

# 日本落叶松群体的叶绿体SSR分析 Analysis of Genetic Structure in Population of Larix Kaempferi by Chloroplast SSR Markers

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## 摘要

利用叶绿体微卫星 (cpSSR) 分子标记对日本国内的7个日本落叶松 (Larix kaempferi) 群体遗传结构进行了研究。11对cpSSR引物中筛选出的3对多态性引物, 共产生10个长度不同片段, 在197个样品中组合出现10个不同的单倍型 (haplotype)。各群体的单倍型差异较大。cpSSR基因座揭示了日本落叶松的遗传变异: 平均等位基因数 A=3.33, 平均有效等位基因数 NE=1.20, 基因多样性 HE=0.17, 群体间变异占总群体变异的5.37%, 遗传变异主要来自群体内个体间。Abstract: Genetic structure of seven populations in Larix kaempferi in Japan was studied by use of cpSSR markers. Ten different length fragments in and ten different kinds of haplotypes were reduced in 197 samples based on 3 pairs of polymorphic primers screened from 11 pairs of primers. There were significant variant haplotypes among the populations. The genetic variation in the populations of Larix kaempferi was detected by using cpSSR with the number of average loci A=3.33, the number of average efficient loci NE=1.20, gene diversity HE=0.17 and 5.37% variation from different populations. The genetic variation was mainly from individuals in population.

关键词 [叶绿体微卫星](#) [日本落叶松](#) [单倍型](#) [群体遗传结构](#) Key words [cpSSR](#) [Larix kaempferi](#) [haplotype](#) [population](#) [genetic structure](#)

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