

植物保护—研究报告

中国甘薯小象甲的rDNA ITS-1遗传变异及入侵来源研究

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摘要:

甘薯小象甲是国内外重要检疫性害虫, 明确中国不同地区甘薯小象甲的遗传多样性可为甘薯小象甲的鉴别检疫提供依据。本文通过对中国6个地区甘薯小象甲种群rDNA ITS-1序列的遗传变异分析探讨了中国6个地区种群的入侵来源。结合世界其他地区已公布35个甘薯小象甲种群序列, 经系统发育分析表明, 甘薯小象甲起源于印度次大陆, 在亚洲地区随甘薯的调运而自东南向西北扩展, 构建的系统发育树分为印度地区分支和亚洲东部分支两个大的分支, 而亚洲东部分支又进一步划分为东南部和东北部两个亚支, 中国的甘薯小象甲种群分别位于东北部分支的两个亚分支上, 说明中国6个地区甘薯小象甲种群至少通过两个不同地区侵入中国, 并在中国定居。

关键词: 侵入来源

The Study on rDNA ITS-1 Variation of *Cylas formicarius* (Coleoptera: Brentidae) Populations and its Invasive Sources in China

Abstract:

Sweet potato weevils (*Cylas formicarius*) are important quarantine pest both in the world. Understanding the genetic diversity of sweet potato weevils in different areas of China can provide the basis for its identification and quarantine. Genetic variations of the ITS-1 region were examined to probe the invasive sources for 6 populations from different areas in Southern China. Phylogenetic analysis on those sequences together with 35 known *C. formicarius* sequences showed that sweet potato weevil originated in India, then spread all over Asia from southeast to northwest along with the transportation of sweet potatoes. The phylogenetic tree consisted of two main clades (India and East Asia). The East Asia clade was further divided into two subclades (Northeast and Southeast). Chinese populations were all in two subclades of the Northeast subclade. It suggested that the 6 populations in China might come from the two origins and settled in China.

Keywords: invasive sources

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