**Dynamics of Duplicated Networks in Polyploids**

Polyploidy is a widespread phenomenon throughout eukaryotes. The duplication of genetic materials immediately reshapes the architecture of biological networks, and sets in motion the evolutionary changes of network components and their interacting relationships, which ultimately affects how molecules generate phenotypes with important ecological

and evolutionary consequences. Although co-expression network analysis has been fruitful to underlie the genotype to phenotype equation for many systems, the analysis in polyploid species poses unique challenges due to the technical difficulty in estimating duplicated gene expression levels. To address these challenges and pitfalls in the use of RNA-seq data for duplicated gene expression and co-expression network analyses, we exemplify the analytic workflow and define reasonable practice for revealing the dynamics of duplicated gene networks in allopolyploid cotton. By examining network topological changes within and between sub-genomes by allopolyploidization, a significant increase of inter-connection between sub-genomes was observed. While no global bias was found within each sub-genome in terms of gain or loss of network connections, asymmetrical sub-network topology was identified implicating the functional and regulatory divergence of duplicated genes. These results demonstrate the potential for duplicated network analysis for understanding the regulatory architecture of complex genomes and phenotypes.