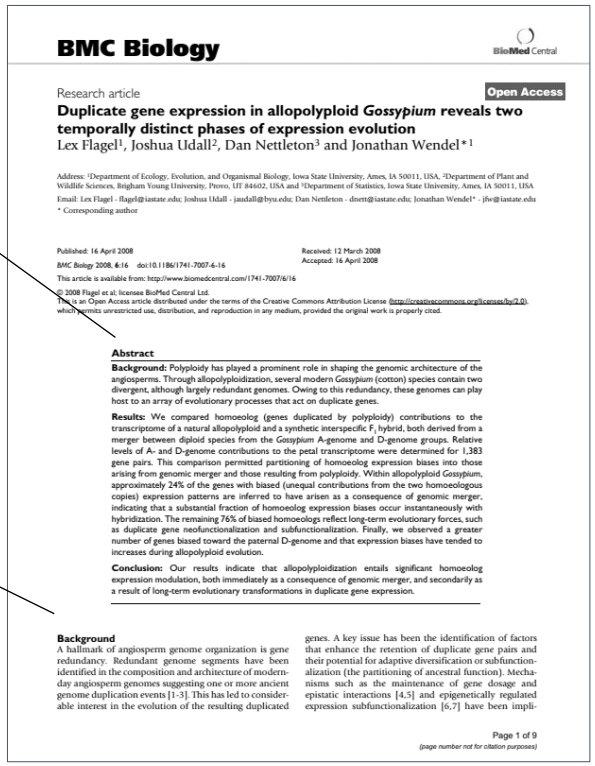
How to Read a Scholarly Article

Do scholarly articles confuse you? You're not alone. Here's a tip: stop reading academic articles like you would your favorite novel from start to finish, and instead, navigate them strategically, recognizing which parts of the article are most important for your needs. Academic articles generally follow a predictable outline, which you can use to your advantage.

1. Read the Abstract

The abstract provides an overview of the paper, a synopsis of the main research question, and a summary of any major findings. Read this first to decide if the article will be useful to you.



BMC Biology

Research article

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Duplicate gene expression in allopolyploid *Gossypium* reveals two temporally distinct phases of expression evolution

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Abstract

Background: Polyploidy has played a prominent role in shaping the genomic architecture of the angiosperms. Through allopolyploidization, several modern *Gossypium* (cotton) species contain two divergent, although largely redundant genomes. Owing to this redundancy, these genomes can play host to an array of evolutionary processes that act on duplicate genes.

Results: We compared homoeolog (genes duplicated by polyploidy) contributions to the transcriptome of a natural allopolyploid and a synthetic interspecific F_1 hybrid, both derived from a merger between diploid species from the *Gossypium* A-genome and D-genome groups. Relative levels of A- and D-genome contributions to the petal transcriptome were determined for 1,383 gene pairs. This comparison permitted partitioning of homoeolog expression biases into those arising from genomic merger and those resulting from polyploidy. Within allopolyploid *Gossypium*, approximately 24% of the genes with biased (unequal contributions from the two homoeologous copies) expression patterns are inferred to have arisen as a consequence of genomic merger, indicating that a substantial fraction of homoeolog expression biases occur instantaneously with hybridization. The remaining 76% of biased homoeologs reflect long-term evolutionary forces, such as duplicate gene neofunctionalization and subfunctionalization. Finally, we observed a greater number of genes biased toward the paternal D-genome and that expression biases have tended to increases during allopolyploid evolution.

Conclusion: Our results indicate that allopolyploidization entails significant homoeolog expression modulation, both immediately as a consequence of genomic merger, and secondarily as a result of long-term evolutionary transformations in duplicate gene expression.

Background

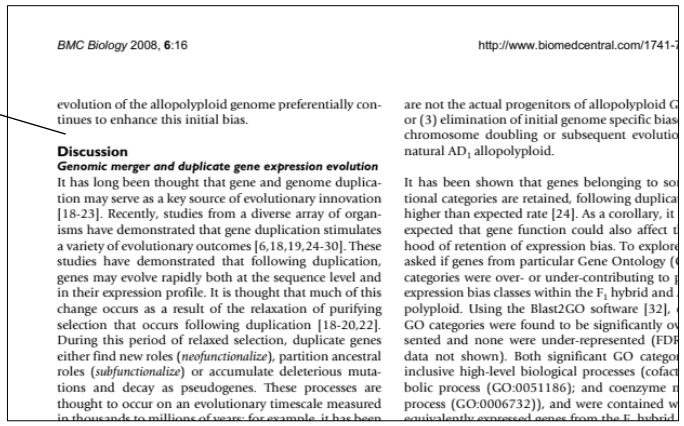
A hallmark of angiosperm genome organization is gene redundancy. Redundant genome segments have been identified in the composition and architecture of modern-day angiosperm genomes suggesting one or more ancient genome duplication events [1-3]. This has led to considerable interest in the evolution of the resulting duplicated genes. A key issue has been the identification of factors that enhance the retention of duplicate gene pairs and their potential for adaptive diversification or subfunctionalization (the partitioning of ancestral function). Mechanisms such as the maintenance of gene dosage and epistatic interactions [4,5] and epigenetically regulated expression subfunctionalization [6,7] have been impli-

2. Read the Introduction/Background

The introduction details the background and context for the research. Identify the research question and the researchers' hypothesis.

3. Read the Discussion/Conclusion

Skip down to the discussion section to read the findings of the research. Look for the significance and application of these findings, as well as any further research ideas proposed by the authors.



evolution of the allopolyploid genome preferentially continues to enhance this initial bias.

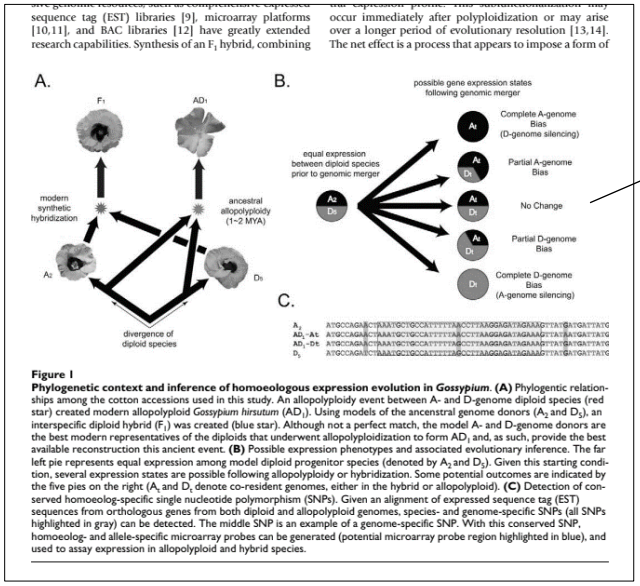
Discussion

Genomic merger and duplicate gene expression evolution

It has long been thought that gene and genome duplication may serve as a key source of evolutionary innovation [18-23]. Recently, studies from a diverse array of organisms have demonstrated that gene duplication stimulates a variety of evolutionary outcomes [6,18,19,24-30]. These studies have demonstrated that following duplication, genes may evolve rapidly both at the sequence level and in their expression profile. It is thought that much of this change occurs as a result of the relaxation of purifying selection that occurs following duplication [18-20,22]. During this period of relaxed selection, duplicate genes either find new roles (*neofunctionalize*), partition ancestral roles (*subfunctionalize*) or accumulate deleterious mutations and decay as pseudogenes. These processes are thought to occur on an evolutionary timescale measured

are not the actual progenitors of allopolyploid G
or (3) elimination of initial genome specific bias
chromosome doubling or subsequent evolutio
natural AD_1 allopolyploid.

It has been shown that genes belonging to so
tional categories are retained, following duplica
higher than expected rate [24]. As a corollary, it
expected that gene function could also affect t
hood of retention of expression bias. To explor
asked if genes from particular Gene Ontology (
categories were over- or under-contributing to
expression bias classes within the F_1 hybrid and
polyploid. Using the Blast2GO software [32],
GO categories were found to be significantly ov
sented and none were under-represented (FDR
data not shown). Both significant GO categor
inclusive high-level biological processes (cofact
bolic process (GO:0051186); and coenzyme m
process (GO:0006732)), and were contained w
equivalently expressed genes from the F, hybrid



sequence tag (EST) libraries [9], microarray platforms [10,11], and BAC libraries [12] have greatly extended research capabilities. Synthesis of an F_1 hybrid, combining

occur immediately after polyploidization or may arise over a longer period of evolutionary resolution [13,14]. The net effect is a process that appears to impose a form of

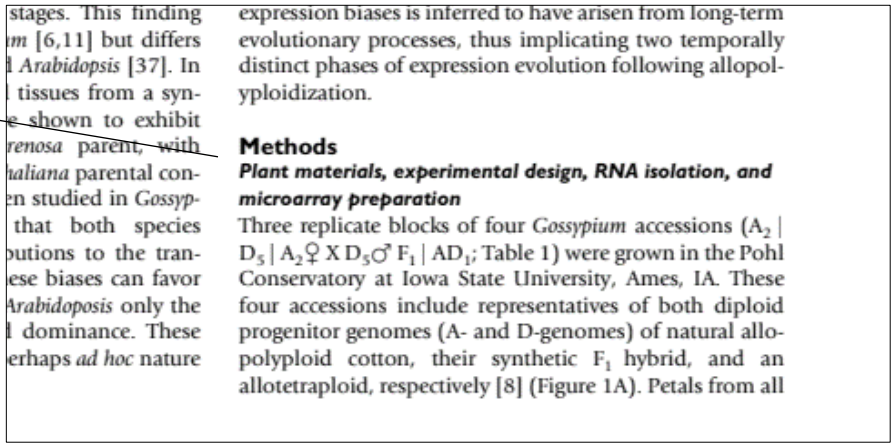
Figure 1
Phylogenetic context and inference of homoeologous expression evolution in *Gossypium*. (A) Phylogentic relationships among the cotton accessions used in this study. An allopolyploidy event between A- and D-genome diploid species (red star) created modern allopolyploid *Gossypium hirsutum* (AD_1). Using models of the ancenstral genome donors (A_2 and D_5), an interspecific diploid hybrid (F_1) was created (blue star). Although not a perfect match, the model A- and D-genome donors are the best modern representatives of the diploids that underwent allopolyploidization to form AD_1 and, as such, provide the best available reconstruction this ancient event. **(B)** Possible expression phenotypes and associated evolutionary inference. The far left pie represents equal expression among model diploid progenitor species (denoted by A_2 and D_5). Given this starting condition, several expression states are possible following allopolyploidy or hybridization. Some potential outcomes are indicated by the five pies on the right (A_t and D_t denote co-resident genomes, either in the hybrid or allopolyploid). **(C)** Detection of conserved homoeolog-specific single nucleotide polymorphism (SNPs). Given an alignment of expressed sequence tag (EST) sequences from orthologous genes from both diploid and allopolyploid genomes, species- and genome-specific SNPs (all SNPs highlighted in gray) can be detected. The middle SNP is an example of a genome-specific SNP. With this conserved SNP, homoeolog- and allele-specific microarray probes can be generated (potential microarray probe region highlighted in blue), and used to assay expression in allopolyploid and hybrid species.

4. Look at Figures

Most research articles contain figures like graphs or charts, often accompanied by a short caption describing their contents. They may be helpful as they concisely display the research findings.

5. Skip the Methods

This section will explain the authors' experimental methods. You can skip it unless you need to know exactly how the experiment was performed or replicate it yourself.



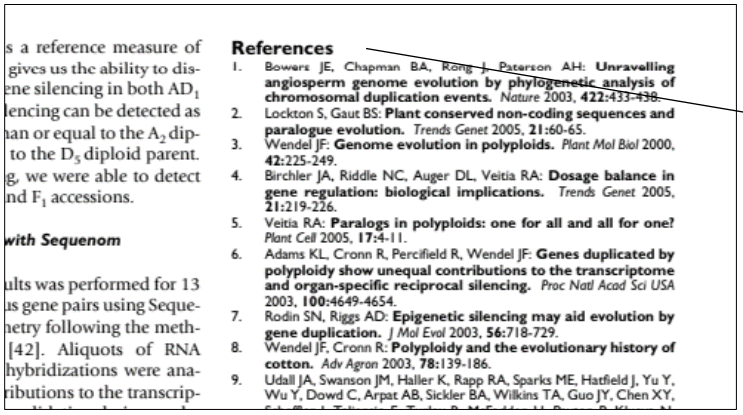
stages. This finding
m [6,11] but differs
Arabidopsis [37]. In
tissues from a syn-
shown to exhibit
renosa parent, with
haliana parental con-
n studied in *Gossyp-*
that both species
butions to the tran-
ese biases can favor
Arabidopsis only the
dominance. These
erhaps *ad hoc* nature

expression biases is inferred to have arisen from long-term evolutionary processes, thus implicating two temporally distinct phases of expression evolution following allopolyploidization.

Methods

Plant materials, experimental design, RNA isolation, and microarray preparation

Three replicate blocks of four *Gossypium* accessions (A_2 | D_5 | A_2♀ X D_5♂ F_1 | AD_1; Table 1) were grown in the Pohl Conservatory at Iowa State University, Ames, IA. These four accessions include representatives of both diploid progenitor genomes (A- and D-genomes) of natural allopolyploid cotton, their synthetic F_1 hybrid, and an allotetraploid, respectively [8] (Figure 1A). Petals from all



s a reference measure of
gives us the ability to dis-
ene silencing in both AD_1
lencing can be detected as
an or equal to the A_2 dip-
to the D_5 diploid parent.
g, we were able to detect
nd F_1 accessions.

with Sequenom

ults was performed for 13
as gene pairs using Seque-
netry following the meth-
[42]. Aliquots of RNA
hybridizations were ana-
ributions to the transcrip-

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6. Check the Bibliography/References

Glance at the bibliography to see what articles and authors are cited. This is a great way to find more articles that are relevant to your research topic.