47th World Congress on Microbiology

September 10-11, 2018 | London, UK

A Genomic Infection Control Study For Staphylococcus aureus In Two Ghanaian Hospitals

Prof Eric Sampane-Donkor Dept. of Medical Microbiology, University of Ghana

Staphylococcus aureus is a notorious hospital acquired pathogen and is implicated in several serious infections such as meningitis, bacteraemia and pneumonia. Whole genome sequencing analysis (WGSA) provides the best resolution for typing of bacterial isolates and has the potential for identification of transmission pathways. We used WGSA to study carriage, environmental and clinical isolates of S. aureus from Korle-Bu Teaching Hospital (KBTH) and Lekma hospital (LH) in Ghana where suspected outbreaks of the organisms had recently occurred. The isolates belonged to diverse sequence types (ST) with ST15 and ST152 most common. All isolates carried the blaZ gene, with low prevalence of tetK and dfrG genes also observed. All isolates were mecA negative. The pvl genes were common and observed in distinct lineages that revealed diverse Sa2int phages. The genomics data indicated contamination of various surfaces in the paediatric emergency ward of KBTH by strains of ST15 and highlights the need for a more rigorous disinfection of environmental surfaces at this hospital.

ericsdon@hotmail.com