**Comparative study of *Pseudomonas syringae* pv. syringae strains isolated from mango trees distributed worldwide with over 25 years apart.**

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Mango (*Mangifera indica* L.) is one of the most important fruit crops in the world. In 1992, the bacterial apical necrosis (BAN) disease of mango was described for the first time in southern Spain. BAN disease is caused by the phytopathogenic bacterium *Pseudomonas syringae* pv. syringae (Pss) and is mainly associated with Mediterranean climate. In addition, BAN 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 in depth to decipher their virulence and epiphytic fitness mechanisms. In this sense, different genes associated with these biological characteristics have been described: *mbo* operon involved in the mangotoxin production, *cop*ABCD or *cus*CBA operons involved in copper resistance, as well as the production of cellulose by *wss* genes. On the other hand, phylogenetic studies have revealed the presence of a differentiated phylotype of the Pss strains isolated from mango and characterized by mangotoxin production. Therefore, the main aim of this study comprise an epidemiological and evolutionary analysis of different Pss isolates from mango from different growing areas worldwide (Spain, Portugal, Italy, Israel, Australia), isolated by the year 2000 (UMA lab collection) and new isolates obtained in 2016 and 2017. We will perform a selection of the most representative strains of each collection in order to carry out a comparative genomic analysis to unravel the evolutionary processes which have been take place throughout these more 25 years.

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**Session topic:** Wood diseases in fruit crops in the Mediterranean area