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Perspective

Meiosis, The Master Driver of Gene Duplication in Higher Plants?

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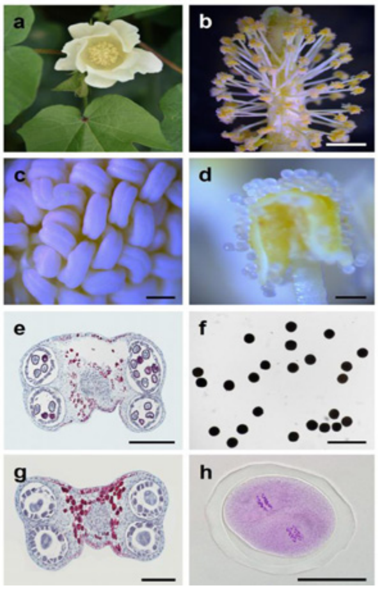
Perspective

Gene duplicationis a common and abundant event in plants; on average, 65% of annotated genes in plant genomes have a duplicate copy [1]. Gene duplication remains of specific interest because of both the abundance of duplicate genes in plants and their potential to contribute to plant evolution in nature [2-5]. The angiosperms (flowering plants) are of particular interest to study the impact of gene duplication on plant reproduction and evolution in nature (e.g., Upland cotton in this study, 2n=4X=52, 2.5 GB). Compared to mammals and most other plant genomes, angiosperms undergo gene duplication events more frequently [6,7]. It is unknown what major selective forces are associated with plant genome-wide gene duplication. The biological processes to which gene duplication primarily contributes during growth and development in plants is a vitally important question, the answer to which will indicate the major evolutionary force for gene duplication. Meiosis is a critical biological process for reproduction and genetic variation in higher plants. Gene duplication is a prominent feature of plant genomic architecture. Meiosis and gene duplication are of fundamental importance in unraveling the nature of genetics and evolution. The ideas and findings in this letter demonstrate highly significant connection between the meiosis and gene duplication, which bring together these two disparate study fields and highlight the importance of the meiosis for understanding evolutionary success of flowering plants. These insights and opinions opens a new area and points a significant way to illustrate the impact of duplicated genes on the meiosis during reproduction and fitness in higher plants, as well as their ultimate evolutionary, ecological, and agronomic impacts in light of challenges due to global climate change. This letter addresses short reports of novel and topical ideas and viewpoints in plant developmental genomics and evolution. Reproduction is pivotal for plant survival and for evolution of life in nature. We are now beginning to understand which life cycle stage and which duplicate genes have dominantly contributed to reproductive evolution in plants at the genome scale.Interestingly, transcriptome analysis in our studyshowed that the expression of genome-wide duplicated genes during the stage of meiosis (close to 50%) was significantly higher than that during the stages of pollen development and vegetative growth



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Transcriptome Samples	Useful Reads	Total Mapped Reads	Total Mapped %	Multiple Mapped Reads	Multiple Mapped %	Uniquely Mapped Reads	Uniquely Mapped %
Gh-Ve-1	45845402	36977089	80.66	6683685	18.08	30293404	81.92
Gh-Ve-2	46791598	36431133	77.86	4790618	13.15	31640515	86.85
Gh-Ve-3	46611562	35889337	77.00	6880202	19.17	29009135	80.83
Gh-De-1	41226376	32751554	79.44	6036506	18.43	26715048	81.57
Gh-De-2	46223520	35842722	77.54	6459117	18.02	29383605	81.98
Gh-De-3	43180102	33753332	78.17	5312051	15.74	28441281	84.26
Gh-Me-1	42297582	33629933	79.51	16279943	48.41	17349990	51.59
Gh-Me-2	46043530	36726948	79.77	16560535	45.09	20166413	54.91
Gh-Me-3	44773010	35758541	79.87	17308324	48.40	18450217	51.60

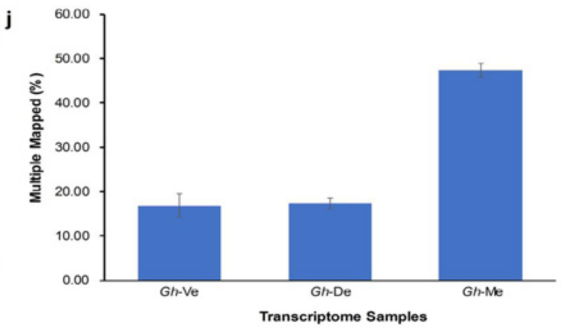

Figure 1: Developmental staged male gametophyte and meiosis specific expression shoot up of duplicate genes in flowering plant.
a) Blooming flower of angiosperm cotton. B) Stamen in bloom, *Bar*= 5 mm**.** c) Undehisced anther, *Bar*= 1mm**.** d) Dehisced anther in bloom, *Bar*= 500μm**.** e) Developed pollen staged anther histological section, *Bar*= 500μm**.** f) Fertility detection of developed pollen grains, *Bar*= 500μm**.** g) Meiosis staged anther histological section, *Bar*= 100μm**.** h) Meiosis staged microspore mother cell, *Bar*= 25μm. i) Statistics of multiple mapped duplicate genes from the transcriptomes. j) Duplicate genes expression is significantly overrepresented in meiosis. Error bars denote SD of three biological replicates.
Gh: Gossypiumhirsutum; Ve: Vegetative tissue of shoot apex; De: Developed pollen stage; Me: Meiosis stage

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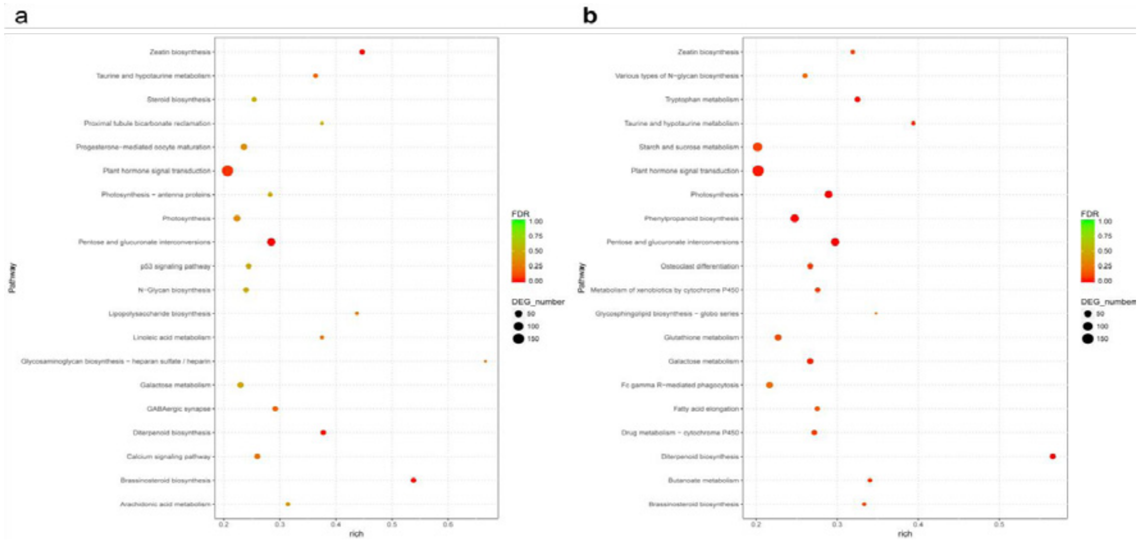

Figure 2: KEGG pathway enrichment on meiosis specific expressed duplicate genes. a) Developed pollen versus meiosis stage. b) Vegetative tissue versus meiosis stage.
FDR: False Discovery Rate; Corrected P-Value; DEGs: Differentially Expressed Genes

(both less than 20%) (Figure 1). Our data unequivocally present an increase in the expression of genome-wide duplicated genes in the stage of meiosis, but not in the stage of mature pollen development. Our letter suggests that meiosis, the key stage of plant reproduction, is the major associated selective force for gene duplication during plant evolution. Moreover, the duplicate genes over represented during meiosis in our study are annotated and predominantly enriched in critical pathways of plant hormone signal transduction (Figure 2). This finding is consistent with the gene balance hypothesis, which suggests that the expression levels of duplicate genes encoding members of the components of signal transduction pathways need to be maintained for correct function [8]. Meiosis occurring during male gametogenesis is potentially under more stringent selection than other phases of the life cycle in plants because cells undergo intense competition as haploids following the pollen development processes. Thus, the gene balance would be more critical in the highly sensitive meiosis stage. These data suggest that meiosis places exceptional demands on plant hormone signal transduction, so that much higher selection pressure on appropriate gene balance results in retention and expression of a greater proportion of duplicated genes in meiosis during plant reproduction. This letter provides direct evidence that suggests that meiosis during plant male gametogenesis is the master driver for gene duplication in angiosperms. These findings thus highlight the importance of meiosis to the evolution of gene duplication in higher plants and provide a significant opportunity for understanding the biological basis of the function and evolution of genome-wide duplicate genes. Understanding the contribution of plant gene duplication to the evolution, ecology and agriculture is important in light of the environmental challenges, including the old problems of diversity, adaptation and grain yield concerning food security, as well as new issues related to global climate change. Considering the critical role of the meiosis in genetic variation and sexual reproduction in plants, the finding of the connection between the meiosis and gene duplication in this letter open a new avenue to illustrating the impact of duplicated genes on the meiosis for plant reproduction, as well as their ultimate evolutionary, ecological, and agronomic impacts.

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