

Longitudinal assessment of antibiotic resistance gene profiles from the infant gut microbiome

CURRENT STATUS: ACCEPTED

BMC Infectious Diseases  BMC Series

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DOI:

10.21203/rs.2.18486/v1

SUBJECT AREAS

Infectious Diseases *Pediatrics*

KEYWORDS

Antibiotic resistance genes, resistome, infancy, birth cohort, ESBL producing Enterobacteriaceae

Abstract

Background: The rapid spread of multidrug- resistant pathogenic bacteria is a worldwide public health concern. Given the high carriage rate of extended spectrum beta-lactamase (ESBL)- producing Enterobacteriaceae in Asia, we aimed to evaluate community prevalence and dynamics by studying the longitudinal changes in antibiotic resistance gene (ARG) profiles and prevalence of ESBL-producing *E. coli* and *K. pneumoniae* in the intestinal microbiome of infants participating in the Growing Up in Singapore Towards Healthy Outcomes (GUSTO) study, a longitudinal cohort study of pregnant women and their infants.

Methods: We analysed the antibiotic resistance genes profile in the first year of life among 75 infants who had stool samples collected at multiple timepoints using metagenomics.

Results: The mean number of ARGs per infant increased with age. The most common ARGs identified confer resistance to aminoglycoside, beta-lactam, macrolide and tetracycline antibiotics; all infants harboured these antibiotic resistance genes at some point in the first year of life. Few ARGs persisted throughout the first year of life. Beta-lactam resistant *Escherichia coli* and *Klebsiella pneumoniae* were detected in 4 (5.3%) and 32 (42.7%) of subjects respectively.

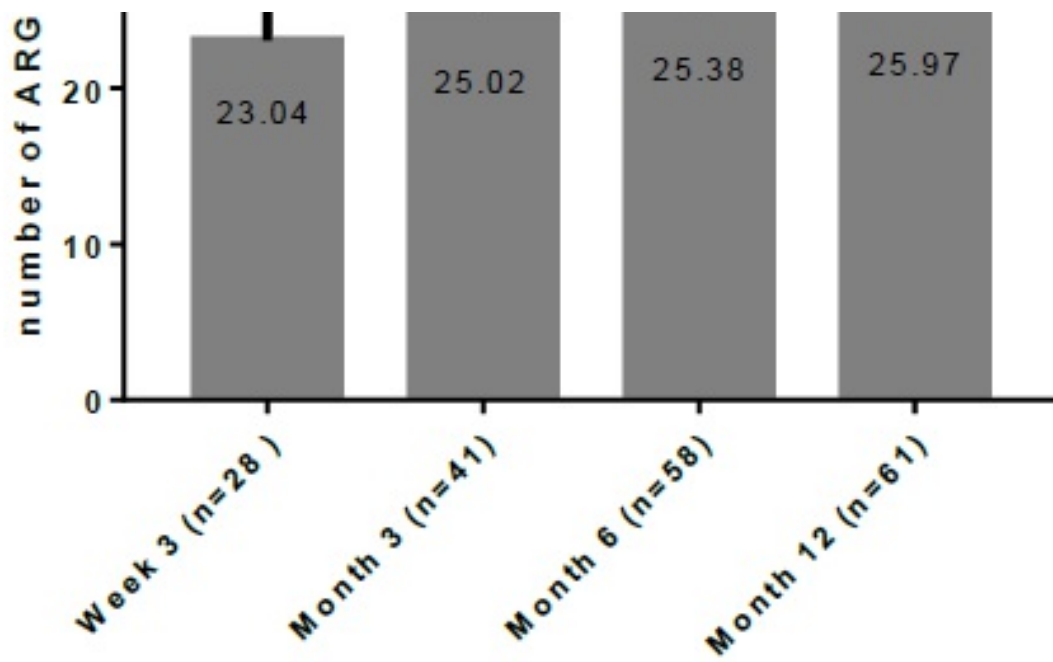
Conclusion: In this longitudinal cohort study of healthy infants living in a region with high endemic antibacterial resistance, we demonstrate that majority of the infants harboured a number of antibiotic resistance genes in their gut and showed that the infant gut resistome is diverse and dynamic over the first year of life.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures





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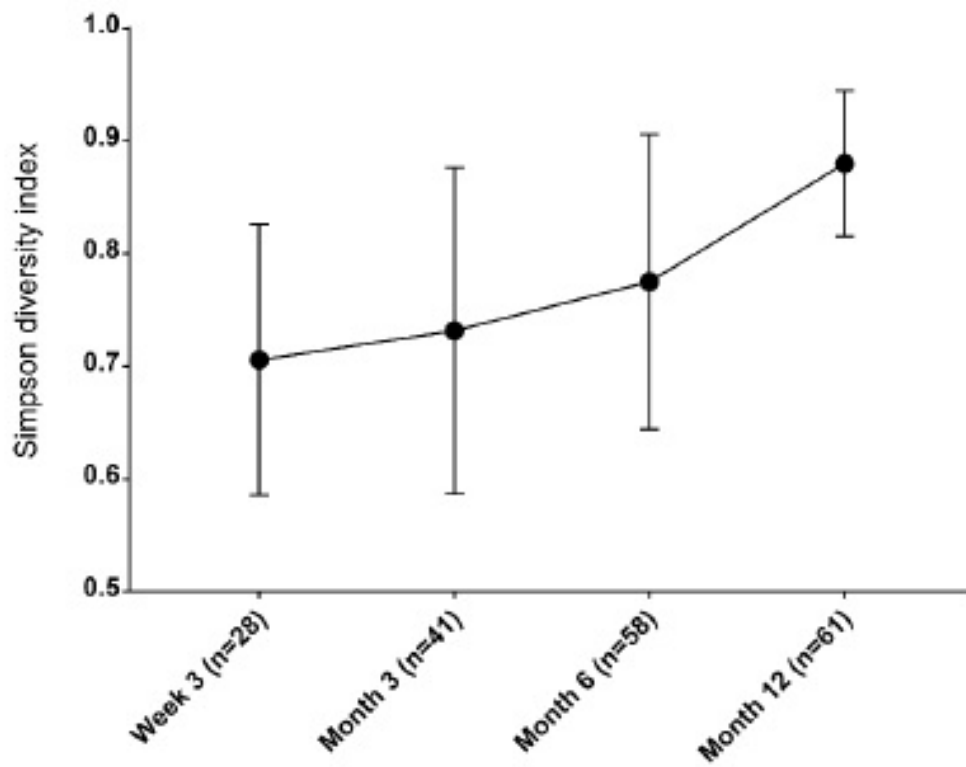


Figure 1

1a. Mean number of ARGs per infant over time. 1b Microbial diversity of stool samples over

time as determined by Simpsons Diversity Index.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

[ARGpaper_Additional Data_271119.pdf](#)