Sensitive and specific detection method for *Pseudomonas savastanoi* isolates from *Mandevilla sanderi*

Eltlbany, N.[1,4], Prokscha, Z.-Z.[1], Castañeda-Ojeda, M.-P.[3], Krögerrecklenfort, E.[1], Heuer, H.[1], Wohanka, W.[2], Ramos, C.[3], Smalla, K.[1].

[1] Julius Kühn-Institute, Federal Research Centre for Cultivated Plants (JKI), Institute for Epidemiology and Pathogen Diagnostics, Braunschweig, Germany.
[2] Geisenheim Research Center, Section Phytomedicine, Geisenheim, Germany.
[3] Área de Genética, Facultad de Ciencias, Universidad de Málaga, Instituto de Hortofruticultura Subtropical y Mediterránea La Mayora (IHSM-UMA-CSIC), Málaga (Spain).
[4] Suez Canal University, Faculty of Agriculture, Ismailia, Egypt.
Email of corresponding author: namis.eltlbany@jki.bund.de

The ornamental plant *Mandevilla sanderi* originating from Middle and South America has become increasingly popular over the last decade mainly because of its copiously formed red flowers. In 2008 breeders of *Mandevilla sanderi* observed for the first time large necrotic lesions with chlorotic rings on leaves and tumor formation on stems. The potential causal agents isolated from the lesions of leaves of diseased plant material were identified initially by metabolic profiling (BIOLOG) as *Pseudomonas savastanoi* pv. glycinea or pv. nerii. Several pathovars of *P. savastanoi* infect woody plants, e.g., *P. savastanoi pv.* savastanoi is known as an important pathogen of olive trees (*Olea europaea)* in the Mediterranean area. The BOX fingerprints were similar for *P. savastanoi* isolates from different host plants, plasmid restriction patterns and sequencing of plasmid-located pathogenicity determinants revealed that *Mandevilla* isolates contained similar plasmids distinct from those of other isolates. A *repA*-based detection method was established. The present study was carried out to do molecular characterization of *Pseudomonas savastanoi* isolates from *Mandevilla sanderi* in comparison to isolates originating from olive trees, oleander, jasmine and privet. This information can be used as a basis for the development of a sensitive and specific detection method for the pathogen from total community DNA.