

Abstract

Flowering time is a major adaptive trait in plants and an important selection criterion in the breeding for genetic improvement of crop species. QTLs for the time of flower opening and days to flower were identified in a cross between a short duration domesticated cowpea (*Vigna unguiculata* (L) Walp.) variety, 524B, and a relatively long duration wild accession, 219-01. A set of 159 F7 lines was grown under greenhouse conditions and scored for the flowering time associated phenotypes of time of flower opening and days to flower. Using a LaD threshold of 2.0, putative QTLs were identified and placed on a linkage map consisting of 202 SSR markers and four morphological loci. A total of five QTLs related to the time of flower opening were identified, accounting for 8.8%-29.8% of the phenotypic variation. Three QTLs for days to flower were detected, accounting for 5.7%-18.5% of the phenotypic variation. The major QTL of days to flower and time of flower opening were both mapped on linkage group J. The QTLs identified in this study provide a strong foundation for further validation and fine mapping for developing an efficient way to restrain the gene flow between the cultivated and wild plants.