

Estimation of Double Reduction in Segmental Allotetraploid Peanut

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The vast majority of eukaryotes historically went through at least one polyploidization event. Polyploidy can confer evolutionary advantages and is thought to be favored during domestication and crop evolution. Such advantages of polyploidization are evident for tetraploid peanut (*Arachis hypogaea* L.), which is characterized by increased adaptability attributable to the fixation of the heterotic state. On the other hand, polyploidization reduced peanut genetic diversity which is one of the main limitations for crop improvement in modern peanut breeding programs. Genetic mechanisms characteristic of polyploids, such as tetrasomic recombination and double reduction spontaneously generate genetic diversity and provide a route to circumvent the genetic bottleneck associated with polyploidy. Double reduction is a special circumstance in polyploids where an individual carrying a locus in a single dosage can produce gametes disomic for this locus. In order for double reduction to manifest, three events need to occur during meiosis: multivalent pairing of chromosomes during prophase I followed by crossing-over between non-sister chromatids, and a subsequent non-disjunctional chromosomal separation during anaphase I and II. In plants, polysomic inheritance and multivalent pairing are typical of autopolyploids since high similarities are shared among the different sets of chromosomes. Conversely, allopolyploids, which were derived from the hybridization of two different species, are typically characterized by disomic inheritance and bivalent pairing. Thus, double reduction has only been inferred in autopolyploid plants. Instead, peanut is an allotetraploid species with a mostly AABB type genome ($2n = 4x = 40$), that follows a third genetic model, segmental allopolyploidy. Hence, it exhibits a mostly disomic pairing, but with significant levels of multivalent pairings and tetrasomic recombination. In this study, for the first time, we estimate the rate of double reduction in an allopolyploid organism, the segmental allotetraploid peanut, by genotyping a BC₁ population of 184 individuals. This population has the neotetraploid [*A. magna* x *A. stenosperma*]^{4x} as the donor parent, and *A. hypogaea* as the recurrent parent. Surprisingly, about 20% of the studied individuals showed at least one clear case of double reduction in the male parent, resulting in unbalanced genomic compositions (AAAB) in the progeny. All these events occurred in chromosomes 4 and 6.