研究论文

韭不同倍性及其非整倍体的LTS序列变异研究

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对不同倍性及其非整倍体非Allium tuberosum和野非Allium ramosum核糖体DNA的内部转录区(ITS)进行了 PCR扩增和克隆,并测定10个ITS1和ITS2的序列,用ITS1+ITS2的序列探讨Allium tuberosum和Allium ramosum的 系统发育关系。研究表明,Allium tuberosum与Allium ramosum种间的平均Kimura遗传距离仅为0 0146,二者是<mark>▶加入我的书架</mark> 一对近缘种。虽然韭经历了长期的人工选择和自然选择,但与野韭的分化仍然较小。韭不同倍性及其非整倍体之 间,其ITS序列亦无明显差异。

韭 野韭 ITS序列 多倍体 非整倍体 关键词

分类号

Studies on Variation of ITS Sequences with Different Ploidy and Its **Aneuploid in Allium tuberosum**

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Abstract

The ITS regions of 2 closely related species Allium tuberosum Rotuer. ex Spreng. and Allium ramosum L. in Allium Sect. Rhiziridium G. Don were amplified, cloned and sequenced. The genetic re-lationships among 10 materials of diploid, triploid, tetraploid and aneuploid in Allium tuberosum and All-lium ranwsum were reconstructed based on ITS1 + ITS2 sequences. The results demonstrated that the aver-age Kimura pairwise distance between Allium tuberosum and Allium ramosum was 0.0146. They are a pair of closely related species. Although it was gone through evolution by artificial selection and natural selec-tion, Allium tuberosum kept little differentiation from Allium ramosum. Sequences of ITS region show that there are no evident differentiation among the various diploid, triploid, tetraploid and aneuploid of Allium tuberosum.

Key words Allium tuberosum Allium ramosum ITS sequence Polyploidy Aneuploid

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