

INTEGRATIVE AND CONJUGATIVE ELEMENTS (ICEs) AND GENOMIC ISLANDS (GIs) REVEALS  
POTENTIAL EVOLUTIONARY IMPACT TO ENHANCE THE FITNESS AND PATHOGENICITY IN THE  
*Ralstonia* SPECIES COMPLEX

GONÇALVES, O.S.; SANTANA, M.F.

INSTITUTO DE BIOTECNOLOGIA APLICADA À AGROPECUÁRIA (BIOAGRO), UNIVERSIDADE  
FEDERAL DE VIÇOSA (AVENIDA PETER HENRY ROLFS, S/N, CAMPUS UNIVERSITÁRIO, CEP 36570-  
900, VIÇOSA -MG, BRAZIL)

**ABSTRACT**

*Ralstonia solanacearum* is one the most devastating plant pathogenic bacteria worldwide, able to infect a great diversity of host range. This soil-borne pathogen is composed of a very large group of strains varying in their geographical origin and pathogenic behavior, known as *Ralstonia* Species Complex (RSC). The observation of this heterogeneous group has led to the hypothesis that the mobile genetic elements (MGEs) may play an important role in shaping the structure of RSC diversification. Here, we performed genome mining in 121 RSC genomes and comparative genomic analysis based in the integrative and conjugative elements (ICEs) and Genomic islands (GIs). Overall, our results provide a collective dataset of 41 GIs and 12 ICEs in the RSC, these elements constitute a large fraction of the *Ralstonia* genomes (about 5%) and are phylogenetically related, which might indicate their ancestral acquisition. We also found that the majority of GIs and ICEs identified are preferentially associated with *R. pseudosolanacearum* strains. In addition, ICEs and GIs carry a repertoire of genes with potential impact in the *Ralstonia* fitness and pathogenicity such as stress response and candidate virulence genes as several type III effector proteins, which may enable the bacteria a rapid evolution and infect a wide range of hosts. Altogether, our results provide novel insight in RSC diversified adaptation and further perspectives to better understand how these elements may affect the fitness and pathogenicity traits of this important plant pathogen.

**Keywords:** Genome evolution, microbial genomics, mobile DNA, plant pathogen

**Development Agency:** CAPES, CNPq and Fundação Arthur Bernardes (Funarbe)