

Spontaneous Generation of Diversity in *Arachis* neopolyploids (*A. ipaënsis* x *A. duranensis*)^{4x} as a Model for the Early Stages of Peanut Evolution

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Polyploidy is considered a driving force in plant evolution and domestication. For the genus *Arachis*, several diploid species were cultivated for their seeds. However, it was only the allotetraploid peanut, *Arachis hypogaea*, that became the successful, widely spread legume crop. This suggests that polyploidy has given a selective advantage for domestication of peanut. We studied induced allotetraploid (neopolyploid) lineages obtained from peanut's progenitor species, *A. ipaënsis* and *A. duranensis*, at earlier and later generations. We observed plant morphology, seed dimensions, chromosome makeup (by FISH and GISH) and performed analyses of genome wide SNPs. These neopolyploid lineages show more variable fertility and morphology than their progenitors and cultivated peanut. They also showed high sexual and somatic genome instability. Instability was manifest by changes of number of detectable 45S rDNA sites, mosaic chromosomal patterns and extensive homeologous recombination, that is, allele recombination between component subgenomes. Genome instability was not randomly distributed across the genome: more syntenic chromosomes had more homeologous recombination. Based on the observations of this study, we conclude that early stages of the origin and domestication of the allotetraploid peanut involved two genetic bottlenecks: the first, common to most allotetraploids, is the rare hybridization and polyploidy event, which is followed by sexual isolation between the allotetraploid and its wild diploid relatives. Here we suggest a second bottleneck: the survival of only very few lineages, which had stronger mechanisms in place for controlling genomic instability.