ABSTRACT

Morphological and genetic diversity are important components for cultivar development and are a pre-requisite to cultivar improvement. The probability of producing unique genotypes increases in proportion to the number of genes for which parents differ (genetic distance). The objectives of this study were to determine the morphological and genetic diversity among native blackberry (Rubus L. subgenus Rubus Watson) accessions in selected counties in Kenya and their relationship with Plant Introductions (PIs) using morphological and SSR markers. Eleven out of thirteen available blackberry SSR primer sets were used to screen 90 blackberry accessions in this study. Molecular data were scored in binary fashion for SSR marker loci amplified and were analysed using DARwin 6.0, PowerMarker 3.25 and GenAlEx 6.5 software. Each individual blackberry accession was nested within its county of collection and morphological data were taken in-situ on all the accessions including erect, semi-erect and trailing types. Morphological data were analysed using GENSTAT 15th Edition programme, SAS ver. 9.1 (SAS Institute Inc., Cary, 2001) andR forstatistical computing version 3.4.1 software.Both molecular and morphological data analysed detected considerable diversity within and among the blackberry accessions studied. Analysis of Molecular Variance (AMOVA) showed that much of the genetic diversity existed within the accessions (95%) with estimated genetic variation of 4.12. The expected heterozygosity (HE) of the blackberry accessions ranged from 0.48 to 0.89. Principal component analysis(PCA) conducted on morphological data generated 10 axes, out of which, 7 had a cumulative variation of 96.30%, with the first two axes having a discriminatory variance of 52.71 % sufficient to identify variables able to differentiate blackberry accessions in Kenya. Further, out of the 10 important morphological traits subjected to PCA, 8 were able to differentiate the collected accessions and were considered as variables capable of discriminating them on the basis of morphology. Molecular data cluster analysis using the Jaccard's similarity coefficient grouped the accessions into three classes; I, II and III consisting of 31, 52 and 7 accessions, respectively, while a phylogenetic tree constructed for morphological data, using the Gower's coefficient, grouped the accessions into two classes; I and II consisting of 1 and 89 accessions, respectively. Both clusters were random and did not group the accessions according to their geographical origin, indicating that the accessions found in Kenya are closely related. This study revealed high levels of within genetic diversity in the blackberry genetic resources studied which can be used in blackberry breeding programs.