

Abstract

Bambara groundnut is an indigenous African legume grown mainly in sub-Saharan Africa; it is an important source of protein to the rural majority. There are no established varieties and subsistence farmers grow locally adapted landraces which are generally low yielding. Bambara groundnut is a predominantly self-pollinating crop and is expected to exist as non-identical inbred lines, although the previous lack of co-dominant markers has prevented a formal assessment of heterozygosity within bambara groundnut genotypes.

A total set of 75 microsatellites that were characterised in this study were used to investigate the genetic diversity of a set of 24 bambara groundnut, to provide an evaluation of the markers for polymorphism and provide a link with DArT marker data that were previously analysed.

Sixty eight microsatellites were identified that were found to be consistent and reproducible, from which a set of markers were selected and used for genetic variability studies of bambara groundnut, to compare the use of molecular markers with morphological markers, and to investigate using SSR markers in pure line selection.

The genetic diversity of bambara groundnut was assessed based on morphological characters for two seasons; in a glasshouse experiment at the University of Nottingham, Sutton Bonington Campus, UK and in a field experiment that was conducted at the Botswana College of Agriculture (Notwane farm), Gaborone in a randomised block design with three replicates. The landraces were characterised for 24 quantitative and 13 qualitative characters. The results indicated considerable variation for quantitative characters, while significant morphological differences were also recorded for most characters. Multivariate data analysis was conducted using principal component analysis, cluster analysis and heritability estimates were developed. The low cost, simplicity and agricultural relevance of morphological characterisation makes it an important tool in germplasm genetic variation studies.

Thirty four lines from field experiments were investigated for genetic diversity based on 20 microsatellites. The expected heterozygosity (H_e) had an average of 1 in agreement with the fact that bambara groundnut is predominantly self-pollinating. Both cluster analysis and principle component analysis (PCoA) grouped landraces based mainly on their areas of origin.

A thorough molecular analysis of genetic and morphological variation in bambara groundnut was conducted to investigate the relationship between the two assessment techniques. This comparison will assist in breeders making informed decisions as to which approach is best to use in germplasm characterisation and plant breeding and how best to apply such knowledge in practical situations. DNA markers could then aid with the selection of germplasm for breeding, quality control within breeding programmes and, potentially, direct selection via Marker Assisted Selection (MAS). Euclidean distance estimates for morphological data and (Nei's 1972) genetic distance estimates for SSR data were strongly correlated ($r = 0.7$; $P < 0.001$) in the agronomy bay and ($r = 0.6$; $P < 0.001$) in the controlled growth room. These results suggest the two approaches are generating the same pattern of genetic diversity, and as such can be used as a surrogate for each other.