

研究报告

基于分离亚群体QTL定位的模拟研究

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摘要

在数量性状QTL的精细定位中, 通过数量性状目标QTL的近等基因系可构建分离群体。在目标QTL效应较大的情况下, 数量性状表型值可反映目标QTL的基因型。若目标QTL附近的标记密度大时, 大样本才能定位该QTL。但是, 这增加了试验费用。为节约试验经费, 若只利用QTL纯合隐性基因型植株的分子标记信息, 也可比较准确地定位该QTL。利用极大似然法, 分别推导出F₂、BC、DH以及RIL群体中重组率及其标准误的估计公式。Monte Carlo模拟研究表明, 基于定位群体中全部数据或隐性纯合基因型数据所获得的重组率估计值是一致的, 且在相同样本容量条件下, 二者精度相当。

关键词 [连锁](#) [标记](#) [极大似然方法](#) [重组率](#)

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A Simulated Study on Mapping QTL in a Segregating Sub-population

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Abstract

For mapping QTLs, phenotypes of the traits in segregating population derived from the cross between two isogenic lines of the targeted QTL may reflect its genotype if the effect of the QTL is relatively large. In order to map the QTL, it is necessary to use a large sample under the high density of markers around the QTL. However, it increases experimental costs. In order to save the costs, it is possible to map the QTL using the sub-population that consists of plants with homogenous recessive. In this paper, the sub-population was used to estimate the recombination fraction between the marker and the QTL, and its standard error for F₂, backcross (BC), double haploid (DH) and recombinant inbred lines (RIL) populations, respectively. The results from Monte Carlo simulation showed that the estimation of recombination fraction based on the sub-population is consistent with that obtained from the full population, and the precision of the former is same as that of the later under the same sample size.

Key words [linkage](#) [marker](#) [maximum likelihood method](#) [recombination fraction](#)

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