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[Browse by Type](#)
[Poster Categories](#)
[Meeting Information](#)
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P1034
Evidence of Mixed Disomic and Polysomic Inheritance in Allotetraploid Peanut

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Cultivated peanut and wild synthetic are allotetraploid ($2n=4x=40$) with two homeologous sets of chromosomes. Genetic mapping in tetraploid peanut is usually performed considering a diploid-like meiotic behavior. However, a recent study points out the occurrence of partial tetrasomic behavior. In this study, we investigated the meiotic inheritance of the allotetraploid peanut using 380 SSR markers and 93 F_2 progenies derived from the cross between *Arachis hypogaea* cv Fleur11 (AABB) and ISATGR278/18 (AAKK), a wild synthetic with a K genome reported to pair with the cultivated B genome during meiosis. As results, the analysis of the segregation for 34 SSR markers, revealed unexpected null band among some progenies, unexplainable under disomic inheritance. Chi-square tests for these loci indicated a 1:34:1 segregation ratio consistent with a tetrasomic inheritance rather than the 1:2:1 Mendelian ratio for disomic inheritance. A linkage map was constructed. It consists of 365 loci aligned into 20 linkage groups (LGs) with a total length of 1928 cM, averaging 5.1 cM between markers. Interestingly, among the ten homeologous sets of LGs, one set consisted of markers that all segregate in a tetrasomic pattern, 6 in a likely disomic pattern and the 3 remaining in a mixed pattern with disomic and tetrasomic loci, clustered on the same LG. Our findings provided evidence that the meiotic behavior of allotetraploid peanut is neither fully disomic nor fully tetrasomic, but rather mixed. In addition, we reported a conversion of homeologous chromosomes for some progenies. This opens new horizons for peanut breeding.

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[<< Previous Poster](#) | [Next Poster >>](#)