

Antimicrobial Resistance Patterns of Commensal *Staphylococcus haemolyticus* From the Skin Microbiome

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Structured Abstract

Background: *Staphylococcus haemolyticus* (*S. haemolyticus*) is a commensal species of the coagulase negative staphylococcus (CoNS) that colonizes the human skin. *S. haemolyticus* is normally nonpathogenic but can become an opportunistic pathogen when its host skin microbiome is disturbed or upon entry into the blood. One factor that may contribute to this pathogenicity is the development of antimicrobial resistance (AMR). *S. haemolyticus* is one of the nosocomial pathogens that has developed resistance to multiple antibiotics, but there is limited data on its antimicrobial resistance pattern in Malaysia. In this research, the objectives are to determine the antimicrobial resistance pattern of commensal *S. haemolyticus* isolated from the skin microbiome, to compare the AMR patterns with other *Staphylococcus* species from the skin microbiome and to confirm the identity of selected CoNS isolates using *sodA* gene sequence analysis.

Methods: *S. haemolyticus* samples were taken from the armpits of UiTM undergraduate students. Samples were cultured for preliminary identification using several biochemical tests and tested for antimicrobial resistance to oxacillin, kanamycin, rifampicin, erythromycin, chloramphenicol and linezolid. Two isolates with high levels of antibiotic resistance were selected for confirmation of species identity using *sodA* sequence analysis.

Results: The study showed that 15 *S. haemolyticus* commensal isolates only demonstrate resistance against oxacillin (6.67%), kanamycin (6.67%), and linezolid (6.67%). One isolate demonstrated coresistance to all three antibiotics. In comparison, *S. epidermidis* showed high resistance to kanamycin (47.37%), but not linezolid (5.26%). *S. hominis* showed high resistance to erythromycin (60.00%) and low resistance to kanamycin (20.00%) whereas *S. lugdunensis* showed resistance to kanamycin (11.11%) and linezolid (11.11%). Thus, *S. haemolyticus* appears to show similar level of antibiotic resistance compared to other common CoNS species.

Conclusion: In conclusion, the findings of this study indicated that there is considerable potential in the limitations of biochemical tests and the potential ambiguous species identification may hinder progress of CoNS identification

Keywords: *S. haemolyticus*, coagulase negative staphylococcus (CoNS), antimicrobial resistance (AMR), co-resistance, *sodA* gene

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