Miniature Inverted Repeat Transposable Element Based Sequence Capture for Next Generation Sequencing and Marker Development in Peanut (*Arachis hypogaea* L.).

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Cultivated peanut (*Arachis hypogaea* L.) is an allotetraploid plant with a large genome size (~ 2800 Mbp) and minor status as a crop, factors that have delayed whole genome sequencing. An alternative to sequencing the entire genome is capturing and sequencing the gene rich regions of the genome. One approach to target such regions is to capture sequences contiguous with Miniature Inverted Repeat Transposable Elements (MITEs) which are known to insert near genes. Peanut genomic DNA enriched for MITE-containing fragments was sequenced on the Illumina Next-Generation sequencing platform to generate sufficient coverage to identify polymorphic insertion sites between three cultivars and two irradiation-induced mutants. Several polymorphic markers have already been obtained among cultivated genotypes using Sanger generated sequences of captured MITE-containing inserts. Deep sequencing of gene-rich regions should significantly expand the number of available markers since cultivated peanut has so far shown very little polymorphism at the molecular level in spite of morphological and agronomic variations. Low levels of polymorphism between peanut cultivars have thus far limited the application of marker-assisted selection/molecular breeding in peanut.