

Amplified Fragment Length Polymorphism Analysis and Genetic Variation of the Pinewood Nematode, *Bursaphelenchus xylophilus* in South Korea¹

Jongwoo Jung² · Hyerim Han³ · Sung-Hee Ryu² · Won Kim^{2*}

ABSTRACT

The pinewood nematode *Bursaphelenchus xylophilus* causes pine wilt disease and is a serious economic concern for the forest industry of South Korea. To achieve effective control with limited resources, it is necessary to clarify the transmission routes and mechanisms of dispersal of this organism. Highly polymorphic and easy-to-use molecular markers can be used for investigating this aspect. In this study, we evaluated the usefulness of amplified fragment length polymorphisms (AFLPs) for investigating the genetic variations of *B. xylophilus* and related individuals from China, Japan, and South Korea. The AFLP patterns obtained in our study were similar to the microsatellite patterns reported in a previous study; our AFLP patterns indicated high genetic variability and cryptic genetic structure, but did not indicate any peculiar geographic structure. Moreover, the genetic distances between individuals suggested that the Korean population was affected to a greater extent by the Chinese population than the Japanese population. Further, the gene flow among the related species appeared to be limited; however, there may be also the possibility of genetic introgression among species. These results confirm the usefulness of AFLPs for understanding the epidemiology of pine wilt disease, thereby contributing to the effective control of this disease.

Keywords : AFLPs, Pinewood Nematode, *Bursaphelenchus xylophilus*, Pine wilt disease, Genetic variation

¹ Received on October 16, 2009

Accepted on March 8, 2010

² Seoul National University, Seoul 151-747, Korea

³ Korea Forest Research Institute, Seoul 130-712, Korea

* Corresponding author E-mail : wonkim@plaza.snu.ac.kr