

研究论文

普通小麦籽粒黄色素含量的QTL分析

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摘要 小麦面粉黄色度b*值是反映面粉颜色的重要指标, 主要与籽粒黄色素含量有关。利用122对SSR引物、4对贮藏蛋白STS引物和10对AFLP引物组合, 分析了中优9507/CA9632的71个DH系, 构建了由173个位点组成的遗传连锁图, 在小麦21个连锁群上覆盖2 881 cM。将该群体种植2年共计5个地点, 测定籽粒黄色素和面粉黄色度b*值含量。采用复合区间作图法(CIM)进行了籽粒黄色素含量和面粉黄色度QTL分析。结果表明, 面粉黄色度b*值的QTL位于染色体1DS、2DL、3A、4D、5D、6AL、6D和7AL上, 其中7AL的QTL效应最大, 贡献率为12.9%~37.6%; 籽粒黄色素含量的QTL位于染色体2DL、3DL、4A、5A和7AL, 其中7AL的QTL效应最大, 贡献率为12.1%~33.9%。面粉黄色度b*值与籽粒黄色素含量共同的QTL位于7AL, 与Xgwm264b紧密连锁, 遗传距离分别为0~3.9 cM和0~0.9 cM。

关键词 [普通小麦](#) [面粉黄色度 b*值](#) [籽粒黄色素含量](#) [分子标记](#) [QTL分析](#)

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QTL Mapping for Kernel Yellow Pigment Content in Common Wheat

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Abstract Flour yellowness b* is a major criterion to estimate flour colour, which is basically determined by yellow pigment content in wheat grains. A doubled haploid (DH) population with 71 lines derived from a cross between Zhongyou 9507 with lower flour yellowness b* and CA9632 with higher flour yellowness b*, was sown for two years in 5 locations. A total of 173 loci including 122 SSR, 4 STS of storage protein genes and 10 AFLP markers were used to construct a linkage map, covering 2 881 cM of whole genome at 21 linkage groups. With the method of composite interval mapping (CIM), 8 putative major QTL of yellowness b* were detected on chromosomes 1DS, 2DL, 3A, 4D, 5D, 6AL, 6D and 7AL (Table 2), and 5 putative QTL of yellow pigment content were detected on chromosome 2DL, 3DL, 4A, 5A and 7AL (Table 3), respectively. The QTL on 7AL was common for yellowness b* and yellow pigment content, accounting for 12.9% - 37.6% and 12.1% - 33.9% of the phenotypic variance across different environments, respectively, which was closely linked to Xgwm264b. The genetic distance between Xgwm264b and the QTL of flour yellowness b* and grain yellow pigment on chromosome 7AL were 0 - 3.9 cM and 0 - 0.9 cM, respectively. It can be used as a molecular marker in wheat breeding program.

Key words [Common wheat \(Triticum aestivum L.\)](#) [Flour yellowness b*](#) [Kernel yellow pigment](#)
[Molecular marker](#) [Quantitative trait loci \(QTL\)](#)

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