Multilocus sequence typing and molecular detection of phenol-soluble modulin in biofilm-positive *Staphylococcus Epidermidis* isolated from paediatric blood culture

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Abstract

Aim: *Staphylococcus epidermidis* is a significant coagulase-negative staphylococci obtained from blood culture samples. However, there is limited information about phenol-soluble modulin (PSM), which is associated with virulence in *S. epidermidis* and its genetic relatedness in Nigeria. This study observed the presence of phenol-soluble modulin mec *(psm-mec)* gene and the multilocus sequence typing (MLST) of biofilm-positive *Staphylococcus epidermidis* (BPSE).

Method: Twenty-two biofilm-positive *S. epidermidis* isolates obtained from paediatric blood culture at three hospitals in north-west and north-central Nigeria were evaluated for the molecular detection of the *psm-mec* gene using conventional polymerase chain reaction (PCR). The biofilm formation was previously assessed by molecular detection of the intercellular adhesion *(icaA)* gene and the methicillin resistance using cefoxitin disk agar diffusion. Internal fragments of the respective seven housekeeping genes was sequenced for 21 BPSE strains and matched with the central MLST database.

Results: Out of 22 BPSE, only 4.5% had the *psm-mec* gene and it was methicillin resistant. About 91% methicillin resistance was observed among the *psm-mec* negative BPSE strains. Twenty-one BPSE strains were

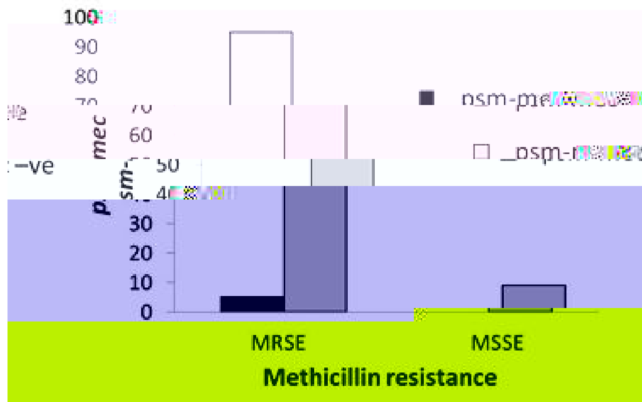
Y PSMs belongs to the amphipathic phenol-soluble modulin family and it is the only staphylococcal toxin encoded by the *psm-mec* gene localized in the SCCmec element, which also contains the *mecA* genes, regulatory elements, recombinase genes, and some resistance genes [4,8].

Multilocus sequence typing (MLST) is a reference genotyping method that is suitable for analysing the evolution and population

Yinternal fragments of the seven housekeeping genes (*arcC, aroE, gtr, mutS, pyrR, tpi, and yqiL*) were Ua d`] YX by PCR, using the gdYW/ Wprimers with varying amplicon size and annealing temperature (Table 1) with the di f] YXPCR products as the DNA template [18].

A collection of 21 V|c `a producing *S. epidermidis* isolates were analysed by MLST protocol. Y PCR was performed with 25 µl reaction volume, composed of 1 µl each of the forward and reverse primer, 12.5 µl of Midas mix and 9.5 of RNAse/DNase free sterile water.

Y conditions for running the PCR Ua d`] W]cb involved an initial denaturation of 95°C for 3 min; 30 cycles of 95°C for 30 s,



100
90
80
70
60
50
40
30
20
10
0
MRSE
MSSE
Methicillin resistance

at a g][b] Wbh toxic level. Y strains analysed are genetically related to each other.

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