



Chapter

Genomic Islands in Helicobacter Species

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S.s. Meenambiga · Varsha K · Sowmya Hari · Sakthiselvan Punniavan

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Abstract

Horizontal gene transfer mechanisms help in the transfer of distant genes generating pathogens with different types of virulence. Genomic Islands (GI) are the evidence representing microbial genome evolution. These genes are acquired by HGT process. It determines their adaptation to the environment, compatibility, and other gene expression mechanisms. The pathogenicity islands which are a subclass of Genomic Islands contribute to the virulent nature of the pathogen. Helicobacter pylori known for its colonization in the stomach and the intestinal regions poses the most genetic diversity among the pathogenic species of the bacterial community. H. pylori has the ability to adapt to the host system by changing its gene members. Chronic infections show the maximum genetic differential ability of H. pylori. The strains are categorized into type 1 and type 2 in which each secretes certain antigens and cytotoxin enhancing its virulence. Numerous computational tools have been advanced to recognize and categorize these genomic islands. One such tool is Island viewer which enables the user to access published and GIs. It is also linked with external databases like NCBI. GIs can be predicted based on genomes. GIs do not frequently replicate like plasmids and they serve as markers for identifying evolutionary pathways. However, real-time tracking is still under research and needs to be developed.

Keywords: Horizontal gene transfer, Genomic Islands, Pathogenicity islands, Helicobacter pylori, Antigens, Cytotoxins, Genomes, NCBI, Plasmids

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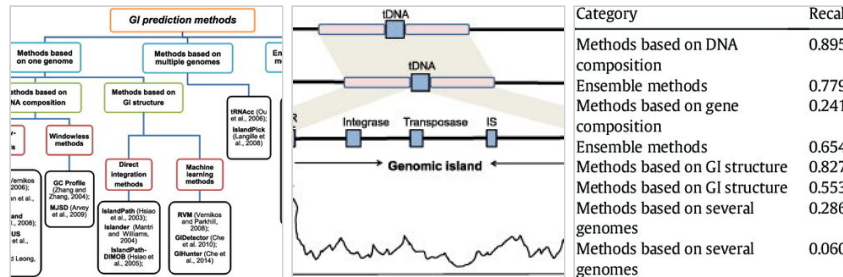
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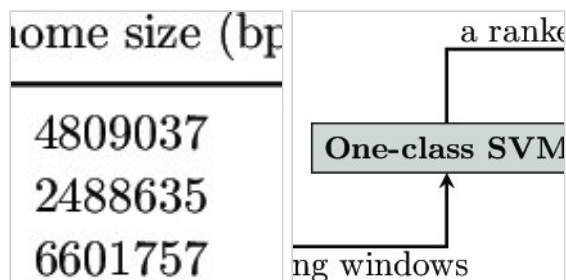
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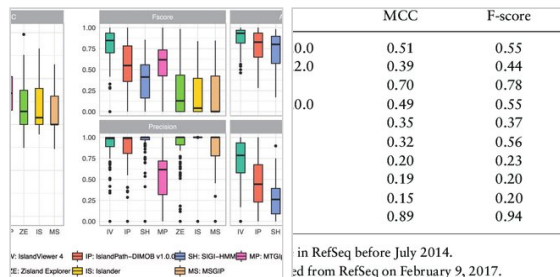
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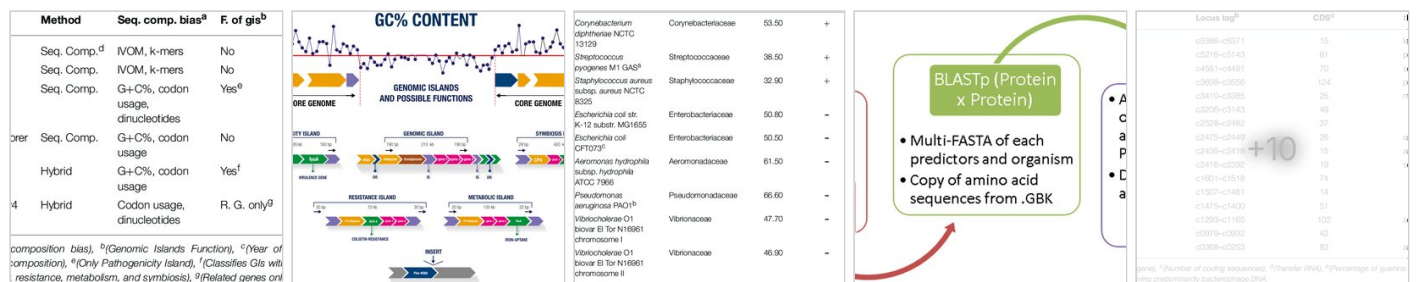
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