

不同生态环境下稻米淀粉RVA谱特征值的QTL定位分析

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Identification of QTL for Rice Starch RVA Profile Properties under Different Ecological Sites

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摘要

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摘要 利用2个直链淀粉含量相似的水稻品种93-11和日本晴为亲本, 采取单粒传法创建由190个家系组成的重组自交系群体, 并构建了包含202个SSR、CAPs和STS标记的遗传连锁图谱。采用复合区间作图法, 在3个不同生态环境下(陵水、合肥和怀远)对RVA谱特征值(峰值黏度、热浆黏度、崩解值、冷胶黏度、消减值、峰值时间、起浆温度和回复值)的8个特征性状进行了定位分析。共定位到57个QTL, 单个性状QTL数目在1~14个之间, 说明RVA谱特征值是多基因控制的数量性状。13个QTL在3个不同环境中被2次或3次检测到, 其中 $qCPV-3$ 、 $qCPV-10b$ 、 $qSBV-10b$ 、 $qCSV-3b$ 、 $qCSV-10b$ (贡献率分别为, 26.9%、29.5%、29.7%、25.2%、28.3%)被3次检测到, 稳定性较高。16个QTL具有一因多效性, 单个QTL位点控制的性状一般在2~6个之间, 第10染色体RM25032~RM1375区段控制峰值黏度、热浆黏度、冷胶黏度、消减值、峰值时间和回复值等6个性状。

关键词: 水稻 RVA谱特征值 数量性状 QTL稳定性 QTL多效性

Abstract: Two rice varieties with similar apparent amylose content, Nipponbare (*japonica*) and 93-11 (*indica*), were used as parents to establish a recombinant inbred lines population consisting of 190 lines by single seed descent method. The genetic linkage map was constructed with 202 SSR, CAPs and STS markers. Quantitative trait loci (QTLs) were identified for eight rice starch RVA profile properties including peak paste viscosity(PKV), hot paste viscosity(HPV), cool paste viscosity(CPV), breakdown viscosity(BDV), setback viscosity(SBV), consistency viscosity(CSV), peatime (PeT), pasting temperature (PaT) by composite interval mapping method in three different ecological sites (Lingshui, Hefei, and Huaiyuan). A total of 57 QTLs were identified, with 1 to 14 for each trait, indicating that rice starch RVA profile properties were controlled by multiple genes. Thirteen stable QTLs were detected at two or three sites, among which $qCPV-3$, $qCPV-10b$, $qSBV-10b$, $qCSV-3b$, and $qCSV-10b$ (explaining, 26.9%, 29.5%, 29.7%, 25.2%, and 28.3% of variance) were detected in all the three sites. Sixteen QTLs were found to have pleiotropy with a single QTL controlling two to six traits (RVA profile properties), the interval RM25032 - RM1375 on chromosome 10 controlling six traits (PKV, HPV, CPV, SBV, PaT and CSV).

Keywords: Rice RVA profile properties Quantitative trait locus QTL stability QTL pleiotropy

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