

ABSTRACT

The pathogenic microorganisms are responsible for causing infectious diseases. These microorganisms include bacteria, viruses, fungi and parasites. The infectious diseases account for large number of deaths and the most identifiable infectious diseases are Invasive bacterial diseases, Melioidosis and Ebola virus disease. *Streptococcus pneumoniae* and *Haemophilus influenzae* are the most common community-acquired bacterial pathogens and causes great extent of invasive bacterial diseases and respiratory tract infections (meningitis, septicemia, pneumonia, bronchitis, and sinusitis). These pathogens exhibit increased resistance against commonly administered antibiotics which are used to treat these infections. Melioidosis awareness is surprisingly low among physicians and health care workers in endemic regions in spite of its higher prevalence. Ebola virus disease represents a miniscule fraction of the major infectious diseases and causes an acute febrile illness that is widely associated with the high mortality rates. Thus, these diseases impose a serious burden on human health care systems throughout the world. There is an immediate requirement to afford organism specific annotations for these organisms to scientific community. In view of above, *Streptococcus pneumoniae* Genome Database (SPGDB), *Haemophilus influenzae* Genome Database (HIGDB), Melioidosis Database (MDB) and *Ebolavirus* Database (EDB) are developed for *S. pneumoniae*, *H. influenzae*, Melioidosis and Ebola virus disease respectively. These databases will act as universal single point resources for complete proteomic and genomic data. In addition, these databases provide various tools to compare the gene and protein sequences. The comparative analysis of their genomes may be useful to identify the immunogenic targets and drug candidates by finding out the genes involved in virulent activity. These databases can be used to predict the DNA/RNA motifs within their genomes, to analyze the phenotypic variations and also to perform comprehensive genomic and proteomics studies. These databases are available through the following URL:

- SPGDB - <http://pranag.physics.iisc.ernet.in/SPGDB/>
- HIGDB - <http://bioserver1.physics.iisc.ernet.in/HIGDB/>
- MDB - <http://bioserver1.physics.iisc.ernet.in/MDB/>
- EDB - <http://bioserver1.physics.iisc.ernet.in/EDB/>