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Chromosomal evolution in Brassicaceae: Allopolyploidy, aneuploidy and transgene transmission

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Polyploidy is a eukaryotic phenomenon common to plants that serves as an evolutionary mechanism for speciation. Diploid species undergo polyploidization through single genome duplication (autopolyploidy) or by the hybridization of genomes from two or more distinct progenitor species (allopolyploidy). Aneuploidy can arise where offspring possess extra or fewer chromosomes than their progenitors. Over successive generations, changes in chromosomal number and rearrangement can lead to speciation or differentiation of ecotypes within a species. Using advanced molecular cytogenetics and fluorescent *in situ* hybridization (FISH), we can distinguish chromosomes and genomic markers among different ecotypes and species. In the agricultural industry where genetically modified organisms (GMOs) are used, aneuploidy and homoeologous recombination of transgenic elements presents a potential mechanism of moving transgenes from GMO crops into the genomes of wild diploids. These wild diploids then have the potential to become "superweeds" that can disrupt ecological systems. The goal of this study was to investigate the movement of a transgene from an allopolyploid to a diploid in controlled greenhouse crosses.

Transgenic *Brassica napus* allopolyploid plants (AACC) were backcrossed to natural *Brassica rapa* (AA) recurrently over three generations. We examined each of the three backcross generations for chromosome number and gene transmission. Molecular cytogenetic analysis was performed on flower buds from each backcross, chromosome numbers were recorded and gene transmission was analyzed by PCR. As expected, we found aneuploidy in *Brassica napus* x *Brassica rapa* hybrids suggesting potential for homoeologous recombination of transgenes into non-transgenic diploid species.

Surprisingly, despite aneuploidy, we also found a high rate of both germination and transmission of the transgene into wild *Brassica rapa*, suggesting the need to find safe sites in *Brassica napus* to insert transgenes.