BELGIAN CO-ORDINATED COLLECTIONS OF MICRO-ORGANISMS BACTERIA COLLECTION

New insights in the taxonomy of plantpathogenic and plant-associated bacteria in the *Enterobacteriaceae* 

#### Dr. Ilse Cleenwerck





# **ENTEROBACTERIACEAE**

- family within the Gammaproteobacteria
- contains many plant-pathogenic and plant-associated bacteria, as well as pathogens to humans & animals

- > Erwinia
- Pectobacterium
- > Pantoea
- Brenneria
- Samsonia
- » Dickeya

- Escherichia
- Salmonella
- > Klebsiella
- > Enterobacter 🔶
- 🕞 Serratia 🔶

+ Also plant-associated or plant-pathogenic isolates

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# **ENTEROBACTERIACEAE**

- phenotypically similar → difficult to identify some taxa using commercial ID kits
- eg. species of *Pantoea, Erwinia* and *Enterobacter* cannot be accurately identified
- incorrect classification of numerous strains
- many taxonomic rearrangements





## TAXONOMY OF PP AND PA ENTEROBACTERIACEAE

- plant pathologists → species according to disease, not phylogenetic relationship
- eg. the genus *Erwinia* was created in 1920 to unite all G<sup>-</sup>, fermentative, non-sporulating, peritrichously flagellated plant pathogenic bacteria
- end of 1998, most species of this genus were reclassified into new or existing genera





# TAXONOMY

"... one of the goals of any taxonomy is to create a classification scheme that reflects the genealogy of the organisms, thus circumscribing all taxa in monophyletic groups" – Ramon Rossello-Mora (Ed. Syst Appl Microbiol)

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## TAXONOMY OF PP AND PA ENTEROBACTERIACEAE

- 16S rRNA gene sequence analysis → many genera not monophyletic
- such as:
- > Enterobacter
- > Serratia
- Pantoea
- Frwinia
- > Pectobacterium
- » Brenneria

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## TAXONOMY OF PP AND PA ENTEROBACTERIACEAE

- housekeeping gene sequences → phylogenies more compatible with the "accepted classifications"
- eg. Serratia was monophyletic based on gyrB (Dauga, 2002)
- phylogenies should be based on sequences of several genes encoding different functions, as comparisons of a single housekeeping gene can provide misleading results

## BCCM/LMG – FABI/UNIV. PRETORIA

 MLSA study of plant-pathogenic and plantassociated *Enterobacteriaceae* based on partial sequences of four house keeping genes:

*atpD* (ATP synthase β subunit) *gyrB* (DNA gyrase) *infB* (initiation translation factor 2) *rpoB* (RNA polymerase β subunit)



## OUR INTEREST IN ENTEROBACTERIACEAE

- FABI: Forestry and Agricultural Biotechnology Institute, Univ. of Pretoria, SA
- Isolation campaigns/field trips in Africa, Asia and South America
- *Eucalyptus* + bacterial blight and dieback
  → Pantoea
- Community studies of diseased vs. healthy *Eucalyptus* seedlings → *Enterobacter* (?)









## OUR INTEREST IN ENTEROBACTERIACEAE

- Onion + centre rot  $\rightarrow$  *Pantoea*
- Maize + stalk rot  $\rightarrow$  Pantoea
- Potato + soft rot  $\rightarrow$  *Dickeya*
- Collaboration with University of Perugia (Italy)
  - Olive trees + knots  $\rightarrow$  Pantoea/Erwinia
- Collaboration with Forest Research (UK)

Oak + Acute Oak Decline (AOD)  $\rightarrow$  close to Serratia and Brenneria



MLSA STUDY OF PP AND PA ENTEROBACTERIACEAE

- BILA (Belgium-SA), BOF, UGent (2006-2008)
  - → focus on *Pantoea* from *Eucalyptus* and onion
- Post Doctoral Fellowship for non-EU researchers (2009)
  - → plant pathogenic and plant-associated bacteria in the *Enterobacteriaceae* and their relationships with other representatives of the family

## MLSA STUDY OF PP AND PA ENTEROBACTERIACEAE

- included:
- genera such as *Pantoea*, *Erwinia*, *Brenneria*, *Pectobacterium*, *Dickeya*, *Samsonia*, *Serratia* and *Enterobacter*
- strains of closely related genera containing (mainly) isolates from clinical origin, such as *Tatumella*, *Citrobacter*, *Klebsiella*, *Kluyvera*, *Leclercia*, *Raoultella*, *Yokenella*
- unidentified new isolates from trees/plants

#### Pantoea-Erwinia

atpD, gyrB, infB, rpoB

 $\cap$ 

#### Br HG

- > ||
- > IV
- > V

#### isolates from:

- > Eucalyptus
- > Onion
- Maize
- > Olive tree knots



Carrie L. Brady et al. Int J Syst Evol Microbiol







Carrie L. Brady et al. Syst Appl Microbiol 2014;37:417-422





#### Dickeya

#### isolates from potato





## MLSA STUDY OF PP AND PA ENTEROBACTERIACEAE

- successfully constructed an MLSA scheme that included all plant-pathogenic and plant-associated genera of the family *Enterobacteriaceae*
- MLSA phylogeny was partially congruent with 16S rRNA phylogeny
- using MLSA data, several genera were less polyphyletic
- MLSA data suggested the reclassification of some established species into existing or new genera
- the proposed taxonomic rearrangements were supported by DDH data, FAMES and phenotypic data

## MLSA STUDY OF PP AND PA ENTEROBACTERIACEAE

- MLSA is more reliable than 16S rRNA gene sequences for classification of new *Enterobacteriaceae* isolates at the genus and species level
- MLSA of the isolates enabled to identify them at the species level or suggested the existence of new species
- closely related plant-associated and clinical bacteria should not be studied separately

## MLSA STUDY OF PP AND PA ENTEROBACTERIACEAE

- distinction between PA and clinical bacteria is becoming more vague
  - Erwinia
  - Pectobacterium
  - > Enterobacter +
  - > Serratia +
  - 🖻 Rahnella 🔶
  - 🔊 Tatumella 🔶
  - 🗵 Pantoea 🔶
  - Saccharobacter
  - > Brenneria
  - > Samsonia
  - > Raoultella

- » Dickeya
- Mangrovibacter
- Lonsdalea
- Phaseolibacter
- 🛌 Gibbsiella 🔶
- Rosenbergiella
- 🗵 Kosakonia 🔶
- > Lelliottia
- 🖻 Pluralibacter 🔶
- Franconibacter
- Siccibacter

+ Also isolates from human/clinical samples

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