

# Skin and gut colonisation with *Staphylococcus haemolyticus* in term and preterm neonates

Hanna Kadri Metsvaht<sup>1</sup>, Tuuli Metsvaht<sup>2</sup>, Imbi Eelmäe<sup>2</sup>, Mirjam Merila<sup>3</sup>, Mari-Liis Ilmoja<sup>4</sup>, Irja Lutsar<sup>1</sup>, Hiie Soeorg<sup>1</sup>

<sup>1</sup>Department of Microbiology, University of Tartu, Tartu, Estonia; <sup>2</sup>Pediatric Intensive Care Unit, Tartu University Hospital, Tartu, Estonia; <sup>3</sup>Department of Neonatology, Children's Clinic, Tartu University Hospital, Tartu, Estonia; <sup>4</sup>Pediatric Intensive Care Unit, Tallinn Children's Hospital, Tallinn, Estonia

## Background

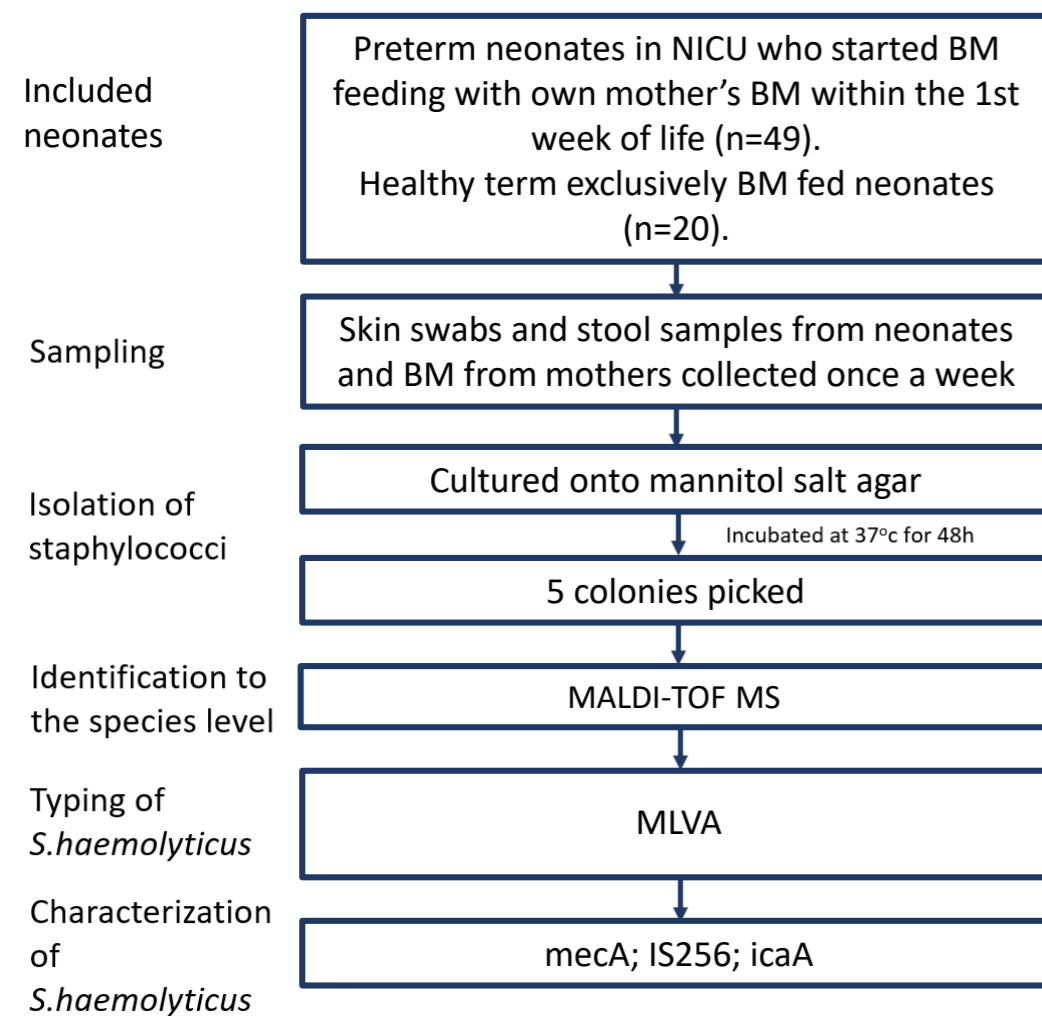
- Among coagulase-negative staphylococci *Staphylococcus haemolyticus* (SH) is the second commonest cause of late-onset sepsis (LOS) in preterm neonates. Clones spread in NICUs has been described.
- SH colonisation is poorly described. Understanding the mechanisms of SH colonisation may hold potential to develop strategies for prevention of invasive infection

## Aim

To compare SH colonisation of healthy term and hospitalized preterm neonates in terms of:

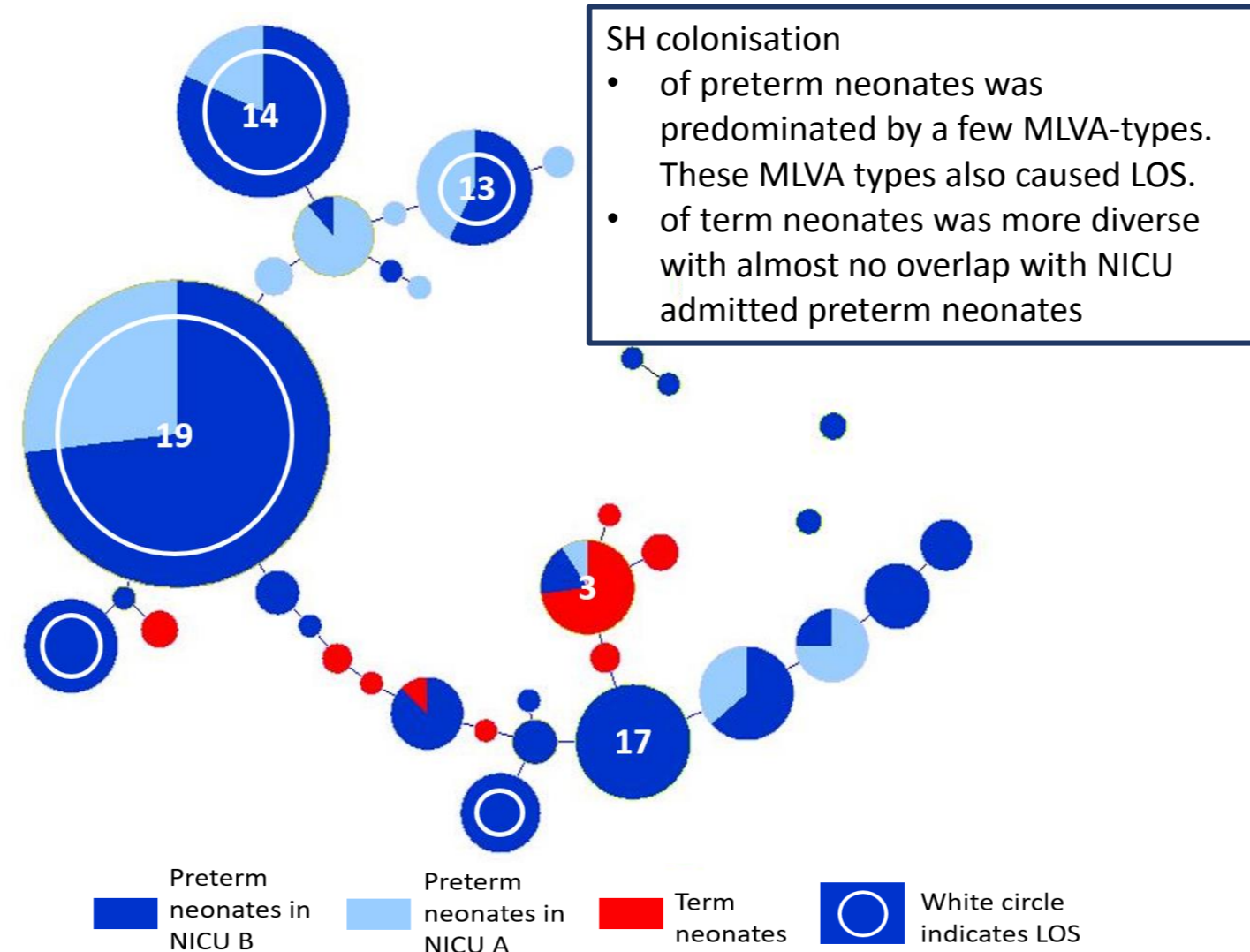
- the prevalence and multilocus variable-number tandem-repeats analysis (MLVA) type distribution
- the prevalence of virulence factors

## Material and Methods



## Results

- Median (range) gestational age and birthweight of included term and preterm neonates was 40 (39-40) and 28 (25-30) wks; 3651 (3324-3970) and 1154 (814-1564) g
- Colonisation with SH was
  - more likely in preterm than term neonates (45/49 vs 11/20; OR 9.2; 95%CI 2.4-35.5)
  - equally likely in gut and on skin (55/69 vs 51/69; OR 1.4; CI 0.6-3.1).
- In unit A 15/19 and in unit B all neonates were colonised with SH ( $p=.018294$ )
- 621 isolates represented 41 MLVA-types, 32 present in preterm and 12 in term neonates, with only 3 colonising both term and preterm.



**Figure: MLVA-types colonising term and preterm neonates.** Each node represents a distinct MLVA-type and the size of the node is proportional to the number of isolates of the MLVA-type. Numbers in nodes represent 5 most common MLVA-types. MLVA-types yielding multiple bands in loci Sh1 and Sh2 ( $n=7$ ) were excluded.

- MLVA-types colonising preterm compared with term neonates carried more likely virulence genes
  - mecA* (153/185 vs 1/27; OR 124.3; 95%CI 16-950)
  - IS256 (95/185 vs 0/27; OR 58; 95% CI 3-966)
- None of tested isolates were *icaA* positive.
- Five MLVA-types (Figure 1)
  - Colonised 69% (34/49) of preterm, but none of term neonates
  - Caused 7 episodes of LOS in 6 preterm neonates. (Table)

**Table: LOS cases.**

Patient	MLVA-type	Age during first isolation from blood (days)	Isolated from SKIN before LOS (days)	Isolated from GUT before LOS(days)
	14	7	=	*
B10	19	17	*	3
B16	15	10	4	*
B20	13	11	2	5
B21	18	6	*	*
B22	19	7	5	5
C07	19	15	5	5

Each MLVA-type is presented in a different color. If MLVA-types colonised gut or skin prior to or at the same time as blood, it is colored accordingly.

= isolated on the same day as LOS

\* Isolated later than from blood or not found on this site

## Conclusion

- NICU environment may be responsible for higher colonisation with more virulent SH strains in preterm.
- Control of virulent NICU clones may hold potential to reduce the burden of invasive infections.