Letter

Differential lineage-specific amplification of transposable elements is responsible for genome size variation in Gossypium

Jennifer S. Hawkins,1 HyeRan Kim,2 John D. Nason,1 Rod A. Wing,2 and Jonathan F. Wendel1,3

1Iowa State University, Department of Ecology, Evolution and Organismal Biology, Ames, Iowa 50011, USA; 2University of Arizona, Department of Plant Sciences, Arizona Genomics Institute, Tucson, Arizona 85721, USA

The DNA content of eukaryotic nuclei (C-value) varies ~200,000-fold, but there is only a ~20-fold variation in the number of protein-coding genes. Hence, most C-value variation is ascribed to the repetitive fraction, although little is known about the evolutionary dynamics of the specific components that lead to genome size variation. To understand the modes and mechanisms that underlie variation in genome composition, we generated sequence data from whole genome shotgun (WGS) libraries for three representative diploid (n = 13) members of Gossypium that vary in genome size from 880 to 2460 Mb (IC) and from a phylogenetic outgroup, Gossypioideae kirkii, with an estimated genome size of 588 Mb. Copy number estimates including all dispersed repetitive sequences indicate that 40%–65% of each genome is composed of transposable elements. Inspection of individual sequence types revealed differential, lineage-specific expansion of various families of transposable elements among the different plant lineages. Copia-like retrotransposable element sequences have differentially accumulated in the Gossypium species with the smallest genome, G. raimondii, while gypsy-like sequences have proliferated in the lineages with larger genomes. Phylogenetic analyses demonstrated a pattern of lineage-specific amplification of particular subfamilies of retrotransposons within each species studied. One particular group of gypsy-like retrotransposon sequences, Gorge3 (Gossypium retrotransposable gypsy-like element), appears to have undergone a massive proliferation in two plant lineages, accounting for a major fraction of genome-size change. Like maize, Gossypium has undergone a threefold increase in genome size due to the accumulation of LTR retrotransposons over the 5–10 Myr since its origin.

[The sequence data described in this paper have been submitted to the GSS Division of GenBank under accessions DX390732–DX406528.]
cies. Other mechanisms posited to be responsible for genome size expansion include variation in intron size (Deutsch and Long 1999), expansion of tandemly repetitive DNA sequences (Ellegren 2002; Morgante et al. 2002), segmental duplication (Blanc et al. 2000; Ku et al. 2000; Vision et al. 2000; Wendel 2000; Bancroft 2001), accumulation of pseudogenes (Zhang 2003), and transfer of organellar DNA to the nucleus (Adams and Palmer 2003; Shalmuradov et al. 2003). However, these mechanisms generally do not appear to have a large impact on genome size differences among closely related species.

Although it has been suggested that organisms may have a “one-way ticket to genomic obesity” (Bennetzen and Kellogg 1997), it is possible that differences in genome size are not only the outcome of an organism’s tolerance for accrual of non-essential DNA, but also its efficiency in removal of non-essential DNA (Petrov and Hartl 1997; Petrov et al. 2000; Petrov 2002a; Wendel et al. 2002b). Many organisms with smaller genomes are striking in their relatively small proportion of non-essential DNA. Evidence of a deleterious bias among organisms with smaller versus larger genomes (Bennett and Leitch 1997; Petrov and Hartl 1997; Kirik et al. 2000; Petrov et al. 2000) has led to the “mutational equilibrium model” of DNA loss (Petrov 2002b). Other suggested mechanisms of DNA loss include unequal intrastrand homologous recombination between two tandem repeats in the same orientation, such as the LTRs of retrotransposable elements (Shepherd et al. 1984; SanMiguel et al. 1996; Chen et al. 1998; Vicent et al. 1999; Benetzen et al. 2002), illegitimate recombination (Devo et al. 2002; Wicker et al. 2003; Ma et al. 2004; Benetzen et al. 2005), and double-stranded break repair (Kirik et al. 2000; Orel and Puchta 2003; Filkowski et al. 2004).

To effectively study genome size evolution from a phylogenetic perspective, it is necessary to exploit a system in which the closely related species vary widely in genome size and for whom phylogenetic relationships are well understood. A good example in this respect is the monophyletic genus *Gossypium* (Malvaceae), which is composed of ~50 species of small trees and shrubs with an aggregate distribution that encompasses many tropical and subtropical semi-arid regions of the world (Fryxell 1992; Seelanan et al. 1997; Cronn et al. 2002; Wendel and Cronn 2003). Diploid members of the genus are divided into eight groups based on chromosome pairing behavior and fertility in interspecific hybrids (Beasley 1941; Endrizzi et al. 1985). All diploid members of the genus have 13 chromosomes, yet genome sizes range approximately threefold, from a median estimate of 885 Mb per haploid nucleus in the American D-genome species, to 2572 Mb per haploid nucleus in the Australian K-genome species (Fig. 1; Hendrix and Stewart 2005). An even larger range in genome size is observed in the tribe to which *Gossypium* belongs (the *Gossypieae*), from only 590 Mb in *Gossypioides kirkii* and *Kokia drynariae* to 4018 Mb in *Thebesia populnea* (Wendel et al. 2002b). The wide range in genome size observed across closely related diploid species and the well-established phylogeny makes *Gossypium* an excellent system for the study of genome size evolution.

To better appreciate the relevance of genome size variation to organismal fitness and evolution, it is first necessary to enhance our understanding of the quantity and quality of the genomic components that distinguish two or more genomes, as well as the modes and mechanisms by which these differences arise. This insight may derive from comparative sequence analysis of specific genomic regions or from using more global approaches. An example of the former is the recent study by Grover et al. (2004), who compared ~104 kb of aligned sequence surrounding the *CesA1* gene from the D- and A- genomes of tetraploid cotton. In this case, both gene content and intergenic regions were largely conserved, and hence there was no evidence of the mechanisms responsible for the twofold size variation that characterizes these genomes. Here, we employ the second approach, utilizing whole genome shotgun (WGS) libraries constructed for three members of *Gossypium* that range threefold in genome size, and one outgroup species, *Gossypioides kirkii*. Copy number estimates for several *Gossypium* transposable elements suggest that different types of repetitive sequences have accumulated at different rates in different plant lineages. Additionally, the results suggest that different families within a repetitive sequence type proliferate differentially. Indeed, the major fraction of the genome size variation observed in *Gossypium* is largely due to recent, lineage-specific amplification of one particular group of gypsy-like retrotransposon sequences, *Gorge3* (*Gossypium* retrotransposable gypsy-like element), within the larger-genome *Gossypium* species.

![Figure 1. Evolutionary relationships among diploid members of *Gossypium*. *Gossypium* is a monophyletic genus composed of ~50 species that are widely distributed throughout many tropical and subtropical regions. Diploid species have a haploid complement of 13 chromosomes. *Gossypium* is divided into eight genome groups based on cytogenetic data and level of fertility in interspecific hybrids (Endrizzi et al. 1985). Multiple molecular data sets support the phylogenetic relationships indicated, including the outgroup relationship of *Gossypioides kirkii* (Wendel and Albert 1992; Seelanan et al. 1997; Small et al. 1998, 1999). Despite conservation of chromosome number among the diploids, genome size varies threefold, from an average of 885 Mb in the New World D-genome species to an average of 2576 Mb in the Australian K-genome species (Hendrix and Stewart 2005).](image-url)
Results

Library construction and sequence analysis

The Gossypioideae kirkii (outgroup), Gossypium raimondii (D), G. herbaceum (A), and G. exiguum (K) libraries contained 1920, 3072, 6048, and 10,368 clones, of which 1464, 2722, 4864, and 6747 were successfully sequenced, respectively (Table 1). The percent of each genome sequenced (0.19%–0.24%) was determined by multiplying the number of successfully sequenced clones by the average high-quality sequencing read length, divided by the estimated genome size. Sequences were queried against GenBank using BLASTX and against each other using BLASTN, and sequences were classified as described (see Methods). All types of dispersed repetitive sequences identified via this procedure were categorized into 1) gypsy-like, 2) copia-like, 3) LINE-like, 4) Muta-tor-like, 5) hAT-like, 6) En/Spm-like, and 7) unknown repetitive sequences. Gypsy- and copia-like LTR retrotransposons, in addition to LINE-like retroposons, were abundant in all four species (Table 2; Fig. 2). Class II DNA sequences and tandem repeats were less abundant. Some classes of dispersed repetitive sequences, such as MITEs and SINEs, were not identified in the libraries. However, because of the lack of conserved domains for these two types of sequences, they may be present in Gossypium and unidentifiable via BLAST. Copy number estimates suggest a minimum of 44%, 54%, 52%, and 60% of the G. kirkii, G. raimondii, G. herbaceum, and G. exiguum genomes, respectively, are occupied by repetitive sequences alone.

Several conserved coding domains for diverse repetitive sequences were recovered from the WGS libraries when queried against Arabidopsis and Brassica databases. A total of 427 gypsy-like reverse transcriptase sequences were identified. Phylogenetic analysis of 373 of these sequences confirmed the existence of three distinct classes of gypsy-like retrotransposons among the four libraries identified in the initial BLAST search (Fig. 3, and see Figure 2). Copy number estimates for repetitive sequences in Gossypium. Copy numbers for repetitive sequences recovered in the WGS libraries were estimated as described (see Methods). The majority of repetitive sequences are LTR retrotransposons, particularly in the larger-genome species. In both the A and K genomes, massive amplification of Gorge3 gypsy-like sequences has occurred, contributing predominantly to genome size expansion in these two lineages. In the smallest Gossypium genome, G. raimondii (D genome), and copia-like sequences have proliferated and are primarily responsible for genome size expansion in this lineage. Class II sequences were less abundant and appear to contribute little to genome size evolution in the genus. Tandem repeats are approximately evenly distributed among all four species, with pXP1–80 sequences slightly elevated in G. exiguum (K genome).

Table 1. Library construction and sequencing effort for three species representing different Gossypium genomes and one phylogenetic outgroup

<table>
<thead>
<tr>
<th>Taxon.genome group</th>
<th>Genome size* (in Mb)</th>
<th>No. clones in library</th>
<th>Successfully sequenced</th>
<th>Average read (bp)</th>
<th>% genome sequenced</th>
<th>No. Mb sequenced</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gossypioides kirkii Outgroup</td>
<td>588</td>
<td>1920</td>
<td>1464</td>
<td>753</td>
<td>0.19%</td>
<td>1.10</td>
</tr>
<tr>
<td>Gossypium raimondii D genome</td>
<td>880</td>
<td>3072</td>
<td>2722</td>
<td>770</td>
<td>0.24%</td>
<td>2.10</td>
</tr>
<tr>
<td>G. herbaceum A genome</td>
<td>1667</td>
<td>6048</td>
<td>4864</td>
<td>704</td>
<td>0.21%</td>
<td>3.42</td>
</tr>
<tr>
<td>G. exiguum K genome</td>
<td>2460</td>
<td>10368</td>
<td>6747</td>
<td>704</td>
<td>0.19%</td>
<td>4.75</td>
</tr>
</tbody>
</table>

*Genome size from Wendel et al. (2002b) for G. kirkii and from Hendrix and Stewart (2005) for G. raimondii, G. herbaceum, and G. exiguum.

Figure 2. Copy number estimates for repetitive sequences in Gossypium. Copy numbers for repetitive sequences recovered in the WGS libraries were estimated as described (see Methods). The majority of repetitive sequences are LTR retrotransposons, particularly in the larger-genome species. In both the A and K genomes, massive amplification of Gorge3 gypsy-like sequences has occurred, contributing predominantly to genome size expansion in these two lineages. In the smallest Gossypium genome, G. raimondii (D genome), and copia-like sequences have proliferated and are primarily responsible for genome size expansion in this lineage. Class II sequences were less abundant and appear to contribute little to genome size evolution in the genus. Tandem repeats are approximately evenly distributed among all four species, with pXP1–80 sequences slightly elevated in G. exiguum (K genome).
is similar to those of published centromere repeats from (23,795/11506 2004). Several other tandem repeats of unknown identity were (178 bp), wheat (192 bp), rice (155 bp), and maize (156 bp). G. herbaceum — G. kirkii — 80 were comparable between three of the four mates for pXP1–libraries. Similar to the 5SrDNA repeats, copy number esti-

This 170- to 172-bp repeat was present in all four of the WGS libraries. One of these tandem repeats was identified as a pre-

sequences identified by TRF = 1), and (transposons (Benson 1999). Sequences identified by Tandem Repeat Finder = 2), Mutator-like (n = 1), and En/Spm-like (n = 15) transposable elements were also retained for further analysis.

Tandem repeats were identified using Tandem Repeat Finder (Benson 1999). Sequences identified by TRF as tandemly repeti-

Copy number estimates and lineage specific amplification

Tandem repeats

Sequences with high identity to previously described Gossypium 5SrDNA repeats were identified in all four libraries. Estimates for D- (7675 ± 3826) and A- (5073 ± 3379) genome 5SrDNA copy numbers are in agreement with previously published estimates (Cronn et al. 1996) of 4730 ± 893 for G. raimondii and 3415 ± 807 for G. herbaceum, those of the latter study being based on Southern hybridization data. Estimated copy numbers for 5SrDNA sequences among the four libraries fall well within the same 95% CI (Table 2). Several other tandem repeats were recovered. One of these tandem repeats was identified as a previously published Gossypium sequence, pXP1–80 (Zhao et al. 1998).

This 170- to 172-bp repeat was present in all four of the WGS libraries. Similar to the 5SrDNA repeats, copy number esti-

Table 2. Repetitive element copy number and density estimates

<table>
<thead>
<tr>
<th>G. kirkii Outgroup</th>
<th>G. raimondii D genome</th>
<th>G. herbaceum A genome</th>
<th>G. exiguum K genome</th>
</tr>
</thead>
<tbody>
<tr>
<td>S5RNA</td>
<td>4279 ± 3227</td>
<td>7675 ± 3826</td>
<td>5073 ± 3379</td>
</tr>
<tr>
<td>pXP1–80</td>
<td>12,264 ± 6098</td>
<td>6573 ± 3956</td>
<td>10,101 ± 5392</td>
</tr>
<tr>
<td><strong>Class II transposons</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>En/Spm-like</td>
<td>120 ± 138</td>
<td>835 ± 326</td>
<td>343 ± 216</td>
</tr>
<tr>
<td>−0.2%</td>
<td>−0.9%</td>
<td>−0.2%</td>
<td>&lt;0.1%</td>
</tr>
<tr>
<td>hAT-like</td>
<td>305 ± 352</td>
<td>81 ± 163</td>
<td>263 ± 304</td>
</tr>
<tr>
<td>−0.2%</td>
<td>−0.1%</td>
<td>&lt;0.1%</td>
<td>&lt;0.1%</td>
</tr>
<tr>
<td><strong>Class II Total</strong></td>
<td>3.5 Mb</td>
<td>12 Mb</td>
<td>5 Mb</td>
</tr>
<tr>
<td>&lt;0.1%</td>
<td>1.0%</td>
<td>&lt;0.1%</td>
<td>1.0%</td>
</tr>
<tr>
<td><strong>Class I retrotransposons</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>copia-like</td>
<td>17,006 ± 5765</td>
<td>57,956 ± 9300</td>
<td>43,181 ± 8774</td>
</tr>
<tr>
<td>LINE</td>
<td>16,006 ± 5597</td>
<td>13,011 ± 4502</td>
<td>30,000 ± 7335</td>
</tr>
<tr>
<td>5.1%–10.6%</td>
<td>2.8%–5.7%</td>
<td>4.0%–6.5%</td>
<td>2.4%–4.1%</td>
</tr>
<tr>
<td>GORGE1 gypsy-like</td>
<td>4502 ± 2992</td>
<td>1971 ± 1762</td>
<td>5900 ± 3273</td>
</tr>
<tr>
<td>2.4%–11.9%</td>
<td>0.2%–3.9%</td>
<td>1.5%–5.2%</td>
<td>0.8%–3.2%</td>
</tr>
<tr>
<td>GORGE2 gypsy-like</td>
<td>2500 ± 2233</td>
<td>3154 ± 2227</td>
<td>3181 ± 2403</td>
</tr>
<tr>
<td>0.4%–7.5%</td>
<td>1.0%–5.7%</td>
<td>0.4%–3.2%</td>
<td>1.6%–4.7%</td>
</tr>
<tr>
<td>GORGE3 gypsy-like</td>
<td>5502 ± 3305</td>
<td>8674 ± 3683</td>
<td>48,181 ± 9257</td>
</tr>
<tr>
<td>3.9%–13.9%</td>
<td>5.3%–13.6%</td>
<td>22.0%–32.6%</td>
<td>28.8%–38.6%</td>
</tr>
<tr>
<td><strong>Class I Total</strong></td>
<td>255 Mb</td>
<td>465 Mb</td>
<td>865 Mb</td>
</tr>
<tr>
<td>42%</td>
<td>53%</td>
<td>52%</td>
<td>58%</td>
</tr>
</tbody>
</table>

below). Reverse transcriptase sequences from copia-like retro-

The three major superfamilies of Class II DNA transposons pre-

The most highly represented group of repetitive sequences

Within the Gossypium genome, Class II transposons occupy <2% of the Gossypium genome (Table 2). En/Spm-like sequences occupy <1% of the genome in each of the four species, comprising ~0.2% of the G. kirkii (~120 copies) and G. herbaceum (~343 copies) genomes, but increasing in copy number in the smallest (G. raimondii — 0.9%, ~835 copies) and largest (G. exiguum — 1.0%, ~2515 copies) genomes. Similarly, hAT-like sequences occupy <1% of the genome in each of the four species. hAT-like sequence comprise only 0.2% of the G. kirkii (~300 copies) genome, and an even smaller portion of the G. raimondii (0.03%, ~80 copies) and G. herbaceum (0.06%, ~260 copies) genomes. However, a large in-

The most highly represented group of repetitive sequences

Within all four WGS libraries is the Class I elements (Fig. 2). Estimated total Class I copy numbers range 4.4-fold, from 45,515 ± 9241 in Gossypiodae kirkii to ~197,294 ± 18,935 in the K genome species, Gossypium exiguum. When multiplied by an
The most striking example of differential lineage-specific amplification of specific groups of repetitive sequences is found among the gypsy-like sequences. BLAST analysis led to the discrimination of three different types of gypsy-like sequences present in the WGS libraries, and copy-number estimates for each of these are shown separately in Table 2. Phylogenetic analysis of 373 gypsy-like reverse transcriptase sequences assembled from all four of the WGS libraries confirmed the existence of three distinct classes, here designated Gorge1, Gorge2, and Gorge3, for Gossypium retrotransposon gypsy-like elements (Fig. 2). The Gorge1 group is similar to the Arabidopsis gypsy sequence athila, Gorge2 is similar to maize cinful1, and Gorge3 is similar to del1–46 from Lilium henryi and dea1 from Ananas comosus. Copy number calculations for the three types of sequences revealed relatively stable copy numbers for Gorge1 and Gorge2 across all four species, although the copy number estimate for Gorge1 in the D genome (1971 ± 1762) is somewhat lower than that of the other three species, and Gorge2 copy number is slightly elevated in the K genome (8220 ± 3983) (Table 2). In contrast to this relative stability for Gorge1 and Gorge2, there is a profound increase in copy number of Gorge3 gypsy elements in the larger-genome species. Whereas copy numbers for Gorge3 are similar in G. raimondii and G. exiguum (5502 ± 3305 and 8674 ± 3683, respectively), a striking increase in copy number has taken place in both the A (48,181 ± 9257) and K (88,492 ± 12,904) genome lineages. There is a sixfold increase of Gorge3 copy number from the D to the A genome, and copy number in the A genome is nearly doubled in the K genome. The impact of this proliferation on genome size is apparent from density calculations: Gorge3 occupies ~9% of both the G. kirkii and D genomes, but 27.3% and 33.7% of the A and K genomes, respectively.

Unidentified repetitive fraction

Clones with no similarity to any sequence deposited in GenBank were placed in a separate database as the “unidentified fraction” of repetitive fraction.
of each of the WGS libraries. These sequences were queried against each other using BLASTN to identify repetitive sequences that were missed during the initial BLAST search. Any sequence with >80% sequence to at least three other clones from the same library was considered repetitive. A total of 43, 129, 364, and 603 clones from the G. kirkii, D, A, and K libraries, respectively, were considered repetitive under this criterion. The percentage of each library composed of these unidentified repetitive sequences is as follows: G. kirkii (OG)—3%; G. raimondii (D)—5%; G. herbaceum (A)—7.5%; and G. exiguum (K)—9%.

Discussion
Variation in nuclear DNA content observed within and between organisms has been a topic of interest dating back to the early 1900s, but was specifically defined and named the “C-value paradox” by Thomas in 1971 (Thomas 1971). Investigations over the past half century have revealed multiple sources of genome size variation, most commonly the differential accumulation or deletion of transposable elements. Repetitive DNA constitutes 80% of angiosperm genomes with haploid DNA content >5.0 pg (Flavell et al. 1974). Approximately 60% or more of the maize (SanMiguel et al. 1996, 1998; Meyers et al. 2001), wheat (Wicker et al. 2001), and barley (Vicien et al. 1999; Shirasu et al. 2000) genomes are composed of transposable elements. Nearly 25% of the maize genome consists of five classes of LTR retrotransposons alone (SanMiguel et al. 1996), and LTR retrotransposon accumulation is responsible for nearly doubling the maize genome in as little as 3 Myr (SanMiguel and Bennetzen 1998). Roughly 80% of the wheat genome is repetitive DNA, mainly LTR retrotransposons (Kumar and Bennetzen 1999). These observations have led to an interest in the effects of repetitive DNA on genome size variation and its significance to plant fitness. Relatively little is known, however, about the evolutionary dynamics of transposable element accumulation among closely related species and how this varies among TE classes.

We constructed WGS libraries for three Gossypium and one outgroup species that range approximately fourfold in genome size in order to describe their overall genomic composition and to determine the sequences that contribute to genome size variation. Congruent with results from taxa studied to date, we found that the majority of the Gossypium genome consists of dispersed repetitive sequences. Density estimates based on previously reported repetitive sequence lengths suggest that the Gossypium genome is composed of ~45%–60% repetitive sequences when considering only those sequences with positive BLAST matches to previously identified repetitive elements in Gossypium or in other species. This number is in agreement with estimates from other species with large genomes, such as maize, barley, and wheat (SanMiguel et al. 1996; SanMiguel and Bennetzen 1998; Kumar and Bennetzen 1999; Vicien et al. 1999; Shirasu et al. 2000; Meyers et al. 2001; Wicker et al. 2001), but differs from estimates for smaller-genome species such as Arabidopsis (~14%) and rice (~26%) (The Arabidopsis Genome Initiative 2000; Jiang and Wessler 2001; Jiang et al. 2004). Additionally, given the number of repetitive sequences of unknown identity recovered in the self-BLAST searches, 45%–60% clearly is an underestimate of the actual repetitive fraction.

Also in agreement with results from other well-studied taxa, the majority of the identified repetitive fraction consists of Class I retrotransposon sequences. As expected based on reported estimates from many grasses and a few well-studied eudicots, Class II sequences were less abundant and constituted a minor fraction of the Gossypium genomes (2%). This estimate is comparable to that from Arabidopsis (2%–3%) (The Arabidopsis Genome Initiative 2000), whose genome is almost five times smaller that of G. kirkii (88 Mb), as well as maize (2%) (Meyers et al. 2001), whose genome is only slightly larger than that of G. exiguum (2460 Mb). However, this result is in contrast with that from Brassica and rice, whose genomes harbor ~6% and 12% Class II DNA transposons, respectively (Jiang and Wessler 2001; Jiang et al. 2004).

Lineage-specific transposition
A key conclusion of the present study is that genome size variation in a single genus of plants reflects not only the differential amplification of diverse types of repetitive sequences, but that specific families within a repetitive sequence type proliferate differentially as well. From a purely quantitative standpoint, much of the genome size variation observed in Gossypium is a consequence of the propagation of one particular family within the larger class of gypsy-like retrotransposons, i.e., Gorge3. Recently, a gypsy-like retrotranspon (“G45” and “G84”) that is transcriptionally active was reported in the tetraploid G. barbadense (Zaki and Ghany 2004). Comparisons of this active gypsy with sequences recovered in the present study revealed a maximum of 96.1% and 80.9% amino acid sequence identity between the best BLAST hit to an A-genome Gorge3 and G45 and between A-genome Gorge3 and G84, respectively. Additionally, 165 out of 150,322 Gossypium ESTs show >60% sequence similarity over >75 bp to Gorge3 (c-value cut-off of e-20, data not shown). Based on this high level of sequence identity to G45 and G84, presence in the Gossypium EST libraries, and overabundance of Gorge3 in the WGS libraries, we believe Gorge3 is a recently active, major constituent of the cotton genome that, like LTR retrotransposons in maize, has triggered a threefold increase in genome size over the 5–10 Myr since the diversification of the major Gossypium clades following the origin of the genus (Cronn et al. 2002).

It is interesting to note that other repetitive sequences that are less common than Gorge3 have also been subject to lineage-specific amplification during diversification of the genus. For example, little amplification of LINE retrotransposons has occurred in the D genome lineage, but these sequences have proliferated in the A and K genome species. Similarly, accumulation of copia-like retrotransposons has occurred in the D genome lineage, yet these repetitive elements have been suppressed in the remainder of the genus, with the proportion of the genome occupied by copias in the remaining three species being between 10% and 20%. Indeed, G. raimondii is the only studied Gossypium species in which there are more copia-like than gypsy-like sequences (Fig. 2).

The most parsimonious interpretation of the copia data would invoke differential amplification in the D genome lineage. However, we cannot discount the possibility of unequal rates of DNA loss. Some species appear to be more efficient at removal of non-essential DNA, such that genome size may reflect, at least in part, differential rates of DNA loss (Petrov and Hartl 1997; Kirik et al. 2000; Petrov et al. 2000; Orel and Puchta 2003). With respect to the present study, LINE-like sequences recovered in the WGS libraries are often highly degraded and hence difficult to identify. Although the most parsimonious interpretation of our copy-number estimates is a single amplification event in the common ancestor of the A and K genome lineages, a formal alternative is that LINE-like sequences existed at an ancestrally high copy
number and have subsequently been differentially eliminated from the species with smaller genomes (D genome and the outgroup G. kirkii).

**Genome size evolution in Gossypium**

At present relatively little is known about the genomic locations at which genome size evolution takes place in Gossypium. The data presented here show that specific families and classes of dispersed repetitive elements have differentially proliferated in different Gossypium lineages. Given the propensity of many high-copy-number LTR retrotransposons to accumulate in heterochromatic regions of the genome (Kumar and Bennetzen 1999), we suspect that much of the evolutionarily rapid genome size change that has arisen during the global radiation of Gossypium has occurred in these gene-poor regions. Consistent with this notion, Grover et al. (2004) investigated genome size evolution in 104 kb of contiguous sequence surrounding the CesA1 gene in the Gossypium A and D genomes from tetraploid cotton. Within this genomic region of the Gossypium genome, no evidence of genome size variation was apparent, suggesting that genome size evolution in Gossypium takes place in heterochromatic regions located between highly conserved, euchromatic gene islands. Evaluation of this hypothesis will require additional comparative sequence and mapping data, the latter including visualization techniques such as fluorescent in situ hybridization (FISH) of various transposable elements.

In addition to transposable element accumulation, other suggested mechanisms of genome size change include variation in intron length, expansion/contraction of tandem repeats, illegitimate recombination, indel bias, and unequal intraspecies homologous recombination (Petrov and Wendel 2006). Contrary to suggestions that plants with smaller genomes carry smaller introns (Deutsch and Long 1999; Vinogradov 1999), there is no apparent correlation between genome size and intron length in Gossypium (Wendel et al. 2002a; Grover et al. 2004). In fact, intron length has been shown to be highly stable across 28 orthologous sets of genes from A and D genome diploid species and the outgroup species, G. kirkii (Wendel et al. 2002a). In the present study, we find no major difference between copy numbers for tandem 5SrDNA and pXP1–80 repeats, although there is a small increase in copy number in larger genomes. However, Cronn et al. (1996) reported a 20-fold variation in 5SrDNA copy number among Gossypium species, reflecting both array expansion and contraction. Grover et al. (2004) found no evidence of an indel bias, and although there was some evidence of illegitimate recombination marked by flanking repeats of 2–15 bp in length, the resulting deletions encompass approximately the same proportion of sequence in each genome. Similar studies from other genomic loci in Gossypium will be necessary to determine if this result is a local or global occurrence.

**Conclusions**

Comparative studies of genome size variation among phylogenetically characterized and closely related species serve an important role in clarifying the patterns and processes that underlie the striking genome size variation that characterizes eukaryotes in general and plants in particular. With respect to the latter, we note that the genomic architecture of most plant species remains to be elucidated, and hence mechanisms that characterize one group of plants may not be universal to, say, angiosperms in general. Our data, demonstrating that different families of different classes of TEs have differentially accumulated among closely related clades of a single plant genus, underscores what we believe will be a generality, namely, that mechanisms of genome size evolution are highly variable among even closely related lineages. Our appreciation of plant genomic architecture will continue to be enhanced as comparable studies in other plant groups accumulate. These investigations will generate a deeper understanding of the genomic landscape of different plant lineages, the scale, scope, and pace of evolutionary change responsible for the observed patterns, and insights into the mechanisms that underlie the differential accumulation of different sequence types among genomes.

**Methods**

**Construction and sequencing of WGS libraries**

WGS libraries were constructed according to Meyers et al. (2001) with minor modifications and sequenced at the Arizona Genomics Institute, University of Arizona. Briefly, total genomic DNA extracted from young leaves of a single individual was randomly sheared using a HydroShear (Thorstenson et al. 1998) (GeneMachine), an automated hydrodynamic point-sink–based DNA shearing device (Oefner et al. 1996), at speed code 13 for 25 cycles at room temperature to obtain fragments from G. herba-ceum (JMS), G. raimondii (JFW stock), G. exiguum (Gos 5184), and G. kirkii (JFW stock) (Fig. 1). Sheared fragments between 2500 and 6000 bp were excised and converted to blunt-ended DNA fragments using the “End-it” DNA end repair kit (Epigen) containing T4 DNA polymerase (for 5′→3′ polymerase and 3′→5′ exonuclease activities) and T4 Polynucleotide Kinase (for phosphorylation of 5′-ends of blunt DNA), followed by ligation into pBluescriptII KS+ (Strategene) and electroporation into Escherichia coli strain DH10B T1 phase-resistant electrocompetent cells (Invitrogen). WGS library clones were sequenced from one direction using the T7 primer (5′-TAATACGACTCACTATAGGG-3′) and BigDye Terminator v3.1 (Applied Biosystems, ABI) according to manufacturer’s instruction. Cycle sequencing was performed using PTC-200 thermal cyclers (MJ Research) in a 384-well format with the following regime: 35 cycles of 30 sec at 96°C, 20 sec at 50°C, and 4 min at 60°C. After the cycle-sequencing step, the DNA was purified by ethanol precipitation.

Samples were eluted into 20 µL of water and separated using ABI 3730×1 DNA sequencers (ABI). Sequence data were collected and extracted using sequence analysis software (ABI). The sequencing data were base-called using the program Phred (Ewing et al. 1998). Vector and low-quality sequences were removed by the program Lucy (Chou and Holmes 2001) and then submitted to the GSS division of GenBank under accessions DX390732–DX406528.

**Analytical framework**

The number of sequences needed to generate 95% confidence that at least one member of a given class of sequences will be sampled was determined for each species using the following equation:

\[
N_{95} = \ln (0.05) / \ln [1 − n \{ l + 2m + c\}/(G − e)]
\]

where \(N_{95}\) is the sampling effort required to be 95% confident that at least one target sequence will be sampled, \(n\) is the number of targets present in the genome, \(l\) is the length of the target sequence, \(m\) is the estimated minimum length required to identify the sequence in a BLAST search, \(c\) is the number of base pairs sequenced from each insert, and \(G\) is genome size. By using this
equation we were able to estimate the sampling intensity needed to detect at least one repetitive sequence of an estimated length and copy number in each of the four genomes. Published data for diverse types of repetitive elements, such as Ty3-gypsy, Ty1-copia, LINE retroposons, SINES, and MITEs of various estimated lengths ($l$) and copy numbers ($n$) were used to calculate $N_{\text{seq}}$ in order to determine how many clones should be sequenced from each library. The value for $m$ was conservatively estimated at $m = 200$ bp, which in a BLASTX analysis would equal sequence similarity over $\geq 66$ amino acids. We estimated $e$ to be 700 bp, based on the average high-quality sequencing read length reported from the Arizona Genomics Institute. Based on these estimates, libraries were constructed that contain 1.5% (based on $\sim 5$ kb plasmid insert length) of the genome from each species. One-pass sequencing from one end of the insert ($e \sim 700$ bp) was performed, which, when totaled across the number of clones sequenced, yielded sequence data for $\sim 0.2\%$ of each haploid genome (Table 1).

Data analysis and copy number estimation
Because of rapid sequence divergence of repetitive DNA and the limited database of repetitive sequences available in GenBank for plants closely related to *Gossypium*, sequences from the WGS libraries were subjected to BLASTX (amino acid) in addition to BLASTN (nucleotide) analyses at the NCBI Web site. Hits of e-5 or better were retained for further analysis. In addition, libraries were queried against themselves in an attempt to identify families of repetitive elements not recognized in the initial search. In this self-BLAST analysis, sequences with $>80\%$ identity over 100 bp were considered related. Clones were assigned to a general category according to their best BLAST hit. These general categories were (1) nuclear, (2) chloroplast, (3) mitochondrial, (4) repetitive, and (5) unknown.

Plant transposable elements are broadly divided into three main lineages: the “Transposons” consisting of the Class II DNA elements, the “Retrotransposons” containing the LTR Class I elements, and the “Retroposons” consisting of the non-LTR Class I elements (Eickbush and Malik 2002). Class I elements transpose via a duplicative mechanism, in which an RNA intermediate formed from the parental copy is reverse transcribed, and the newly translated copies are inserted into new positions in the genome. Class I LTR retrotransposons are subdivided into two classes, gypsy and copia-like, based on the position of the integrate coding domain. The non-LTR retrotransposons consist of autonomous Long Interspersed Nuclear Elements (LINES) and the non-autonomous Small Interspersed Nuclear Elements (SINES). Class II DNA elements transpose via a cut-and-paste mechanism in which the element is excised and inserted into a new area of the genome. DNA elements characterized contain terminal inverted repeats (TIR) ranging from 11 to a few hundred base pairs in length, and families of elements are defined by these TIR sequences (Bennetzen 2000b). Class II transposons can be divided into three main superfamilies: hAT (holo from Drosophila, Activator of maize, and Tam from Snapdragon), Mutator, and En/Spm, both first described in maize (Kidwell 2002). Therefore, dispersed repetitive sequences recovered from the WGS libraries were placed into the specific categories 1) gypsy-like, 2) copia-like, 3) LINE-like, 4) hAT-like, 5) En/Spm-like, and 6) Mutator-like. DNA sequence alignments were performed with published sequences of the same type to confirm sequence identity.

Tandem repeats were identified using the program Tandem Repeat Finder (Benson 1999). Searches were performed using the default settings. Any tandem repeat present in more than three clones with a score $>500$ was retained for further analysis. These sequences were queried against GenBank using BLASTN to search for sequence similarity to known sequences deposited in GenBank. Sequences were queried against another to identify sequences that were shared among the libraries.

Copy numbers ($n$) for various repetitive elements recovered from the WGS libraries were estimated according to the following equation:

$$n = (X_{\text{obs}} / N)(G - e)(1 / (l - 2m + e))$$

where $X_{\text{obs}}$ is the observed number of copies, $N$ is the total number of sequence reads, and the other variables are as before: $n$ is the number of targets in the genome; $l$ is the length of target sequence; $m$ is the estimated minimum length required to identify sequence in a BLAST search; $e$ is the number of bp sequenced from each insert; and $G$ is genome size. Published sequences for various repetitive elements were used to estimate $l$. Similar to average copia sequences in rice ($5\sim6$ kb) (McCarthy et al. 2002), an $l$ of 5.3 kb was used for copia-like sequences based on published data from *Gossypium* (Grover et al. 2004). Also in agreement with rice data for gypsy-like sequences ($11\sim13$ kb) (McCarthy et al. 2002), $l$ for gypsy-like sequences in *Gossypium* was set at 9.7 kb (C.E. Grover, unpubl.). Because no data exist for other dispersed repetitive sequences in *Gossypium*, the estimated lengths for the remaining repetitive sequences were established according to their closest BLAST hit from GenBank and are assigned as follows: LINE retroposon 3.5 kb (GenBank accession no. NP_92230 from *O. sativa*); En/Spm with high identity to Tam1 (Nacken et al. 1991) (GenBank accession no. X57297) 15.2 kb; and hAT with high identity to Tam3 (Hehl et al. 1991) (GenBank accession no. X55078) 3.6 kb. Published lengths for Mutator-like sequences are highly variable (in *Arabidopsis* these range from 444 to 19,397 bp) (Yu et al. 2002); therefore, we did not attempt to estimate Mutator-like copy numbers. A recent manuscript by Rabinowicz et al. (2005) used WGS libraries to estimate gene number in various plant species. When using their data for *Arabidopsis* and rice in our equation, we recover comparable results to those published for these two sequenced genomes, suggesting that our equation results in reasonably accurate estimates of copy numbers.

Phylogeny reconstruction
Sequences were queried against coding domains of various repetitive sequences from *Arabidopsis thaliana* and *Brassica oleracea* obtained from S. Wessler and F. Zhang (Univ. Georgia). Amino acid sequences with an e-value of e-5 or better were imported into BioEdit (Hall 1999) and aligned using ClustalW (Johnson et al. 1994). Neighbor-Joining analysis was performed in Paup* (Swofford 2001) using the default settings.

Acknowledgments
We thank Curt Brubaker for providing *Gossypium exiguum* seeds and DNA; S. Wessler and F. Zhang for sharing a repetitive sequence database; Jordan Swanson for assistance with data analysis; Ryan Percifield, Corrinne Grover, and Ryan Rapp for helpful discussion; and the anonymous reviewers for their comments. This work was funded by the National Science Foundation Plant Genome program.

References


SanMiguel, P. and Bennetzen, J.L. 1998. Evidence that a recent increase in maize genome size was caused by the massive amplification of intergene retrotransposons. *Ann. Bot. (Lond.)* 82: 37–44.


Received March 3, 2006; accepted in revised form May 22, 2006.
Differential lineage-specific amplification of transposable elements is responsible for genome size variation in Gossypium


Genome Res. 2006 16: 1252-1261
Access the most recent version at doi:10.1101/gr.5282906