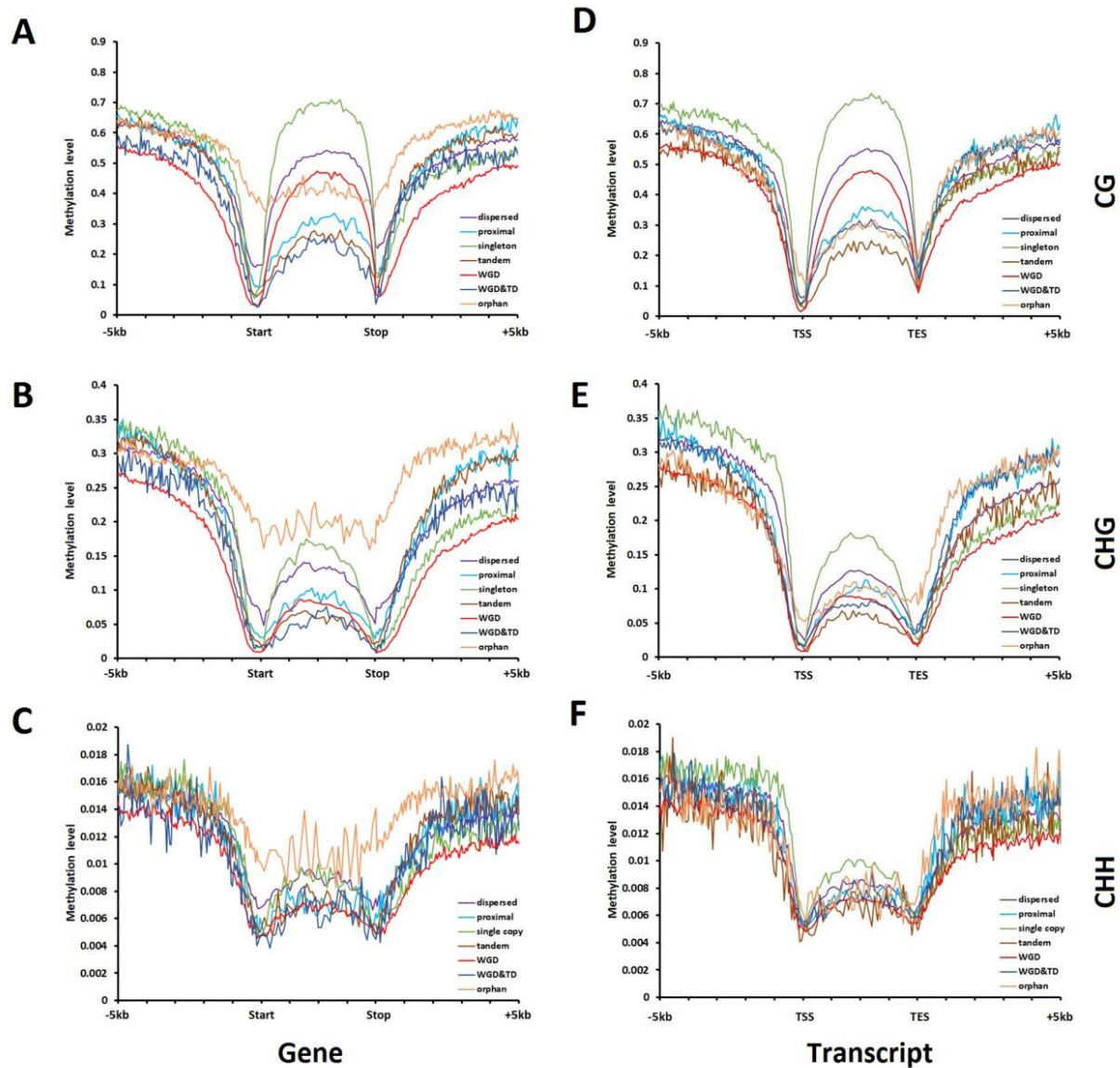


Gene fate after single whole-genome duplication in angiosperm

July 1 2020, by Zhang Nannan



CG, CHG and CHH methylation patterns of the lotus genes with different

duplication status (fate after a WGD). Credit: SHI Tao

Multiple whole-genome duplications (WGDs) are found in most sequenced angiosperms. WGDs help plants to survive in extreme environments and contribute to phenotypic innovations. Duplicated genes following WGD often have different fates: They can quickly disappear again, be retained for long(er) periods, or subsequently undergo small-scale duplications. But why do different genes have different fates following a WGD? How can different expression, epigenetic regulation, and functional constraints be associated with these different gene fates following a WGD? To answer these questions requires a model plant with a single WGD during its evolutionary past.

Researchers from the Wuhan Botanical Garden of the Chinese Academy of Sciences (CAS), Ghent University, University of Maryland and Sun Yat-sen University have investigated the lotus, an angiosperm with a single WGD during the K-pg boundary.

Relying on an improved intraspecific-synteny identification by a high-throughput chromosome conformation capture (Hi-C)-based [genome assembly](#), transcriptome, and bisulfite sequencing, the researchers explored not only the fundamental distinctions in genomic features, expression and methylation patterns of [genes](#) of different fates after a WGD, but also what shaped post-WGD expression divergence and expression bias between duplicates.

Also, they found biases in [expression levels](#) between different subgenomes reflecting subgenome dominance, which were associated with the bias of subgenome fractionation. Based on the observed subgenome pattern, they suggest that the lotus might be an ancient allopolyploid.

This study on the genome duplication of lotus emphasizes the impact of functional constraints on gene fate and post-WGD duplicates divergence in plants.

The article, titled "Distinct expression and methylation patterns for genes with different fates following a single whole-genome duplication in flowering plant," has been published in *Molecular Biology and Evolution*.

More information: Tao Shi et al. Distinct expression and methylation patterns for genes with different fates following a single whole-genome duplication in flowering plant, *Molecular Biology and Evolution* (2020). [DOI: 10.1093/molbev/msaa105](https://doi.org/10.1093/molbev/msaa105)

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