

A novel gene cluster involved in high tolerance to copper compounds has been detected in *Pseudomonas syringae* pv. *syringae*

José A. Gutiérrez-Barranquero, Francesca Aprile, Francisco Cazorla and Antonio de Vicente.

Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora" (IHSM-UMA-CSIC), Departamento de Microbiología, Facultad de Ciencias, Universidad de Málaga, Spain.

*Pseudomonas syringae* pv. *syringae* (Pss), is the most polyphagous bacterium of the *P. syringae* complex, based on its wide host range, that severely affects woody and herbaceous plants. Pss has been described as the causal agent of bacterial apical necrosis (BAN) on mango crops, an important threat that drastically reduces the mango fruit yield in the Mediterranean region. Copper compounds have traditionally been used as standard bactericides to manage woody plant diseases, being the spraying of copper compound known as Bordeaux mixture (BM), the conventional treatment for controlling BAN disease. The extensive use of copper compounds can lead to many problems, and among them, the emergence of copper-resistant strains is one of the most serious. Pss strains isolated from mango trees harbour at least, two different genetic structures (*copABCD* and *copABCD* modified) encoded by plasmids that are involved in copper detoxification. Determination of the minimum inhibitory concentration of copper, together with a phylogenetic distribution analysis performed in a collection of Pss strains isolated from mango trees revealed a phylogenetic group of Pss strongly associated with high levels of copper resistance. Genome mining and functional characterization of one Pss strain present in this group have uncovered a novel gene cluster of chromosomal location that could be playing a major role in high levels of copper resistance during the epiphytic survival of Pss on mango tree surfaces.