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Talk

Computational analysis of an integrative and conjugative element in a biodegrader bacterium

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ABSTRACT

In this study, we explore a shared sequence of an integrative and conjugative element (ICE) in Sphingopyxis granuli strain TFA. ICEs are significant mobile genetic elements, which are integrated into the bacterial chromosome and encode a fully functional conjugation machinery, making them self-transmissible between bacterial cells. ICE cargo genes can confer host selective advantages such as antibiotic resistance and virulence factors (Delavat et al., 2017). S. granuli strain TFA is a member of the Sphingomonadaceae family, has garnered attention for its metabolic capabilities, particularly in the degradation of aromatic compounds such as tetralin. This strain has been characterized through genomic analyses that reveal its potential for environmental adaptability and resistance mechanisms (García-Romero et al., 2020). For these reasons, the presence of ICEs in the S. granuli genome has been identified and confirmed using the ICEfinder tool (Liu et al., 2019). A unique sequence has been selected that does not occur in all other S. granuli strains but in other bacteria in which the conserved sequence is found with more than 99% identity and 80-96% coverage using skani, which is a program for calculating average nucleotide identity (ANI). Each of the genes present in the shared ICE was annotated using BLAST (Basic Local Alignment Search Tool) from NCBI. In addition, structural annotation of all genomes and shared ICE was performed using Bakta (Schwengers et al., 2021). Raw sequencing data have been used to confirm the integration site of the shared ICE. The ends of the ICE are currently being investigated with an evolutionary approach, a set of genetic elements around the ICE known as genetic archipelago is conserved among bacteria.

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