

## OP 16

### **Distribution of chlorhexidine resistance *qacA/B* genes among Coagulase negative *Staphylococcus* isolated from central venous catheters of intensive care patients**

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**Background:** Chlorhexidine is a widely used skin antiseptic in hospital setting. Bacterial resistance to chlorhexidine, especially among *Staphylococcus* species is an emerging concern as this can lead to a rise in hospital acquired infections. Efflux pumps encoded by plasmid-borne ‘*qac*’ (quaternary ammonium compound) genes are responsible for chlorhexidine resistance in these bacteria. Catheter-Related Bloodstream Infections (CRBSI) are nosocomial infections with high morbidity and mortality rates. Coagulase-negative *Staphylococcus* (CoNS) are among the commonest microorganisms associated with CRBSI and Central Venous Catheter (CVC) colonization. Chlorhexidine resistance in CoNS will cause adverse consequences in prevention and management of CRBSI.

**Objective:** This study was designed to detect the distribution of *qacA/B* gene which causes chlorhexidine resistance, in CoNS isolated from CVC of the intensive care unit patients at two tertiary care hospitals in Colombo, Sri Lanka.

**Methods & Materials:** Eighty-two CoNS isolates from CVC were included in the study. Eight were isolated from patients with CRBSI and 74 from colonized CVC without evidence of blood stream infection. The species identification was done using API ® Staph system (BioMérieux, France). *qacA/B* gene was detected by the polymerase chain reaction.

**Results:** *qacA/B* gene was detected in 13/82 (16%) isolates. The commonest species was *Staphylococcus haemolyticus* (34/82; 41%). The proportion of the presence of *qacA/B* gene among them was 18% (6/34) followed by 50% (3/6) in *S. chromogenes*, 18% (2/11) in *S. hominis*, 11% (1/9) in *S. epidermidis*, and 50% (1/2) in *S. lugdunensis*. *S. cohnii* (n=9), *S. capitis* (n=4), *S. saprophyticus* (n=3), *S. sciuri* (n=2), *S. kloosii* (n=1), and *S. xylosus* (n=1) were also isolated from the CVC. However, *qacA/B* gene was not detected in them.

**Conclusion:** In this population distribution of *qacA/B* gene in CoNS from CVC is 16%. Rates of the resistance gene shows variations among different species. Immediate attention should be given to curtail antiseptic resistance among bacteria in health care settings.

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