

## 探討臺灣褐根病菌族群結構及病害傳播模式

### Assessing the genetic structure of *Phellinus noxius* and the dissemination pattern of brown root rot disease in Taiwan

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#### 摘要

褐根病菌 (*Phellinus noxius*) 寄主範圍相當廣泛，可感染包括樟樹、榕樹、臺灣欒樹、鳳凰木等超過二百種木本植物，是 1990 年代起臺灣極受重視的樹木病原菌。植物罹患褐根病後，初期不易看出明顯病徵，但感病後期常因根系組織、木質部逐漸腐朽，養分和水分吸收以及運輸功能嚴重受損，導致罹病樹木萎凋、死亡或風倒，不僅破壞景觀，也可能造成公共安全疑慮。為擬定有效的防治策略，必須對褐根病菌的生物學及散播流行趨勢有所瞭解。本研究首先針對一個由臺灣宜蘭採集之褐根病菌子實體上分離所得之單一擔孢子菌株，進行 Illumina 次世代定序與 de novo 組裝，初步獲得 15,966 contigs 共約 40 Mb 之基因體資料，以及 10,554 個簡單重複性序列 (simple sequence repeat, SSR) 區域，並據以設計出 76 個褐根病菌 SSR 分子標誌，經測試後進一步篩選出增幅效率高、適用於區分褐根病菌遺傳變異的 16 個 SSR 分子標誌。本研究共分析 1989-2012 年間，由臺灣 13 個縣市的市區或田間發現之罹病樹木 (超過 70 個樹種) 上所分離之 ~320 個褐根病菌菌株。基因分型結果顯示，全臺褐根病菌族群呈現高度遺傳變異，即使由單一校區內採集之褐根病菌株，除了部分栽植位置相近的罹病樹木外，自其他樹木上分離的菌株皆屬於不同的無性繁殖系，由此可知臺灣樹木褐根病之發生，並非由單一或少數高致病力之強勢小種所引起。依據現有之分子證據，可推測褐根病菌可能藉由根接觸而短距離傳播，其長距離之傳播，則可能由擔孢子飛散、罹病樹木或種苗移動、人員活動等綜合因素所造成。此外，本研究中不同地理區域之樣本，並無顯著的族群分化現象，亦不符合距離隔離 (isolation-by-distance) 模式。

**關鍵詞：**褐根病、簡單重複性序列、微衛星、族群遺傳、無性繁殖系

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### ABSTRACT

Since 1990s, brown root rot caused by *Phellinus noxius* has become a major tree disease in Taiwan. This fungal pathogen has a very wide host range, including *Cinnamomum camphora*, *Ficus microcarpa*, *Koelreuteria henryi*, and *Delonix regia*. When infecting trees, it can not only destroy bark and wood structure, but also seriously impair nutrient transportation and water uptake. In the early stage of infection, the infected trees may not show any obvious symptom, but as the disease develops, the tree may decline and eventually fall down or die within few or ten more years, thereby resulting in considerable economic loss and causing public danger. For effective control of the disease, it is important to know how the pathogen is disseminated and how new infection center of brown root rot is established. As a first step to decipher the biology of *P. noxius*, we performed Illumina sequencing and *de novo* assembly of a single basidiospore isolate originated from a basidiocarp collected from an infested *Ficus* tree in Ilan, Taiwan. We obtained an approximately total of ~40 Mb genome comprising 15,966 contigs. Sequence analysis identified a total of 10,554 SSR regions throughout the *P. noxius* genome. Accordingly, 76 SSR markers were developed and evaluated on the basis of their amplification efficiency and discrimination capacity. A set of 16 SSR markers was then chosen for subsequent analyses of 320 *P. noxius* isolates collected from 70 tree species from urban/agricultural areas in 13 cities/counties all around Taiwan during 1989-2012. The results revealed a high level of allelic diversity and the presence of a variety of fungal clones, even within a small campus. The *P. noxius* clones exist as discrete patches, suggesting that the occurrence of brown root rot was most likely caused by multiple clones rather than a single predominant strain of *P. noxius*. Isolates collected from diseased trees nearby each other tend to have similar genotype(s), indicating that *P. noxius* may spread to adjacent trees through root-to-root contact. There seems little

to no barrier to gene flow throughout the *P. noxius* population in Taiwan, which may be attributed to a combined effect of basidiospore dispersal, the migration of *P. noxius* via infected trees/seedlings from different nurseries, and other human activities.

**Key Words:** Brown root rot, simple sequence repeat (SSR), microsatellite, population genetics, clonality