Molecular genetic variation in cultivated peanut cultivars and breeding lines revealed by highly informative SSR markers.

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Groundnut or peanut (*Arachis hypogaea* L.) is an economically important crop worldwide as a source of protein and cooking oil, particularly in developing countries. Because of its narrow genetic background and shortage of polymorphic genetic markers, molecular characterization of cultivated peanuts especially released cultivars and breeding lines is very limited, even though there are some genetic diversity studies for cultivated germplasm and wild species. The objective of this study is to investigate the genetic variation of the released peanut cultivars and breeding lines from China and the United States for future molecular genetics and breeding studies, such as genetic mapping population construction and marker-assisted selection in cultivated peanut. Recently, two sets of highly informative SSRs developed by ICRISAT (199 SSRs) and the University of Brasilia (66 SSRs) with higher PIC over 0.5 have been reported. We are using these markers to genotype 48 peanut popular cultivars and breeding lines representing top producing regions from China (Henan Province and Shandong Province) and USA (Georgia and Texas). Genetic relationship analysis will be studied and correlate the current pedigree and taxonomical classification of subspecies and varieties. Thus the highly informative markers could contribute to several genetic studies and marker-assisted improvement of peanut in the future.