

plan is necessary to contain *X. fastidiosa* impacts, and this requires specific and sensitive diagnostic tools. PCR-based methods are favoured for their sensitivity and specificity, but these require laboratory facilities. Advantages might be gained from moving testing closer to sampling sites. A diagnostic assay based on loop mediated isothermal amplification (LAMP) was developed to detect *X. fastidiosa*. This assay, optimized on the portable instrument Genie II (Optigene, UK) and based on RimM target region, can recognize the pathogen DNA with high levels of specificity, identifying only *X. fastidiosa*, and sensitivity, detecting DNA as little as 0.128 pg/μL, equaling results obtained with the compared *X. fastidiosa* qPCR assay. The LAMP method used for detecting *X. fastidiosa* on symptomatic and asymptomatic samples could assist checking of imported and exported live plants, limiting the uncontrolled spread of this pathogen. Simplicity, sensitivity and specificity, high speed (only 30 min) and minimum required equipment make the assay ideal for field applications, helping routine plant testing in cities and forests.

Wood, root and foliar diseases in fruit and forest crops in the Mediterranean region

Pine wilt disease: insights into the biology of *Bursaphelenchus xylophilus*-associated *Serratia*. C.S.L. VICENTE¹, K. HASEGAWA², M. MOTA¹. ¹ICAAM – Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal. ²Department of Environmental Biology, Chubu University, Kasugai, Japan. E-mail: coicente@uevora.pt

Pine wilt disease (PWD) is caused by the parasitic nematode *Bursaphelenchus xylophilus* (pinewood nematode; PWN), which infects mainly *Pinus* species with the aid of an insect-vector, *Monochamus* sp.. Bacteria isolated from *B. xylophilus* are being considered as a fourth element in this disease complex. Their precise roles of these organisms in this interaction are unclear, as both beneficial and pathogenic bacteria have been found associated with PWD. Previously, we have shown the high oxidative stress tolerance of the PWN-associated bacteria *Serratia* sp. LCN16 and *Serratia marcescens* PWN146, and their beneficial effects towards the nematode under harsh

oxidative stress conditions. Here, we present a detailed analysis of the genome sequences of these two PWN-associated bacteria and provide new insights into their biology and contributions to PWD and the PWN. *Serratia* sp. LCN16 is phylogenetically most closely related to the phytosphere group of *Serratia*, and shares many features with endophytes (plant-associated bacteria). These include genes coding for plant polymer degrading enzymes, iron uptake/transport, siderophore and phytohormone synthesis, aromatic compound degradation and detoxification enzymes. *Serratia marcescens* PWN146 can also withstand and colonize the plant environment, without having any deleterious effects towards *B. xylophilus* nor to the nematode model *C. elegans*. PWN146 has the potential to interfere with plant metabolism via hormonal pathways or nutritional acquisition (i.e. iron), and to be competitive against other bacteria and fungi, through resource acquisition or production of antimicrobial compounds.

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Comparative study of *Pseudomonas syringae* pv. *syringae* strains isolated from mango trees distributed worldwide with over 25 years apart. F. APRILE, J.A. GUTIERREZ-BARRANQUERO, F.M. CAZORLA, A. DE VICENTE. Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora” (IHSM-UMA-CSIC), Departamento de Microbiología, Facultad de Ciencias, Universidad de Málaga, Spain. E-mail: aprile@uma.es

Mango (*Mangifera indica* L.) is one of the most important world fruit crops. In 1992, the disease bacterial apical necrosis (BAN) of mango was described for the first time in southern Spain. BAN is caused by *Pseudomonas syringae* pv. *syringae* (Pss), and is mainly associated with Mediterranean climate. The disease has been described in other mango-producing areas with similar weather (Portugal, Italy, Israel, Egypt, Florida and northeast Australia). Different Pss isolates from mango have been studied for years, to decipher their virulence and epiphytic fitness mechanisms. Genes associated with these biological characteristics have been described: *mbo* operon involved in the mangotoxin production, *copABCD* or *cusCBA*