27th ECCMID Vienna, Austria 22 – 25 April 2017
The congress of ESCMID

Session: P079 Mycobacteria and other fastidious microbes

Category: 4c. Molecular bacterial typing methods

25 April 2017, 12:30 - 13:30
P1598

Whole-genome sequencing and analysis of Burkholderia cepacia complex clinical isolates from India

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Background:

Burkholderia cepacia complex (Bcc) comprises twenty phenotypically similar but genetically distinct species. Members of Bcc are recognised as an important pathogen in immunocompromised, cystic fibrosis (CF) and hospitalised patients causing mainly life-threatening bacteraemia, urinary tract infections and respiratory tract infections. In our recent study to understand the population structure of Bcc from India, we found that there are two lineages by multilocus sequence analysis (Gautam, V. et al. 2016). Further to understand genomic diversity, species status by modern taxonomic criterions, variation by horizontal gene transfer, candidate virulence loci and its resistome we aimed to carry out whole genome sequencing on this collection of Bcc. Whole genome sequencing and analysis of the eleven representative isolates (Blood; n=9, Respiratory specimen; n=2), including one CF isolate was carried out.

Material/methods:

Whole genome sequencing was carried out by using Illumina Miseq platform with pair-end sequencing strategy. Reads were De-novo assembled into the high-quality draft genome using CLC Genomic Workbench 9.5.2 and annotated by using RAST. The species of the Bcc isolates was confirmed by calculating Average Nucleotide Identity (ANI) and Digital DNA-DNA hybridization (dDDH) by JSpecies and Genome to genome distance calculator respectively. We screened these genomes for the presence of the key virulence features, transmissibility marker genes like *cblA*, *emsR* and genomic islands. Genome alignments with reference strains were carried out by using Mauve and BRIG.

Results:

The genome size ranging from the 6.6 to 9.1 Mb with GC content around 67%. Based on the modern genome based taxonomic criterion ANI and dDDH, the isolates 30379, 7216, 1125, 22565, 7142, 1168 belongs to *B. cenocepacia* and isolates 5310, 4613, 31178, 8947 belonged to *B. cepacia*. The species status is consistent with as identified by MLSA except for CF isolate 1236 which is a taxonomic outlier with *B. cenocepacia*. Interestingly, it was found that 8947, harboured transmissible marker *cbl* gene cluster thus it belonged to the ET12 lineage, which is highly transmissibility lineage in the US, UK and Canada. Further 1125, 22565 also harboured *esmR* gene called as *Burkholderia cepacia* epidemic strain marker (BCESM). When compared with the reference genomes *B. cenocepacia* J2315 and *B. cepacia* ATCC 25416 genomic variations were observed between the genomes. Comparative genomic analysis of these isolates, to examine the genomic differences and their correlations with clinical metadata are currently being performed.

Conclusions:

The present study highlights the genome diversity and dynamics of the Bcc isolates from India, which has never been studied before. Further genome sequencing and analysis of the isolates is ongoing in order to understand the genome based biology of this important pathogen.