

QTLs for oil yield components in an elite oil palm (*Elaeis guineensis*) cross

ABSTRACT

Increased modern farming of superior types of the oil palm, *Elaeis guineensis* Jacq., which has naturally efficient oil biosynthesis, has made it the world's foremost edible oil crop. Breeding improvement is, however, circumscribed by time and costs associated with the tree's long reproductive cycle, large size and 10–15 years of field testing. Marker-assisted breeding has considerable potential for improving this crop. Towards this, quantitative trait loci (QTL) linked to oil yield component traits were mapped in a high-yield population. In total, 164 QTLs associated with 21 oil yield component traits were discovered, with cumulative QTL effects increasing in tandem with the number of QTL markers and matching the QT+ alleles for each trait. The QTLs confirmed all traits to be polygenic, with many genes of individual small effects on independent loci, but epistatic interactions are not ruled out. Furthermore, several QTLs maybe pleiotropic as suggested by QTL clustering of inter-related traits on almost all linkage groups. Certain regions of the chromosomes seem richer in the genes affecting a particular yield component trait and likely encompass pleiotropic, epistatic and heterotic effects. A large proportion of the identified additive effects from QTLs may actually arise from genic interactions between loci. Comparisons with previous mapping studies show that most of the QTLs were for similar traits and shared similar marker intervals on the same linkage groups. Practical applications for such QTLs in marker-assisted breeding will require seeking them out in different genetic backgrounds and environments.

Keyword: *Elaeis guineensis*; Oil palm; Genetic linkage map; SSR; QTL mapping; QTL effects