



## **Diversity of *Xanthomonas hortorum* pv. *carotae*, the agent of bacterial leaf blight of carrot and the need for a new pathotype strain**

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*Xanthomonads* are plant-associated bacteria responsible for diseases of considerable economic importance. While these bacteria spread by aerosols and mechanical means like infected pruning tools, the movement of contaminated seeds and other propagation material generally represents the main inoculum source for diseases due to xanthomonads. Plant health management of these diseases through sanitation practices and plant resistance mainly depends on reliable detection and identification tools. The genus *Xanthomonas* has been subject to numerous taxonomical and phylogenetic studies, but its taxonomy is still under active debate. Some of the relationships between pathovars and species have not been thoroughly clarified. Strains formerly part of one pathovar are now found in two different species, some pathovars need pathotype strains and others were left with unsuitable pathotypes. Bacterial leaf blight of carrot (*Daucus carota* L. subsp. *sativus*) is caused by *Xanthomonas hortorum* pv. *carotae* (*Xhc*), a seed-borne pathogen with a worldwide distribution. The pathotype for this pathovar was reported to be unsuitable in 1991. In order to test plant genetic material for resistance to this pathogen, we study the genetic diversity of strains within this pathovar. A large collection of *Xhc* strains and *Xhc* look-alikes isolated from carrots was established. A multilocus sequence analysis (MLSA) targeting six housekeeping genes revealed that *Xhc* strains cluster in two close genetic lineages sharing a common ancestor. Pathogenicity of strains representative of these lineages was confirmed. The low polymorphism revealed by these genes does not allow a thorough typing of strains. In contrast, a multilocus variable number of tandem repeats analysis (MLVA) yielded a large genetic diversity among strains of this pathovar that is useful for molecular epidemiology study of this disease. In contrast with *Xhc* strains, look-alikes split in various parts of the *Xanthomonas* phylogenetic tree. These strains are not pathogenic on carrots but most generally induce hypersensitive reaction on tobacco and possess a hrp-Type Three Secretion System. This polyphasic analysis of *Xhc* and look-alikes offer the opportunity to designate a neopathotype strain for *Xhc*, which will help future studies of strains belonging to this pathovar.

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## Liens

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