植物数量性状遗传体系检测中回交或自交家系重复试验数据的分析方法
Detection of Genetic System of Quantitative Traits Using Backcross and Selfing Families

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摘要   为提高主基因+多基因混合遗传分析的精度,降低试验误差,采用重复内分组随机区组设计,对低遗传力性状的B1:2和B2:2或F2:3家系平均数资料进行遗传分析.通过AIC准则和适合性检验比较无主基因(A-0)、1对主基因(A)、2对主基因(B)、多基因(C)、1对主基因+多基因(D)和2对主基因+多基因(E)模型以鉴定其遗传模式.采用IECM算法估计混合模型参数.通过油菜HSTC14×宁油7号初花期F2:3家系平均数资料阐明该方法。

abstract:To improve the precision in the genetic analysis of quantitative traits,the B1:2 and 132:2,or F2:3 families in a randomized blocks design were used to identify the mixed major gene plus polygene inheritance model while error variance was estimated from the analysis of variance.Five kinds of genetic models were established,including:one-major-gene model,two-major-gene model,polygene model,mixed one-major-gene plus polygene model,and mixed two-major-gene plus polygene model.The AIC value and a set of tests of goodness-of-fit were used to identify the most fitted model among the possible ones.The iterated ECM (IECM) algorithm was used to obtain maximum likelihood estimates of the parameters in sample likelihood function.An example of the genetic analysis of days from planting to flowering of a rape cross was used to illuminate the above procedure.

Abstract

Key words

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