



Development of multilocus variable-number tandem repeat analysis (MLVA) for *Xanthomonas arboricola* pathovars

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Titre	Development of multilocus variable-number tandem repeat analysis (MLVA) for <i>Xanthomonas arboricola</i> pathovars
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Auteur	Cesbron, Sophie [1], Pothier, Joel [2], Gironde, Sophie [3], Jacques, Marie-Agnès [4], Manceau, Charles [5]
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Résumé en anglais	<p><i>Xanthomonas arboricola</i> is an important bacterial species, the pathovars of which are responsible for bacterial blight diseases on stone fruit, hazelnut, Persian walnut, poplar, strawberry, poinsettia and banana. In this study, we evaluated variable number tandem repeats (VNTR) as a molecular typing tool for assessing the genetic diversity within pathovars of <i>X. arboricola</i>. Screening of the <i>X. arboricola</i> pv. <i>pruni</i> genome sequence (CFBP5530 strain) predicted 51 candidate VNTR loci. Primer pairs for polymerase chain reaction (PCR) amplification of all 51 loci were designed, and their discriminatory power was initially evaluated with a core collection of 8 <i>X. arboricola</i> strains representative of the different pathovars. Next, the 26 polymorphic VNTR loci present in all strains were used for genotyping a collection of 61 strains. MLVA is a typing method that clearly differentiates <i>X. arboricola</i> strains. The MLVA scheme described in this study is a rapid and reliable molecular typing tool that can be used for further epidemiological studies of bacterial diseases caused by <i>X. arboricola</i> pathovars.</p>
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Liens

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