



## First report of molecular identification of 'Candidatus Phytoplasma pyri' in pear trees in Belgium

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Pear decline phytoplasma (PD) is a quarantine pest ('harmful organism') for the European Union that has been assigned to the *Candidatus* taxon, '*Candidatus Phytoplasma pyri*'. In October 2010, 137 samples consisting of leaves or roots from symptom-bearing pear trees showing early yellow or red discoloration (Fig. 1) were collected in pear production orchards in northeast Belgium.

Total DNA was extracted from 0.5 g of leaf midribs using a simplified CTAB extraction method (ANSES, 2010). Total DNA was used as a template for phytoplasma testing in a direct PCR assay using the universal primer pair fU5/rU3 (Lorenz *et al.*, 1995) that targets the phytoplasma 16S rRNA gene. Amplified 16S rDNA fragments of expected size (approximately 880 bp) were directly sequenced and each obtained sequence was compared to those of reference phytoplasmas in GenBank by BLAST. In order to further study the genetic diversity of the phytoplasma isolates, some positive samples were additionally amplified and directly sequenced using the fHf1B3\_1/rHf1B3 primer pair (Seemüller *et al.*, 2011) that targets the putative transmembrane metalloprotease gene (Hf1B) for phytoplasmas.

Out of the 137 samples, approximately 15% gave positive results for '*Ca. Phytoplasma pyri*' through PCR and sequencing. BLAST analysis of the consensus fU5/rU3 sequence (HF547271) revealed a 100% of sequence identity with that of '*Ca. Phytoplasma pyri*' isolates (16SrX group, subgroup C). Four Hf1B amplicons of expected size (approximately 530 bp) from samples of four different municipalities were directly sequenced. The obtained sequences were 100% identical in the available regions, and

the consensus Hf1B sequence (HE984352) showed 98.3% sequence identity with that of '*Ca. Phytoplasma pyri*' partial Hf1B gene, strain PD1 (GenBank Accession No. FM201271). To our knowledge this is the first report of the molecular identification of '*Ca. Phytoplasma pyri*' in Belgian pear orchards.

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### References

ANSES, 2010. Détection des phytoplasmes responsables de l'enroulement chlorotique de l'abricotier, de la prolifération du pommier et du dépérissement du poirier. Protocole MOA 004 version a: 1-22.

Lorenz KH, Schneider B, Ahrens U, Seemüller E, 1995. Detection of the apple proliferation and pear decline phytoplasmas by PCR amplification of ribosomal and nonribosomal DNA. *Phytopathology* **85**, 771-776.

[<http://dx.doi.org/10.1094/Phyto-85-771>]

Seemüller E, Kampmann M, Kiss E, Schneider B, 2011. Hf1B gene-based phytopathogenic classification of '*Candidatus Phytoplasma mali*' strains and evidence that strain composition determines virulence in multiply infected apple trees. *Molecular Plant-Microbe Interactions* **24**, 1258-1266.

[<http://dx.doi.org/10.1094/MPMI-05-11-0126>]



Figure 1

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