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松属植物遗传多样性研究进展 Review on Genetic Diversity in Pinus

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摘要 研究松属遗传多样性的方法涉及表型、同工酶、染色体、DNA等多层面。 松树表型性状变异广泛，其不同树种不同性状的遗传力（或遗传率）均存在差异。到目前为止，同工酶仍是检测松树遗传多样性的最常用方法，一般而言，松属树种群体内等位酶多样性程度高，群体间分化较低，但各树种的情形也不尽相同。松属树种染色体水平的变异很低，其核型高度一致。核DNA组较一般阔叶树大，遗传多样性丰富，但叶绿体等质体DNA则多样性较低。影响遗传多样性的因素很多，其中自身的交配系统和外部的生长环境是影响它的两个主要因素。最后，回顾了松树的起源及其遗传多样性保护策略等方面的研究。

Abstract:The ways of probing genetic diversity of pines involve many aspects, such as morphology, chromosome, isozyme, DNA, etc. The phenotypic characteristics in pines vary widely and the differences of inheritability(h2) are obvious among characteristics and among species. Up to now, isozyme is still the most common means to measure genetic diversity of pines. Generally, there are high allozyme diversity within populations and low differentiation coefficient among populations, but differences exist between species in Pinus. The variations of chromosome among pines are very low and the karyotypes of pines are consentaneous, but the genomes of pines in cell nucleus are much larger than that of broadleaves. Diversity of pines are abundant at nucleus DNA level but are poor at plastid DNA level, such as ctDNA. There are many factors that will affect genetic diversity of pines, in which mating system and environment are two main factors. Finally, we reviewed the research on origin of Pinus and conservation strategy of genetic diversity, etc.

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