

In silico identification of Integrative and Conjugative Elements (ICEs) in bacteria of the genera *Ciceribacter*, *Georhizobium*, *Shinella* and *Xaviernesmea*

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Members of the Rhizobiaceae family are described in different ecosystems, with the genera *Shinella*, *Ciceribacter* and *Xaviernesmea* found in terrestrial environments, either in association with plants, in the soil, or in rhizosphere sediments, while the genus *Georhizobium* is reported in marine environments. Integrative and Conjugative Elements (ICEs) are mobile genetic elements propagated passively, by the replication of the host bacteria's chromosome, and actively via conjugation mechanisms. These elements can carry accessory genes important for the cell's fitness. The objective of this work was to investigate the presence and possible impact of ICEs in the genomes of the four aforementioned genera. For this, 14 complete genomes were downloaded from the NCBI (National Center for Biotechnology Information) database, 1 genome for *Ciceribacter*, 1 for *Georhizobium*, 7 for *Shinella*, and 5 for *Xaviernesmea*. The established work direction began with the use of the ICEfinder software, which predicts ICE signature sequences, such as integrase genes, T4SS, and the oriT sequence. oriTfinder was used to detect conjugative transfer origin sequences that are required for the mobilization of ICEs. Finally, the antiSMASH program was used to identify genetic accessories related to secondary metabolites. 23 putative ICEs were identified, present in genomes of the genera *Georhizobium* (1), *Shinella* (17), and *Xaviernesmea* (5). The oriT region was found in only 4 possible ICEs within the genera *Shinella* and *Xaviernesmea*. Relaxases, enzymes responsible for cutting the DNA strand to be transferred, were found in 22 ICEs, with sizes ranging from 315aa to 1193aa. All ICEs have a Type IV Secretion System (T4SS), the machinery responsible for combining the elements. The T4CP machinery was found in all ICEs except of 1 belonging to the genus *Shinella*. As a secondary metabolite, the volatile compound hserlactone was found, which plays an important role in intercellular communication through *quorum sensing*, coordinating the expression of specific genes. Another secondary metabolite found was terpene, whose function may be related to defense against environmental stress and chemical signaling for intercellular communication. Our results indicate the existence of a relatively large number of ICEs in the genomes of the genera studied when compared to other genera, such as pathogenic bacteria. However, the function of these elements has not yet been elucidated in the genera analyzed here. Therefore, new studies will be carried out *in vivo* to better understand the possible relationship between ICEs and the adaptive advantages of some genera of bacteria from the Rhizobiaceae family.

Key words: Integrative and Conjugative Elements; Mobile genetic elements; Rhizobiaceae.

Identificação *in silico* de Elementos Integrativos e Conjugativos (ICEs) em bactérias do gênero *Ciceribacter*, *Georhizobium*, *Shinella* e *Xaviernesmea*

Os gêneros *Ciceribacter*, *Georhizobium*, *Shinella* e *Xaviernesmea* são encontrados em diferentes ecossistemas. Elementos Integrativos e Conjugativos (ICEs) são elementos genéticos móveis propagados passivamente ou ativamente, podendo carregar genes importantes para o fitness da célula. O objetivo deste trabalho foi investigar a presença e possível impacto de ICEs em genomas dos quatro gêneros supracitados por meio de estudos *in silico* utilizando os softwares ICEfinder, oriTfinder e antiSMASH. Dentre os 14 genomas baixados no NCBI, foram identificados 23 putativas ICEs. Como metabólitos secundários foram encontrados o terpene e o hserlactone. A função desses elementos ainda não foi elucidada nos gêneros aqui analisados.

Palavras-chave: Elementos genéticos móveis; Elementos Integrativos e Conjugativos; Rhizobiaceae.