

Isolation and characterization of the bacteriophages infecting *Xanthomonas arboricola* pv. *juglandis*

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Bacterial blight of walnut (*X. arboricola* pv. *juglandis*, Xaj) is one of the most destructive diseases that annually reduces the fruit production in most walnut growing regions in the world. The disease control is challenging, since abundant use of copper-based compounds in walnut orchards resulted in the emergence of highly copper resistant isolates and, therefore, reduced the efficacy of copper-based sprays. Existence of genetic diversity among Xaj strains from different geographical areas in the world is well known and recorded that the geographic location can influence the genomic rearrangement and the heterogeneity of Xaj populations. Some studies also reported that diversity could be linked with the virulence of the pathogen. The aim of this study was to isolate and characterize novel lytic bacteriophages specific to Xaj, with the main idea to evaluate their interaction with pathogenic Xaj strains isolated from different locations in Italy, Serbia and Turkey with diverse virulence. Bacteriophages were collected from different substrates. To increase the potential of Xaj-specific phage isolation, substrate samples were subjected to incubation with target bacteria in 50 ml Nutrient Broth amended with 2.5 g CaCO₃. The phage isolates were characterized by host-range, plaque morphology, thermal inactivation and sensitivity to pH, UV light and chloroform. Phage life cycle was studied by a one-step growth procedure. A host specificity assay was performed using 15 bacterial isolates of Xaj collected from symptomatic walnut trees in different years and countries, and possessing a different virulence degree. Parameters, such as country of isolation, type of substrate and different virulence of strains, were evaluated. Extended characterisation of bacteriophages represents, therefore, the basis for the implementation of innovative methods to control the bacterial blight of walnut in commercial groves.