DUMP: DATABASE OF UNIQUE METABOLIC PATHWAYS

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Bacteria are present everywhere, on objects, in air, and usually found inside and outside the human body. Pathogenic bacteria are those which cause infections in the host organism. They can infect host by multiple ways, wounds, contaminated water and food, etc. Spread of infections is very common due to globalization and frequent traveling by one part of the world to the other. The success of a pathogen in host cell depends upon multiple factors. The existence of unique metabolic pathways (not present in host) to survive in unfavourable conditions exhibited by pathogenic (i.e. resistance to antibiotics) is another alarming situation in recent times. Pathogen's ability to multiply and propagate to the other parts of the host largely depends upon the interaction with the host molecular machinery. Pathogen's normal metabolic mechanism can be disturbed by the drug or antibiotic, administered to cure the disease. However, the pathogen has capability to bypass and display unique metabolic pathways to survive in that acute unfavourable condition, and hence resulted in resistance. DUMP has all pathogenic bacteria which were reported in KEGG (Kyoto Encyclopedia of Genes and Genomes) and were selected by further confirmation provided by VFDB (virulence factor database). After having a list of pathogenic bacteria, unique metabolic pathways of pathogenic bacteria were identified (pathways that did not appear in host but were present in pathogen were called as unique metabolic pathways). For this purpose, in-house bash-shell scripting was used to iterate the process of identifying the unique metabolic pathways of all pathogenic bacteria. User can download the files consisting of a list of pathogenic bacteria, list of unique metabolic pathways of pathogenic bacteria and list of enzymes involved in unique metabolic pathways in text format.

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