

Genetic structures of *Bursaphelenchus xylophilus* and *Monochamus alternatus* in a seriously damaged maritime pine forest of Japan

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Genetic structures of *Bursaphelenchus xylophilus* and *Monochamus alternatus*, the pathogen and its vector of pine wilt disease, was sympatrically investigated using SSR markers. We configured six sampling sites scattering east to west at 300-1000 m intervals in a seriously damaged maritime pine forest at Shizuoka prefecture, Japan and sampled 1459 nematodes and 220 vectors from 53 and 15 dead *Pinus thunbergii* (Japanese black pine) respectively. These genetic structures were analyzed hierarchically between or within sites and trees. Nematode subpopulations within trees usually had low F_{IS} and expected heterozygosity, and hierarchical analysis of molecular variance (AMOVA) for *B. xylophilus* showed significant differentiation between trees within sites (43% of total variance). These results indicated the founder effect occurred within each tree. Nematodes subpopulations between sites also differentiated (21 % of variance) and Mantel test between trees among the whole site was significantly positive. Therefore, it was revealed gene flow of nematodes beyond sites border was limited. In the case of *M. alternatus*, subpopulations within trees showed high expected heterozygosity and low F_{IS} . Although hierarchical AMOVA showed subpopulations between trees were differentiated within sites (11% of variance), there was not significant differentiation between sites subpopulations. Mantel test between trees among the whole site was not significantly positive. This sympatric analysis showed although *B. xylophilus* was vectored by *M. alternatus*, both genetic structures were much different, especially in dispersal range beyond sites border.

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