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生物安全 · 生物多样性

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### 云南松口蘑的ISSR遗传多样性研究

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### The Genetic Diversity of *Tricholoma matsutake* by ISSR in Yunnan Province

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摘要

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**摘要** 本文利用16条ISSR引物,对来自云南香格里拉、大理、楚雄和昆明的4个松口蘑居群共42个个体的遗传多样性进行研究。结果表明,ISSR PCR共扩增出76条条带;总多态性位点百分率PPB=61.04%,多态位点百分率依次为56.76%, 67.75%, 70.27%和50.00%;总的基因多样性指数(Ht)为0.3215,居群内的Nei遗传多样性指数(Hs)为0.2447, Shannon多样性指数(I)为0.4717,居群间的遗传分化系数Gst为0.2471,基因流Nm为1.5234,这说明云南松口蘑具有较高的遗传多样性,且主要存在于居群之间,居群内的变异较小;遗传距离表明4个居群中香格里拉和昆明的亲缘关系最远,大理和楚雄的亲缘关系最近

**关键词:** 松口蘑 遗传多样性 分子标记 ISSR

**Abstract:** Genetic diversity of 42 individuals belonging to four populations of *Tricholoma matsutake* from Shangri-la, Dali, Chuxiong and Kunming in Yunnan Province was detected by using 16 ISSR primers. The results showed that 76 DNA bands were amplified by 16 primers above mentioned and the total percentage of polymorphic bands (PPB) was 61.04%. The PPBs of Shangri-la, Dali, Chuxiong and Kunming were 56.76%, 67.75%, 70.27% and 50.00%, respectively. The total genetic diversity (Ht) was 0.3215, the genetic diversity within population (Hs) was 0.2447, Shannon's diversity index (I) was 0.4717, the coefficient of gene variation was 0.2471 and the gene flow among populations was 1.5234. It was implied that a higher genetic diversity of *T. matsutake* mainly existed among populations, and a lower degree of genetic variation occurred within populations. The genetic relationship was the farthest between Shangri-la and Kunming, and it was the closest between Dali and Chuxiong in the genetic distance.

**Keywords:** *Tricholoma matsutake* genetic diversity molecular marker ISSR

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