Assessment of Oil Content and Fatty Acid Variability in Peanut Wild Relatives.

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Peanut wild relatives contain useful alleles and can be potentially used as a secondary gene pool for improving cultivated peanuts. The variability of oil content and fatty acid composition in these peanut wild relatives were not well assessed. Sixty accessions representing 40 species within Arachis genus covering different genomes (A, B, and D) with different chromosome numbers (18 – 40) and ploidy levels (2x – 4x) were selected from the USDA peanut germplasm collection and evaluated for their oil content and fatty acid composition with nuclear magnetic resonance (NMR) and gas chromatography (GC). Significant variability of oil content and fatty acid composition has been identified among these peanut wild relatives. The information obtained in this study would be useful for further screening peanut wild relatives and introgression of wild species alleles into cultivated peanut in breeding programs.