First record of Xanthomonas arboricola pv. corylina on hazelnut and Xanthomonas arboricola pv. juglandis on walnut in Poland



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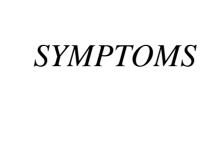
In Poland, the hazelnut (*Corylus avellana*) and walnut (*Juglans regia*) had been grown mostly by amateur growers in home gardens and small orchards. Recently their production has become more profitable. This popularity resulted in the establishment of large commercial plantations. Symptoms resembling diseases caused by bacteria from the genus *Xanthomonas* have been observed in various hazelnut and walnut growing regions in the country. The aim of our study was to elucidate the etiology of the observed disease symptoms.

HAZELNUT







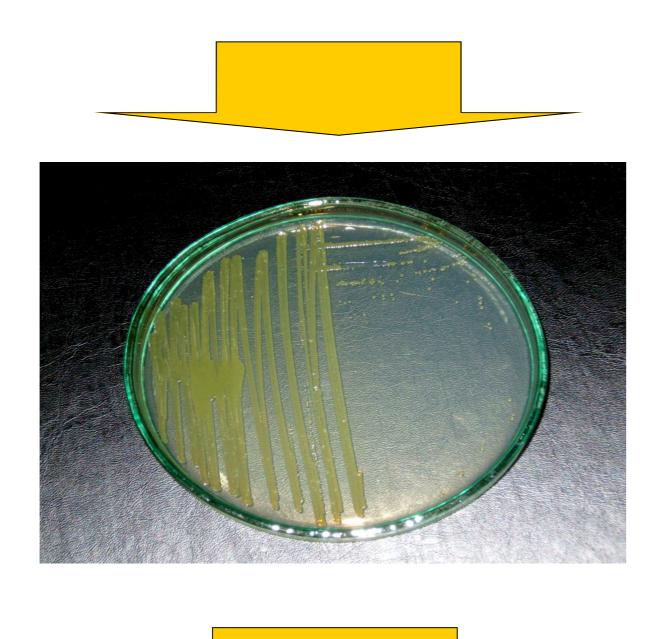




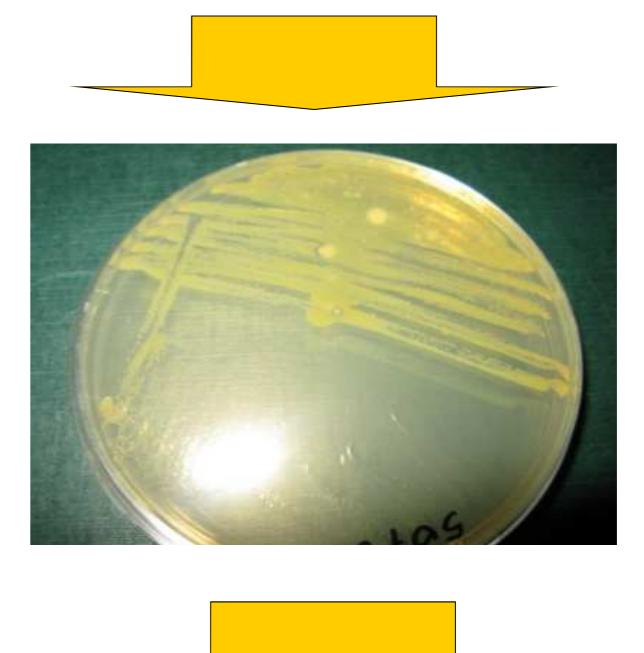


WALNUT









Based on results of:

- O PCR with Primer X1X2 specific do genus *Xanthomonas* (Maes 1993);
- biochemical and physiological tests (Anonymous, 2004);
- Fatty Acids Methyl Esters analysis;
- gyrB gene sequence analysis;
- opathogenicity test on young leaves of potted hazel plants in greenhous;

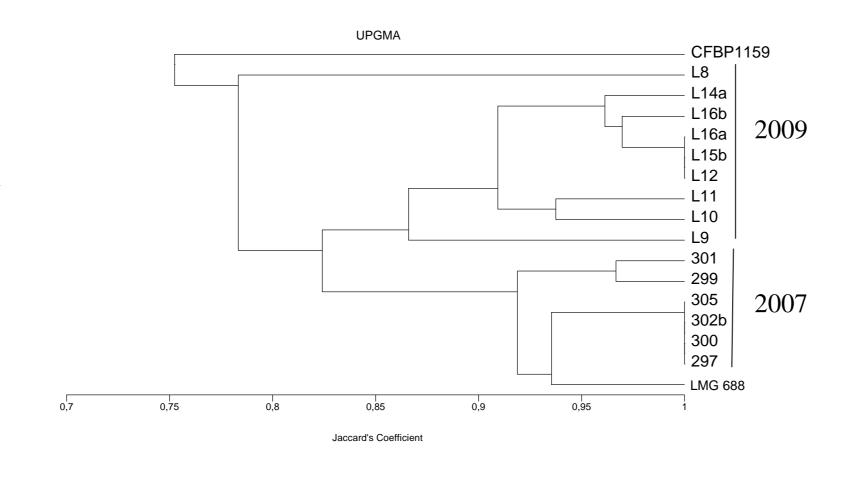
Koch postulates were fulfilled

Isolated bacteria were identified as

Xanthomonas arboricola pv. corylina

Analysed isolates showed **BOX, ERIC and REP-PCR** patterns similar to those of reference *Xac* strains (LMG 688, CFBP 1159). However, patterns of isolates obtained in 2009 were slightly different from those isolated in 2007.

Fig.1. Dendrogram of genetic similarity of *Xan-thomonas arboricola* pv. *corylina* originated from hazelnut as results of the combined data set of ERIC, REP and BOX-PCR primers using UP-GMA analysis and Jaccard's coefficient



IDENTIFICATION

Based on results of:

- PCR with Primer X1X2 specific do genus *Xanthomonas*;
- Biochemical and physiological tests—test on BS and SQ medium, hydrolysis of esculine, growth at 35°C
- BOX, REP and ERIC analysis;
- Pathogenicity test on unripe walnut fruits; Koch postulates were fulfilled

Isolated bacteria were identified as

Xanthomonas arboricola pv. juglandis

Analysis of concatenated sequences of partial *fyuA*, *gyrB* and *rpoD* genes showed that Polish *Xaj* isolates create 3 different lineages related to their origin of isolation

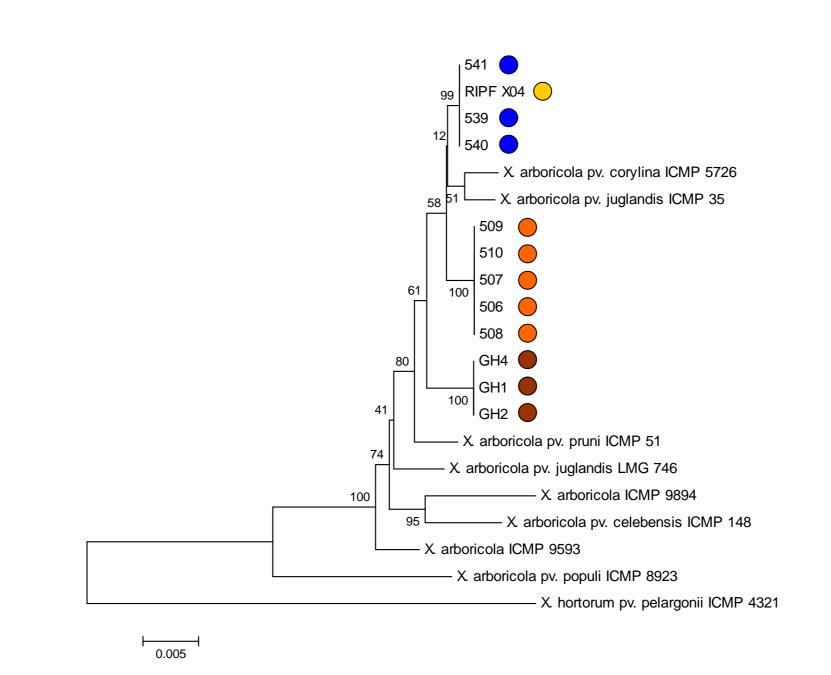




Fig.2. NJ tree of concatenated nucleotide sequences for partial *fyuA*, *gyrB* and *rpoD* genes of Polish *Xaj* isolates. For comparison, concactenated sequences of the same genes of other *Xanthomonas* strains are included.