

鹅掌楸属种质资源遗传多态性及其形成机制研究*

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摘要:【目的】揭示鹅掌楸属种质资源遗传多态性及其形成机制, 为物种保护、遗传改良及生态恢复提供科学依据。【方法】根据 LcDHN-like、LcDHN-like1、LcDHN-like2、LtNCED1、LtNCED3、Ltosmotin-like 6 个适应性相关基因在鹅掌楸属各自然群体中的序列变异信息, 探讨鹅掌楸属各个群体遗传多态性及其形成机制, 分析鹅掌楸属群体的群体结构和遗传分化及其影响因素。【结果】群体遗传结构分析结果显示, 两个种之间存在显著的分化, 鹅掌楸种内普遍存在遗传混合, 但仍可将其区分为东部和西部群体; 而北美鹅掌楸种内的群体遗传结构则不明显。6 个基因在鹅掌楸与北美鹅掌楸两个群体之间的平均遗传距离分别为 0.0481 ± 0.0050 、 0.0386 ± 0.0037 、 0.0251 ± 0.0040 、 0.0146 ± 0.0024 、 0.0264 ± 0.0033 、 0.0196 ± 0.0046 ; Nst 分别为 0.547、0.887、0.873、0.818、0.772、0.746; Gst 分别为 0.011、0.019、0.080、0.023、0.019、0.086; Fst 分别为 0.543、0.885、0.871、0.817、0.770、0.744。鹅掌楸与北美鹅掌楸中 6 个基因的遗传多态性的分布几乎是均质的, 结合祖先地理分布重建推测过去两个种存在多个避难所, 大多数鹅掌楸表现为在分布区内原地或就近居留在多个避难所, 北美鹅掌楸则在采样点分布区原地或就近居留在多个避难所。鹅掌楸可能的避难所在东部主要位于大别山、天目山脉、武夷山脉、仙霞岭山脉及其周边, 西部主要位于大巴山、大娄山、武陵山脉、雷公山脉、云贵高原东侧一带。【结论】结合祖先地理分布重建推测, 长期的地理隔离和环境隔离导致鹅掌楸与北美鹅掌楸存在显著的遗传分化, 大多数鹅掌楸表现为在分布区内原地或就近居留在多个避难所, 长期的隔离导致东部和西部群体的分离, 种内各群体间基因交流出现限制。北美鹅掌楸则在采样点分布区原地或就近居留在多个避难所, 之后北美鹅掌楸没有东西走向山脉的阻隔, 群体之间基因仍可交流。孤立的鹅掌楸小群体和连续分布基因交流频繁的北美鹅掌楸群体的种质资源遗传多态性的分布几乎是均质的。就鹅掌楸而言, 其种质资源在不同地理区域内表现出显著的遗传多样性和分化, 保护策略应注重保护不同区域的种群及其周边环境, 北美鹅掌楸应注意保护其基因交流通道。

关键词: 鹅掌楸属; 适应性基因; 群落遗传结构; 遗传分化; 冰期避难所

Study on Genetic Polymorphism and Formation Mechanism of Germplasm Resources in Liriodendron Species

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Abstract:【Objective】To reveal the genetic polymorphism and formation mechanisms of germplasm resources in Liriodendron species, providing scientific basis for species conservation, genetic improvement, and ecological restoration. 【Method】Based on the sequence variation information of six adaptation-related genes (LcDHN-like,

LcDHN-like1, LcDHN-like2, LtNCED1, LtNCED3, Ltosmotin-like) in various natural populations of *Liriodendron* species, this study explores the genetic polymorphism and formation mechanisms of different populations, and analyzes the population structure, genetic differentiation, and influencing factors of *Liriodendron* populations.

【Result】 The analysis of population genetic structure shows significant differentiation between the two species. Despite the widespread genetic admixture within *L. chinense*, it can still be distinguished into eastern and western populations, whereas the population genetic structure within *L. tulipifera* is not obvious. The average genetic distances of six genes between the populations of *L. chinense* and *L. tulipifera* are 0.0481 ± 0.0050 , 0.0386 ± 0.0037 , 0.0251 ± 0.0040 , 0.0146 ± 0.0024 , 0.0264 ± 0.0033 , and 0.0196 ± 0.0046 , respectively. The *Nst* values are 0.547, 0.887, 0.873, 0.818, 0.772, and 0.746, respectively. The *Gst* values are 0.011, 0.019, 0.080, 0.023, 0.019, and 0.086, respectively. The *Fst* values are 0.543, 0.885, 0.871, 0.817, 0.770, and 0.744, respectively. The distribution of genetic polymorphism for the six genes in *L. chinense* and *L. tulipifera* is almost homogeneous. Based on the reconstruction of ancestral geographic distribution, it is inferred that there were multiple refugia for both species in the past. Most *L. chinense* populations remained in situ or nearby refugia within their distribution range, while *L. tulipifera* populations also remained in situ or nearby refugia within their sampling distribution range. The possible refugia for *L. chinense* in the east are mainly located in the Dabie Mountains, Tianmu Mountains, Wuyi Mountains, Xianxialing Mountains, and surrounding areas, while in the west, they are mainly located in the Daba Mountains, Dalou Mountains, Wuling Mountains, Leigong Mountains, and the eastern side of the Yunnan-Guizhou Plateau.

【Conclusion】 Based on the reconstruction of ancestral geographic distribution, long-term geographic and environmental isolation has led to significant genetic differentiation between *L. chinense* and *L. tulipifera*. Most *L. chinense* species tend to stay in situ or nearby refugia within their distribution range. Prolonged isolation has resulted in the separation of eastern and western populations, with restricted gene flow between intra-species populations. In contrast, *L. tulipifera* populations remain in situ or nearby refugia at sampling points, and without east-west mountain barriers, gene flow between populations is still possible. The genetic polymorphism distribution of isolated small *L. chinense* populations and continuously distributed *L. tulipifera* populations with frequent gene flow is almost homogeneous. For *L. chinense*, its germplasm resources exhibit significant genetic diversity and differentiation across different geographic regions. Conservation strategies should focus on protecting populations in different regions and their surrounding environments, while *L. tulipifera* should pay attention to preserving its gene flow corridors..