Abstract

Cowpea (*Vigna unguiculata* (L.) Walp.) is a grain legume commonly grown and consumed in many parts of the tropics and subtropics. A genetic linkage map was constructed using simple sequence repeat (SSR) markers and a recombinant inbred (RI) population of159 individuals derived from a cross between the breeding line 524B, a California Blackeye, and 219-01, a perennial wild cowpea from Kenya. Out of 912 primer combinations predicted to amplify SSRs in cowpea, 639 reliably produced amplification products in PCR assays and 202 (31.6%) were polymorphic between the two parents. These polymorphic SSRs were used to construct a genetic map consisting of 11 linkage groups (LGs) spanning 677 cM, with an average distance between markers of 3 cM. Agronomic traits related to domestication (seed weight, pod shattering) were analyzed together with the genotypic data. Six quantitative trait loci (QTL) for seed size were revealed with the phenotypic variation ranging from 8.9 to 19.1%. Four QTL for pod shattering were identified with the phenotypic variation ranging from 6.4 to 17.2%. The QTL for seed size and pod shattering mainly cluster in two areas of LGs 1 and 10, facilitating the use of marker-assisted selection to eliminate undesirable wild phenotypes in breeding activities involving introgression of traits from wild germplasm. The generation of an SSR-based molecular map and additional trait-linked markers also contributes to the expanding tool kit available to cowpea breeders, especially in Africa.