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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.

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Background

***S. capitis* NRCS-A strain** has emerged as a global cause of late onset sepsis (LONS) in neonatal intensive care units (NICUs)[1]. 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

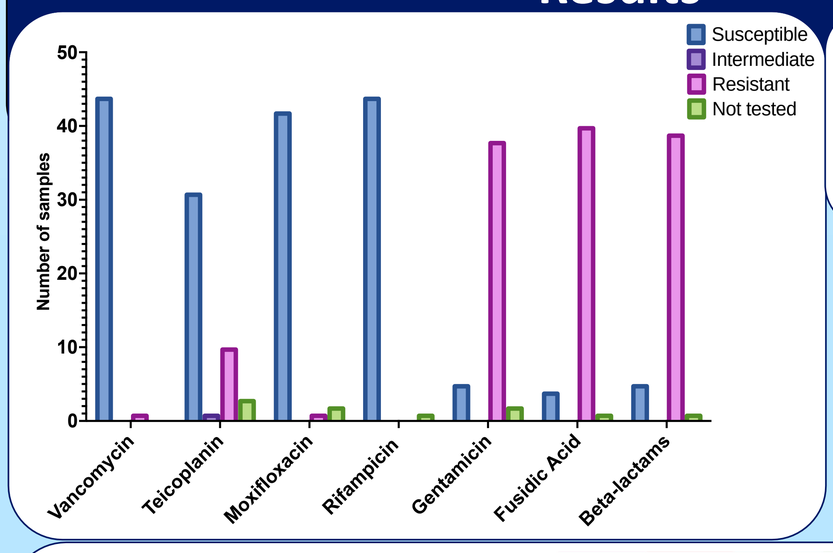

Figure 1: Left: Antibiotic susceptibilities observed in local NICU *S. capitis* blood culture isolates, matched that of reported NRCS-A strains

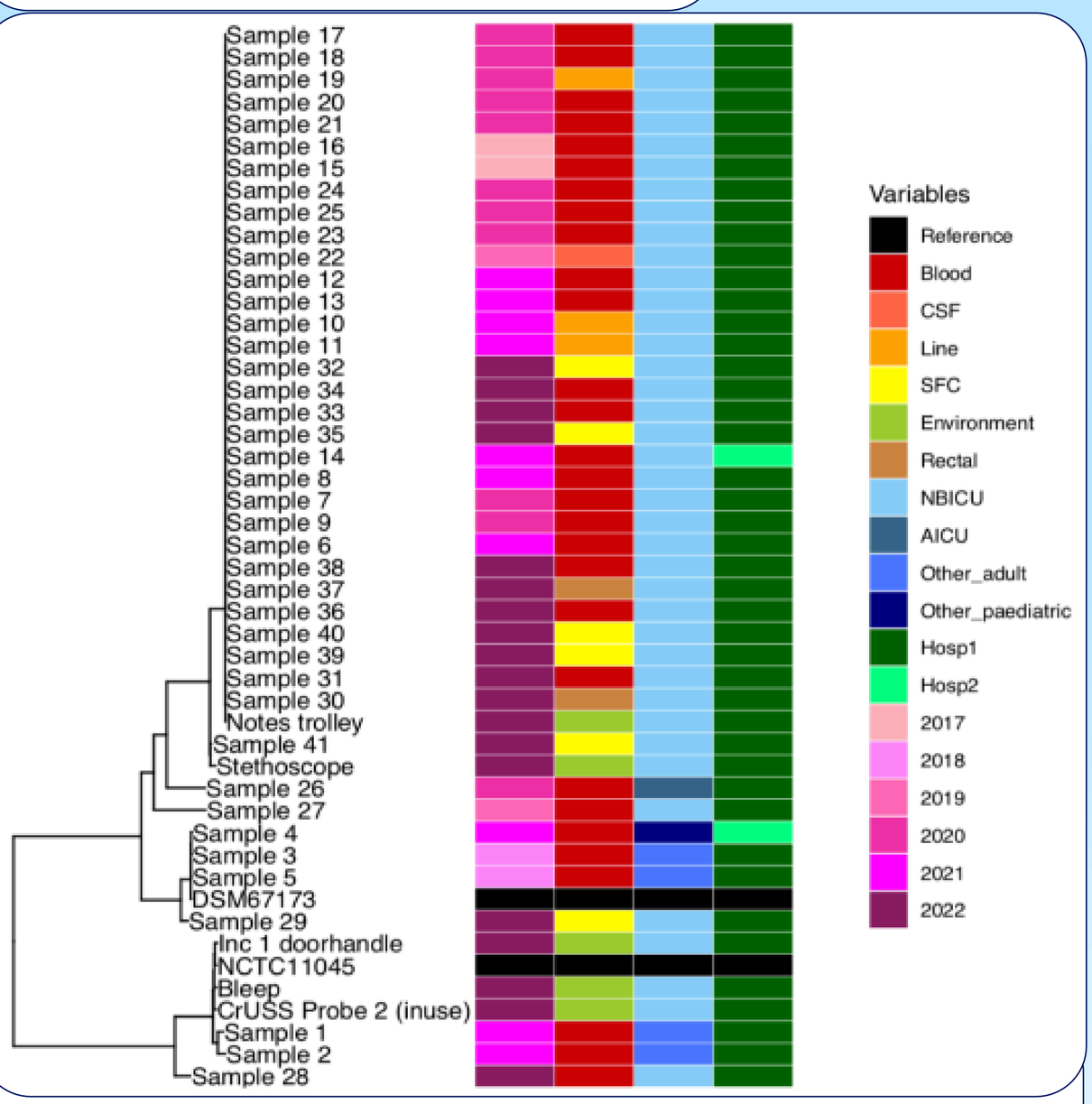

Figure 2: Above: Sequences obtained from *S. capitis* isolates formed a cluster with limited diversity for 24/26 NICU isolates, most closely related to the UK NRCS-A strain. 1/5 *S. capitis* isolates from sites within the NICU 1 fell within the cluster. 3/5 *S. capitis* isolates from skin cultures fell within the NRCS-A cluster, 2 isolates obtained from rectal cultures, both fell within this cluster; both patients developed *S. capitis* sepsis.

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 Illumina sequencing.
- Sequences mapped to a reference genome, and phylogenetic trees created.

Discussion and Conclusion

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-A *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.

Future investigations

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

References

[1] Rasigade, J.-P. *et al.* (2012) 'Methicillin-resistant Staphylococcus capitis with reduced vancomycin susceptibility causes late-onset sepsis in intensive care neonates', *PLoS ONE*, 7(2). doi:10.1371/journal.pone.0031548.

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