of 80% of nucleotide identity over 80% of the read length were considered. Genome sizes were listed in Noirot et al. (2003) and Razaftinario et al. (2012).
of 38,772 predicted LTR-retrotransposons were found (supplementary data S13, Supplementary Material online). After filtering, a total of 373 candidates were found distributed among 23 different monocotyledonous and dicotyledonous plant genomes (fig. 5). Detailed analysis of candidates TR-GAG elements confirmed the structures previously discovered in the C. canephora genome.

Detection of TR-GAG Families in Genomes Using HMM
In order to validate the detection of TR-GAG by LTR_STRUC, we developed HMM to recognize GAG motifs (retrotrans_gag, UBN2, UBN22, UBN23) surrounded by direct repeats. The new model was used in Banana (Musa acuminata, angiosperm, monocots), Cacao (Theobroma cacao, angiosperm, dicots), coffee (C. canephora, angiosperm, dicots), Ectocarpus (Ectocarpus siliculosus, brown algae; Cock et al. 2010), Chondrus (Chondrus crispus, red algae; Collen et al. 2013), and Drosophila (Drosophila melanogaster, insect) genomes. Although TR-GAG elements were found in all angiosperm and brown algae genomes, no potential candidate was predicted in red algae and Drosophila genomes. Twenty-five TR-GAG families were detected for Banana and one of them shows a high copy number (~700 copies, supplementary data S14, Supplementary Material online). In brown algae (Ectocarpus), the presence of one TR-GAG-like sequence was previously reported (Cock et al. 2010, in supplementary material, Supplementary Material online). Using our detection approach, four TR-GAG families were finally predicted in this genome (Cock et al. 2010, in supplementary material, Supplementary Material online).

Discussion
The identification and classification of the whole spectrum of LTR-retrotransposon structures is particularly a complex process in plant genomes due to the huge number and variety of defective LTR-retrotransposon structures. Although most of the defective structures, deriving from a wide variety of rearrangement mechanisms, lead to inactive elements, some of them remain mobile like TRIM, LARD, and BARE2 elements (Witte et al. 2001; Kalender et al. 2004; Tanskanem et al. 2007). These known nonautonomous LTR-retrotransposon structures redefined our view of the definition of what is really an active element in genomes, and raised new questions about their precise classification and their mechanisms of mobility. The discovery of such exceptional diversity of nonautonomous structures opened the door to the large-scale in

Fig. 5.—Identification of TR-GAG families in available plant genomes. (A) Dot-plot of predicted TR-GAG sequences from 23 plant genomes against themselves. TR-GAGs were predicted by LTR_STRUC and filter out according to features described for TR-GAG1. Sequences were clustered by plant genomes. (B) Detailed structure of one TR-GAG family for seven different plant genomes.
silico exploitation of plant genome sequences to seek novel nonautonomous structures.

The novel element called TR-GAG belongs to such type of nonautonomous structures and brings new insight on TE and genome evolution. TR-GAG elements clearly belong to LTR-retrotransposons order of TEs (Wicker et al. 2007). TR-GAG can be identified using de novo LTR-retrotransposons finding programs like LTR_STRUC (McCarthy and McDonald 2003), as they share key structural features with them, like LTR domains, PPT and PBS motifs and a 5-bp TSD at their insertion sites in the host genome. TR-GAGs appear generally smaller (<4 kb) than typical full-length Copia and Gypsy LTR-Retrotransposons (5–20 kb) in plants. Several signs suggest that TR-GAGs are active elements in Coffea species in spite of the absence of an internal polyprotein domain: 1) RT-PCR and RNA-seq data show the transcription of TR-GAG families. Although TR-GAG1 is mainly expressed at a low level in vegetative tissues, other families (TR-GAG2 and TR-GAG3) show a significant expression in reproductive tissues suggesting that new insertions could be vertically transmitted to the progeny; 2) the copy number of TR-GAG elements in C. canephora and the different TSD motifs found for each copy suggests an amplification mechanism that can be achieved by the lifestyle cycle of mobile LTR-retrotransposons; 3) the high conservation of sequence and structure between each TR-GAG copy in the C. canephora genome; and 4) their insertion time patterns.

TR-GAG elements lack a polyprotein domain involved in the mobility, but carry a GAG precursor, which is usually processes by protease into protein subunits (matrix, capsid, and nucleocapsid) (Freed 1998). This structure is the strict opposite of the described BARE-2 nonautonomous elements in barley, lacking only the GAG domain. It remains mobile as a two-component system: A nonautonomous elements (BARE2) and an autonomous counterpart (BARE-1) providing by complementation-like a functional GAG precursor (Tanskanem et al. 2007). For TR-GAG1 elements, no full-length autonomous element similar to the TR-GAG1 sequence was found in the draft genome sequence of C. canephora, suggesting that either the mobility of TR-GAG1 is driven in trans by a compatible but different full-length autonomous elements, or the complete element appears as absent due to incompleteness of the sequenced genome or it has been specifically lost in the studied and sequenced genotype. The presence of a functional GAG precursor in TR-GAG elements also raises the question to know their potential role in the cycle of other LTR-retrotransposon elements. The capsid (CA) and nucleocapsid (NC) protein subunits of GAG precursors are, respectively, implicated in the transposition and in the assembly packaging, reverse transcription, and integration mechanisms. More generally GAG proteins appear to be able to engage interactions with a wide spectrum of molecules such as proteins, DNA, RNA, and lipids (Freed 1998). The GAG peptides encoded by TR-GAG elements may drive in trans the mobility of a variety of other LTR-retrotransposons that lack functional GAG domain similarly to the BARE2. Additional molecular experimental data will be required to precisely understand the function of GAG domain in TR-GAG elements.

Five different families of TR-GAG were identified in C. canephora. They carry GAG domains that show similarities with both Copia and Gypsy superfamily related GAG domains suggesting that TR-GAG structures have been generated with a frequent and common mechanism for all LTR-retrotransposon superfamilies certainly involving unequal recombination events (Ma et al. 2004). In C. canephora, all five TR-GAG families show different complete, fragmented and solo LTR copy numbers, suggesting distinct levels of proliferation control by the host genome. Interestingly, TR-GAG2 that shows the highest copy number is nonrandomly distributed along the C. canephora pseudomolecules and targets preferentially TE-rich regions.

The TR-GAG2 family shows high variation in copy number among the ten Coffea species we analyzed. These variations are in agreement with the three botanical sections (or groups) defined by Chevalier (1942), strongly suggesting that TR-GAG2 copy number proliferation is associated with the evolution of botanical groups of Coffea. These botanical sections correspond also to genetically differentiated groups as obvious from fertility of FI interspecific hybrids (Louarn 1993), mean genome sizes (Noirot et al. 2003; Razafinarivo et al. 2012), and from genetic diversity revealed by simple sequence repeat markers (Razafinarivo et al. 2013).

Finally, the presence of TR-GAG structures in 23 different plant genomes from dicotyledonous and monocotyledonous species, as well as in basal Angiosperms (Amborella) and one algae species, indicates that these elements are ubiquitous mobile elements. Comparisons between all predicted TR-GAG elements in plants (fig. 5) show the absence of conservation between species suggesting that TR-GAG elements were originated from distinct pool of full-length autonomous LTR-retrotransposons. The notable exception is the conservation of one TR-GAG family between Cicer arietinum and Lotus japonicus genomes (fig. 5). Such significant conservation of TEs over different plant families suggests that TR-GAG elements could also be subjected to events of horizontal transfer like LTR-retrotransposons (Fortune et al. 2008; Roulin et al. 2008, 2009).

**Conclusions**

In conclusion, TR-GAG elements are a new nonautonomous element ubiquitous in plant genomes. TR-GAG elements are potentially active indicating that they are associated to functional full-length LTR-retrotransposons to achieve their life cycle. Considering their significant copy numbers TR-GAG elements could play an important role in chromosome...
structure, alteration of coding region expression, and genome evolution in plants.

**Supplementary Material**

Supplementary data S1–S14 are available at Genome Biology and Evolution online (http://www.gbe.oxfordjournals.org).

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**Literature Cited**


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