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ABSTRACT OF ETB WORKSHOP

濒危植物望天树的遗传多样性和居群遗传结构

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摘要

龙脑香科（Dipterocarpaceae）濒危植物望天树（*Parashorea chinensis*）目前仅局限分布于热带亚洲北部边缘, 目前已受到特别的保护, 但有关其遗传特性的研究很少。在本研究中, 使用随机扩增多态性 DNA（RAPD）技术对望天树 7 个天然居群进行了遗传多样性和群体遗传结构的研究。望天树 7 个天然居群（194 个个体）用 20 个随机引物进行了扩增, 48.22%的 RAPD 位点为多态位点, 平均每个居群的多态位点百分比为 20.84%。居群内的平均基因多样度为 0.7870（用 Shannon 表型多样性指数来测量）, 整个物种的基因多样度为 1.4100, 居群内的基因多样度为 55.82%, 居群间的基因多样度为 44.18%。G_{ST}平均值为 0.4448。AMOVA 分析表明 37.67%的遗传变异存在于地区间, 11.40% 存在于地区内的居群间, 而 50.93% 则存在于居群内。结果揭示了望天树低水平的遗传多样性和很强的地区居群分化, 这可能是由于望天树在其进化历史上, 居群不断的减小及再扩张所引起的居群瓶颈所造成的。相关分析没有检测到居群大小和遗传多样性大小的正相关, 而居群间的遗传距离和地理空间距离检测到了显著的正相关。所得结果对该物种保护策略的制定有指导作用。

关键词

保护遗传学, 龙脑香科, 居群遗传学, RAPD, 望天树

Genetic Diversity and Population Genetic Structure of Endangered *Parashorea chinensis*

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ABSTRACT

Parashorea chinensis is an endangered dipterocarp, narrowlly ranged on the north edge of Tropical Asia, and now subjects to special protect in natural reserve and *ex situ* conservation programme, while almost nothing is known about its genetic feature. Random amplified polymorphic DNA（RAPD）markers were used to investigate the genetic diversity and population genetic structure of seven natural populations of P. *chinensis*. 194 individuals in seven natural populations of P. *chinensis* were amplified with 20 random primers. 48.22% of RAPD loci were polymorphic across the whole species, while only 20.84% on average on population levels. Mean population gene diversity within populations (measured by Shannon's index of phenotypic diversity) was 0.7870, and total was 1.4100 for the whole species. 55.82% of the total gene diversity was distributed within populations, and 44.18% was among populations. Mean G_{ST} value arcoss loci was 0.4448. AMOVA analysis revealed 37.67% of the total genetic variation was attributed among regions, 11.40% among populations within regions, and 50.93% within populations. These results suggested low levels of genetic diversity in this species and strong regional population differentiation, which might be the results of population bottleneck resulting from the repeated extinction and recolonization in its evolutionary history. Correlation analysis did not detect positive correlation between population size and the amount of genetic diversity, while significant positive correlation between genetic distance between populations and geographical spatial distance was demonstrated. The implications of these results to conservation strategies of this endangered species were also discussed.

KEYWORDS

Conservation genetics, *Dipterocarpaceae*, Population genetics, RAPD, *Parashorea chinensis*