

Opinion Article

Genetic sequences in microorganisms

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DESCRIPTION

The term “Horizontal Gene Transfer” (HGT) describes how organisms pick up foreign genes. It is expected that the presence of HGT among environmental bacteria will have an impact on how risky genetically modified bacteria are when discharged into the environment. First, native microorganisms could be exposed to imported genetic sequences from a genetically engineered bacterium, changing their ecological niche as a result. Second, the genetically altered bacteria may take up Mobile Genetic Elements (MGE) from local microorganisms, which could increase their ecological potential. Understanding the degree of HGT and genome plasticity of bacteria in the environment is crucial for risk assessment. The current level of knowledge on HGT between bacteria, a key process promoting bacterial adaptability and variety, is outlined in this study. In this article, we specifically focus on the prevalence and function of MGE in soil and plant-associated bacteria as well as the variables affecting gene transfer in light of the usage of GM crops and microbes in agricultural contexts.

When numerous antibiotic resistances to pathogens were shown to be caused by “infectious heredity,” the relevance of HGT between bacteria was first understood. A genome examination of eight free-living bacteria revealed that members of such “exchange communities” tend to be similar in terms of traits including genome size, genome G/C composition, carbon usage, and oxygen tolerance. HGT can only influence bacteria that readily exchange genes. There is now a lot of evidence that horizontal gene transfer is an ongoing process that plays a key role in the real-time ecological adaptation of prokaryotes. While genome sequences have provided retrospective evidence of horizontally acquired genes over long time periods and their importance in bacterial evolution. By influencing bacterial genomes, encouraging intra-species diversity, and dispersing functional genetic modules among exchange communities, MGE play a crucial part in this process. The HGT of genetic

modules that enable quick adaptation to such variables is encouraged by dynamically shifting selection forces. In order to adapt to rapidly changing biotic interactions, HGT of genetic modules was frequently seen. Examples of these interactions include the production of antibiotics by microbes or the use of antibiotics by humans, which leads to the spread of antibiotic resistance, the release of xenobiotics or new secondary metabolites and the spread of derivative genes and pathway assembly, or pathogenic and symbiotic interactions and the spread of genomic islands.

Transformation, transduction, and conjugation are the three main mechanisms that cause Horizontal Gene Transfer (HGT) between bacteria. The crucial vehicles in the latter two processes are Mobile Genetic Elements (MGEs), which include plasmids, bacteriophages, integrative conjugative elements, transposons, ARE elements, integrons, gene cassettes, and genomic islands. The defining characteristics of MGEs are briefly outlined. Plasmids, prophages, pathogenicity islands, and integrons are only a few of the MGEs found in soil and plant-associated bacteria thanks to the application of genomic techniques. A significant fraction of bacteria from various settings were found to carry plasmids, according to surveys on the presence of plasmids isolated from plant-associated or soil bacteria. Plasmids were discovered in about 18% of the bacterial isolates from the sugar beet phytosphere. The limited nutrients that soils typically offer to enable microbial growth lead to low population densities and activity levels. In turn, this limits microbial activities that depend on density and activity, like all HGT.

It is now well acknowledged that HGT was crucial to the development of bacterial genomes. It is also a key method for bacteria to adapt in the present. The mosaic structure that can be seen in many sequenced bacterial genomes reflects the pressure for genetic flexibility. The potential for and, more crucially, the likelihood of any negative impacts of HGT on microorganisms in the environment must be taken into account when evaluating the risks associated with genetically modified organisms.

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