

论文

侵染云南烟草的粉虱传双生病毒的分子鉴定及其卫星DNA β 的遗传多样性分析

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摘要 为了研究侵染云南烟草的粉虱传双生病毒的种类及其伴随的致病性卫星分子DNA β 的遗传多样性, 从云南各地区表现为曲叶、曲叶耳突的烟草上获得病毒分离物Baoshan1, Baoshan2, Baoshan3, Baoshan4, Dali, Lijiang, Yuanmou1和Yuanmou2。通过双生病毒DNA-A基因间隔区和部分外壳蛋白基因的引物及其卫星分子DNA β 设计的引物分别进行PCR扩增。序列分析发现Baoshan、Yuanmou1和Yuanmou2为烟草曲茎病毒, Baoshan1、Baoshan2及Baoshan4为番茄黄化曲叶病毒, Dali和Lijiang为中国番茄黄化曲叶病毒, 且不同地点的分离物种类差异较大。分离物伴随的DNA β 也存在差异, 序列相似性在51.3%到99.7%之间。其中Baoshan1的DNA β 与烟草曲茎病毒Y98的DNA β 相似性最高(98.7%), Baoshan4的DNA β 与云南赛葵黄脉病毒的DNA β 相似性最高(98.7%), 其余分离物Baoshan2, Baoshan3, Dali, Lijiang, Yuanmou1和Yuanmou2的DNA β 与中国番茄黄化曲叶病毒各分离物DNA β 的相似性最高, 分别为94.4%, 91.8%, 99.2%, 99.3%, 98.7%和98.9%。系统进化树分析DNA β 与云南其它分离物的DNA β 关系较近, 而与其它省份、亚洲以及亚洲以外国家的病毒分离物的DNA β 关系较远, 表现明显的地理分布差异。

关键词 [粉虱传双生病毒; 烟草; 遗传多样性](#)

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Molecular Identification and DNA β Genetic Diversity Analysis of Whitefly Transmitted Geminiviruses Infecting Tobacco in Yunnan

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Abstract

To investigate the species and satellite DNA genetic diversity of whitefly transmitted geminiviruses (WTGs) infecting tobacco, virus isolates of Baoshan1, Baoshan2, Baoshan3, Baoshan4, Dali, Lijiang, Yuanmou1 and Yuanmou2 that obtained from leaves showing leaf curl and enation symptoms were collected from different regions of Yunnan. PCR was performed with primers based on DNA-A intergenic region and partial CP gene and primers of total sequence of DNA β . Sequence analysis showed that Baoshan3, Yuanmou1 and Yuanmou2 belong to Tobacco curly shoot virus (TbCSV), Baoshan1, Baoshan2 and Baoshan4 belong to Tomato yellow leaf curl virus (TYLCV), Dali and Lijiang belong to Tomato yellow leaf curl China virus (TYLCCNV). There were considerable differences among virus species from different regions. Differences also existed among DNA β associated with virus isolates, the DNA β s of isolates shared sequence identities from 51.3% to

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99.7%. DNA β s of Baoshan1 and TbCSV shared the highest sequence (98.7%) , and DNA β s of Baoshan4 and Malvastrum yellow vein Yunnan virus (MYVYNV) showed the highest sequence identity (98.7%) , DNA β of Baoshan2, Baoshan3, Dali, Lijiang, Yuanmou1 and Yuanmou2 shared 94.4%, 91.8%, 99.2%, 99.3%, 98.7% and 98.9% sequence identity with that of TYLCCNV, respectively. Phylogenetic analysis of DNA β revealed that these DNA β s had closer relationship with that of other WTGs isolates of Yunnan than those isolates from other provinces of China, Asia and other countries, suggesting there might be typical geographical distribution characterization among DNA β .

Key words [Whitefly transmitted geminiviruses;](#) [Tobacco;](#) [Genetic diversity](#)

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