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## A genomic infection control study for *Staphylococcus aureus* in two Ghanaian hospitals

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*Staphylococcus aureus* is a notorious hospital acquired pathogen and is implicated in several serious infections such as meningitis, bacteremia 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 isolates of *S. aureus* from the pediatric emergency ward of Korle-Bu Teaching Hospital (KBTH) in Ghana where a suspected outbreak had recently occurred. The dominant clone of *S. aureus* identified among the isolates was sequence (ST) 15. The genomics data indicated cross contamination of multiple surfaces in the emergency ward by multiple lineages of ST 15 with the door handle of the ward implicated as a potential transmission route. The data also suggests that ST 15 is widely disseminated at KBTH, as it was found in multiple infections in the hospital (during the period of the outbreak) that were unrelated to the transmission events in the pediatric emergency ward. This investigation highlights the need for proper disinfection of environmental surfaces at KBTH.

### Biography

Eric S Donkor has done his Doctoral degrees in Infectious Diseases and Public Health from the London School of Hygiene and Tropical Medicine, and University of Iceland, respectively. He holds Master degrees in Molecular Biology and Animal Microbiology from Birkbeck College, University of London and University of Ghana, respectively. He has received several research fundings and has published 50 peer reviewed articles in the areas of infectious diseases, food safety and environmental health. Currently, he is an Associate Professor of Public Health Microbiology at the University of Ghana, Ghana.

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