

Genetic diversity of soft rot enterobacteriaceae

Dr L. Moleleki, University of Pretoria
IBSG13052718289

The Soft Rot Enterobacteriaceae (SRE) are of significant importance due to their broad host spectrum and economic importance in crop production. The SRE are important phytopathogens infecting a wide range of economically important crop and ornamental plants. One of the best studied hosts of the SRE is potato, which is considered the 3rd most important crop plant after rice and wheat. They also infect maize which is one of the most important grain crops in Southern Africa. The SRE were formerly known as *Erwinia carotovora* and *Erwinia chrysanthemi*. The global advent of molecular tools for identification and phylogeny used for characterisation of many phytopathogenic bacteria has resulted in reclassification and taxonomic changes. As a result, within the SRE, the former *E. carotovora* has now been reclassified into the genus *Pectobacterium* while *E. chrysanthemi* has now been reclassified into the genus *Dickeya*. Furthermore, the use of molecular phylogeny has facilitated the identification of new species within both the genus *Dickeya* and *Pectobacterium* worldwide. Presence of some members of the SRE in South Africa was first reported in 1991 by Serfontein and co-workers under the old nomenclature (*E. carotovora* and *E. chrysanthemi*). Since adoption of the new nomenclature, we have reported on occurrence of two new species in potatoes, namely *P. wasabiae* and *P. brasiliense* (van der Merwe et al., 2010; Moleleki et al., 2013). However, there has been no real survey conducted to understand the biodiversity of SRE in South Africa particularly according to the new nomenclature. The aim of this study will be to conduct a DNA phylogenetic survey of the different SRE present in South Africa, to identify new species previously not reported as well as to compile a comprehensive database consisting of SRE and identification of host plants from which they were isolated.