**Thirteen genome sequences representing the entire subgenus Houzingenia (Gossypium): insights into evolution of the New World diploid cottons**

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Abstract

Keywords

**Background**

The American diploid “D-genome” cottons (subgenus *Houzingenia*) comprise a monophyletic clade of cytogenetically and morphologically distinct species largely distributed from Southwest Mexico to Arizona, with additional disjunct species distributions in Peru and the Galapagos Islands which citations here, (Endrizzi, Turcotte, and Kohel 1985). Among the 13-14 species currently included in the D-genome (Ulloa et al. 2013) is a source of cytoplasmic male sterility in cotton, *G. harknessii*, and the model diploid progenitor to wild and domesticated allopolyploid cotton, *G. raimondii* (reviewed in (Jonathan F Wendel and Grover 2015)). The close relationship of *Houzingenia* species to the agronomically important polyploid cottons, combined with the relative ease of sampling this subgenus for early cotton taxonomists, facilitated much of the current understanding of the relationships among D-genome species.

These early taxonomists divided subgenus *Houzingenia* into two sections and six subsections whose species alliances have largely been retained by subsequent phylogenetic studies (R C Cronn et al. 1996; Seelanan, Schnabel, and Wendel 1997; R L Small and Wendel 2000; J F Wendel and Albert 1992; J F Wendel, Schnabel, and Seelanan 1995; Álvarez, Cronn, and Wendel 2005). Several molecular datasets have been used to evaluate these relationships, including chloroplast restriction sites [citation]; simple sequence repeat (SSR) and expressed sequence tag (EST)-SSR markers [citation]; random amplified polymorphic DNA (RAPD) markers [citation]; internal transcribed sequences (ITS) [citation]; and few single-copy nuclear genes [citation]. Relationships among the six subsections, however, remain unclear despite numerous, and often conflicting, studies (R C Cronn et al. 1996; Liu et al. 2001; R L Small and Wendel 2000). Determining the closest living relative of the D-genome ancestor to the polyploid, however, has been met with greater success. Early morphological and cytogenetic comparisons using intergenomic hybrids quickly identified *G. raimondii* as the closest living relative to the D-genome ancestor of polyploid cotton species (reviewed in J F Wendel and Cronn 2003). Subsequent analyses have largely supported this observation (Abdalla et al. 2001; Richard C Cronn, Small, and Wendel 1999; Liu et al. 2001; R C Cronn et al. 1996; Seelanan, Schnabel, and Wendel 1997; Randall L Small et al. 1998; R L Small and Wendel 2000), with few conflicts (see, however, (J F Wendel, Schnabel, and Seelanan 1995)).

A secondary outcome of this research has been the elucidation of multiple instances of hybridization among the D-genome cottons (R. Cronn and Wendel 2004), and, in one remarkable case (i.e., *G. gossypioides*), between a *Houzingenia* species and another, geographically isolated subgenus from Africa (either A-, B-, E-, or, F-genome; (R. Cronn and Wendel 2004; R. Cronn et al. 2003)). Notably, *G. gossypioides* is multiply introgressed, with a subsequent hybridization to a member of the *G. raimondii* lineage resulting in chloroplast, if not further (and cryptic), nuclear introgression (R. Cronn et al. 2003). Cytoplasmic introgression, and possibly cryptic nuclear, is also present in some populations of *G. aridum*; i.e., the Mexican Colima populations of *G. aridum* possess a *G. davidsonii*- or *G. klotzschianum*-like cytoplasm.

Modest attempts at understanding the evolution of the repetitive fraction of this genus support the inference of African introgression in G. gossypioides (Zhao et al. 1998); however, little else is understood with respect to the evolution of the non-genic fraction of Houzingenia. The D-genome cottons possess the smallest genome sizes in the genus, ranging only ~1.11 fold, from 841 Mb – 934 Mb. Notably, the distribution of genome sizes among the subsections suggests that this subgenus has experienced differential growth and/or reduction in genome size among species; however, the patterns the characterize sequence gain and loss have not been characterized. While the differences in genome size are not dramatic, there is evidence that the transposable element types which have accumulated in *G. raimondii* are different than those that have achieved higher copy numbers than the remainder of the genus (Jennifer S Hawkins et al. 2006; Corrinne E Grover et al., n.d.; Renny-Byfield et al. 2016). Furthermore, research comparing the two sister genera to cotton (i.e., *Kokia* and *Gossypioides*; (Corrinne E Grover et al., n.d.)) reveals that their apparently static genome sizes belies both gain and loss of repetitive sequence, a result similar to that of the extant members of the A-genome (subgenus Gossypium), whose small change in genome size (~1.05X) masks differences in element accumulation (Renny-Byfield et al. 2016; Corrinne E Grover et al., n.d.).

Modern sequencing techniques make it easy to produce a substantial amount of genomic sequencing suitable for addressing basic molecular evolutionary questions in a more genomically comprehensive manner. Here we use modest coverage Illumina sequencing to present an in-depth view of the evolution subgenus Houzingenia, the cotton D-genome clade. We leverage newly generated genome and plastome sequences, representing the first for many species, to address questions surrounding genome evolution in a monophyletic group of closely related species. We characterize the patterns of molecular evolution of both genes and repetitive sequences to provide insight into the pace and pattern of evolution in this subgenus. For the first time, intergenic regions are evaluated to characterize the amount of divergence outside of genes, and due to indels or single-nucleotide polymorphisms (SNPs). Finally, we revisit the phylogeny of the D-genome, both adding additional insight into the relationships among species using hundreds of nuclear genes, as well as addressing questions regarding sequence gain and loss among closely related species. The genomes characterized here not only provide insight into molecular evolution on a relatively recent timeframe, but they also provide resources for comparative research and the cotton community at large.

**Results**

**Genome assemblies and annotation**

Approximately 22-65X raw coverage libraries were sequenced for at least one representative of each D-genome species (Table Assembly\_reads), resulting in an average of 169.4 M reads per accession. Quality filters further reduced the number of reads per sample to an average of 136.9 M (range: 87.2 – 260.2 M), representing an average of 33X coverage per sample. All accessions (except *G. thurberi* accession 2) were assembled via ABySS using multiple k-mer values (see methods) and the assembly with the greatest E-size (Salzberg et al. 2012) was selected to represent each species. These representative assemblies were improved with the reference-based scaffolder Chromosomer (Tamazian et al. 2016) using the closely related, gold-standard *G. raimondii* genome (Paterson et al. 2012), producing assemblies which range in size between 585 – 775 Mbp (average 643 Mbp) and cover 67 – 85% of each genome (Table Assembly Stats; Figure Assembly Stats). These metrics are comparable to those generated by the subgenus *Houzingenia*-derivedgold-standard reference genome (Paterson et al. 2012).

Assemblies from all accessions were annotated resulting in between 20,522 and 45,244 gene models per accession (min=26,492 for improved assemblies), similar to the number of primary transcripts published for *G. raimondii* (Paterson et al. 2012)*.* BUSCO (Simão et al. 2015) analysis recovered over 80% of BUSCOs from nearly 80% of the improved assemblies, where a gene was considered present if more than 67% of the gene was recovered from that accession. This suggests a general completeness of the gene space, with an average of 87% complete BUSCOs recovered from each accession and less than 3.5% redundancy on average (Table\_BUSCO).

Chloroplast reads were also recovered from the raw reads, representing an average of 3% (range: 1.46 – 7.27%) of the filtered sequencing reads. These were used in reference guided assemblies against the published *G. hirsutum* chloroplast genome (Lee et al. 2006). The chloroplast genome alignment (excluding positions with ambiguity in any sequence) size was 158,996 bp, which is comparable to previously published cotton chloroplast genomes (Chen et al. 2016, 2017; Richard C Cronn et al. 2002). Chloroplast sequences were retained for phylogenetic analyses, and are available under WHAT-PRJNA

**Phylogenetics, divergence, and molecular evolution**

Phylogenetic relationships among *Houzingenia* species were revisited using a concatenation of 7,595 dispersed nuclear genes containing a minimum of one accession per species. After removing any alignment position with >10% ambiguity, >20.3 million nucleotides derived from all 13 chromosomes remained for 28 *Houzingenia* accessions and for the outgroup, *G. longicalyx* (subgenus *Longiloba*). Maximum likelihood reconstruction of the phylogenetic relationships among species largely recapitulate established section and subsection relationships (Figure\_phylogeny.png). As previously reported, while the two sections which comprise the subgenus, i.e., *Houzingenia* and *Erioxylum* exhibit polyphyly, the individual subsections are either monophyletic or monotypic (Figure phylogeny). Species relationships are largely congruent with the most recent treatise of the subgenus using nuclear genes (Álvarez, Cronn, and Wendel 2005), both of which differ from the subgenus SSR dendrogram (Ulloa 2014) in the placement of several taxa, including *G. raimondii*, *G. davidsonii*, and *G. gossypioides*. Coalescent analysis of the same data converge on the same relationships established by the concatenated phylogeny, with the exception of the relationships among individuals of the same species, and, notably, in the placement of *G. schwendimanii* versus *G. laxum*, whose positions are reversed in the coalescent phylogeny (data not shown).

Notably, one of the two *G. aridum* accessions included (D4-12C from Colima, Mexico; PI 530897) is placed basal within the arborescent cottons of subsection *Erioxylum* and not sister to the *G. aridum* accession from Jalisco (Álvarez, Cronn, and Wendel 2005). This observation recapitulates that of Alvarez et al (2006) , which used AFLPs to evaluate 143 individuals from 50 populations of subsection *Erioxylum* species and the related subsection, *Integrifolia*, which was previously identified as a source of cytoplasmic introgression in Colima *G. aridum* accessions (Dejoode 1992). Indeed, phylogenetic analysis of the entire chloroplast for *Houzingenia* species concurs with previous chloroplast restriction site analysis (J F Wendel and Albert 1992), which suggest that the Colima *G. aridum* accession (D4-12C) has an *Integrifolia* derived cytoplasm. It is interesting to note that diversity analyses of subsection *Erioxylum* using SSR markers (Ulloa 2006, Ulloa 2014, Feng 2011) suggest that the circumscription of *G. aridum* may include previously undescribed species, an potential alternate hypothesis to introgression. SNP analyses of the two *G. aridum* accessions included here suggest that the Colima accession does retain evidence of nuclear introgression. To evaluate the presence of nuclear introgression, we conducted an ABBA-BABA test (Korneliussen, Albrechtsen, and Nielsen 2014; Sousa and Hey 2013) using both accessions of *G. aridum* (H1 and H2); *G. davidsonii* as the source of introgression (H3); and *G. gossypioides* as the ancestral state (outgroup) which confirms nuclear introgression from *G. davidsonii* into *G. aridum* Colima (Z=-3.64). To further characterize the extent of nuclear introgression in *G. aridum* Colima, we compared the number of inferred introgressed SNPs (i.e., *G. aridum* Colima shares a derived SNP with *G. davidsonii*) against the number of SNPs where *G. aridum* Jalisco (non-introgressed) shares a derived state with *G. davidsonii*. This tabulation recapitulates the results of the ABBA-BABA test (chi-square p-value = 0) to further confirm the retention of nuclear introgression in *G. aridum* Colima from Integrifolia. When the data are partitioned by chromosome, about half of the chromosomes show an excess of derived SNPs compared to their counterpart in the non-introgressed *G. aridum* Jalisco (Table Introgression). Although the number of genes showing derived SNPs, and hence a residue of introgression, is not significantly different between the two *G. aridum* accessions, the Colima *G. aridum* does exhibit an excess of SNPs *in genes*. The latter is important in that these SNPs, while limited, both have high confidence in their orthology and recapitulate the broader genomic conclusions of nuclear introgression in Colima *G. aridum*.

In addition to the evidence for introgression detected in Colima *G. aridum* accessions, comparison between the nuclear and chloroplast phylogenies recapitulates previous observations of Austroamericana-derived introgression in section Selera, i.e. *G. gossypioides*. *G. gossypioides* is unusual within *Houzingenia* as it has likely undergone two separate instances of introgression: (1) the more recent chloroplast introgression noted here and elsewhere (R. Cronn et al. 2003; R. Cronn and Wendel 2004), and (2) nuclear introgression, as evidenced by the presence of African cotton-like ITS (J F Wendel, Schnabel, and Seelanan 1995) and repetitive DNA (Zhao et al. 1998). Clear evidence of chloroplast-nuclear conflict is seen in the analyses here, congruent with previous observations. Evidence for nuclear introgression is less clear (see below) and warrants additional, in depth analyses beyond the scope of the present.

Divergence times were calculated for the thirteen extant *Houzingenia* species (Figure ancGS) using the *chronos* function in the R package {ape}; see methods. Subgenus *Houzingenia* diverged an estimated 6.58 mya from the remaining cotton subgenera (here represented by *Longiloba*), which falls within prior estimates for the basal radiation of cotton lineages (Senchina et al. 2003). The basal-most radiation of the genus is represented by the divergence of *G. gossypioides* from the rest of the subgenus, approximately 2.56 mya (Figure AncGs), although we note that there may be additional error in this estimation arising from cryptic nuclear introgression in *G. gossypioides*. For this reason, the time estimates for all nodes (including *G. gossypioides*) were based on the estimated divergence time range for the next most-basal node, which separates section *Erioxylum* subsection *Erioxylum* from the remaining subgenus. Most species have diverged relatively recently, within the last 0.5-2 my, with the notable exception of *G. davidsonii* and *G. klotzschianum* here estimated an order of magnitude more recent than previously suggested by allozyme and chloroplast restriction site analysis (J F Wendel and Percival 1990). Their near identical nature is reflected in both their estimated nuclear branch lengths (0.0003 substitutions per site versus 0.0018 to 0.0065 on other terminal branches) and their rates of substitution (0.0000 to 0.0048 dS and 0.0000 dN; Table dnds). While this close relationship between *G. davidsonii* and *G. klotzschianum* has been reported previously (J F Wendel and Percival 1990), this is the first modern estimate of genome-wide divergence between these two species.

Genome-wide rates of molecular evolution among *Houzingenia* species were calculated for all species comparisons (Table dnds). As expected, pairwise synonymous mutation rates (dS, average = 0.0213 substitutions/site) were approximately an order of magnitude greater than the nonsynonymous mutation rates (dN, average = 0.0026; Table dN). Synonymous mutation rates varied from 0.0000 between the two extant members of subsection Integrifolia, *G. davidsonii* and *G. klotzschianum*, to 0.0287 between *G. aridum* and the basal-most diverging member of *Houzingenia*, *G. gossypioides*. When considering divergence time between species, the dS range narrows to between 0 and 0.017 substitutions/site/million years (my) with 94% of the comparisons falling between dS/my=0.009-0.013. A single dS comparison, *G. davidsonii* and *G. klotzschianum*, was less than this range. No pattern was seen in the four values that exceeded this range. Similarly, dN varied from 0.000 between *G. davidsonii* and *G. klotzschianum* to 0.0033 between *G. lobatum* and *G. gossypioides*, again reflecting the basal nature of *G. gossypioides*. When standardized by time, the range narrows to dN=0-0.0018, with 90% between dN=0.0011-0.0015. Again, the Integrifolia species occupied the lowest dN value; however, notably, the dN value for *G. turneri* versus *G. harknessii* was similarly small (dN=0.0002). This stands in contrast to the dS value for the pair, which was comparably large at dS=0.0148 (Table dNdS).

**Transposable element characterization**

Similar to previous reports, repetitive DNAs contribute roughly half of the total genome sequence for all species in subgenus *Houzingenia*, from an average of 44.5% in *G. lobatum* to 52% in *G. anomalum*. Like most flowering plants, a vast majority of this sequence is due to the occupation of class II *gypsy* elements, which comprise 32.7 - 37.9% of the total genome size for any *Houzingenia* species (Figure TEamounts). Multi-dimensional transposable element profile visualization using both log transformed and percent-genome size standardized counts showed considerable overlap among species, and even among subsections (Figure Ordination). Multivariate t-distribution confidence ellipses for each subsection overlap with at least one other subsection. Even those subsections where insufficient sampling precludes the generation of a confidence ellipse (i.e., Selera and Integrifolia), the plotted data points are contained within the occupied space of another subsection (Figure Ordination). Selera, for example, is contained within the confidence ellipse for both Caducibracteata and Houzingenia; likewise, Integrifolia is within Houzingenia and Austroamericana. Likewise, few repetitive elements (15 elements at p<0.5, 13 *gypsy* and 2 *copia*) differ significantly in copy number among *Houzingenia* species. This apparent overlap in repetitive element profiles is also suggested by the relative amounts of each transposable element category among subsection; however, to formerly compare the overlap among subsections, we performed a Procrustes ANOVA with complex linear models, as implemented in the R package [geomorph]. For this analysis, we compared each subsection using all representatives of that subsection as indicators of variance. Few comparisons showed statistically significant differences, with the patterns of repetitive abundance differing only in Austroamericana versus both Caducibracteata and Erioxylum (p<0.05). Interestingly, the variation in repetitive elements found in monotypic Selera, i.e., *G. gossypioides*, was not distinct from the remainder of subgenus Houzingenia. This stands in contrast to previous reports (Zhao et al. 1998), which noted the presence of repeats derived from "African cottons" (here represented by subgenera *Gossypium* and *Longiloba*, i.e., A- and F-genome species). This result is further apparent when including the African subgenera in the ordination (Figure African Ordination); that is, *G. gossypioides* is clearly lumped with the other Houzingenia species. While perhaps in contrast to expectations, given previous reports, this analysis does not preclude African-like repeats in the New World *G. gossypioides* genome; however, evidence for this phenomenon is not evident in the present repeat data. Analysis of individual clusters reveals only two clusters (i.e., *gypsy* clusters 186 and 368) where *G. gossypioides* is significantly different in copy number from the rest of *Houzingenia*, and *G. gossypioides* is also significantly different from the African representatives for these clusters. Copy numbers for those clusters suggest an increase in copy number for *G. gossypioides* relative to both the rest of *Houzingenia* and the African subgenera, and therefore are not part of the repeats that distinguish *G. gossypioides* from the African subgenera, as reported by Zhao (1998). BLAST analysis of the repeats reported by Zhao (1998) suggest the closest cluster is *gypsy* cluster CL63 (e-value: 4e-100); however, this cluster is not enriched in *G. gossypioides* versus the rest of *Houzingenia* (average 161.5 kb versus average 214.7 kb, respectively). This lack of enrichment is also reflected when the repetitive clones from Zhao (1998) are used to mask each *Houzingenia* genome; that is, neither repetitive clone masks a greater fraction of the *G. gossypioides* genome than any of the other assembled genomes.

The absolute amount of sequence attributable to each type of TE category is similar among *Houzingenia* species and distinguishable from the African subgenera only in amount of putative *gypsy* and MULE/MuDR-like elements (Figure TE\_amounts) in opposing directions. The total amount of *gypsy* elements predicted for the African species is far greater (average 907 Mb versus 309 MB, respectively), which is expected given previous analyses of cotton transposable elements (Jennifer S Hawkins et al. 2006; J. S. Hawkins et al. 2009; C.E. Grover et al. 2007). The total amount of predicted MULE/MuDR-like elements, however, is greater for *Houzingenia* (average 6.3 Mb versus 2.4 Mb in the African subgenera) even despite the large difference in genome size, an observation not previously reported. These patterns persist even when comparing TEs as a function of genome size (Figure TE\_amounts.GS), with two additional observations. The large error bars for *gypsy* amount in *G. raimondii* become more pronounced. Inspection of the total amounts for this species suggest that there is a single accession (D5-6; Table Assembly Stats) which has remarkably more *gypsy* elements than the remaining conspecifics. While approximately 35% of *gypsy* clusters in *G. raimondii* accession 6 are found in excess (relative to the other accessions), less than half contribute > 1 Mb additional sequence. Interestingly, however, a single *gypsy* cluster (cluster 62) comprises 11.3 Mb additional sequence in *G. raimondii* accession 6 relative to the conspecific with the closest amount (19.7 Mb in *G. raimondii* accession 6 versus 8.4 Mb in accession 8). The average for this cluster, including *G. raimondii* accession 6, is only 6.7 Mb. These observations suggest that the *gypsy* element represented by cluster 62 has been recently active in the *G. raimondii* genome, achieving significant success in at least one lineage.

A second notable observation from the genome size standardized TE amounts is that while the amount of sequence attributable to *copia* elements is similar between subgenera *Houzingenia, Gossypium,* and *Longiloba*, this element type represents a larger portion of the genome in *Houzingenia* than in the two African subgenera. This observation reflects either lack of both *copia* element colonization and degradation since divergence of the three subgenera (i.e., stasis of *copia* elements), or convergence of absolute amount that belies element turnover. Ancestral state reconstructions (Figure copia\_anc) suggest that the latter is more likely, as both reduction and increase in copy numbers for the annotated *copia* elements are observed, both for the *Houzingenia* species, as well as the African species (represented by *Longiloba*). Dynamics of *copia* elements in *Houzingenia* were broadly characterized with respect to their aggregate effect on genome size (Supplementary Figure magnitude.gainloss.copia), using the reconstructed ancestral amount for each as a baseline. Interestingly, while *copia* elements comprise a higher proportion of the genome for *Houzingenia* species than for other cottons surveyed (Figure TE amounts), these elements generally seem to be in decline (Table copia.gainloss.tbl), as 67% of accessions experienced a net loss attributable to *copia* elements.

Previous research on *G. raimondii* (subsection Austroamericana) demonstrated a relative lack of lineage-specific amplification with concomitant removal of a prolific cotton *gypsy* element as a mechanism for genome downsizing in *G. raimondii* (J. S. Hawkins et al. 2009). Congruent with these results, most of the clusters recovered here (78%; range 76.5 – 79.7% per species) are composed primarily of “older” reads, i.e., reads more divergent than expected for recently active transposable elements. Ancestral state reconstruction of individual clusters, however, demonstrate both amplification and removal concomitant with the inferred changes in overall genome size (Figure phylogeny; Supplementary Figure grid.anc). Generally speaking, however, most clusters are “older” and even the most recently amplified repeats are inferred to be active at the base of the subgenus (Supp Figure all histogram), with a small number (20) that appear to be recently active in terminal lineages.

**Genome differentiation via indel and copy number evolution**

Small-scale insertions and deletions are a common form of sequence variation which have the potential to rapidly generate evolutionarily significant evolutionary differences among closely-related taxa (Britten et al. 2003). While this is particularly true for large-scale, TE-associated indels (e.g., transposable element insertions), the formation of smaller indels can also vary among related species. Accordingly, we evaluated the extent of indel evolution among *Houzingenia* species, using the gold-standard *G. raimondii* genome (Austroamericana) as the reference state and polarized using *G. longicalyx* (subgenus Longiloba). Phylogenetics analysis of coded indels as multistate characters (see methods) recapitulates the nuclear phylogeny, suggesting that indel formation largely corresponds to species relationships. In total, small indels were present at 214,222 position in at least one of the 24 accessions evaluated. The range in number of indels per chromosome spans over 7,800 events, from 11,703 indels on chromosome 12 to 19,586 on chromosome 9; however, relative to the length of each chromosome, the gap narrows to between 227 indels/Mb on chromosome 5 to 330 indels/Mb on chromosome 12.

Generally speaking, insertions outweigh deletions for each chromosome/accession combination, with the exception of chromosomes 8 and 9 for subsection Integrifolia (*G. klotzschianum* and *G. davidsonii*; Table Indels). Chromosome 9, in particular, appears susceptible to deletions, as the only chromosome where the total length in deletions outweigh insertions for more than half (60%) of the accessions. While the total amount of sequence change is relatively small (maximum gain = 61 kb and maximum loss = -31 kb), this belies the number (average 106,016 events per accession) and amount of sequence involved (average 540,196 inserted or deleted).

Compared to the rate of nucleotide substitution, SOMETHING. Ru = ratio of unpaired nucleotides due to indels versus substitutions

Recently, the extent of variation in gene content within and among plant species has been expanded to include the concept of the “pan-genome”, which refers to the suite of genes present within or among closely related species. Here we begin to evaluate the scope of a *Houzingenia*-specific pan-genome by modeling copy number evolution. Homologous gene clusters generated via OrthoFinder were used as input in Count (Csurös 2010), which has been developed to conduct evolutionary analyses of homologous family sizes in a phylogenetic context, and random re-sampling of the data was used to generate bootstrap replicates. Within a lineage, the inferred rate of loss for a given lineage was consistently greater than the rate of gainas might be expected, and exhibited lineage-based variability,.

Our knowledge of gene duplications at the phylogenetic, functional and genomic levels is impressive. Hardly any aspect of genome evolution or function is not somehow linked to gene duplications, which occur in all kinds of life forms[1](https://www.nature.com/articles/nrg2689#ref1) and have taken place since before the last universal common ancestor[2](https://www.nature.com/articles/nrg2689#ref2). Some genomes contain large numbers of genes owing to whole-genome duplications[3](https://www.nature.com/articles/nrg2689#ref3) or lineage-specific gene expansions[4](https://www.nature.com/articles/nrg2689#ref4). The duplication of genes may form a cornerstone in the evolution of biological complexity[5](https://www.nature.com/articles/nrg2689#ref5). Finally, gene duplications segregate in high numbers in natural populations, and some cause disease[6](https://www.nature.com/articles/nrg2689#ref6) or confer an adaptive advantage[7](https://www.nature.com/articles/nrg2689#ref7). These and other aspects of gene duplications have been continuously reviewed and their importance has been emphasized[2](https://www.nature.com/articles/nrg2689#ref2),[3](https://www.nature.com/articles/nrg2689#ref3),[4](https://www.nature.com/articles/nrg2689#ref4),[8](https://www.nature.com/articles/nrg2689#ref8).

By contrast, our current understanding of the selective and evolutionary mechanisms involved in the emergence, maintenance and evolution of gene duplications is preliminary and fragmented. There are two main reasons for this discordance between theory and data. First, the literature contains many different models of and hypotheses about the evolution of gene duplications, which have not been described in a systematic way. Second, the development of theory on gene duplications has been driven by data, without attempts to stringently test hypotheses. Consequently, although many models for the evolution of gene duplications have been proposed, we still do not know their relative importance for describing general trends in the evolution of gene duplications or their applicability to specific gene copies.

Genes in evolutionarily stable modules have lower gene-duplication rates and tend to be involved in environmental interactions[20](https://www.nature.com/articles/nrg2267#ref20). However, one has to be careful in applying this criterion for assessing th

**Discussion**

**Evolution of coding regions: content variation and molecular evolution among closely related species**

**Evolution of noncoding regions: SUBHEADING (includes TEs and indels)**

D6 repeats – why didn’t we find Af specific repeats? Idk. Only 2 A-genome like repeats were reported in D6 (pxp 095 and pxp271). Of Andy’s repeats, first is A-specific and the second is A-enriched. Neither hits any proteins by blastx

**Conclusions**

**Methods**

Sequence generation and initial processing

DNA was extracted from (LEAVES) using (WHAT KIT), and sent to (WHERE) for library construction and sequencing. Sequencing was completed on the Illumina (WHAT MACHINE) using (WHICH SEQUENCING). The data were trimmed and filtered with Trimmomatic v0.32 [citation] with the following options : (1) sequence adapter removal, (2) removal of leading and/or trailing bases when the quality score (Q) <28, (3) removal of bases after average Q <28 (8 nt window) or single base quality <10, and (4) removal of reads < 85 nt. Detailed parameters can be found at https://github.com/IGBB/D\_Cottons\_USDA. [Let's port this repo to a lab site after and give the new url]

Genome assembly and annotation

The trimmed data was independently assembled for each species via ABySS v2.0.1 (Simpson et al. 2009), using every 5th kmer value from 40 through 100. A single assembly with the highest E-size (Salzberg et al. 2012) was selected for each species and subsequently annotated with MAKER v2.31.6 (Holt and Yandell 2011) using evidence from: (1) the NCBI *G. raimondii* EST database [citation], (2) *G. raimondii* reference genome predicted proteins, as hosted by CottonGen.org (Paterson et al. 2012), and (3) three *ab initio* gene prediction programs, i.e. Genemark v4.30 (Genes et al. 2003), SNAP v2013-11-29 (Korf 2004), and Augustus v3.0.3 (Stanke et al. 2006). Both the SNAP and Augustus models were trained using BUSCO v2.0 (Simão et al. 2015). Chromosomer version 0.1.3 (Tamazian et al. 2016 10.1186/s13742-016-0141-6), a reference-assisted scaffolder, was used to scaffold the selected assemblies against G. raimondii genome and transfer the previous annotation to the new scaffolds.

Gene stuff

Gene orthology and family designations were determined via OrthoFinder [citation]...

Phylogenetics and ancestral state reconstruction

Trimmed reads from the genome assembly were mapped against the *G. raimondii* reference sequence (Paterson et al. 2012) using BWA v0.7.10 (Li and Durbin 2009), post-processed with samtools (which version) (Li et al. 2009), and individual genes were independently assembled for each species/accession via BamBam v 1.4 (Page, Gingle, and Udall 2013) in conjunction with the *G. raimondii* reference annotation (Paterson et al. 2012). Alignments were pruned for genes and/or alignment positions with insufficient coverage, i.e., too many ambiguous bases, using filter\_alignments (https://github.com/IGBB/D\_Cottons\_USDA/). Parameters were set to remove sequences with more than 10% ambiguous bases within species and to remove aligned positions with more than 10% ambiguity among species. Genes were additionally filtered by length, to retain only those genes between a minimum of 500 bp (cite Mirarab 2016) and a maximum of 4051 bp, the latter of which represents the *G. raimondii* genome-wide mean plus three standard deviations. Only those genes with a minimum of one accession per species were retained for phylogenetic and molecular analyses.

Species trees were estimated from individual gene trees via SNaQ (citation) and MP-EST (citation) using Bayesian and Maximum Likelihood analyses, respectively. Bayesian analyses were generated using MrBayes v (which version) (Huelsenbeck and Ronquist 2003) under GTR gamma with the following parameters: four runs with four chains for 1 million generations and using a burn-in fraction of 25%. Concordance among individual gene trees was assessed via BUCKy (Ané et al., 2007; Larget et al., 2010) with 3 runs, each with 4 chains and 1 million iterations, and default parameters. Quartet MaxCut was used to estimate the starting tree, and SNaQ was run using this starting tree and the concordance factors estimated by BUCKy. Visualization of networks….

Maximum likelihood (ML) analyses were performed using RaxML v(which version) (Stamatakis 2014)using the basic general time reversible model with gamma distribution (GTRGAMMA), 10000 alternative runs on distinct starting trees, and rapid bootstrapping with consensus tree generation. The ML trees were rooted with a member of subgenus *Longiloba*, *G. longicalyx* (African F-genome). MP-EST (citation) was used to estimate the species tree from the population of gene trees. Visualized how

Measures of molecular evolution were all calculated in R v(which version) (R Core Team 2017). Species divergence estimates were calculated via the [chronoMPL] package (citation), using the (which time estimates?) (citation). Trees were visualized using the [ape] package (Paradis, Claude, and Strimmer 2004). Ancestral state reconstructions for genome size were completed using [fastAnc]. Indels and SNPs were characterized among Houzingenia] using the Genome Analysis ToolKit (gatk) and the *G. raimondii* reference sequence (Paterson citation). Distance measures of aligned intergenic regions were estimated via [ape], and indels were characterized by (???).

**Repetitive characterization**

Reads from only one of the paired-end files (i.e., R1) were filtered and trimmed via Trimmomatic version 0.33 (Bolger, Lohse, and Usadel 2014) to a uniform 95nt (https://github.com/IGBB/D\_Cottons\_USDA), and then randomly subsampled to represent a 1% genome size equivalent (GSE) for each individual (Hendrix and Stewart 2005; Jonathan F Wendel et al. 2002). These 1% GSEs were combined as input into the RepeatExplorer pipeline (Novák, Neumann, and Macas 2010; Novák et al. 2013), which has been successfully used to profile genomic repeats using low-coverage, short read sequencing. Only clusters which contain at least 0.01% of the total input sequences (i.e., 387 reads from a total input of 3872016 reads) were retained for annotation as per Grover (in revision), which uses the RepeatExplorer implementation of RepeatMasker (Smit, Hubley, and Green, n.d.) and a custom cotton-enriched repeat library. Genome occupation of each broad repeat type was calculated (in megabases; Mb) for each genome/accession based on the 1% genome representation of the sample and the standardized read length of 95 nt.

Broad patterns of repeat occupation per genome were determined by using the abundance of each cluster in a multivariate dataset. Initial visualization of the data was conducted using both calculated in R (R Core Team 2017) using both Principle Coordinate Analysis on read counts, either log normalized (to compare overall patterns of repeats) or normalized by genome size (to compare proportional cluster occupation). Differential abundance in cluster occupation was iteratively calculated in increasing phylogenetic depths to understand the evolution of repeat types throughout the evolution of the subgenus; that is, differentially abundant clusters were determined (1) within species, (2) between sister taxa, and (3) between deeper phylogenetic nodes. For each cluster, the ancestral state was reconstructed and used for comparison in the next analysis. Ancestral state reconstructions were completed using [fastAnc] for reconstruction (Revell 2012) and the fitContinuous function of [Geiger] (Harmon et al. 2008) for visualization. All analyses are available at (https://github.com/IGBB/D\_Cottons\_USDA).

Repeat heterogeneity and relative age

Relative cluster age was approximated using the among-read divergence profile of each cluster, as previously used for Fritillaria (Kelly et al. 2015), dandelion (Ferreira de Carvalho et al. 2016), and *Kokia*/*Gossypioides* (Corrinne E Grover et al., n.d.), sister outgroup genera to *Gossypium*. Briefly, cluster-by-cluster all-versus-all BLASTn (Boratyn et al. 2013; Camacho et al. 2009) searches were conducted using the same BLAST parameters implemented in RepeatExplorer. A pairwise percent identity histogram was generated for each cluster, and regression models were used to describe the trend (i.e., biased toward high-identity, “young” or lower-identity, “older” element reads) using Bayesian Information Criterion (Schwarz 1978) to select the model with the most confidence; specific parameters can be found in (Corrinne E Grover et al., n.d.) and at https://github.com/IGBB/D\_Cottons\_USDA. The read similarity profile was automatically evaluated for each cluster to determine if the reads trend toward highly similar “young” or more divergent “older” reads. These profiles generally consist of six different trends: (1) positive linear regression ("young"); (2) absence of linear regression ("old"); (3) negative linear regression ("old"); (4) positive quadratic vertical parabola, trend described by right-side of vertex ("young"); (4b) positive quadratic vertical parabola, trend described by left-side of vertex ("old"); (5) negative quadratic vertical parabola, trend described by right-side of vertex ("old"); and (6) negative quadratic vertical parabola, trend described by left-side of vertex and vertex at >99% pairwise-identity ("old"; Figure WHATEVER). We note that young" and "old" are relative designations and not indicative of absolute age.

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Figure legends

Figure\_phylogeny: G. thurberi (By Katja Schulz from Washington, D. C., USA (Arizona Wild Cotton) [CC BY 2.0 (http://creativecommons.org/licenses/by/2.0)], via Wikimedia Commons) – also used = D10, D4, D3d