

P1418 **Whole-genome sequencing reveals recently acquired virulence islands in *Ralstonia mannitolilytica* isolated from high-risk patients**

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Background: *Ralstonia mannitolilytica* is a Gram-negative bacteria found in moist environments, such as water, soil and plants. It has been rarely associated with nosocomial infections. However it has an ability to survive in different types of disinfectants and to pass through 0.2-µm filters which are used to sterilize solutions. Thus, it is still a potential agent for healthcare associated infections that can even result in outbreaks.

Materials/methods: Two patients with lymphoma hospitalized in bone marrow transplantation unit developed clinical signs of infection and *Ralstonia mannitolilytica* strains were cultivated from blood samples of the Intravascular catheter. Pathogen isolation and identification was done using standard microbiological procedures. Whole genome DNA sequencing of one strain was performed using Illumina MiSeq and Oxford Nanopore MinION technologies. The genomes were assembled by SPAdes 3.11. RAST annotation server was used to predict genes and annotate the protein functions. Mauve whole genome aligner was used to conduct comparative genomics analyses.

Results: A total of 4777 Open Reading Frames were found from 5,082,331 bp genome. Comparing the genome against previously sequenced *Ralstonia mannitolilytica* strains, similar antimicrobial gene profile (identical Beta-lactamase, fluoroquinolone resistance, and Multidrug Resistance Efflux Pumps genes) was detected. The sequenced strain contains abundant phage-related islands and transposable elements. We have detected that these islands harbour Type VI protein secretion systems and pathogenicity island “nu Sa beta2” which do not exist in the previously sequenced *Ralstonia mannitolilytica* isolates.

Conclusions: We have detected *S. aureus* related pathogenicity island in a *Ralstonia mannitolilytica* pathogen for the first time, which might indicate a potentially more virulent human pathogen. The bioinformatics analysis reveals that this is due to a phage-mediated recent horizontal transfer.