

Extraordinary high allelic diversity in a groundnut (*Arachis hypogaea* L.) germplasm collection assayed by robust and informative SSR markers

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The ability to identify genetic variation is indispensable for effective management and use of genetic resources in crop breeding. Genetic variation among 189 groundnut (*Arachis hypogaea* L.) accessions comprising landraces (31), cultivars (34), mutant (1), advanced breeding lines (64) and others (59; unknown genetic background) representing 29 countries and 10 geographic regions was assessed at 25 microsatellite or simple sequence repeat (SSR) loci. A higher number of alleles (265) were detected in the range 3 (Ah1TC6G09) to 20 (Ah1TC11H06) with an average of 10.6 alleles per locus. The PIC value at these loci varied from 0.38 (Ah1TC6G09) to 0.88 (Ah1TC11H06) with an average of 0.70. A total of 59 unique alleles and 127 rare alleles were detected at almost all the loci assayed. Cluster analysis grouped 189 accessions into four clusters. In general, genotypes of South America and South Asia showed higher level of diversity. Extraordinary level of allelic diversity reported here provides opportunities to the groundnut community to make better decisions and define suitable strategies for harnessing the genetic variation in groundnut breeding.