

## 西花蓟马EST-SSR信息分析、标记筛选及其与Genomic-SSR的多态性比较

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Characterization and molecular marker screening of EST-SSRs and their polymorphism compared with Genomic-SSRs in *Frankliniella occidentalis* (Thysanoptera: Thripidae)

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**摘要** 西花蓟马 *Frankliniella occidentalis* 是一种世界性入侵昆虫, 近年来传入我国并不断扩散蔓延。基于简单重复序列 (simple sequence repeats, SSRs) 的西花蓟马种群遗传结构研究对于揭示其传播途径等具有重要的指导价值。本研究对来源于西花蓟马的13 839条EST序列进行了uni-EST组装、EST-SSR信息分析以及标记筛选, 并比较了EST-SSR与Genomic-SSR在分析遗传多样性方面的差异。结果表明: 在7 707个singlets中共找到2 623个SSR位点, 分布于1 930个uni-EST中, 平均每2.21 kb就出现一个SSR位点。重复单元中, 以单碱基重复单元为主(83.00%), 其次是四碱基重复单元(11.17%), 而二、三、五和六碱基重复单元所占比例较低(分别为1.41%, 0.80%, 2.02%和0.91%)。设计出的22对EST-SSR引物中, 4对引物能稳定扩增出清晰的目的条带; 荧光标记毛细管电泳发现3对引物表现出多态性。西花蓟马EST-SSR与Genomic-SSR多态性分析表明, 这3对多态性EST-SSR引物揭示的多态信息含量(PIC)为0.48~0.69, 比5对多态性Genomic-SSR引物揭示的PIC(0.88~0.92)略低。本研究结果可为今后更深入开展西花蓟马的种群遗传结构分析提供帮助。

**关键词:** 西花蓟马 分子标记 EST-SSR Genomic-SSR 荧光标记毛细管电泳 多态性

**Abstract:** The western flower thrips (WFT), *Frankliniella occidentalis* Pergande (Thysanoptera: Thripidae), is an important agricultural pest worldwide. In recent years, it has spread into many provinces since its first detection in China. The research of the population genetic structure based on microsatellite marker (simple sequence repeats, SSRs) will contribute to revealing its invasion pathway. In this study, we analyzed the characteristics of SSRs from expressed sequence tags (ESTs) in *F. occidentalis*, screened PCR primers for EST-SSRs and tested the diversity of EST-SSR primers with the capillary electrophoresis. The results showed that 2 623 EST-SSRs were distributed in 1 930 uni-EST sequences, with an average of 1 SSR in every 2.21 kb of uni-EST sequence. Among mono- to hexa-nucleotide repeat types, mononucleotide repeats are the dominant type (83.00%), and tetranucleotide repeats are the second dominant type (11.17%). Furthermore, 4 of 22 pairs EST-SSR primers designed produced discernable PCR products. The capillary electrophoresis revealed that 3 of 4 pairs of EST-SSR primers are polymorphic. The average polymorphism information content (PIC) with the 3 polymorphic EST-SSR primers (0.48-0.69) is lower than that with 5 polymorphic Genomic-SSR primers (0.88-0.92). This study may contribute to further research on the analysis of genetic structure of *F. occidentalis* populations in future.

**Key words:** *Frankliniella occidentalis* molecular marker EST-SSR Genomic-SSR capillary electrophoresis polymorphism

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