Abstract

Brassica mustard species represent one of the most important oilseed crops in India, nevertheless, their genetic diversity is barely known. A better understanding on this topic is essential for the proper utilization of genotypes in breeding programmes. We evaluated the genetic diversity among 44 Indian mustard (Brassica juncea) genotypes including varieties/purelines from different agro-climatic zones of India and few exotic genotypes (Australia, Poland and China). For this, we used A and B genome specific SSR markers and phenotypic data on 12 yield and yield contributing traits. Out of the 143 primers tested, 134 reported polymorphism and a total of 355 alleles were amplified. Dendrograms based on Jaccard’s similarity coefficients and Manhattan dissimilarity coefficients were generated based on an average linkage algorithm (UPGMA) using marker data and phenotypic data. Genotypes were grouped into four clusters based on genetic distances. Both the clustering patterns based on Jaccard’s similarity and Manhattan dissimilarity coefficients, independently, discriminated the genotypes effectively as per their pedigree and origin. PCoA revealed that, the grouping of genotypes based on SSR marker data is more convincing than phenotypic data, however, the correlation between phenotypic and genetic distance matrices was observed to be very low (r=0.11). Hence, for diversity studies reliability on molecular markers is worth proving and SSR markers are the stronger tools than quantitative traits in discriminating B. juncea genotypes. Rev. Biol. Trop. 61 (4): 1919-1934. Epub 2013 December 01.

Keywords

Brassica juncea, genetic diversity, quantitative traits, SSR markers.