北京地区黄栌枯萎病菌群体遗传多样性分析

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摘要: 黄栌枯萎病是一种由大丽轮枝菌（*Verticillium dahliae*）侵染黄栌（*Cotinus conggygria* Scop.）引起的病害。黄栌是一种重要的观赏树木，在北京市得到推广种植，对北京市的景观建设起到了重要的作用。但是，由于大丽轮枝菌（*V. dahliae*）是一种土传植物病原真菌，具有土壤中存活时间长、缺乏寄主抗性等特点，目前还缺乏有效地防治措施，严重影响了北京市的生态环境建设。为了明确北京地区黄栌枯萎病的群体遗传多样性，及其群体遗传结构，并为该病害的防治提供理论支持，本研究主要以来自北京地区黄栌枯萎病菌为研究对象，并以山东省的菌株为对照，将试验菌株根据不同的采集地点分为 6 个群体 ，采用 SSR 分子标记的方法进行群体遗传多样性研究。本研究结果如下：

1. 根据已知大丽轮枝菌的微卫星位点设计合成了 51 对 SSR 引物，利用 10 个来自不同采集点的菌株用于多态性筛选，并结合适合黄栌枯萎病菌群体遗传研究的 SSR 分子标记体系，获得了 6 对多态性丰富的引物，为后续的群体遗传研究奠定基础。

2. 采用筛选出的 6 对多态性 SSR 引物对 179 个菌株进行 SSR 分析。共得到 26 个多态性位点，每对引物的扩增条带数在 2~7 之间，平均为 4.33。有效等位基因数（*Ne*）、Nei 基因多样性指数（*H*）和 Shannon 信息指数（*I*）分别为 1.4399、0.2715 和 0.4251，表明大丽轮枝菌群体中存在遗传多样性，其中，昌平群体的遗传多样性水平最高，百望群体的遗传多样性水平最低。

3. 黄栌枯萎病菌群体间和群体内都存在一定的遗传分化，总的遗传多样性（*Ht*）为 0.2748，群体内的遗传多样性（*Hs*）为 0.2410，群体内和群体间的遗传变异分别占总遗传变异的 87.70%和 12.30%，群体内遗传多样性明显大于群体间遗传多样性，群体内的遗传变异对总的遗传变异起主要作用。群体间具有较高的基因流（*Nm*=3.5665），使各群体趋向于一致。

4. 根据遗传距离和遗传相似系数对各群体进行 UPGMA 聚类分析，当遗传相似系数为 0.95 时，将 6 个群体分为 2 大类。延庆群体和历城群体聚为一类，其他四个北京地区的群体

聚为另一类，没有表现出明显的与地理距离的一致性。

关键词：黄栌，大丽轮枝菌，SSR 标记，群体遗传多样性

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Genetic Diversity Analysis of *Verticillium dahliae* Population on *Cotinus conggygria* in Beijing Region

Abstract：Smorke-tree *(Cotinus conggygria* Scop.) which can be infected by *Verticillium dahliae* is an important kind of ornamental tree species and play an important role in the landscape construction in Beijing. *V. dahliae* is a soil-borne plant pathogenic fungus. It is survival in soil with a long time and there is not a useful control management. In order to analysis population genetic diversity of *V. dahliae* on smoke-tree, 179 isolates coming from Beijing and Shandong province were used and divided into six populations by the different geographical origin. Population genetic diversity was studied based on the SSR molecular marker, and provided the theoretical support to control the smoke-tree wilt. Main results are as follows:

1. 51 pairs of SSR primers were designed by the reported SSR loci and used to and the validity of resulting primer pairs was detected by amplifying 10 isolates of *V. dahliae* from different geographical origins. Under the established SSR reaction system, 6 primer pairs which produced effective and polymorphic fragments were selected to analyze the genetic diversity of 179 *V. dahliae* isolates.

2. On the 6 SSR loci, a total of 26 alleles were detected in 179 isolates. At each locus, 2~7 alleles were detected with an average of 4.22. On the level of species, effective number of alleles (*Ne*) was 1.4399, Nei's gene diversity was 0.2715, Shannon's information index was 0.4251, the results indicated the genetic diversity existed among the populations. The highest one was found in Changping population and the lowest in Baiwangshan population.

3. The result of genetic differention among 6 populations showed that it could be found within and among populations. The gene diversity in the species (*Ht*) was 0.2748 and the gene diversity within populations (*Hs*) was 0.2410. The majority of genetic variation occurred within populations. Gene flow among populations was high (*Nm*=3.5665) and made the populations had the trend to be consistent.

4. According to the genetic similarity coefficient, the six populations were clustered into two groups by UPGMA method. One group included Yanqing population and Licheng populaton. Other four populations coming

from Beijing were in the other group. It implicated that the population genetic diversity was not consistent with the geographic distance.

Key words: *Cotinus coggygria*, *Verticillium dahliae*, SSR marker, population genetic diversity