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The *clfA*- R domain based objective molecular typing of methicillin resistant *Staphylococcus aureus* isolates from patients and screening procedures reveal dominant host-specific clonal lineages in a tertiary care hospital in Buraidah, Qassim, KSA

Kamaleldin B Said

Carleton University, Canada

Despite enormous efforts, the molecular mechanisms of specialization and emergence of invasive methicillin-resistant *Staphylococcus aureus* (MRSA) in a clonal background has been quite elusive. In an effort to contain the devastating outbreaks, significant research has been conducted that included many controversies and inconsistent reports. We have previously shown that a reason for this to occur when genotypes used for vertical analysis were determined based only on the DNA pattern of the marker irrespective of its function, the host and the strain factors. Furthermore, major genome based subtyping processes often fail to recognize minor differences in clonal genomes. We have established in recent years through multicenter collaborations that the use of adaptation-sensitive repeats in subtyping followed by subsequent genome wide expressions yielded relevant data on host and clonal differentiations. In this study, application of *clfA*- R-domain genotyping of clinical *Staphylococcus aureus* isolates revealed 14 different repeat types (RTs) designated, A to L, and Q and X while eight sequenced strains belonged to 3 types A, C and Q. The most dominant types were D (24 isolates, 57 copies), X (19 isolates, 52 copies), B (13 isolates, 60 copies), E (11 isolates, 55 copies) and F and Q (8 isolates 49, 47 copies each). Interestingly, the genotypes showed long-variable and short-clonal copy numbers reflective of the length and functional properties of *clfA* in human-specific and animal-associated lineages, respectively. Furthermore, presence of resistant phenotypes of the global genotype X among human isolates suggested potential transmission of bovine lineage to human hospital. Thus, we have shown the dominant types as well as the potential transmission lines of MRSA in a tertiary care hospital. Future vertical analysis and genome-wide sequence expression profiling of host-specific lineages would reveal potential candidates for vaccine and therapeutic developments.

Biography

Kamaleldin B Said has completed his PhD in Molecular Microbiology and Genomics from McGill University in Montreal, Canada. He continued at McGill to work on projects involving molecular typing and comparative genomic hybridizations of pathogens shortly before accepting a contract position at Qassim University, College of Pharmacy as an Assistant Professor. He has published significantly on the development and validation of molecular markers for host and organ-specific strain typing as well as genome-wide expression profiling for vaccine and therapeutic gene candidates. He is currently a Visiting Scholar at Systems Biology, Carleton University and has many projects underway and many manuscripts ready for publication.

kamal.said@mail.mcgill.ca

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