Ultrasound should be used as an adjunct in the diagnosis.

Empiric therapy covering *Staphylococcus aureus* is prudent pending culture reports.

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Virulence gene profile and SCCmec types of clinical MRSA isolates: Is there a fitness cost involved?

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Background: The success of methicillin resistant *Staphylococcus aureus* as a pathogen is attributed to its extraordinary repertoire of virulence factors. Based on SCC*mec* types, MRSA isolates can be classified as hospital (HA-MRSA) or community acquired (CA-MRSA). Association of certain virulence genes with particular SCC*mec* types has been previously reported. For instance, *pvl* gene is associated with *SCCmec* types IV or V (CA- MRSA types).

Methods & Materials: Two hundred non-repetitive isolates of MRSA from clinical specimens were screened for virulence genes such as *pvl*, *tsst*, *hlg*, enterotoxin A (*sea*), exfoliative toxin A (*eta*), intercellular adhesion (*ica*) genes by PCR. SCC*mec* typing was carried out by multiplex PCR. An attempt was made to find the association between virulence genes and the clinical presentation as well as with the SCC*mec* types to establish the fitness cost, if any.

Results: A total of 192 isolates (96%) carried one or more virulence genes while 8 (4%) had none. The commonest virulence gene encountered was *ica* (90%) followed by *hlg* (83%), *sea* (78%), *pvl* (53%), *eta* (12%) and *tsst* (2%). Out of 200 MRSA isolates, only 40% carried single SCC*mec* type, whereas 59% carried multiple SCC*mec* types including a combination of classical HA and CA types. The predominant SCC*mec* type found in our study was III followed by SCC*mec* V. *eta* and *pvl* toxins were mainly encountered in isolates from severe skin and soft tissue infections whereas the isolates which were negative for the virulence genes tested were obtained from mild skin infections. Notably, all the blood isolates (n=12) were negative for *pvl* and *eta*, whereas all were positive for *hlg*. *pvl* gene positivity was significantly associated with SCC*mec* type V followed by type III. Majority of the blood isolates and all the *tsst* positive MRSA isolates carried SCC*mec* III. The single isolate with SCC*mec* type II was negative for all the virulence genes tested.

Conclusion: This study documented the presence of virulence genes in various combinations in majority of the clinical MRSA isolates. No strong evidence for fitness cost of SCC*mec* was established as the isolates negative for virulence genes belonged to diverse SCC*mec* types.

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The human microbiome research in Africa – A systematic review

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Background: The explosion of interest in the human microbiome research was sparked in part by two research initiatives launched in 2008, the European and Chinese-led Metagenomics of the Human Intestinal Tract Consortium and the National Institutes of Health (NIH)-sponsored Human Microbiome Project. The new knowledge provided by these initiatives and others worldwide are transforming our understanding of the pathogenesis of several diseases, including asthma, inflammatory bowel diseases, obesity and Type 1 diabetes, as well as the development of the immune response linked to some vaccines. However, African populations are understudied in these initiatives, and there is no "African Microbiome Initiative". This systematic review aimed to summarize and discuss the state of research on the human microbiome in Africa, including the therapeutic role of the microbiome for the management of certain local diseases.

Methods & Materials: Using predefined keywords, we searched in six electronic databases for human microbiome studies conducted in Africa. In addition, to find additional articles, we checked references cited in eligible studies. Two authors independently selected eligible studies published until 30 September 2015.

Results: Eighty-nine human microbiome papers were identified from six electronic databases and other sources. There were 80 primary microbiome studies (including Khoi San (n= 1) and Hunter-Gatherers (n= 4)) and 9 nested microbiome studies within existing cohorts. 16S rRNA gene sequencing was the technique most widely used to characterize the microbiota. The main body sites studied were the gut (46%), vagina (25%) and the oral cavity (11%). The diseases targeted were malnutrition (n= 4), HIV/AIDS (n= 7), diarrhoea (n= 4), and periodontitis (n= 5). These microbiome studies were performed in individuals of all ages, with most of the studies being conducted in adults. Kenya, Uganda, South Africa and Nigeria were the sites of the majority of studies; however the principal investigators of most of the studies (87%) were from developed countries. The USA NIH was the main funding source (25%), followed by the Bill and Melinda Gates Foundation (9%) and the European Commision (8%).

Conclusion: More studies of the microbiome including African participants, focusing on endemic diseases and led by African researchers are needed.

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