

成熟黄瓜果皮红色性状的遗传分析及其基因定位

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Genetic Analysis and Gene Mapping of Red Mature Fruit in Cucumber

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摘要 以黄瓜 (*Cucumis sativus* L.) 成熟瓜红色果皮自交系 ‘NCG127’ (P_1) 和成熟瓜黄色果皮自交系 ‘9930’ (P_2) 为试验材料构建 F_2 遗传群体, 对成熟瓜红色果皮 R 基因进行遗传分析和基因定位研究。结果表明, 黄瓜果皮红色果皮性状由显性单基因控制, 红色对黄色为显性。以256株 F_2 分离群体为试材, 应用群体分离分析 (BSA) 法筛选得到与 R 基因连锁的20个多态性SSR标记, 构建了 R 基因分子标记连锁图谱, 将 R 基因定位到黄瓜4号染色体上, 物理距离为213.4 kb的区段内, 两侧翼标记为UW019319和UW019203, 与 R 遗传距离分别为0.8 cM和0.7 cM。生物信息学分析表明, 该区段存在30个预测候选基因。

关键词: 黄瓜 红色果皮 遗传分析 SSR标记 基因定位

Abstract: Genetic analysis and gene mapping were carried out on red mature fruit in cucumber (*Cucumis sativus* L.) using ‘NCG127’ (red mature fruit) and ‘9930’ (yellow mature fruit) as experimental materials in this study. The results showed that a single dominant nuclear gene, R , dominates the red mature fruit trait in cucumber. Simple sequence repeat (SSR) marker and bulked segregant analysis (BSA) were conducted on the DNA of F_2 plants, and resulted in screening 20 SSR markers linked to the R gene. The R gene was mapped to a linkage group corresponding to chromosome (Chr.) 4 of cucumber. The flanking markers UW019319 and UW019203 were linked to the R gene with genetic distances of 0.8 and 0.7 cM, respectively. The physical distance between markers UW019319 and UW019203 was 213.4 kb based on the whole genome sequence of ‘9930’ cucumber line, and there were 30 candidate genes in this region.

Keywords: cucumber, red mature fruit, genetic analysis, SSR marker, gene mapping

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