A sustained outbreak of NRCS-A *Staphylococcus capitis* associated with late-onset sepsis in the neonatal intensive care unit: a case-control and environmental genomic survey.

**Background**

*S. capitis NRCS-A strain* has emerged as a global cause of late onset sepsis (LONS) in neonatal intensive care units (NICUs). Identifying outbreaks is critical for improving antimicrobial stewardship and infection prevention.

**Aims**

- Confirm clonal outbreak of NRCS-A *S. capitis* in the NICU.
- Identify potential environmental reservoirs.
- Determine involvement of asymptomatic skin and gut colonisation.

**Results**

*S. capitis* positive blood cultures likely to be clinically significant and represent those with not only central line associated bloodstream infections but also necrotising enterocolitis ( NEC) or gut mucosal injury.

The cluster of NICU *S. capitis* isolates confirms a clonal outbreak of the NRCS-A clone. It is achieving sustained and persistent transmission on the NICU and distinct from diversity seen in adult/paediatric populations.

Presence of both NRCS-A & non-NRCS-*S. capitis* in the NICU environment demonstrates wide dissemination. Presence on sites in direct neonatal contact and the wider area, proves persistence and survival.

NRCS-A isolation from skin cultures confirms its presence on neonatal skin but was not found to be a risk factor for LONS.

Rectal isolation confirms the clone’s presence in the neonatal gut, and an association with *S. capitis* sepsis and NEC.

**Methods**

- Clinical data for neonates of *S. capitis* and other CoNS blood culture isolates reviewed and defined.
- *S. capitis* isolates were obtained from:
  - Clinical blood cultures, cerebral spinal fluid (CSF) and line tip cultures
  - Environmental sampling of the NICU
  - Rectal screening
  - Superficial skin cultures
- DNA extraction: QuickGene DNA extraction kit and/or Qiagen long fragment extraction.
- Sequencing: Oxford Nanopore long-read sequencing and/or short-read Illuma sequencing.
- Sequences mapped to a reference genome, and phylogenetic trees created.

**Discussion and Conclusion**

*Further investigations are necessary to identify an environmental reservoir and further establish the association between presence in the neonatal gut and *S. capitis* sepsis cases.*

**References**