

Characterization of Disomic Alien Addition Lines from an Intersubgeneric Cross between *Glycine max* and *G. tomentella* and Phenotypic Variation within those Lines and their Progenies

Background/Objective

The movement of genes and chromosomes between distantly related plant species is a powerful driver of evolutionary innovation and an important mechanism for expanding genetic diversity in crops. However, fundamental questions remain about how alien chromosomes interact with host genomes, alter gene regulation, and affect chromosome stability across generations. The objectives of this research were to identify differences in gene expression between a hybridization containing disomic addition lines (DAALs) and a DAAL progeny to document the phenotypic variation among the DAAL-derived soybean lines and determine the genetic cause of the variation.

Approach

Using soybean × *Glycine tomentella* disomic alien addition lines (DAALs, 2n=42) as a model system, this study investigated how the presence and subsequent loss of two alien chromosomes influence genome-wide gene expression, chromosome transmission, and the emergence of novel phenotypes. After genomic DNA was extracted, simultaneous hybridization through fluorescent in situ hybridization (FISH) and genomic in situ hybridization (GISH) was performed.

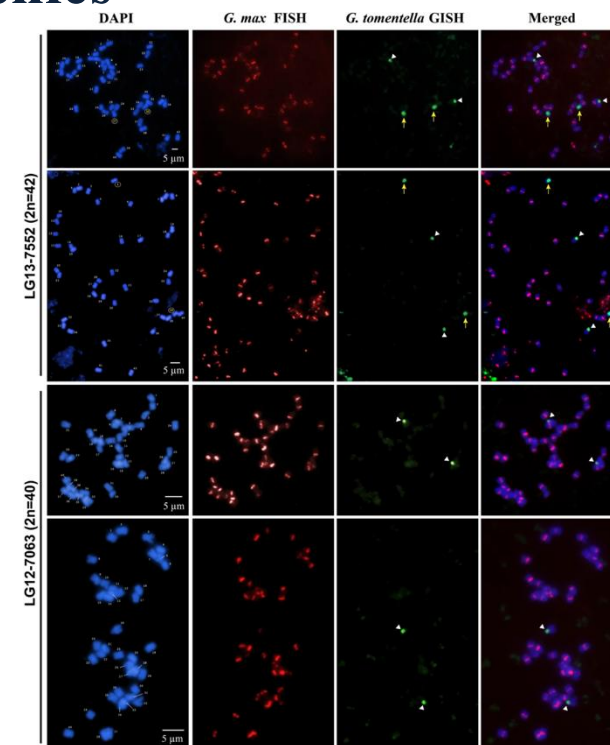
Results

Soybean lines carrying an extra chromosome pair from the wild relative *G. tomentella* proved chromosomally unstable: over multiple field generations, roughly 4% of progeny per year spontaneously reverted to normal soybean's 40 chromosomes, and these revertants showed extensive, unexpected phenotypic and genetic divergence from both parents, likely driven by elevated natural cross-pollination. Supporting genomic and transcriptomic sequence data showed allelic changes and broad gene expression disruption tied to the extra chromosome pair.

Significance/Impacts

This first-of-its-kind tracking of chromosome addition, loss, and resulting genome-wide instability is directly relevant to bioenergy crops: sugarcane, switchgrass, miscanthus, and other feedstocks are polyploid or aneuploidy-prone and often bred via wide interspecific crosses, making this study's tools and findings on chromosomal imbalance a useful template for managing similar instability in bioenergy crop engineering.

Wang et al. 2026. "Characterization of Disomic Alien Addition Lines from an Intersubgeneric Cross between *Glycine max* and *G. tomentella* and Phenotypic Variation within those Lines and their Progenies." *Plant Molecular Biology*. DOI: 10.1007/s11103-026-01727-5.



Fluorescent in situ hybridization (FISH) and genomic in situ hybridization (GISH) of LG13-7552 and LG12-7063.