

云南纵坑切梢小蠹四个地理种群同工酶比较研究 Comparative Studies of Isozymes in Four Geographical Populations of *Tomicus piniperda* L. for Yunnan Province

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摘要 采用不连续聚丙烯酰胺凝胶电泳技术研究了纵坑切梢小蠹(*Tomicus piniperda* L.) 4个自然种群的9个同工酶基因座。4个种群均在Es-1、Es-2、Es-4、Mdh-1、Mdh-2及AAT-1基因座上存在遗传多态现象。路南长湖、楚雄、蒙自3种群间的遗传距离为0.0036~0.0173, 平均值为0.0105, 表明其遗传结构基本相似。丽江种群与上述3种群之间的遗传距离为0.1421~0.2035, 平均值为0.1765, 表明丽江种群与上述三种群已有了遗传分化。丽江种群近交系数较大, 近亲繁殖程度较高。种群遗传结构的差异可能与不同虫害程度之间存在一定的内在联系。

Abstract: Using uncontinued polyacrylamide gel electrophoresis, comparative studies of isozymes between the four geographical populations of *Tomicus piniperda* L. in Yunnan province were carried out in this paper. Among 9 loci, loci Es-1, Es-2, Es-4, Mdh-1, Mdh-2 and AAT-1 exhibited the genetic polymorphs. The Nei's genetic distance (D) among Lunan's, Chuxiong's and Mengzi's populations was 0.0036 and 0.0173 with an average of 0.0105, indicating the similar genetic structure among them. The genetic distance between Lijiang population and other three populations was 0.1421~0.2035 with 0.1765 on average, which implied a certain degree of genetic differentiation between them. Investigation indicated the forest damages by the beetle were high in Lunan, Chuxiong and Mengzi, and was low in other population in Lijiang; whereas inbreeding coefficient was bigger and inbreeding degree was higher in Lijiang, but all low in other three districts. It is so proposed that the differentiation of population in genetic structure is related to the damage levels of *Tomicus piniperda* L.

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