

Background/Objective

- Polyploidy is common in plants, including many of the world's most important crops.
- Genome duplication associated with hybridization, or allopolyploidy, allows chromosome sets to persist as distinct subgenomes.
- Here we present a general method for identifying the subgenomes of a polyploid based on shared ancestry, develop the statistical basis of the method and apply it to several problematic cases in plants.

Approach

First, we identified groups of homoeologous chromosomes based on shared protein-coding genes. Next, we identified nominally subgenome-specific k-mers that are enriched in one member of each homoeologous group. Finally, we collected chromosomes with similar k-mer profiles into subgenomes.

Results

This methodology for identifying subgenomes in allopolyploids is robust in diverse plant and animal systems. Since k-mer analyses are intrinsic to the allopolyploid, subgenomes can be identified without needing to sample the genomes of diploid or other candidate progenitors, which may be extinct.

Significance/Impacts

These results are important for understanding how the genomes of economically and ecologically important species evolved and highlight the need to develop rigorous methodological approaches to study polyploid genomes. We can then apply that knowledge and insight to further develop and improve our targeted polyploid bioenergy crops, including miscanthus, sugarcane, and switchgrass.

Session, A.M., Rokhsar, D.S. June 1, 2023. "Transposon Signatures of Allopolyploid Genome Evolution." *Nature Communications*. DOI: 10.1038/s41467-023-38560-z.

