

## Estimation of Double Reduction in Segmental Allotetraploid Peanut

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Polyploidy can confer evolutionary advantages and seems to be favored during crop evolution and domestication. Such advantages are evident for tetraploid peanut (*Arachis hypogaea* L.), which has increased adaptability attributable to the heterotic state fixation. However, polyploidization also reduced peanut genetic diversity by isolating it from its wild diploid relatives, limiting its improvement in breeding programs. Some polyploid genetic mechanisms spontaneously generate genetic diversity circumventing the bottleneck associated with polyploidy, such as double reduction, which occurs when an individual carrying a locus in a single dosage can produce gametes disomic for this locus. For double reduction to manifest, three events need to happen during meiosis: multivalent pairing, non-sister chromatids cross-over and non-disjunctional chromosomal separation. In plants, polysomic inheritance and multivalent pairing are typical of autopolyploids. Conversely, allopolyploids are characterized by disomic inheritance and bivalent pairing. Thus, double reduction has only been inferred in autopolyploid plants. The allotetraploid peanut, however, follows a third genetic model, segmental allopolyploidy: it mostly exhibits disomic pairing, but significant levels of multivalents. We estimated the rate of double reduction in a BC<sub>1</sub> peanut population of 184 individuals. This population has the neotetraploid [*A. magna* x *A. stenosperma*]<sup>4x</sup> as the donor parent, and *A. hypogaea* as the recurrent parent. Surprisingly, about 20% of the studied individuals showed double reduction in the male parent, resulting in unbalanced genomic compositions in the progeny. All these events occurred in chromosomes 4 and 6. This is the first time that the rate of double reduction is estimated in an allotetraploid organism.