

栓皮栎天然群体SSR遗传多样性研究Genetic Diversity of Microsatellites (SSRs) of Natural Populations of Quercus variabilis

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摘要

利用微卫星(SSR)标记对我国4个省内的5个栓皮栎(Quercus variabilis Bl.)天然群体的遗传多样性进行了研究。16对SSR标记揭示了栓皮栎丰富的遗传多样性: 等位基因数(A)平均8.4375个, 有效等位基因数(Ne)平均为5.9512个, 平均期望杂合度(He)0.8059, Nei多样性指数(h)为0.8041。栓皮栎自然分布区中心地带的群体具有较高的遗传多样性, 而人为对森林的破坏将降低林木群体的遗传多样性。栓皮栎群体的变异主要来源于群体内, 群体间分化较小, 遗传分化系数仅为0.0455。此外, 栓皮栎群体间的遗传距离与地理距离之间存在显著的正相关。这些遗传信息为栓皮栎遗传多样性的保护和利用提供了一定依据。Abstract: Genetic diversity of five Quercus variabilis natural populations in four provinces of China was studied with microsatellite (SSR) markers. A relatively high level of genetic diversity was detected in Q. variabilis species with 16 polymorphic microsatellite loci. Average number of alleles (A) and effective number of alleles (Ne) were 8.4375 and 5.9512 respectively. The mean expected heterozygosity (He) was 0.8059 and Nei diversity index (h) was 0.8041. Higher diversity was found with the populations from the central range of the species in contrast to those from peripheral areas and human activities might decrease the genetic diversity of populations. The majority of genetic variation occurred within populations, which could be concluded from the low coefficient of genetic differentiation (Fst=0.0455). In addition, significant correlation was found between geographical distance and genetic distance. All these results present a basis to the conservation and utilization of genetic diversity of Quercus variabilis.

关键词 栓皮栎 微卫星(SSR) 遗传多样性 遗传分化 Key words Quercus variabilis microsatellite (SSR) genetic diversity genetic differentiation

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