



QTL mapping of soybean oil content for marker-assisted selection in plant breeding program

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ABSTRACT. The present study was undertaken to detect and map the quantitative trait loci (QTL) related to soybean oil content. We used 244 progenies derived from a bi-parental cross of the Lineage 69 (from Universidade Estadual Paulista "Júlio de Mesquita Filho"/Faculdade de Ciências Agrárias e Veterinárias - Breeding Program) and Tucunaré cultivar. A total of 358 simple sequence repeat (SSR; microsatellite) markers were used to investigate the polymorphism between the parental lines, and for the polymorphic lines all the F₂ individuals were tested. Evaluation of the oil content and phenotype was performed with the aid of a Tango equipment by near infra-red reflectance spectroscopy, using single F₂ seeds and F_{2:3} progenies, in triplicate. The data were analyzed by QTL Cartographer program for 56 SSR polymorphic markers. Two oil-content related QTLs were detected on K and H linkage groups. The total phenotypic variation

explained by QTLs ranged from 7.8 to 46.75% for oil content. New QTLs were identified for the oil content in addition to those previously identified in other studies. The results reported in this study show that regions different from those already known could be involved in the genetic control of soybean oil content.

Key words: *Glycine max*; SSR; NIR; Molecular markers