



首页

2023年4月26 星期三 17:22:17

首页 > 科研进展 > 正文

首页

新闻动态

通知公告

科研进展

学术活动

科研平台

媒体报道

QTL Mapping for Leaf Area of Tea Plants (*Camellia sinensis*) Based on a High-Quality Genetic Map Constructed by Whole Genome Resequencing

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Title

QTL Mapping for Leaf Area of Tea Plants (*Camellia sinensis*) Based on a High-Quality Genetic Map Constructed by Whole Genome Resequencing

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Abstract

High-quality genetic maps play important roles in QTL mapping and molecular marker-assisted breeding. Tea leaves are not only important vegetative organs but are also the organ for harvest with important economic value. However, the key genes and genetic mechanism of regulating leaf area have not been clarified. In this study, we performed whole-genome resequencing on "Jinxuan," "Yuncha 1" and their 96 F1 hybrid offspring. From the 1.84 Tb of original sequencing data, abundant genetic variation loci were identified, including 28,144,625 SNPs and 2,780,380 indels. By integrating the markers of a previously reported genetic map, a high-density genetic map consisting of 15 linkage groups including 8,956 high-quality SNPs was constructed. The total length of the genetic map is 1,490.81 cM, which shows good collinearity with the genome. A total of 25 representative markers (potential QTLs) related to leaf area were identified, and there were genes differentially expressed in large and small leaf samples near these markers. GWAS analysis further verified the reliability of QTL mapping. Thirtyone pairs of newly developed indel markers located near these potential QTLs showed high polymorphism and had good discrimination between large and small leaf tea plant samples. Our research will provide necessary support and new insights for tea plant genetic breeding, quantitative trait mapping and yield improvement.

