Chapter 1

Introduction

Infectious diseases (IDs) are disorders or diseases caused by various pathogenic microorganisms such as bacteria, virus, parasites or fungi. Many of these organisms are usually harmless and helpful but under certain circumstances, some organisms infect humans and cause diseases (Wolfe et al., 2007). The term IDs do not indicate the homogenous group of illnesses but assigned to a broad group of broadly different conditions. IDs are one of the most important contributors to human mortality and morbidity. IDs represent the vast extent of death and disability throughout the world and in specific regions; it remains the most imperative reason for ill-health (Lederberg, 1998; Gwatkin et al., 1999). In 2000, the global burden of disease study shows that IDs are accountable for 22% of deaths and 27% of disability worldwide (Murray et al., 2012). In spite of the fact that IDs can affect individuals of all ages, they enforce a particular burden on youngsters remarkably on children below 5 years of age. This is because the younger ones have a lower predominance to non-communicable illnesses and also they have greater susceptibility towards the new infections than adults. The younger ones lack the defensive mechanisms to minimize the impact of these illnesses (Goldmann, 1992; Saiman et al., 2001; Mehnaz, 2009).

The signs and symptoms of IDs may be varied depending upon the organism causing the infection, but frequently it includes fever and weakness. The IDs can be passed from one individual to another individual and sometimes, it can be transmitted by biting of individuals from insects or animals. And others are acquired by the ingestion of contaminated water or food or being exposed to organism present in the environment (Woolhouse, 2002; Jones et al., 2008).

The most common IDs occurring throughout the world are African trypanosomiasis, cholera, dengue, Ebola virus disease (EVD), hepatitis, acquired immune deficiency syndrome, malaria, measles, melioidosis, Invasive Bacterial Diseases (IBD), shigellosis, tuberculosis and typhoid. The precise numbers of instances of IDs are hard to decide as most of these diseases are endemic to developing countries where individuals do not have a modern medical care
approaches (Daszak et al., 2000). Every year World Health Organization (WHO) publishes a list of the most identifiable diseases (McCormick, 1987). IBD, melioidosis and EVD are recognized as the most identifiable IDs for the last 10 years and hence, these three diseases are considered for research work.

The diseases such as meningitis, pneumonia, septicemia, bronchitis and sinusitis are the major IBD. These diseases are responsible for causing high mortality and morbidity among the young children and in the elderly people (Osterholm, 1990). Thus, IBD remains an important public health issue. IBD are caused by invasive bacterial pathogens which includes Streptococcus pneumoniae, Haemophilus influenzae, Neisseria meningitis, Group A & B Streptococcus and Methicillin-resistant Staphylococcus aureus. Among these invasive pathogens, S. pneumoniae and H. influenzae are the major causative agents of IBD (Degani et al., 2008; Meyer et al., 2008).

S. pneumoniae is also known as Pneumococcus and it is a Gram-positive (GP), alpha haemolytic bacterium. It belongs to the member of genus Streptococcus (Jones et al., 2010; Barichello et al., 2012). The organism spreads through quick contact with respiratory discharges from the infected patients as well as from the healthy carriers. S. pneumoniae is accountable for significant mortality both in children and in elderly people (O’Brien et al., 2009). In most of the developed countries, the concern of streptococcal diseases is greatly enhanced with chronic diseases like renal failure, sickle-cell disease, asplenia, liver disease, Mycobacterial and HIV infections, and additionally with aging population (Blasi et al., 2012). The WHO addressed that million instances of pneumococcal disease occurred and results in 8,26,000 deaths in infants aged between one to fifty nine months.

H. influenzae is a Gram-negative (GN) bacterium and it is the first bacterial genome to be sequenced. The organism is one of the most important community-acquired pathogen and it causes respiratory tract infections in children as well as in adults (Kofteridis et al., 2009; Kumar et al., 2014). Among various serotypes of H. influenzae, the type b H. influenzae (Hib) strains are overwhelmingly connected with serious systemic diseases like empyema, pneumonia, meningitis, septicaemia, and septic arthritis (Bae et al., 2010; Okada et al., 2012). The nontypeable H. influenzae
(NTHi) strains are responsible for causing otitis media, sinusitis, conjunctivitis and acute lower respiratory tract infections (Hood et al., 1996; Moghaddam et al., 2011; Marshall et al., 2014). The WHO reported that approximately 3,86,000 deaths occur every year in developed countries because of this organism and especially through meningitis and pneumonia (Chen et al., 2014). Even though, S. pneumoniae and H. influenzae are part of the normal upper respiratory tract flora, these organisms become pathogenic under some conditions like when the immune system of host is quenched (Rodriguez et al., 2011). The prevalence of these organisms and antibiotic resistance is increasing and hence, the optimum treatment for these IDs has become more complicated (Appelbaum, 1992; Tomasz, 1997; Tristram et al., 2007; Kostyanev and Sechanova, 2012).

Melioidosis caused by *Burkholderia pseudomallei* is re-emerging and endemic in tropical countries. *B. pseudomallei* is extremely pathogenic to humans and hence, the Centers for Disease Control (CDC) have categorised this bacterium as a category B agent (Cheng and Currie, 2005; Sarkar-Tyson et al., 2009; Revelli et al., 2012). The signs and symptoms of melioidosis may extend from acute fulminant septicemia to chronic pulmonary disease imitating tuberculosis (Wiersinga et al., 2006; Meumann et al., 2012). The treatment for melioidosis is very difficult as the organism has resistant activity towards large number of antimicrobial agents and the disease requires regular antibiotic treatment and without the treatment, the infection may re-surface in the affected patients (Simpson et al., 1999; Jenney et al., 2001; Cheng et al., 2007; Saravu et al., 2008). Currently, there is no vaccine available for prevention of this deadly disease. Hence, the mortality rate for the disease continues to be remarkably high and it remains a worldwide noteworthy public health problem.

EVD is accountable for extensive number of outbreaks of severe haemorrhagic fever in human beings, and the disease is endemic in Equatorial Africa or Middle Africa (Alvarez et al., 2002; Murray, 2015). EVD has spread over a number of countries, and all of them were exported from Africa. The *Ebolavirus* infections have high case-fatality rates or lethality rates which may be ~42% and it may be differ significantly and likely reflect, partially in the levels of acute care provision, variations in diagnostic accuracy and infecting species (Hoeren et al., 2006; Feldmann and Geisbert, 2011). The ebolaviruses can be transmitted through direct
contact with infected individuals or with dead bodies (Khan et al., 1999). The 

_Ebolavirus_ comprises of five viruses namely Tai Forest virus, Reston virus, Sudan virus, Ebola virus and Bundibugyo virus. Each of these five viruses belongs to a separate species. But, there have been dozens of _Ebolavirus_ outbreaks and yet the agents causing those outbreaks can be assigned to those five species (Bukreyev et al., 2014; Feldmann, 2014). Currently, there is no effective prophylaxis (including vaccine) available for the _Ebolavirus_ infection (Fauci, 2014; Yazdanpanah et al., 2015). The Ebola virus outbreak started in 2013 and it killed more than 2,622 people, including many healthcare workers and as of today, it killed 11,302 people. The number of deaths in current outbreak is greater when compared with that of all earlier outbreaks combined (Baden et al., 2014; Frieden et al., 2014). Thus, these outbreaks serve as an important global public health concern (Baize et al., 2014). In spite of most significant accomplishments in the last two decades to understand the fundamentals of Ebola virus biology, only little information is known about protein and protein precursor functions, and also the major virulent factors responsible for causing the infections are poorly understood.

In recent years, there is an important attention gained towards the comparison of genome of each strain/ species with other strains/ species for these organisms as the number of genome sequencing for these organisms have been amplified manifold. This comparing of genomes contributes knowledge on the strain/species specific characteristics that may play a vital role in virulent and antimicrobial resistance. There is an immediate requirement to afford organism specific annotations to the scientific or research community. However, there are no databases available for _S. pneumoniae, H. influenzae_, melioidosis and _Ebolavirus_. Thus, the objective of this study is to develop universal single platforms for these organisms to provide the complete genomic and proteomic information, to perform simple/advanced Boolean and similarity based searches, to identify the motifs in complete genome of an organism and to visualize the complete genome annotation and protein structures of an organism.