Bacterial leaf spot of ivy: genetic diversity of the pathogen (*Xanthomonas hortorum* pv. hederae)

S. Holcroft and S.J. Roberts

Horticulture Research International, Wellesbourne, Warwick, CV35 9EF, UK



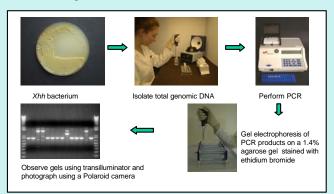
Background

- Ivy is an important crop for nurseries in the UK.
- Bacterial leaf spot causes significant losses for commercial growers of English ivy (*Hedera* spp.) in the UK.
- The disease is caused by the Gram-negative bacterium Xanthomonas hortorum pv. hederae (Xhh).
- No information was available on the genetic diversity of Xhh from the UK.
- We used RAPD-PCR to assess diversity of isolates of Xhh from ivy from the UK in order to assess the population structure.



Bacterial leaf spot of ivy

RAPD-PCR



- Thirty-three Xhh isolates from 10 different sites in the UK, and from the NCPPB (National Collection of Plant Pathogenic Bacteria) from the UK, USA and Denmark were studied. Isolates came from 16 different Hedera spp. and cultivars and from Schefflera arboricola.
- PCR mixture and conditions were optimised using four isolates and primer OPG11 (Operon technologies).
- Ten primers were then used to generate fingerprints for all isolates.
- Fingerprints were analysed and cluster analysis performed on the basis of presence or absence of bands

Results

- All Xhh isolates produced similar fingerprints with eight of the ten primers
- Different banding patterns were produced with primers OPG3 and OPG12.
- All Xhh isolates formed one major cluster which could be divided into two sub-groups at the 80% similarity level.
- Most of the isolates (74%) were contained in sub-group 1.
- Isolates from Schefflera arboricola, reported elsewhere to infect ivy, showed little similarity with each other (43%) and appear unrelated to isolates from ivy (similarity 14%).

Sub-group 1 X. c. pv. campestris X. h. pv. pelargonii P. s. pv. syringae Isolates from Schefflera arboricola Dendrogram showing similarity between isolates of X. h. pv. hederae (Xhh) from different geographical/species of origin. Similarity values were obtained using UPGMA analysis of bands produced from RAPD-PCR using ten oligonucleotide primers.

Conclusions

- Isolates of Xhh from ivy are genetically very similar.
- •There does not appear to be any relationship between the sub-groups within Xhh from ivy and their geographical or cultivar of origin.
- The lack of variability between isolates may suggest there are no races within the pathovar Xhh.
- Given the absence of strain variability and as ivy is propagated vegetatively it seems likely that the disease is disseminated with cuttings and spreads between cuttings/plants during production.
- Infection from wild plants growing locally seems unlikely as more genetic variability would be expected than that observed.



