

FACTORS ASSOCIATED WITH INFANT CARRIAGE OF ANTIMICROBIAL RESISTANCE GENES: A SYSTEMATIC REVIEW



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Introduction

- In recent years carriage of antimicrobial resistance (AMR) genes has increased dramatically among infants.
- Australia's Antimicrobial Utilization Surveillance Program recorded a 2.8% rise from the previous year.
- Children aged 2-4 years had the highest antimicrobial prescribing rate (Australian Commission on Safety and Quality in Health care, 2021).
- The factors driving this rise in AMR in infants are unclear.

Aims

The aim of this review was to evaluate current evidence regarding the association between exposures operating during birth and early infancy and AMR carriage, and to identify the limitations of existing studies and the opportunities for future research.

Methods

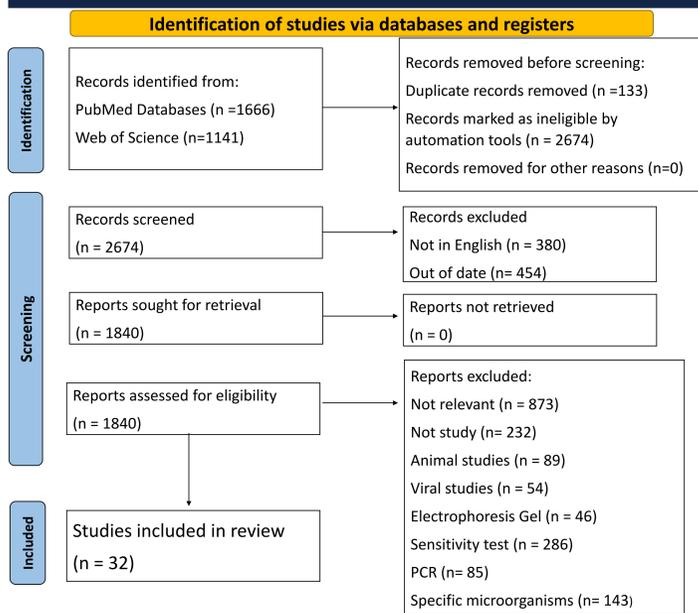


Figure 1: PRISMA Flow chart outline the steps taken to sort through articles identified the final studies that were included.

Results

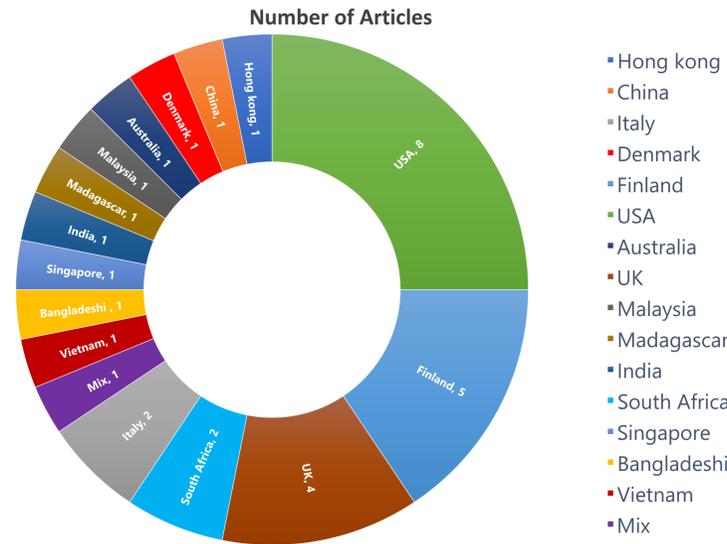


Figure 2. Number of studies reported AMR in infants from across the world. Five were conducted in LMICs, 25 were conducted in HICs, and two in an upper-middle-income country.

Results cont.

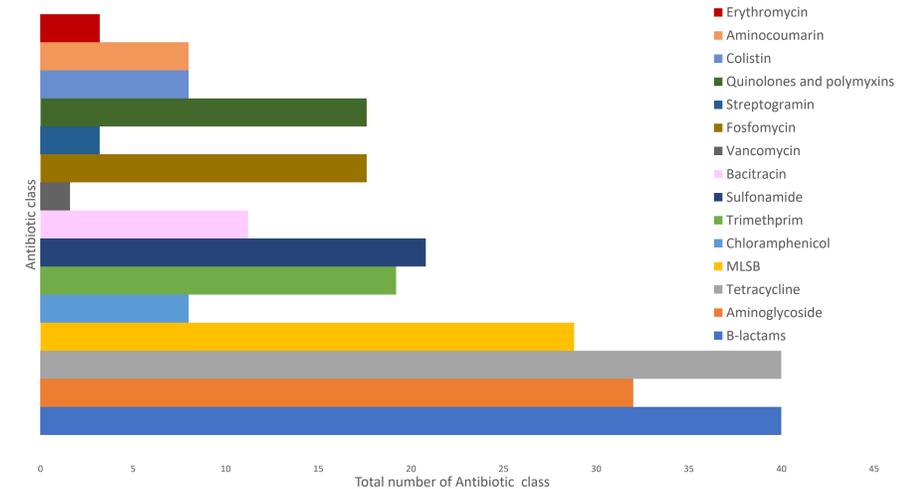


Figure 4. The most common antibiotic resistance classes identified across the studies (Aminoglycoside, β-lactams, macrolide, lincosamide, streptogramin, and tetracycline-class resistance).

Discussion

Overall, the results from this review show:

- Mode of delivery is an important determinant of early intestinal colonization in infants.
- Antibiotics used in infancy directly affect the gut microbiome, including decreased diversity, stability and increases in antibiotic resistance genes following treatments.
- Environmental factors (NICU and hospital ward surface) play a significant role in shaping the infant gut microbiome.
- AMR load were associated with the maturity of the gut microbiome and bacterial composition.
- Aminoglycoside, β-lactams, macrolide, lincosamide, streptogramin, and tetracycline-class resistance were found almost ubiquitous across the studies.
- Bacteria from order Enterobacterales and Bacteroidetes are commonly identified as carrying AMR genes.
- More studies are needed to enhance our understanding of the AMR global burden.

Conclusions

Findings from this systematic review provide evidence from around the world that antibiotics use, delivery by Caesarean section, and admission to a NICU make a fundamental contribution to the problem of AMR acquisition in infants. Early exposure to antibiotics negatively impacts the development of the infant gut microbiome, increases resistant genes and threatening the successful treatment of infectious diseases. AMR determinants' potential long-term adverse consequences on an infant's health also warrant further investigation.

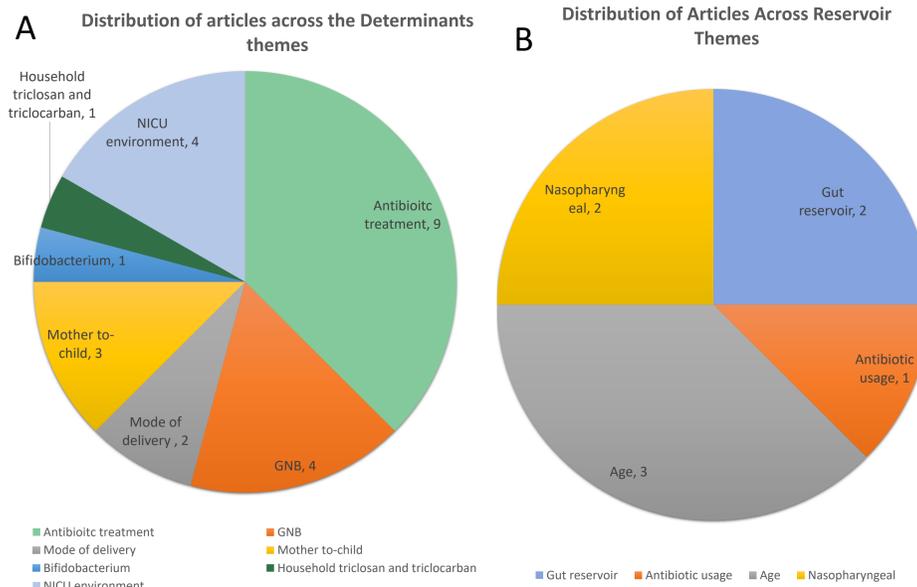


Figure 3. Distribution of articles across the identified themes. A: Determinants themes 24 articles. B: Reservoir themes 8 articles.

Summary of Results

We summarized evidence on AMR determinants among infants by gestational age (disaggregating those >37 weeks and those below), determinant type and reservoir.

References & Acknowledgments

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