

技术与方法

多基因离散性状QTL连锁分析方法

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摘要

动物中有许多重要的离散性状, 与常规的数量性状类似, 其遗传基础受多基因控制且对环境基因子效影响。由于多基因离散性状的复杂性, 利用常规的QTL连锁分析方法易造成假阳性结果, 相应地发展了多基因多元线性模型分析的方法。本文就目前离散性状的QTL连锁分析方法作简要综述, 并对可预期改进方法进行了展望。

关键词

离散性状, QTL, 连锁分析, 多元线性模型

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Methodology of QTL's Linkage Analysis for Discrete Traits Controlled by Polygenes

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Abstract
Discrete characters of biological interest and economical importance that are not inherited in a simple Mendelian fashion vary in a discrete form. These traits are called complex discrete traits. A complex discrete trait is presumably controlled by several genes, and characteristic of the trait is modified by environmental effects. Although methods of mapping QTL for continuous quantitative characters have been well developed, such methods for discrete characters are not available yet. So many non-linear methods were developed under the framework of the generalized linear model. In this paper, we reviewed the recent progress and improvement of the methods for QTL mapping in this field. ©2004-2009

Key words
discrete traits, QTL, linkage analysis, generalized linear models.

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