Higher prevalence of clonal complex 29 among *Staphylococcus haemolyticus* from preterm neonates compared with healthy term neonates and mothers

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Background & Aim

- *Staphylococcus haemolyticus* is common cause of late-onset sepsis (LOS) in preterm neonates.
- Multilocus sequence typing sequence types (STs) belonging to clonal complex 29 (CC29) cause most infections, but whether these STs can be encountered more frequently in hospital than other STs is unknown.
- We aimed to describe STs of *S. haemolyticus* causing LOS and colonizing preterm neonates compared with healthy term neonates and their mothers.

Materials and Methods

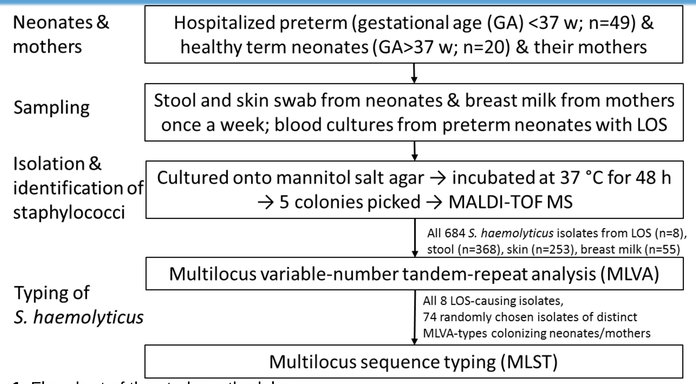

Figure 1. Flowchart of the study methodology

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Results

- Of 82 isolates (Figure 1) 80 were typeable, 2 non-typeable (due to no band in *arc* or SH1431 locus) isolates
- A total of 24 STs (8 previously described, 16 new) among 44 distinct MLVA-types
- Most (81.3%) were CC29 (Figure 2)

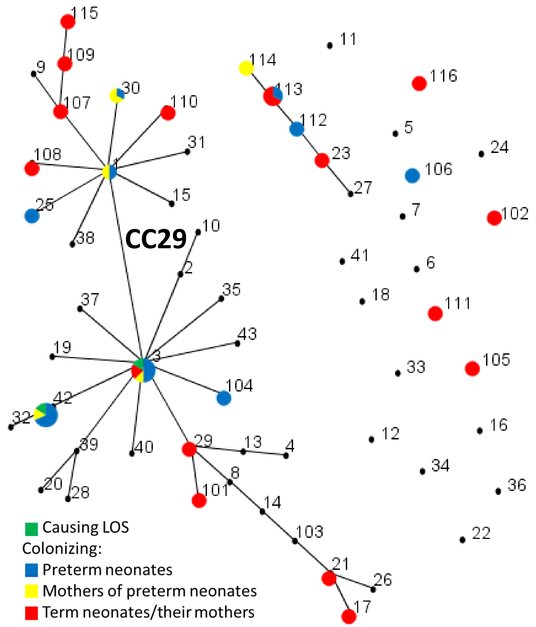

Figure 2. eBURST analysis of *S. haemolyticus* STs

- Most commonSTs causing LOS or colonizing (Figure 3):
  - Preterm neonates/their mothers: ST3, ST42
  - Term neonates/mothers: ST3, two previously undetected STs (ST109, ST113)

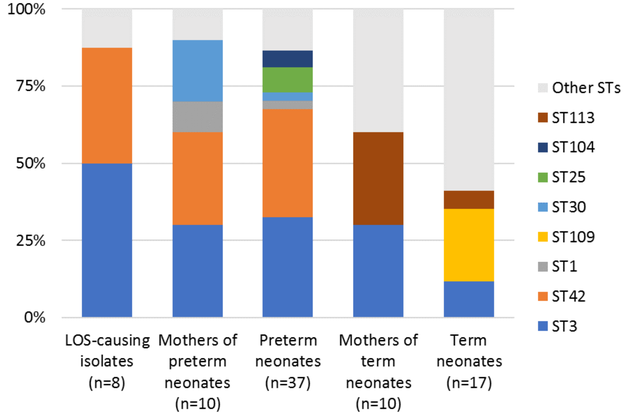

Figure 3. Distribution of STs among isolates from preterm/term neonates/mothers

- Colonizing/LOS-causing isolates from preterm vs colonizing isolates from term neonates/mothers:
  - Less diverse (Figure 4)
  - More often CC29 (Figure 5)

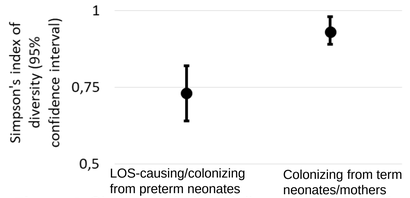

Figure 4. Simpson's index of diversty of isolates from preterm and term neonates/mothers

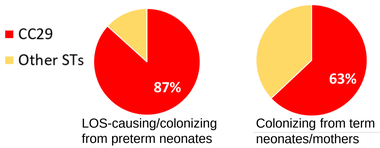

Figure 5. Proportion of CC29 oamong isolates from preterm and term neonates/mothers

Conclusion

- *S. haemolyticus* colonizing or causing LOS in hospitalized preterm neonates belong mostly to CC29, particularly to ST42, suggesting that this is a genetic lineage adapted to hospital environment.

CC29 strains could be with higher virulence and selected from a pool of isolates with diverse genetic background present in community