

基于ITS和*matK*序列探讨新疆野苹果与中国苹果的系统演化关系

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Phylogenetic Relationship Between Xinjiang Wild Apple (*Malus sieversii* Roem.) and Chinese Apple (*Malus* × *domestica* subsp. *chinensis*) Based on ITS and *matK* Sequences

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摘要 以新疆地区不同居群的52份新疆野苹果[*Malus sieversii* (Ledeb.) Roem.]、9份中国苹果品种 (*Malus* × *domestica* subsp. *chinensis* Li.)、1份森林苹果 (*M. sylvestris* Miller) 种质为试材, 进行核糖体DNA内转录间隔区 (ribosomal DNA internal transcribed spacers, ITS) 和叶绿体成熟酶K (*matK*) 基因的测序分析。从GenBank中获取了11个苹果栽培品种、14个塞威士苹果、26个苹果属其它种及1个外类群欧洲梨 (*Pyrus communis*) 的ITS及*matK*序列。利用MEGA (ver. 4.0) 计算不同序列间的碱基组成频率、简约信息位点数、转换/颠换比率、序列间成对距离, 以最大简约法与邻接法进行系统发育分析。结果表明, 采集的“新疆野苹果”与“中国苹果”的ITS序列长度在589 ~ 594 bp, 含有148个简约信息位点, 转换/颠换比率 (R) 为1.029; *MatK*序列长度为1 451 ~ 1 461 bp, 没有复制子II序列, 含有16个简约信息位点, 转换/颠换为1.442。ITS分析将中国苹果、新疆野苹果 (来自中国新疆) 和塞威士苹果 (来自GenBank) 聚类于一个大的发育枝内, 新疆野苹果5个居群的系统演化按新疆、巩留、霍城和塔城的先后次序发生。*MatK*序列的系统发育分析将中国苹果和新疆野苹果聚类在一个大的发育枝内, 但自展支持率低。由此说明, 中国苹果由新疆野苹果驯化而来。*matK*不适于栽培苹果种内的系统发育分析。

关键词: 苹果 新疆野生苹果 中国苹果 ITS *matK* 系统发育分析

Abstract: Revealing the phylogenetic relationship between Xinjiang wild apple (*Malus sieversii* Roem.) and Chinese apple (*Malus* × *domestica* subsp. *chinensis* Li.) at molecular level would help identify the origin and taxonomy of Chinese apple, and provide theoretical basis for preserving and utilizing wild apple resources. The sequence of ribosomal DNA internal transcribed spacers (ITS) and the coding region of the *matK* gene were sequenced from 52 accessions of Xinjiang wild apple, nine cultivars of Chinese apple, and one accession of *M. sylvestris*. Sequences of ITS and *matK* of 11 cultivars of *Malus* × *domestica*, 14 accessions of *Malus sieversii*, 26 of other *Malus* spp., and one of *Pyrus communis* were retrieved from GenBank. The MEGA software (ver. 4.0) was used to analyze the divergences, variable sites, parsim-informative sites, the ratio of transition to transversion (R) and pairwise distances. The phylogenetic analysis was conducted by Maximum parsimony (MP) and Neighbor-joining (NJ) methods. The results showed that the size of ITS sequences of Xinjiang wild apple and Chinese apple ranged from 589 bp to 594 bp containing 148 parsim-informative sites with R of 1.029, whereas their *matK* sequences varied from 1 451 bp to 1 461 bp encompassing 16 parsim-informative sites with R of 1.442. Duplication II was not found in the Xinjiang wild apple and Chinese apple accessions. Phylogenetic trees of ITS showed that Chinese apple, the Xinjiang wild apple (from Xinjiang, China), and *M. sieversii* (from GenBank) fallen into a large clade. The systematic evolution of Xinjiang wild apple appeared to occur in a geographical order of Xinyuan, Gongliu, Huocheng, and Tacheng. The *matK* cladograms grouped Chinese apple and the Xinjiang wild apple into one large clade with weak bootstrap support. These results indicated that Chinese apple was domesticated from Xinjiang wild apple and the *matK* gene was not applicable for phylogenetic analysis in intra-species of *Malus* × *domestica*. The sequence of ribosomal DNA internal transcribed spacers (ITS) and the coding region of the *matK* gene were sequenced from 52 accessions of Xinjiang wild apple, nine cultivars of Chinese apple, and one accession of *M. sylvestris*. Sequences of ITS and *matK* of 11 cultivars of *Malus* × *domestica*, 14 accessions of *Malus sieversii*, 26 of other *Malus* spp., and one of *Pyrus communis* were retrieved from GenBank. The MEGA software (ver. 4.0) was used to analyze the divergences, variable sites, parsim-informative sites, the ratio of transition to transversion (R) and pairwise distances. The phylogenetic analysis was conducted by Maximum parsimony (MP) and Neighbor-joining (NJ) methods. The results showed that the size of ITS sequences of Xinjiang wild apple and Chinese apple ranged from 589 bp to 594 bp containing 148 parsim-informative sites with R of 1.029, whereas their *matK* sequences varied from 1 451 bp to 1 461 bp encompassing 16 parsim-informative sites with R of 1.442. Duplication II was not found in the Xinjiang wild apple and Chinese apple accessions. Phylogenetic trees of

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Keywords: *Malus × domestica* Borkh., *Malus sieversii* (Ledeb.) Roem., *Malus × domestica* subsp. *chinensis* Li Y. N., ITS, *matK*, phylogenetic analysis

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