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Bruker MALDI-TOF: Identification of Coagulase Negative Staphylococci

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Introduction

Coagulase-negative *Staphylococci* (CNS) historically-considered to be commensals or contaminants are now recognized to be pathogens associated with infections of foreign bodies and a major cause of line associated bacteremia. The identification of CNS like *S. lugdunensis* is important to ensure the correct interpretation of susceptibility results.

Objectives

- Determine the ability of the Bruker Maldi-TOF to identify Coagulase Negative *Staphylococci* to the species level compared to VITEK-2 and MIDI gas liquid chromatography

Methods

- Four hundred and eighty five CNS were randomly selected from a bank of CNS previously identified to species level by long tube biochemicals, VITEK-2 and MIDI gas liquid chromatography
- The CNS were identified by the Bruker MALDI-TOF biotyper and was then compared to VITEK-2 and the MIDI gas liquid chromatograph results.
- The following CNS were identified by the Direct Plate Formic Acid (70%) Extraction Method: *S. capitis* subspecies *ureolyticus* (n=50),*S. caprae* subspecies *caprae* (n=50), *S. capitis* subspecies *capitis* (n=50), *S. cohnii* (n=49), *S. epidermidis* (n=90), *S. haemolyticus (n=25), S. hominis (n=17), S. intermedius (n=7), S. lugdunensis* (n=15), *S. saprophyticus* (n=25), *S. schleiferi* (n=22), *S. simulans* (n=24), *S. warneri* (n=24) and *S. xylosus* (n=27).
- The following American Type Culture Collection (ATCC) strains were used for quality control: *Staphylococcus cohnii* ATCC 29974, *S. epidermidis* ATCC 14990, *S. haemolyticus* ATCC 29970, *S. hominis* ATCC 27845, *S. intermedius* ATCC 29663, *S. saprophyticus* ATCC 15305, *S. wameri* ATCC 27836, and *S.xylosus* ATCC 29971.

Results

Staphylocci	**#**	MALDI-TOF % Correct	VITEK-2 % Correct	MIDI % Correct
S. capitis ureolyticus	50	100	54	62
S. caprae caprae	50	**100**	**90**	**88**
S. capitis capitis	50	**100**	**100**	**52**
S. cohnii	49	**100**	**90**	**45**
S. epidermidis	90	**100**	**98**	**22**
S. haemolyticus	25	**100**	**96**	**92**
S. hominis	17	**100**	**96**	**62**
S. intermedius	7	**100**	**76**	**38**
S. lugdunensis	25	**100**	**76**	**88**
S. saprophyticus	25	**96**	**80**	**92**
S. schleiferi	22	**100**	**100**	**92**
S. simulans	24	**100**	**94**	**52**
S. warneri	24	**100**	**96**	**32**
S. xylosus	27	**100**	**94**	**94**
Totals	485	**99.70%**	**86,2%**	**66,2 %**

Discussion

- The Bruker MALDI-TOF identified all of the CNS correctly to the subspecies level with the exception of *S. capitis* subspecies *urealyticus*, where 48 were identified as *S. capitis* subspecies *capitis* and one *S. saprophyticus* which was identified as *S. xylosus*.
- The identification were correct to the species level in 484 of the 485 CNS (99,7%) and to the subspecies level in 436 of 485 CNS (89,9%).
- Vitek-2 identified 86,2% and the MIDI identified 66,2 percent of the CNS correctly to the species level compared to 99,7% by MALDI-TOF.
- Vitek-2 was better at identifying *S. capitis* subspecies *ureolyticus* to the subspecies level than MALDI-TOF (55% vs. 4%).

Conclusion

- The Bruker Biotyper is excellent at identifying CNS to the species level 99,7% compared to the VITEK-2 (86,2%) and the MIDI-GLC (66,2%).
- The identification of the CNS to the subspecies level (89,9%) is superior to the Vitek-2 and MIDI-GLC
- Future software updates to the Bruker Biotyper and updates in the organism identification profile may improve the ability to identify CNS to the subspecies level, the clinical significance of this remains doubtful
- The Bruker Biotyper is an excellent cost effective instrument for the identification of CNS

Disclosure: No Conflict of Interest to Declare