

Abstract

Understanding the genetic basis underlying domestication-related traits (DRTs) of cowpea (*Vigna unguiculata* (L.) Walp.) is important since the genome has experienced divergent domestication and in addition it is also useful to utilize the wild germplasm efficiently for improving different traits of the cultivated cowpea. Quantitative trait loci (QTLs) for DRTs were identified in a population of 159 F₇ recombinant inbred lines derived from a cross between a domesticated cowpea (*V. unguiculata* (L.) Walp.) variety, 524B, and a wild accession, 219. Using the constructed linkage map, QTLs for 10 DRTs were analysed and mapped. QTLs for seed, pod and flower related traits were detected. Subsequently, QTL for ovule number was also identified. To our knowledge, this is the first time a QTL for this trait has been observed. QTLs for DRTs show co-localization on three linkage groups and pleiotropy or close linkage of genes for the traits is suggested in these chromosome regions. The information gained in this study can be used for marker-assisted selection of domestication-related QTLs in cowpea and enhance understanding of domestication in the genus *Vigna*.