Deciphering phenotypic diversity of *Ralstonia solanacearum* strains pathogenic to potato

Cellier G.[ab], Prior P.[ac]
With technical assistance provided by: Baptiste J. M.[a], Cheron J. J.[a], Lebon S.[a]
[a]CIRAD UMR PVBMT-Université de la Réunion, France; [b]AgroParisTech-ENGREF, France; [c]INRA Département Santé des Plantes et Environnement, France.

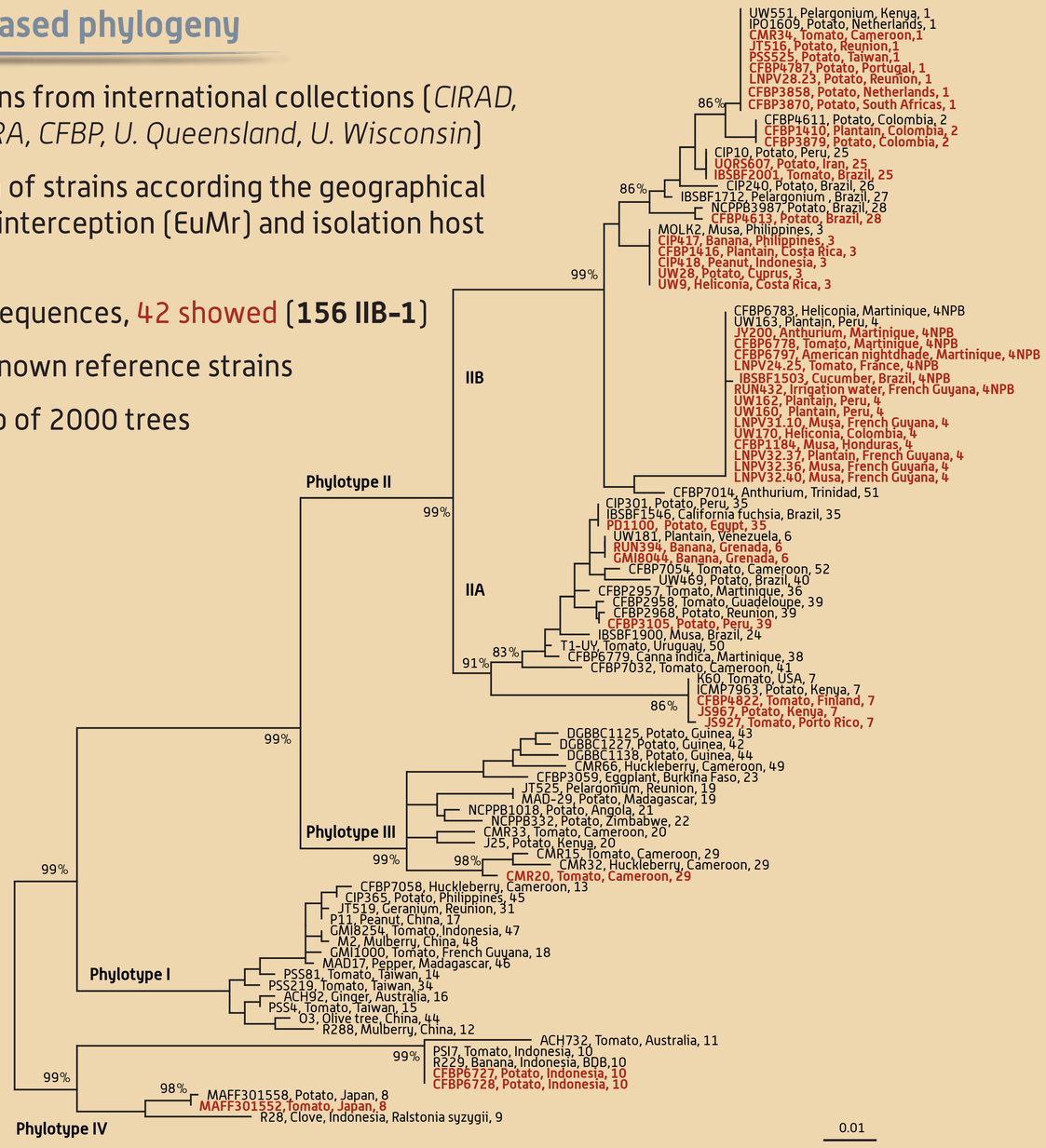
- A soil-borne and a vascular plant pathogenic ß-proteobacterium listed as quarantine organism (European A2 list) and as bioterrorism select agent
- Worldwide geographical distribution and wide host range (at least 54 botanical families)
- Two major ecotypes of economical importance: Brown rot IIB-1 strains on *Solanaceae* and Moko-disease causing IIA-6, IIB-3, and IIB-4 strains on *Musaceae*
- Strains trigger bacterial wilt and are genetically highly heterogeneous and constitute a species complex

Objectives

- Based on phylotype scheme, revisit the genetic diversity among strains pathogenic to *Solanaceae*, with a special attention to potato pathogenic strains from Europe and the Mediterranean
- Revisit and identify virulence patterns of phenotypically divergent while phylogenetically closely related strains within the *R. solanacearum* species complex

egl gene based phylogeny

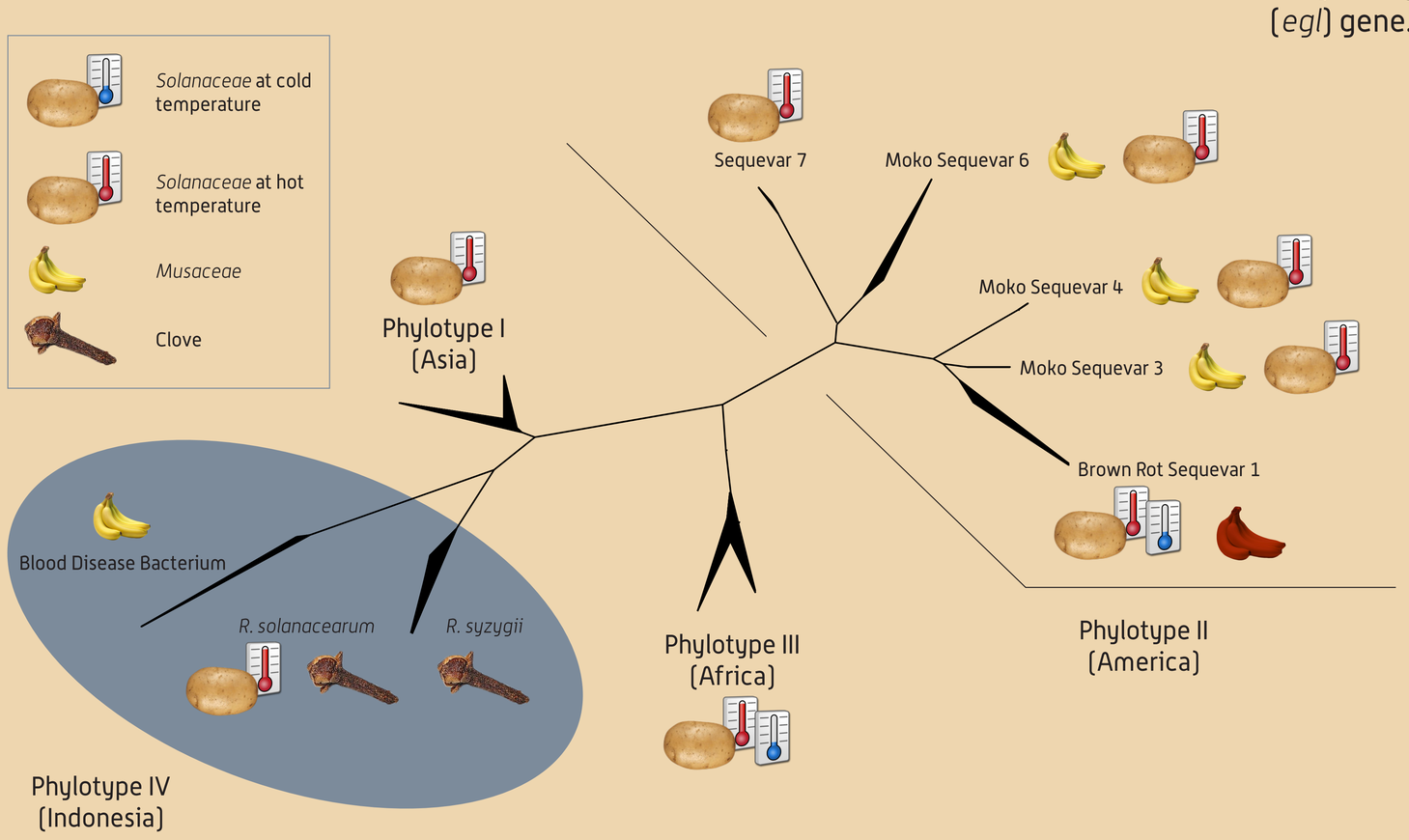
- 450 strains from international collections (*CIRAD, LNPV, INRA, CFBP, U. Queensland, U. Wisconsin*)
- Selection of strains according the geographical origin or interception (EuMr) and isolation host (potato)
- 268 *egl* sequences, 42 showed (**156 IIB-1**)
- 57 well known reference strains
- Bootstrap of 2000 trees



Neighbor-joining phylogenetic tree computed from partial endoglucanase (*egl*) gene. Reference strains are black and collected strains are red

Strains pathogenic to potato were widely distributed among phylotypes while cold tolerant Brown rot strains were monophyletic

- European and Mediterranean (EuMr) strains were mainly (95%) clustered into the Brown rot phylotype IIB-1
- Only five EuMr strains are clustered into other genetic groups:
  - LNPV24.25 (IIB-4NPB) from France / tomato ⚠
  - UW28 (IIB-3) from Cyprus / potato
  - PD1100 (IIA-35) from Egypt / potato
  - CFBP4822 (IIA-7) from Finland / tomato
  - UQRS607 (IIB-25) from Iran / potato



Major pathogenicity lineages within the *R. solanacearum* complex species

Unexpected virulence patterns for well described ecotypes were unraveled

- Cold tolerant Brown rot IIB-1 strains and tropical emergent IIB-4NPB strains were the most aggressive strains
- Unlike BDB, Moko strains (IIA-6, IIB-3, and IIB-4) with the narrowest host range were pathogenic to Solanaceae
- Non-Moko strains, especially Brown rot IIB-1 strains, established into banana as asymptomatic latent infection

Future and prospect

- **Spot the most relevant strains to investigate bacterial speciation towards post-genomic approaches using the in deep pathotypes characterization**
- **Develop a pangenome based Comparative Genomic Hybridization (CGH) approach to investigate gene repertories that might match pathogenicity pattern and design a new diagnosis microarray**

Conclusion

- European and Mediterranean countries are essentially concerned with Brown rot IIB-1 strains but we surveyed (France) the first emerging IIB4-NPB strain in France
- Closely related Brown rot sequevar IIB-1, and Moko-disease causing sequevars IIB-3 and IIB-4 are addressing the question of host adaptation mechanisms which may have undergone a similar bottleneck evolution