

Phylogenetic identification of quarantine bacterial plant pathogens



Funding

Non-competitive funding mechanism. Each funder only pays for the participation of their own national researchers.

Goals

To provide a fully comprehensive validation of phylogenetic identification protocols, based on single-gene sequencing, for a range of plant pathogenic bacteria of quarantine importance.

Research consortium

Austria: AGES; Belgium: ILVO; Bulgaria: NSPP; Czech Republic: NAAR; France: CIRAD, DGAL, INRA; Germany: JKI; Italy: CRA; Netherlands: PD, NAK; Portugal: UIPP; Slovenia: NIB; Spain: DARP, IVIA; UK: Fera, SASA.

Objectives

- To validate published methods for phylogenetic identification of bacterial plant pathogens of plant health importance, including *Ralstonia solanacearum*, *Xanthomonas* spp. and *Dickeya* spp.
- To finish development of new phylogenetic analyses to allow identification of members of the *Pseudomonas syringae* species complex and isolates of *Erwinia amylovora*.
- To standardise methods for the identification of key plant pathogenic bacteria appropriate for use with EPPO diagnostic protocols.
- To facilitate application of phylogenetic identification schemes in routine diagnostics in collaboration with the EU QBOL project (www.qbol.org).

Contact information

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