

IDENTIFICATION OF PROPHAGES AND ITS POTENTIAL ROLE IN EVOLUTION OF THE *Ralstonia* SPECIES COMPLEX GENOMES

GONÇALVES, O.S.; SOUZA, F. O.; ALFENAS-ZERBINI, P.; 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

Prophages can have a positive or negative effect on the host cell, affecting the lifestyle, genomic diversity, and bacterial fitness. However, many basic aspects of how these organisms affect the host cell remain poorly understood. *Ralstonia solanacearum* is a gram-negative plant pathogenic bacterium, encompassing a great diversity of ecotypes regarded as a species complex (*Ralstonia* species complex - RSC), which assign the type strain *R. solanacearum*, *R. pseudosolanacearum*, and *R. syzygii*. It has suggested that *Ralstonia* genome has a mosaic structure containing numerous elements signaling the potential for evolution through horizontal gene transfer. In this study 120 complete genomes of the RSC deposited in NCBI GenBank, were analyzed for the presence of prophage elements. We have identified a great diversity of prophage-like elements and prophages in the RSC genomes. In total, 374 prophage-like elements were found in the chromosome and megaplasmid. These elements encode genes related to host fitness, virulence factor, antibiotic resistance and niche adaptation genes. Our analysis also identified an integration of complete prophages, belonging to Inoviridae, Myoviridae, and Siphoviridae, into RSC genomes, being the Inoviridae family mostly found. Besides complete phages, we also showed the presence of 14 novel putative phages integrated in the RSC genomes. Altogether, our results provide insights into the diversity of prophages in the RSC genomes and have suggested that these elements might deeply affect the shaped the genome evolution among the strains impacting in host-range adaptation.

Keywords: Bacteriophages, genome evolution, microbial genomics, plant pathogen

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