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How diverse is the *Ralstonia solanacearum* species complex in the South-West Indian Ocean?



Photo 1. Leaf epinasty of eggplant

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Photo 2. Brown vascular vessels with bacterial ooze on potato tuber

CONTEXT & OBJECTIVES

Ralstonia solanacearum is a species complex (Rssc), distributed worldwide and economically destructive. This soil borne bacterial plant pathogen encompasses an unusual wide host range, genetic diversity, and virulence. The pathogen invades the roots and colonizes the xylem vessels causing the bacterial wilt (BW) disease (Photo 1 & 2). Strains are distributed into four phylogenetic groups based on ITS sequence called phylotypes linked to their geographical origin of evolution: phylotype I (Asia), phylotype II (America), phylotype III (Africa), and phylotype IV (Indonesia-Japan). Although this pathogen is present in the South West Indian Ocean (SWIO), its genetic diversity, virulence range, and genetic structure of populations are unknown. Our main objectives, through a significant collection of *R. solanacearum* strains sampled in SWIO, are to thoroughly analyze this genetic diversity.

SURVEYS

A total of 2971 *R. solanacearum* strains were collected (2012-2015) mainly from *Solanaceae*: Highlands of Madagascar (n=1224, 74 sites), Reunion (n=789, 41 sites), Mauritius (n=695, 25 sites), Mayotte (n=166, 24 sites), Seychelles (n=92, 9 sites), and Comoros (n=5 historical strains, to be completed).

PHYLOTYPING

Phylotype I (46.6%) is widespread in all SWIO islands, whereas phylotypes II (42.3%) and III (11%) are only present in Madagascar highlands and Reunion Island. We report for the first time the presence of phylotype IV (2 strains) in SWIO (Figure 1).

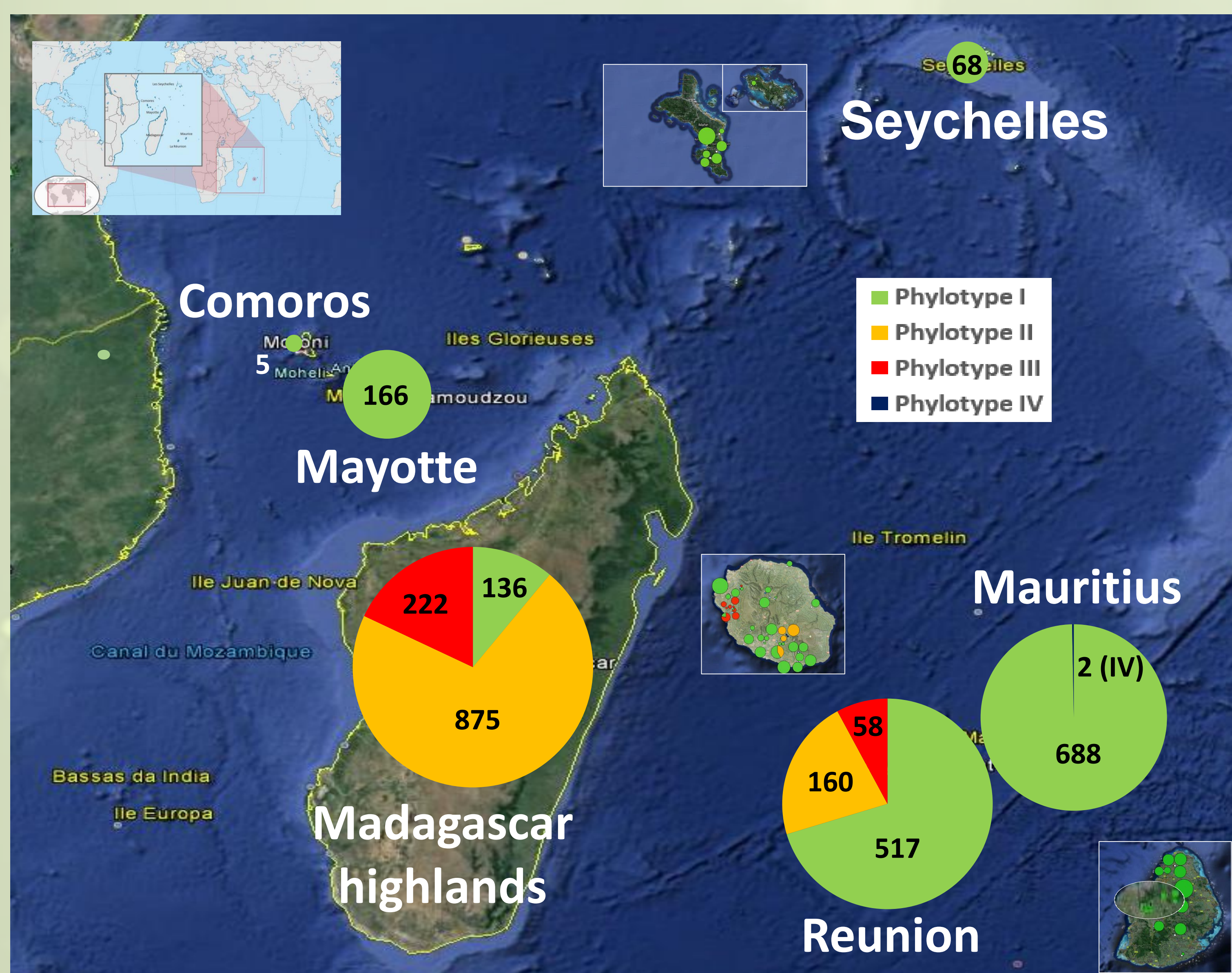


Figure 1. Geographical distribution of newly isolated Rssc strains in the SWIO area (2014-2015)

PHYLOGENETIC ASSIGNMENT OF RSSC STRAINS

Partial endoglucanase (*egl*) gene sequencing (Figure 2) shows that SWIO strains are over represented by only the sequevar I-31.

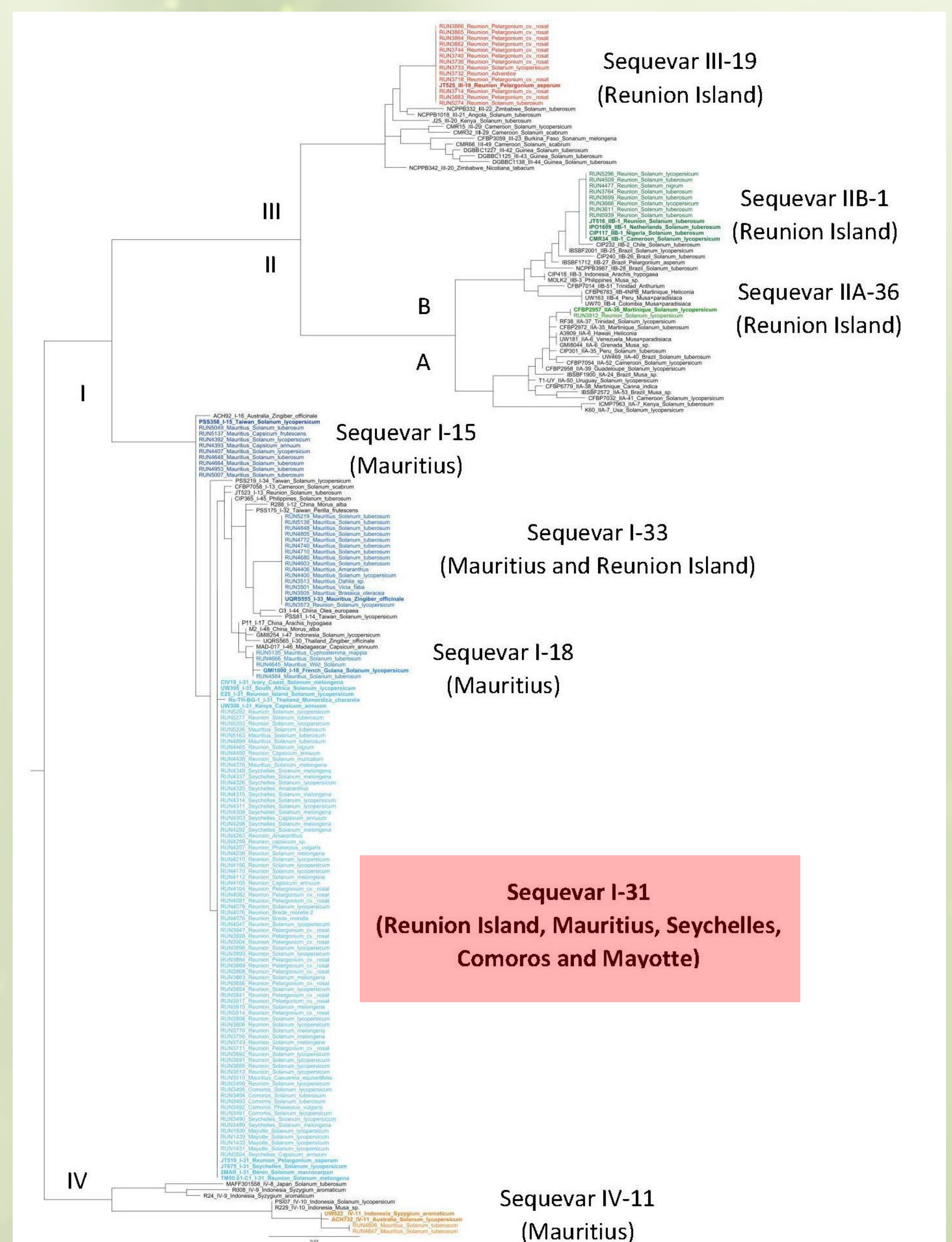


Figure 2. ML tree based on the partial *egl* gene sequences of 128 SWIO Rssc strains, selected to represent one strain / plot / host / phylotype

CONCLUSION & PERSPECTIVES

All phylotypes are present in SWIO, mainly phylotype I sequevar 31.

- Infer phylogeny and evolutionary history of the SWIO Rssc strains through MLSA/MLST and MLVA approaches, and especially on the I-31 strains
- Assess plant genetic resources for BW resistance against the I-31 strains
- Construction of an epidemiosurveillance network (Ralstotracing project) dedicated to Rssc. (Share knowledge, tools and protocols between SWIO research institutions)
- Adaptation of the developed epidemiological tools toward diagnostic applications