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研究论文

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基于转录组数据高通量发掘黄粉甲微卫星引物(英文)

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黄粉甲; 转录组; 微卫星; 遗传标记; 引物

High-throughput discovery of SSR genetic markers in the yellow mealworm beetle, Tenebrio molitor (Coleoptera: Tenebrionidae), from its transcriptome database (In English)

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- 摘要
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全文: PDF (569 KB) HTML (1 KB) 输出: BibTeX | EndNote (RIS) 背景资料

摘要 黄粉虫Tenebrio molitor作为理想的模式研究生物, 虽然已围绕该昆虫在多个研究领域开展了诸多研究, 但是有关其分子和 遗传方面的研究仍知之甚少。为此, 本研究基于前期构建的黄粉甲转录组数据库, 成功发掘获得1 249个微卫星序列。其中, 单 碱基或三碱基序重复列最多, 分别占44.44%和41.15%; A/T型重复序列出现频率最高, 占42.70%。除单核苷酸重复序列外, 重复单元的重复次数以5次最多, 占30.90%。基于鉴定获得的微卫星序列, 共设计获得1 004对微卫星引物, 而且每对引物还设 计了5对替代引物。研究获得的微卫星引物将有助于今后开展黄粉甲功能和比较基因组学方面的研究。

关键词:

Abstract: Tenebrio molitor is a well known model insect. Although a lot of achievements have been made in many research aspects related to this insect, only very few molecular/genetic resources are available. In this study, a high-throughput method was used for discovering the simple sequence repeat (SSR) genetic markers from this beetle. In total, 1 249 SSR genetic markers were developed from the previously constructed trancriptome database. The majority of them contained mono-and trinucleotide motifs (44.44% and 41.15%, respectively), and A/T (42.70%) was the most abundant motif. Except for mononucleotide, the SSRs with five repeat units were the most common, with the frequency of 30.90%. Base on the identified SSRs, 1 004 pairs of primers were designed, of which a maximum of 5 pairs of alternative primers were designed from a single SSR. The SSRs identified here will constitute an important resource for marker-assisted investigation in functional and comparative genomics of T. molitor.

Key words: Tenebrio molitor transcriptome microsatellite genetic marker primer

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