

基于SSR标记的四川野生中国樱桃遗传多样性和居群遗传结构分析

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Assessment of Genetic Diversity and Populations Genetic Structure in Wild Chinese Cherry from Sichuan Province Using SSR Markers

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摘要 采用SSR分子标记技术对四川野生中国樱桃5个居群共133株的遗传多样性水平及居群的遗传结构进行了研究。结果显示: 10对SSR引物共检测到78个等位基因, 平均每位点等位基因7.8个。Nei's基因多样性指数(H)为0.6112~0.6689, Shannon's信息指数(I)为1.1984~1.3786。基于分子方

差分析(AMOVA), 92.53%的变异来自居群内, 7.47%的遗传变异来自于居群间。居群间遗传距离(GD < 0.2416)、遗传一致度(GI > 0.7854)、遗传分化指数(Fst = 0.0844)以及较强的基因流(Nm = 2.7125)均

表明居群间的遗传分化水平较低, 居群内存在显著近交现象(Fis = 0.3986), 且居群在大多数位点上偏离Hardy-Weinberg平衡。基于上述结果, 分析讨论了居群较高遗传多样性和居群间较低遗传分化形成的可能原因, 并提出野生中国樱桃的保护利用策略。

关键词: 野生中国樱桃 SSR 遗传多样性 遗传结构

Abstract: Genetic diversity and genetic structure of five wild Chinese cherry (*Prunus pseudocerasus* Lindl.) populations from Sichuan were investigated using ten SSR markers selected from 31 markers. A total of 78 alleles were successfully amplified, and the number of alleles per locus ranged from 5 to 10, with an average of 7.8. The relatively high levels gene diversity (H: 0.6112-0.6689) and Shannon's diversity (I: 1.1984-1.3786) revealed relatively rich genetic diversity in the five wild Chinese cherry populations. The AMOVA analysis revealed low genetic differentiation among populations, with only 7.47% of total variability partitioned among populations (P < 0.001). This consisted with genetic distance (GD < 0.2416), genetic identity (GI > 0.7854), genetic differentiation (Fst = 0.0844) and strong gene flow (Nm = 2.7125). Five populations showed inbreeding and deviated from Hardy-Weinberg Equilibrium at most loci. Based on these results, the possible formation of the high level genetic diversity and the low genetic differentiation were discussed, and further strategies and suggestions for utilization and conservation of these resources were also proposed.

Keywords: wild Chinese cherry, *Prunus pseudocerasus*, SSR, genetic diversity, genetic structure

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