

7th IBWS

Montevideo – URUGUAY

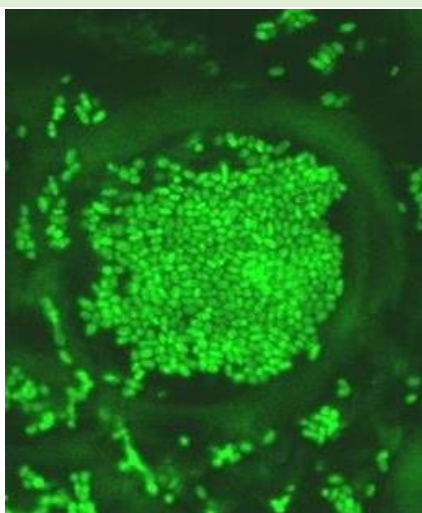
International Bacterial Wilt Symposium

7th International Bacterial Wilt Symposium

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ABSTRACT BOOK



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The *Ralstonia solanacearum* species complex in the age of epidemiology: exploration of its molecular diversity and population structure.

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Long-distance traveling of human beings and movement of goods drastically increase over time in relation with globalization of trade and exchanges, and so is the spread of bacterial pathogens and associated infectious diseases across the globe. Key for improved disease control lies into acquiring a thorough knowledge on factors shaping pathogen populations at fine scales and how they interact with their environment.

In order to show much more clearly how infectious agents are spreading and evolving than sequence data alone, phylogenetic and epidemiological techniques are often use. Bacterial lineage-centered molecular genotyping techniques, such as multilocus variable number of tandem repeats analysis (MLVA), or whole genome sequencing (WGS) techniques are of interest especially when they provide high throughput, a sound phylogenetic signal, and a resolution fitting the spatiotemporal scale investigated. In the case of complex plant pathogen, such as the *Ralstonia solanacearum* species complex (RSSC), several studies achieved molecular characterization of outbreak strains during the last decade mostly using multiplex PCR phylotyping, *egl* partial sequencing, multilocus sequence typing (MLST), MLVA and WGS.

Nevertheless, selecting proper genetic marker and analytical algorithm is vital to apply molecular genetics in a given biological population. Because phylogenetic analysis is inexpensive, especially when sequence data are already available, it is important for molecular epidemiologists to understand, to correctly apply, and to correctly interpret phylogenies and phylogenetic methods. We will then review some key concepts in phylogenetic applied on molecular data associated with the RSSC during this last decade.