

**Phylogenetic Relationships of *Bursaphelenchus xylophilus*
Local Isolates Based on DNA Sequence of
Cytochrome Oxidase 1 Subunit Gene**

**Jae Soon Kang, Kwang Sik Choi¹, Sang Chul Shin¹, Il Sung Moon²,
Yeong Jin Chung¹ and Si Hyeock Lee**

Entomology Program, school of Agricultural Biotechnology, Seoul National University

¹Division Forest Biology, Korea Forest Research Institute

²Nambu Forest Experiment Station, Korea Forest Research Institute

For efficient management of *B. xylophilus*, the accurate prediction of dispersal route is important. For this purpose, genetic variations among local isolates *B. xylophilus* collected from several infected areas (8 domestic and 1 foreign areas) were investigated by analyzing a intraspecific genetic marker, mitochondrial cytochrome oxidase 1 gene (mtCO1 gene), which is known to have many intraspecies variations. According to the sequence results, differences among 8 domestic local isolates were ranged from 0% to 0.9%. The mtCO1 gene sequences from Busan, Jinju, Mokpo and Sinan isolates were homologous each other and completely identical to those of the Japan Shimane isolate (Kanzaki & Futai, 2002), implying that those Korean isolates were initially originated from Japan and spread via the route of Busan, Jinju, Mokpo, and Sinan. Other isolates showed slight variations in mtCO1 gene sequences compared to those of Japan Shimane, suggestive of their different origins and the involvement of man-made factors in the dispersal of *B. xylophilus* besides the natural transmission by *Monochamus alternatus* vector.