

A high density genetic map for underlying the QTLs associated with the main quality and functional components such as catechins, caffeine in tea plant (*Camellia sinensis*)**Liang Chen**

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Flavonoids and methylxanthine are key flavor and functional components of tea. To identify the genetic factors underlying the regulation of catechins and caffeine accumulation in the tender shoots of tea plant, quantitative trait loci (QTL) studies were carried out in a pseudo-testcross population derived from an intraspecific cross between two varieties of *Camellia sinensis*. A high density with more than 6600 SSR/SNP markers interval mapping and restricted multiple QTL model mapping detected a total of 25 QTLs and 13 QTLs associated with catechins and methylxanthine content, respectively. Of the 25 QTL associated with catechins content, nine stable QTLs were validated across years and clustered into four main chromosome regions on LG03, LG11, LG12 and LG15. The population variability explained by each QTL was predominantly at moderate-to-high levels and ranged from 2.4% to 71.0%, with an average of 17.7%. The total number of QTL for each trait varied from four to eight, while the total population variability explained by all QTLs for a trait ranged between 38.4% and 79.7%. Of the 13 QTLs associated with methylxanthine content, including caffeine content (CAF), theobromine content (TBR), total content of caffeine and theobromine (TC), and caffeine-to-theobromine ratio (CTR) over four measurement years. The QTLs detected clustered onto five linkage groups. Among them, one stable QTL (qCAF1) controlling CAF was mapped on LG1 and validated across all years, explaining an average of 18.9% of the phenotypic variance. The other QTL were identified in only one or two years, and of them there were six, two and four QTL for TBR, TC and CTR, respectively. This study presents the first example of QTL detection for methylxanthine related traits in tea plant. The results presented here provide a foundation for further fine mapping and cloning functional genes and elucidating mechanism of flavonoids and methylxanthine accumulation in tea plant.

Biography

Liang Chen has completed his PhD in Tea Science at Zhejiang University, China and Post-doctoral studies at Cornell University, USA. Now, he is an Associate Director of National Center for Tea Improvement at Tea Research Institute-Chinese Academy of Agricultural Sciences. He has published more than 40 papers in reputed journals and has been serving as an Editorial Board Member of reputed.

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