

Antibiotic resistant bacterial colonisation in 4 neonatal units in the UK: part of the NeoIPC Feasibility study

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Background

- Infants on neonatal units are at risk of severe bacterial infections, particularly those born at <32 weeks
- Infants colonised by resistant bacteria have an increased risk of sepsis
- Colonisation pressure; the proportion of infants colonised with resistant bacteria on a neonatal unit, is a major contributor to the spread of resistant bacteria in neonatal units
- We undertook a pre-trial colonisation feasibility study to characterise baseline colonisation pressure at the neonatal unit-level
- We aimed to understand the feasibility of collecting these data using cross-sectional surveys, to inform the frequency of sampling and sample analysis strategy for the NeoDeco trial

Methods

- Sites conducted 4 cross-sectional surveys in a one-month period
- At each survey clinical data, skin swabs and stool samples were collected from all infants present on the unit
- Skin swabs and stool samples were analysed by PCR for the presence of bacterial resistance genes
- Individual data were aggregated to present a unit-level picture
- Proportion of infants ARB colonised at the survey timepoint excludes infants with missing samples or indeterminate PCR results.

Gene targets of interest in stool samples

- Carbapenem resistance: *blaKPC*, *blaNDM*, *blaVIM*, *blaIMP*, *blaOXA-48*
- Extended-spectrum beta-lactamase: *blaCTX-M group1*, *blaCTX-M group9*
- Vancomycin resistance: *vanA*, *vanB*

Gene targets of interest in skin samples

- Methicillin resistance: *mecA*, *mecC*, *orfX*, *nuc*, *SCCmec*

Results

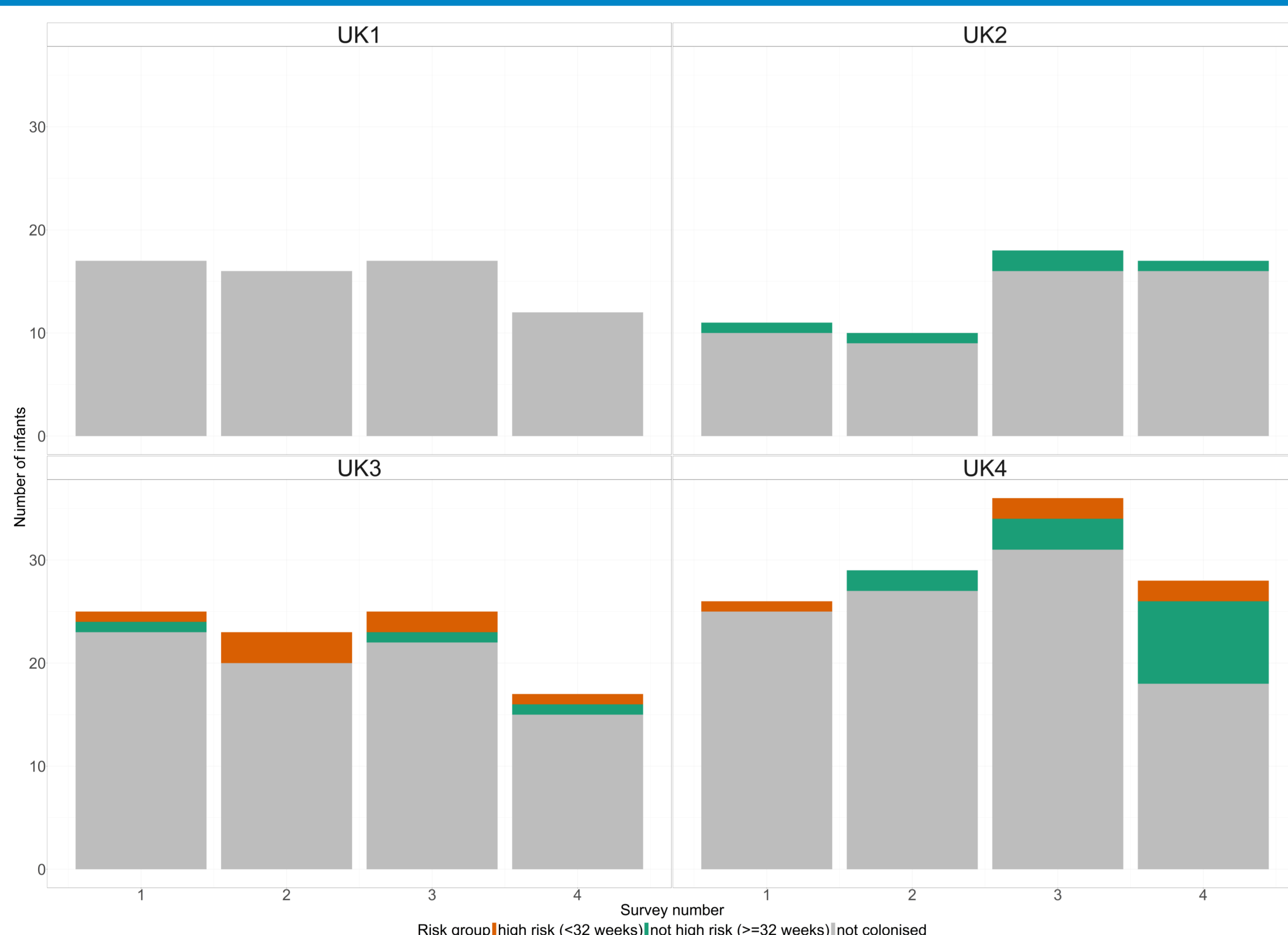


Figure: Number of infants colonised by antibiotic resistant bacteria per survey split by high risk (born <32 weeks gestation) and not high risk (born ≥32 weeks gestation) and total number of infants present on the day of the survey.

- 4 sites had complete sample data from 4 surveys (n=16 surveys)
- 237 infants participated
- 40% (96/237) of infants were born <32 weeks gestation (high risk)
- 44 (18%) of infants were present at all 4 surveys
- Of possible samples to be collected
 - 475/482 (99%) of skin swabs collected
 - 332/482 (69%) of stool samples were collected
- 1% (7/475) skin swabs were positive for MRSA
 - 94% (447/475) were MRCoNS positive
- 8% (26/332) stool samples were positive for any genes of interest
 - 10/26 (28%) of positive samples were in high-risk infants
 - 24/26 samples positive for ESBL genes
 - 2/26 samples positive for carbapenemases
 - 0/26 samples positive for vancomycin resistance genes

Conclusion

- Resistant bacterial colonisation was generally low across UK neonatal units
- Both low- and high-risk infants were colonised
- Findings informed sampling frequency and sample analysis for the NeoDeco trial
- Unit-level IPC interventions target both direct and indirect effects of colonisation regardless of risk status
- Interventions focusing only on infants at high risk of sepsis will miss significant resistant bacterial colonisation in low-risk infants

The NeoDeco trial is a cluster-randomised hybrid implementation-effectiveness trial looking at the impact of implementing optimal kangaroo care on neonatal sepsis and resistant bacterial colonisation prevalence

	Survey Number			
	1, N = 123 ¹	2, N = 113 ¹	3, N = 127 ¹	4, N = 120 ¹
Site number				
UK1	26 (21%)	23 (20%)	26 (20%)	26 (22%)
UK2	15 (12%)	16 (14%)	21 (17%)	23 (19%)
UK3	30 (24%)	29 (26%)	28 (22%)	23 (19%)
UK4	52 (42%)	45 (40%)	52 (41%)	48 (40%)
Gestational age (weeks)	32 (28 - 36)	31 (26 - 35)	31 (27 - 36)	31 (26 - 35)
Birthweight (grams)	1,529 (965 - 2,506)	1,500 (923 - 2,200)	1,500 (924 - 2,478)	1,513 (883 - 2,326)
Postnatal age (days) at survey	18 (9 - 42)	21 (8 - 36)	17 (7 - 45)	21 (8 - 48)
Length of stay on NICU at survey (days)	15 (5 - 35)	16 (5 - 30)	14 (5 - 37)	19 (6 - 37)
Number of infants colonised with ESBL genes	3 (3.8%)	4 (5.1%)	7 (7.2%)	10 (14%)
Number of infants colonised with carbapenemase genes	0 (0%)	1 (1.3%)	0 (0%)	1 (1.4%)
Number of infants colonised with vancomycin resistance genes	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Number of infants colonised with MRSA genes	1 (1.3%)	1 (1.3%)	3 (3.1%)	2 (2.7%)
¹ n (%); Median (IQR)				

