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### 长针科线虫2种传毒种类和3种非传毒种类分子鉴定和亲缘分析

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Molecular characteristics and phylogenetic relationships between three non-virus-vector longidorids and two virus-vector ones

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摘要 裂尾剑线虫*Xiphinema diversicaudatum*和逸去长针线虫*Longidorus elongatus*是植物病毒的重要传毒线虫,具有重要的经济意义,被我国列入入境植物检疫性有害生物名单.通过对上述2种检疫性线虫和中国云南不同地区3种长针科线虫共7个种群rDNA的内转录间隔区(ITS)进行PCR扩增和测序,分别获得1 400~2 100 bp PCR产物片段,通过与Genbank上5种8种群的ITS区序列进行分析,结果发现裂尾剑线虫与包括逸去长针线虫等在内的其他4种线虫的同源性仅有55%,逸去长针线虫与3种长针科非传毒线虫的同源性仅为56%.同种不同种群间的rDNA-ITS的基因变异分别从0~10%不等.

关键词: [长针科线虫](#) [分子鉴定](#) [亲缘分析](#)

Abstract: *Xiphinema diversicaudatum* and *Longidorus elongatus* are economically important plant-parasitic nematodes as virus vectors. Both of them are on the lists of quarantine pests related to the import plants in China. Molecular methods and genetic analyses based on the DNA sequences of nuclear ribosomal DNA ITS were conducted to determine the longidorids species and phylogenetic relationships within 6 taxa 15 populations, including *X. diversicaudatum*, *X. brevicollum*, *X. insigne*, *L. elongatus*, *L. intermedius* as well as *Paralongidorus maximus*. Seven DNA sequences varied from 1400bp to 2100bp for 7 targeted samples collected from Netherlands and Yunnan, China, respectively, both homology tree and phylogenetic tree were set up using MEGA4.0 software. Among them, *X. diversicaudatum* has 55% similarity with the other 4 studied Longidorids nematodes. Similarly, there is 56% genetic divergence between *L. elongatus* and 3 other studied Longidorids. The genetic variation of the studied nematodes had ranged from 10% among *X. diversicaudatum* to zero among *L. elongatus*.

Key words:

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