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Matthew Howes, Rob Baird

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CDI is produced by the Office of Health Protection and Response, Australian Government Department of Health and Aged Care, GPO Box 9848, (MDP 6) CANBERRA ACT 2601

Email:

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Staphylococcus lugdunensis and coagulase-negative staphylococci species characterisation in a tropical climate

Matthew Howes, Rob Baird

Differentiation between coagulase negative staphylococci (CoNS), a heterogeneous group of human and animal colonisers, and their virulent relative *Staphylococcus aureus* was historically important. In recent times, *Staphylococcus lugdunensis* has gained special attention in public health as a human pathogen and has been shown to cause severe invasive disease.¹ Biochemical and genomic identification has become more widely and routinely available, allowing the CoNS species distribution in human clinical samples to be better defined.² We characterised the CoNS species from a single tropical tertiary centre for both swab and blood isolates, and review and compare with previous studies.³ This study was ethics approved: EFILE2022/25273.

Geographically, Royal Darwin Hospital is the tertiary referral hospital for the Top End of the Northern Territory, a region of over 500,000 km² with a tropical climate (latitude 12.5°S). All clinical isolates of CoNS identified from 1 January 2019 to 30 June 2022 were included, with duplicate patient specimens excluded. During this time there were also 7,546 *S. aureus* isolates (including 161 [2.1%] from bloodstream isolates). Isolates were biochemically identified by Vitek 2 (Biomérieux, St Louis USA) and characterised as blood or swab isolates. There were 1,262 isolates collected, of which 203 (16%) were from bloodstream samples. The results are presented in Table 1.

S. epidermidis was predominant, accounting for 30.8% of all CoNS isolates and over 50% of the bloodstream isolates; *S. saprophyticus* was found predominantly in urine; and

S. epidermidis-like organisms (*S. haemolyticus*, *S. capitis* and *S. hominis*) were also frequent in swab and bloodstream isolates.

S. lugdunensis was the second most commonly isolated CoNS species identified with 201 isolates, 15.9% of all isolates. This frequency is far higher than in other published series.⁴ Of the *S. lugdunensis* isolates, 24.0% and 66.3% came from the pelvic and lower body sites respectively, consistent with previous studies.⁵

However, despite the large number of skin swab isolates, there was only a single bloodstream isolate of *S. lugdunensis* detected during this study, from a patient admitted with fever and found to have *S. lugdunensis* in one blood culture bottle only. Repeat blood cultures were negative three days later. The patient had a presumed ileostomy source and received two weeks of intravenous antibiotics for bacteraemia, and the patient remained well on review.

Though it accounted for 15.9% of all CoNS isolates, *S. lugdunensis* represented only 0.5% of CoNS bloodstream isolates, with a low 0.5% rate of blood to swab isolates. Our rate of bloodstream *S. lugdunensis* isolation was much lower than recorded in comparably sized series.² A further retrospective look back over ten years identified only two other bloodstream isolates, both one bottle only, with neither deemed clinically significant. This low incidence of serious bloodstream infection over ten years has not been reported previously from tropical settings.⁶

Our study demonstrates that high rates of *S. lugdunensis* carriage in the tropics does not

Table 1: Characterisation of swab and bloodstream isolates of CoNS between 2019 and 2022

Species	All sites isolates number and frequency N (%)	Blood isolates N (% of total CoNS)	% blood versus all sites isolates
<i>S. epidermidis</i>	389 (30.8)	104 (51.2)	26.7%
<i>S. lugdunensis</i>	201 (15.9)	1 (0.5)	0.5%
<i>S. saprophyticus</i> ^a	193 (15.3)	3 (1.5)	1.6%
<i>S. haemolyticus</i>	184 (14.6)	28 (13.8)	15.2%
<i>S. capitis</i>	55 (4.4)	23 (11.3)	41.8%
<i>S. hom.hominis</i>	44 (3.5)	23 (11.3)	52.3%
<i>S. caprae</i>	38 (3.0)	4 (2.0)	10.5%
<i>S. simulans</i>	36 (2.9)	1 (0.5)	2.8%
<i>S. lentus</i>	29 (2.3)	4 (3)	13.8%
<i>S. pseudintermedius</i>	24 (1.9)	2 (1.0)	8.3%
<i>S. sciuri</i>	21 (1.7)	1 (0.5)	4.8%
<i>S. warneri</i>	14 (1.1)	2 (1.0)	14.3%
<i>S. auricularis</i>	13 (1.0)	4 (2.0)	30.8%
<i>S. cohnii cohnii</i>	10 (0.8)	2 (1.0)	20.0%
<i>S. xylosus</i>	4 (0.3)	0 (0)	0.0%
<i>S. carn.carnosus</i>	3 (0.2)	0 (0)	0.0%
<i>S. schleiferi</i>	2 (0.2)	0 (0)	0.0%
<i>S. gallinarum</i>	1 (0.1)	0 (0)	0.0%
<i>S. kloosii</i>	1 (0.1)	1 (0.5)	100.0%
Total	1262 (100)	203 (16.1)	

a predominantly urine isolates

necessarily translate into invasive disease; this raises the question of whether the tropical environment potentially affects the virulence of the organism. This is something for potential future studies to examine. As a tropical centre, the frequency of isolation of *S. lugdunensis* raises concerns for potential for significant burden on the health service in line with high rates of *S. aureus*, particularly methicillin-resistant strains. We plan to sequence a number of local *S. lugdunensis* isolates to determine the presence of postulated virulence factors, and to compare phylogenetic relationships with known virulent strains, so as to characterise this epidemiological observation.

Author details

Matthew Howes¹
Rob Baird¹

1. Territory Pathology, Royal Darwin Hospital,
Rocklands Drive TIWI NT 0810 Australia

Corresponding author

Matthew Howes

Territory Pathology, Royal Darwin Hospital,
Rocklands Tiwi NT 0810 Australia

email: matthewhowes@doctors.org.uk;
Matthew.Howes@nt.gov.au

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