

Abstract

The tea industry plays significant role to the economies of tea growing countries leading to generation of foreign exchange and improved livelihoods. Efficient breeding and selection of improved tea (*Camellia sinensis* (L.) O. Kuntze) clones require sound knowledge and understanding of genetics associated with desirable attributes. Quantitative trait loci (QTL) mapping for yield and drought tolerance in tea was performed using 42 F₁ clonal progeny derived from a cross between clones TRFCA SFS150 and AHP SI5/10 that had been established at two distinct tea growing regions in Kenya. Of the 260 informative markers identified in the cross, 100 markers that exhibited 1:1 segregation ratio were used to construct a linkage map of tea. The map consisted of 30 (19 maternal and 11 paternal) linkage groups that spanned 1411.5 cM with mean interval of 14.7 cM between loci. Based on the linkage map, QTL analysis was carried out for drought tolerance and yield data recorded between 2003 and 2007 and across the two sites. Twenty-three putative yield QTLs were detected for yield, out of which 16 were identified in 5 different linkage groups for the Timbilil site, 2 in two linkage groups for Kangaita site, while the rest were associated with unlinked markers. On drought tolerance, 13 QTLs were detected of which, 10 were localised to specific linkage groups. None of the QTLs was congruently detected in the two sites owing to $G \times E$ interactions. At least two unassigned markers, EAGC/MCAC-790 and OPO-11-400, consistently associated with yield in Kangaita site for the entire period under investigation indicating their potential as candidate markers for site-specific marker-assisted selection. Markers OPT-18-2500 and OPO-02-900 had pleiotropic effects in that it was significantly associated with traits YLD-T ($P=0.007$) and DT-K ($P=0.003$). Heritability estimates for yield across sites and years varied from 0.2 to 0.88 at Timbilil site, while it remained more or less the same at Kangaita (0.68 to 0.73). The same were however high and stable for drought tolerance in Kangaita and Timbilil at 0.95 to 0.97, respectively. Genetic correlation estimates were highly significant between various years' yield records within site but not between sites save for T06 and K03, K06, K07, ANMK06 and ANMK07, which were weakly significant. The implications of the current study with respect to mapping population, $G \times E$ and marker-assisted selection are discussed.