Larch is a new host for a group 16Srl, subgroup B, phytoplasma in Ukraine

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Abstract

A phytoplasma strain belonging to group 16SrI, subgroup B (`Candidatus Phytoplasma asteris'), the most widely spread phytoplasma worldwide, was detected in diseased larch (Larix sp.) in Ukraine. Detection, identification, and classification of the larch infecting phytoplasma were accomplished through RFLP and sequence analysis of 16S rRNA and ribosomal protein (rp) gene sequences amplified in polymerase chain reactions. The larch infecting phytoplasma was named larch dwarfed needle proliferation (LDNP) phytoplasma. The findings revealed Larix as a previously unknown host of phytoplasma and indicated that ‘Ca. P. asteris’ is capable of infecting a gymnosperm, while raising questions concerning the identity of possible insect vector(s) involved in transmission of ‘Ca. P. asteris’ to larch and perhaps to other gymnosperms.

Key words: Gymnosperm, Pinaceae, proliferation, polymerase chain reaction, mollicute.

Introduction

Class Gymnospermae (gymnosperms) contains several families including Pinaceae, within which are classified diverse woody plants, some of which are highly valuable for their timber (Lin et al., 2010). One genus in the family is Larix (larches), trees 15 to 50 m height that constitute a major component of various forests in cool temperate regions of the northern hemisphere. Indeed, Larix has been cited as one of the most widely distributed tree genera in Eurasia (Lin et al., 2010). Larches are conifers, but unlike members of most genera in the Pinaceae, the genus Larix is deciduous, the leaves, or needles, turning yellow and falling in autumn. In the present study we investigated the possible presence of phytoplasma in diseased larch growing in a public park in Ukraine.

Symptoms similar to those sometimes associated with plant infection by phytoplasma were observed in diseased larch in Oleski park (L’viv region, Ukraine). The trees exhibited general yellowing of needles, dwarfed needles, and proliferation and necrosis of needles. These symptoms, and recent reports of phytoplasma infections in other Gymnosperms (Davis et al., 2010; Paltrinieri et al., 1998; Schneider et al., 2005; Sliwa et al., 2007; Valiuunas et al., 2010), drew our attention to the possibility of phytoplasma-associated disease in larch. Samples of dwarfed needles were collected and analysed for the presence of phytoplasma in diseased larch growing in a public park in Ukraine.

Materials and methods

Samples of symptomatic leaves (needles) from diseased larch were collected and assayed for possible phytoplasma infection. DNA was extracted from the yellowing, dwarfed and proliferated needles using Genomic DNA Purification Kit (Fermentas, Vilnius, Lithuania). Detection of phytoplasma 16S rDNA sequences was accomplished by the use of nested polymerase chain reactions (PCRs) primed by phytoplasma-universal primer pair P1/P7 followed by nested reactions primed by R16F2/R16R2 (F2n/R2) (Lee et al., 1998). Phytoplasma ribosomal protein (rp) gene sequences were amplified from larch DNA templates by using PCR primed by rp gene primer pair rpF1/rpR1. PCR was performed as described previously (Lee et al., 1998). Annealing temperature for amplification of rp gene sequences was 50°C. Products (1.2 kbp, R16F2/R2 segment) of the nested PCR were subjected to enzymatic restriction fragment length polymorphism (RFLP) analysis using restriction endonucleases Alul, HaeIII, Msel, Rsal, HhaI, Hinfl, HpaII. (Fermentas, Vilnius, Lithuania). Detection of phytoplasma 16S rDNA sequences was accomplished through computer-simulated restriction digestion and virtual gel plotting using iPhyClassifier (Zhao et al., 2009).
Amplified 16S rRNA and rp gene products were cloned into *Escherichia coli* by using the TOPO TA cloning kit (Invitrogen, Carlsbad, CA) according to the manufacturer’s instructions and sequenced by automated sequencing of both strands to achieve a minimum of 3-fold coverage per base position.

**Results**

To determine the possible presence of phytoplasmas in diseased larch (*Larix sp.*), we examined total DNA samples prepared from the yellowing, dwarfed and proliferated needles. Two genetic markers (16S rRNA and rp gene sequences) were employed for the detection, identification and classification of phytoplasmas. The product amplified in nested PCR primed by R16F2n/R16R2 from the diseased larch samples was 1.2 kbp in size (data not shown). RFLP analysis of amplified 16S rDNA revealed patterns identical to those of group 16SrI, subgroup B phytoplasmas (‘*Ca. P. asteris*’) (figure 1). Amplification, RFLP and nucleotide sequence analysis of rp gene products confirmed identification of ‘*Ca. P. asteris*’ presence in the larch samples (data not shown). The phytoplasma detected in larch was named larch dwarfed needle proliferation (LDNP) phytoplasma. Amplicons of 16S rDNA and ribosomal protein (rp) genes from strain LDNP were cloned, sequenced and deposited in the GenBank database under accession numbers JF747037 and JF767009, respectively.

![Figure 1. Virtual gel RFLP patterns from analyses of LDNP phytoplasma 16S rDNA R16F2n/R2 fragment.](image)

**Discussion**

Phytoplasma infections in pines (family Pinaceae) have been detected in Spain, Germany, Poland, and Lithuania (Schneider et al., 2005; Sliwa et al., 2007; Valiunas et al., 2010). Symptoms exhibited by the diseased pine trees were shoot-proliferation, dwarfed and proliferated needles, and stunting. The phytoplasma strains detected in pine belonged to group 16SrXXI, subgroup A (‘*Candidatus Phytoplasma pini*’). Group 16SrIII phytoplasma was reported in cypress (Paltrinieri et al., 1998). A juniper (*Juniperus occidentalis*) infecting phytoplasma in Oregon was classified as a ‘*Candidatus Phytoplasma phoenicium*-related strain and a member of group 16SrIX, subgroup E (Davis et al., 2010). Our study revealed infection by a group 16SrI subgroup B phytoplasma in larch. In agreement with concepts expressed previously (Davis et al., 2010), the present and other findings indicate that phytoplasma infections in gymnosperms may be more frequent than previously thought. It will be interesting to learn the identities of insect vectors transmitting the diverse phytoplasmas to gymnosperms and to learn the extent of phytoplasma infections in gymnosperms worldwide.

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