

Ahmad Alhariri, Tusar Kanti Behera, Gograj Singh Jat, Mayanglambam Bilashini Devi, G. Boopalakrishnan, Nada F. Hemeda , Ayaat A. Teleb, E. Ismail and Ahmed Elkordy (2021). Analysis of Genetic Diversity and Population Structure in Bitter Gourd (<i>Momordica charantia</i> L.) Using Morphological and SSR Markers. Plants 10: 1860. https://doi.org/10.3390/plants10091860	البحث الرابع
مشترك مع آخرين بالتخصص وآخرين من خارج التخصص – منشور	4

Title	Analysis of Genetic Diversity and Population Structure in Bitter Gourd (<i>Momordica charantia</i> L.) Using Morphological and SSR Markers.
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ABSTRACT

The present investigation was carried out using 51 diverse bitter gourd accessions as material for studying genetic diversity and relatedness using morphological and SSR markers. A wide variation was observed for morphological traits like the number of days to the first female flower anthesis (37.33–60.67), the number of days to the first fruit harvest (47.67–72.00), the number of fruits/plant (12.00–46.67), fruit length (5.00–22.23 cm), fruit diameter (1.05–6.38 cm), average fruit weight (20.71–77.67 g) and yield per plant (513.3–1976 g). Cluster analysis for 10 quantitative traits grouped the 51 accessions into 6 clusters. Out of 61 SSR primers screened, 30 were polymorphic and highly informative as a means to differentiate these accessions. Based on genotyping, a high level of genetic diversity was observed, with a total of 99 alleles. The polymorphic information content (PIC) values ranged from 0.038 for marker BG_SSR-8 to 0.721 for S-24, with an average of 0.429. The numbers of alleles ranged

from 2 to 5, with an average of 3.3 alleles per locus. Gene diversity ranged from 0.04 for BG_SSR-8 to 0.76 for S-24, showing a wide variation among 51 accessions. The UPGMA cluster analysis grouped these accessions into 3 major clusters. Cluster I comprised 4 small, fruited accessions that are commercially cultivated in central and eastern India. Cluster II comprised 35 medium- to long-sized fruited accessions, which made up an abundant and diverse group. Cluster III comprised 11 long and extra-long fruited accessions. The polymorphic SSR markers of the study will be highly useful in genetic fingerprinting and mapping, and for association analysis in *Momordica* regarding several economic traits.