The Impact of Genomics Evolution and Genomic Island in *Burkholderia pseudomallei*

**Opinion**

*Burkholderia pseudomallei* is a Gram-negative, bipolar, aerobic, motile rod-shaped bacterium [1]. It is a soil-dwelling bacterium endemic in tropical and subtropical regions worldwide, particularly in Thailand and northern Australia [2]. It's a powerful organism, can live in different environments and is also capable to cause a potentially life-threatening infection. It infects humans and animals, and causes disease melioidosis, which caused by Burkholderia pseudomalleus (BP) commonly presenting as an acute septicemic illness, chronic Bp infection is also well recognized which can be confused with TB or malignancy, this confusing happened because of the gene exchange [9].

Many bacterial species exploit specialized secretion systems to transfer macromolecules across bacterial membranes, which by transfer of proteins or nucleoprotein complexes directly mediate pathogenicity and horizontal gene transfer [10].

*B. pseudomallei* has a highly plastic genome and has the ability to acquire new genes horizontally from other microorganisms, especially as the pathogen persists in the environment. A large-scale blast score ratio (LS-BSR).

GIs are one of the major sources of genomic diversity within *B. pseudomallei* and the molecular mechanisms that facilitate horizontally-acquired GIs are common across multiple strains of *B. pseudomallei*. The differential presence of the 71 GIs across multiple strains demonstrates the importance of these mobile elements for shaping the genetic composition of individual strains and populations within this bacterial species [10]. The genomic positions of these GIs are not random, as many of them are associated with tRNA gene loci. In particular, the 3′ end sequences of tRNA genes are predicted to be involved in the integration of GIs [11]. *B. pseudomallei* genes that may cause a predisposition to human disease and that these genes tend to be located on GIs [12].

*B. pseudomallei*, is composed of two chromosomes of 4.07 megabase pairs and 3.17 megabase pairs, each one of them genes have various function. The large chromosome encodes many of the core functions associated with central metabolism and cell growth, whereas the small chromosome carries more accessory functions associated with adaptation and survival in environmental and pathogenic [8]. Example; melioidosis disease which caused by Burkholderia pseudomalleus (BP) commonly presenting as an acute septicemic illness, chronic Bp infection is also well recognized which can be confused with TB or malignancy, this confusing happened because of the gene exchange [9].
different niches. Genomic comparisons with closely and more distantly related bacteria revealed a greater level of gene order conservation and a greater number of orthologous genes on the large chromosome, suggesting that the two replicons have distinct evolutionary origins. A striking feature of the genome was the presence of 16 genomic islands (GIs) that together made up 6.1% of the genome [13]. Unfortunately, almost 35% of the GI genes encode ‘hypothetical’ proteins, meaning that their function is unknown[12].

*B. pseudomallei* genome is widely considered to be ‘open’ (sequencing new strains is always expected to lead to the discovery of new genes), with very high levels of lateral gene transfer, generating the large and moderately diverse genome observed, that recombines at a high frequency, leading to great intra-species diversity within and among pathogen populations. Demonstrated high levels of diversity in *B. pseudomallei* in datasets from MLST (Multi-Locus Sequence Typing) analysis suggesting that genetic exchange has not been limited to GIs. These conserved MLST sites are located at scattered locations along the genome and suggest that homologous exchange occurs extensively throughout the genome and includes presumably core ‘housekeeping’ genes [14].

We can use pathogenicity islands (PAIs) as marker to help identify a certain bacterial pathogen, PAIs are a distinct class of genomic islands (GEIs), which are acquired by horizontal gene transfer. PAIs harbour virulence genes and some, in addition, antibiotic resistance genes. More often genes conferring antibiotic resistance are encoded by GEIs not containing virulence genes. Both types of genetic elements are found in genomes of various human, animal and plant pathogens. There are PAIs and GEIs which are specific for a certain serotype(s), strain, or pathotype of a species. Furthermore, there are also PAIs which are more widespread and found in bacterial pathogens causing a certain pathogenic effect in the host. Even the lack of a certain PAI might be characteristic for a defined subspecies. Obviously, PAIs can be used as markers for diagnostic purposes to help identify a certain bacterial pathogen, subtype it, estimate the pathogenic potential, and in some cases predict its antibiotic resistance [15s].

The genomic structure of bacteria, gives them the ability to survive in new environment and respond to environmental stress and also strengthen the pathogenic effect, so small organism with high life threatening danger.

Acknowledgment

None.

Conflict of Interest

None.