

EVOLUTIVE IMPACT OF INSERTION SEQUENCES IN THE SPECIES COMPLEX OF *RALSTONIA SOLANACEARUM*.

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Ralstonia solanacearum is a bacterium found in soil with the ability to infect 250 plants in different botanic families, being thus considered the most important phytopathogen in the world. This wide host range may be due to its great genetic variability forming species complex of *Ralstonia Solanacearum* (SCRS). In this context, the presence of mobile genetic elements such as insertion sequences (ISs) can play an important role in the genetic variability of this phytopathogen. The ISs are agents of genetic variability because they have the ability to silence and modify gene expression, are sources of ectopic recombination, and can carry accessory genes. This work aimed at identifying inserted ISs in the chromosome of 60 isolates belonging to SCRS and investigate your importance in the genetic diversification of the complex. The ISs present on the chromosome of the 60 complete genomes deposited in National Center of Biotechnology Information (NCBI) were evaluated by BLASTn on the ISfinder program, considering as cut-off e-value $\leq 10^{-5}$. Then, repeated and inverted sequences (TIRs), which delimit the element, the insertion sites and the ORFs within and close to ISs were annotated in the GENEIOUS® program. Overall, 1,588 ISs were identified in the SCRS. The ISs's size ranged from 658bp to 2,731bb. 90 virulence genes were found between 0pb-350pb of the ISs, of which 16,7% (n=15) are secretory factor of type III (SS3), responsible to inject the effector protein inside the host-cell, 3,3% (n=3) are secretory factor of type IV (SS4), associated with degradation of host tissue, and 2,3 % (n=2) are hemolysin, one of the types of toxins secreted by the pathogen. Also, 24.5% (n=22) of the identified ORFs close to ISs are overlapping the TIRs. Furthermore, 8% (n=7) of the factors of virulence as SS3 and hemolysin were stopped by an ISs. Therefore, it is concluded that due to the insertions and or possible changes in the reading frame of genes related to virulence, the ISs can have an important role in genetic variability and consequently in the evolution of SCRS.

Keywords: Insertion sequences, species complex, virulence genes.

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