研究论文

基于单粒观察值的胚乳性状QTL图的构建方法

王伟, 胡治球, 孙长森, 徐辰武

扬州大学江苏省作物遗传生理重点实验室，江苏扬州225009

摘要　　谷物胚乳性状是决定谷物品质的一类重要性状。由于胚乳是由雌性的两个极核和雄性的一个精核受精发育而形成的三倍体组织，因此胚乳性状的遗传基础要比通常的二倍体农艺性状复杂得多。本文根据三倍体胚乳性状的数量遗传模型，提出利用分布于染色体上的所有分子标记对胚乳性状数量基因座位（QTL）进行区间作图的极大似然估计方法。该方法以分离群体中各植株的分子标记基因型以及植株上若干粒种子胚乳性状的单粒观测值为数据模式进行QTL分析。由于该方法充分利用标记基因型内QTL基因型的混合分布特性，因此，它不仅可以精确定位控制胚乳性状的多个QTL，同时还可估计各QTL的两个显性效应。通过计算机模拟数据分析进一步验证了方法的可行性和有效性。

关键词　　胚乳性状　三倍体　区间作图　极大似然估计　EM算法

分类号　Q348

Single Grain Observation-Based Mapping of Quantitative Traits Loci Underlying Endosperm Traits

WANG Wei, HU Zhi-Qiu, SUN Chang-Sen, XU Chen-Wu

Jiangsu Provincial Key Laboratory of Crop Genetics and Physiology, Yangzhou University, Yangzhou 225009, Jiangsu, China

Abstract Endosperm traits are the kind of important traits determining the grain quality in cereals. The endosperm, which is derived from two polar nuclei fusing with one sperm, is a triploid tissue whose genetic constitution is more complex than common diploid tissue. However, current statistical methods for mapping quantitative trait loci (QTL) under diploid genetic control have not been effective for dealing with endosperm traits. Based on the quantitative genetic models for triploid endosperm traits, a new maximum likelihood method implemented via EM algorithm to map QTL underlying endosperm traits was proposed in this paper. The method was established using the DNA molecular marker genotypes of each plant in segregation populations and the single endosperm observation of a few endosperms of each plant. Because of using the mixture distribution property of QTL genotypes within flanking marker genotypes, the method could not only precisely map QTL of endosperm traits, but also estimate two dominance effects of endosperm traits. Efficiency and feasibility of the methods have been verified through Monte Carlo simulation studies. The means and standard deviations of the estimated QTL effects and locations as well as the empirical powers under different QTL heritabilities and sampling strategies were listed in Table 2. These simulation results show that the proposed method provide accurate estimates of both the QTL effects and locations with high statistical efficiency. The next step of endosperm mapping is to consider both the maternal diploid genotype and the triploid endosperm genotypes jointly.

Key words Endosperm traits　Triploid　Interval mapping　Maximum likelihood estimation　EM algorithm

DOI:

通讯作者　徐辰武

扩展功能

本文信息
- Supporting info
- PDF(389KB)
- [HTML全文](0KB)
- 参考文献

服务与反馈
- 把本文推荐给朋友
- 加入我的书架
- 加入引用管理器
- 复制索引
- Email Alert
- 文章反馈
- 浏览反馈信息

相关信息
- 本刊中 包含"胚乳性状"的 相关文章
- 本文作者相关文章
  - 王伟
  - 胡治球
  - 孙长森
  - 徐辰武