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# A physiological explanation for the abundance of transposon DNA in bacteria

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## Abstract

Transposon DNA is highly abundant in genomes, even in microbes. Typically, 1-30% of microbial genomes are active transposons. Surprisingly, the biological role of transposons within microbial genomes remains poorly understood. Transposons are disrupters of genetic information, involved in pseudogenization, the deterioration of genomes and key to the breakdown of product expression in biotechnology. On the other hand, transposons contribute to genetic change and adaptation by their importance for genetic recombination and the generation of beneficial mutations. Here, we experimentally test for biological effects of transposons on a whole-genome level – when they are not transposing. We ask whether transposons are beneficial or deleterious to their host cells in a natural state and how they impact physiology and fitness. For this work, we focus on the group of insertion sequence elements (IS), which are the most abundant group of transposable elements in bacteria. Using genome engineering techniques, we constructed strains with which we can look at the individual IS families (IS1, IS3, IS5 etc.) and their mutants. The strains were validated using hybrid sequencing with Nanopore and Illumina and off-target mutations corrected. This allowed us to measure the biological impact of IS for bacterial growth and competitive fitness, by direct comparison of the strains in mono and co-culture experiments. We find that IS elements are directly beneficial to the physiology of a bacterium. They increase competitive fitness and growth rate. We thus identify a beneficial physiological role of transposon DNA in bacterial cells, providing an explanation for their abundance in bacterial genomes.

**Keywords:** bacteria, IS element, genome engineering

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