

## **Tetrasomic Recombination in a Recombinant Inbred Line Population Confirmed through Whole Genome Re-sequencing**

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Genetic analysis in peanut has generally assumed classic allotetraploid genetic behavior with diploid-like disomic recombination occurring exclusively between homologous chromosomes. However, recently, genetic recombination between homeologous chromosomes has been reported between peanut and wild species-derived allotetraploids. Here we provide evidence of tetrasomic recombination at the molecular level in cultivated peanut, in a set of recombinant inbred lines (RIL). Firstly, the analysis demonstrates historical tetrasomic recombination by the identification of regions where numerous identical SNPs occur in homeologous chromosomes; secondly, we analyze the sporadic occurrence of non-parental genotype calls and show that they are caused by spontaneous recombination between subgenomes. Historical tetrasomic recombination was observed at the ends of chromosomes A04, B04 and A06, B06 where one parent was nulliplex and the other tetraplex for one of the subgenomes. For the second approach, we observed a few RILs with occasional, sporadic non-parental genotype calls distributed in discontinuous regions in most of the chromosomes except by A01, B01, A08, B08 and A10. Using whole genome re-sequencing of the parents and two RILs at ~35X coverage we found compelling evidence that these non-parental calls were caused by genetic exchange between subgenomes. QTL previously identified in this population were found to overlap with regions of tetrasomic recombination in linkage groups A04, A07, B07 and B09. Further investigation will be needed to confirm and analyze the effect of tetrasomic recombination on the inheritance of quantitative traits.