

Abstract

Traditionally red kidney bean landraces from Jamaica are divided into three major groups based on morpho-agronomic methods of such as seed morphology. The diversity of red kidney beans (*Phaseolus vulgaris* L.) were evaluated at the genetic level using random amplified polymorphic DNA (RAPD) PCR-based marker system and screened using four random primers, OPW-04, OPW-07, OPW-10, and OPW-19 (Operon Technologies). The DNA fingerprints were compared using Nei and Li's (1979) similarity coefficient and the cluster analysis using UPGMA to determine the molecular genetic relationship between the 28 bean accessions. The RAPD DNA fingerprinting resulted in a total of 542 amplification products being produced, and were scored as 33 polymorphic and 8 monomorphic markers and dendrograms were constructed for each primer. The DNA fingerprints did not show any correlation with the seed morphology, having mottled varieties being clustered with red coloured seed types, revealing that the indigenous *P. vulgaris* L. cultivars are a highly heterogenous population. In addition to the estimation of the degree of relatedness the fingerprints revealed a unique marker, OPW-19₉₂₄, that was present only in the Ja-17 accession enables its identification. Secondly, OPW-04₁₆₅₀ was unique to the Ja-1-5 accessions that were clustered together. The marker OPW-19₇₉₅ was absent from a single accession, Ja-16, indicating the allele is recessive and would not be amplified since RAPD markers are dominant. Characterization of the seed protein phaseolin among the accessions revealed three allozymes; the 'S' (54%), 'T'

(28%), and the 'C' (18%) types. The existence of both the S and T-type allozymes suggests that the beans found in Jamaica originated from the Mesoamerican and the Andean centres of domestication respectively. The C-type phaseolin, is a rare recombinant of dissimilar subunits of the S and T-type allozymes, resulting from genetic crossing over between the genepools. Studies suggest the genepools met in Columbia; therefore the population originated in two domestication centres and may have been disseminated via Columbia.