

Enteroaggregative *Escherichia coli* (EAEC) colonization in infancy. Evidence of mother-to-child transmission?

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INTRODUCTION

- Escherichia coli* are among the major cause of both hospital and community-acquired infections including bacteremia, sepsis among other syndromes worldwide, with high incidence in developing countries including Mozambique.
- In our study community, Manhica District in southern Mozambique, fatal EAEC O25:4 ST131 has emerged as cause of bacteremia in children younger than 3 years of age, supporting the need of prompt recognition for appropriate management
- Escherichia coli* typically colonizes the gastrointestinal tract of human infants within a few hours after birth. However, gut colonization by enteroaggregative *Escherichia coli* (EAEC) pathotype in neonates and possible mother-to-child transmission remain unknown.
- Poor outcome due to *E. coli* infection are generally associated with septicemic and urinary infection that might precipitate early preterm labor and death in neonates. Herein, we report the possible role of *E. coli* as a contributing factor to mortality in stillbirth's and in children under 5 years .

METHODOLOGY

- As part of Child Health and Mortality Prevention Surveillance (CHAMPS) ongoing at the Manhiça District (since December 2016) in southern Mozambique and other 6 countries (1), stillbirths and under five dead children from a catchment area are submitted to MITS for ascertaining the cause of death after informed consent. (<https://champshealth.org/>)
- CHAMPS aims to track definitive causes of child mortality in sites throughout Sub-Saharan Africa and South Asia and produce and disseminate high-quality data to inform policy and public health action in real time.
- Families of eligible (residing in study area - Manhica District) stillbirths or dead child under 5 years of age occurred at the Manhica District Hospital within 24-36 hours were approached for consent form after death notification by study team
- Tissue samples, blood, cerebrospinal fluid (CSF) were collected and appropriately analyzed by conventional microbiology, Taq Array Card (TAC) technology and histopathology for pathogens detection.
- A total of 24 rectal swabs from stillbirth and dead children under five were analyzed by TAC qPCR (QuantStudio™7 Flex Real-Time PCR System, Applied Biosystems®) for detection of enteric pathogens, including diarrheagenic *E. coli* pathotypes genes after DNA / RNA extraction using MagNAPure (MagNA Pure Compact System, Roche).

RESULTS

Table 1. Demographic characteristics enrolled cases for MITS

Sexo	Age group			Total
	Stillbirth n(%)	Neonates n (%)	Under 5 n (%)	
Female	4/5 (80 %)	4 (36.4%)	2 (25%)	10/24 (41.7%)
Male	1/5 (20%)	7 (63.6%)	6(75%)	14/24 (58.3%
Total	5	11	8	24

CONCLUSIONS

- Overall, we documented high prevalence of *E. coli* strains harboring *aatA*, particularly in still birth and neonates suggesting possible mother-to-child transmission.
- These findings support our early observation and hypothesis that EAEC might be a relevant pathogen colonizing gut of young children and, consequently may explain the high burden of disease (e.g sepsis/bacteremia) arguing prompt recognition and appropriate management to prevent poor patient's outcome.
- This also support the need of further investigation of the role of EAEC related genes in stillbirth and neonates; and probable adoption of appropriate measurement of pregnant women during antenatal visits for infection prevention/control.
- Our findings may also reinforce the urgent need of development of broader strategies for maternal immunization which may consider vaccines also targeting *E. coli* pathotypes.

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Fig. 1. Detection of the enteric pathogens by TAC from rectal swabs of stillbirth and dead under five children

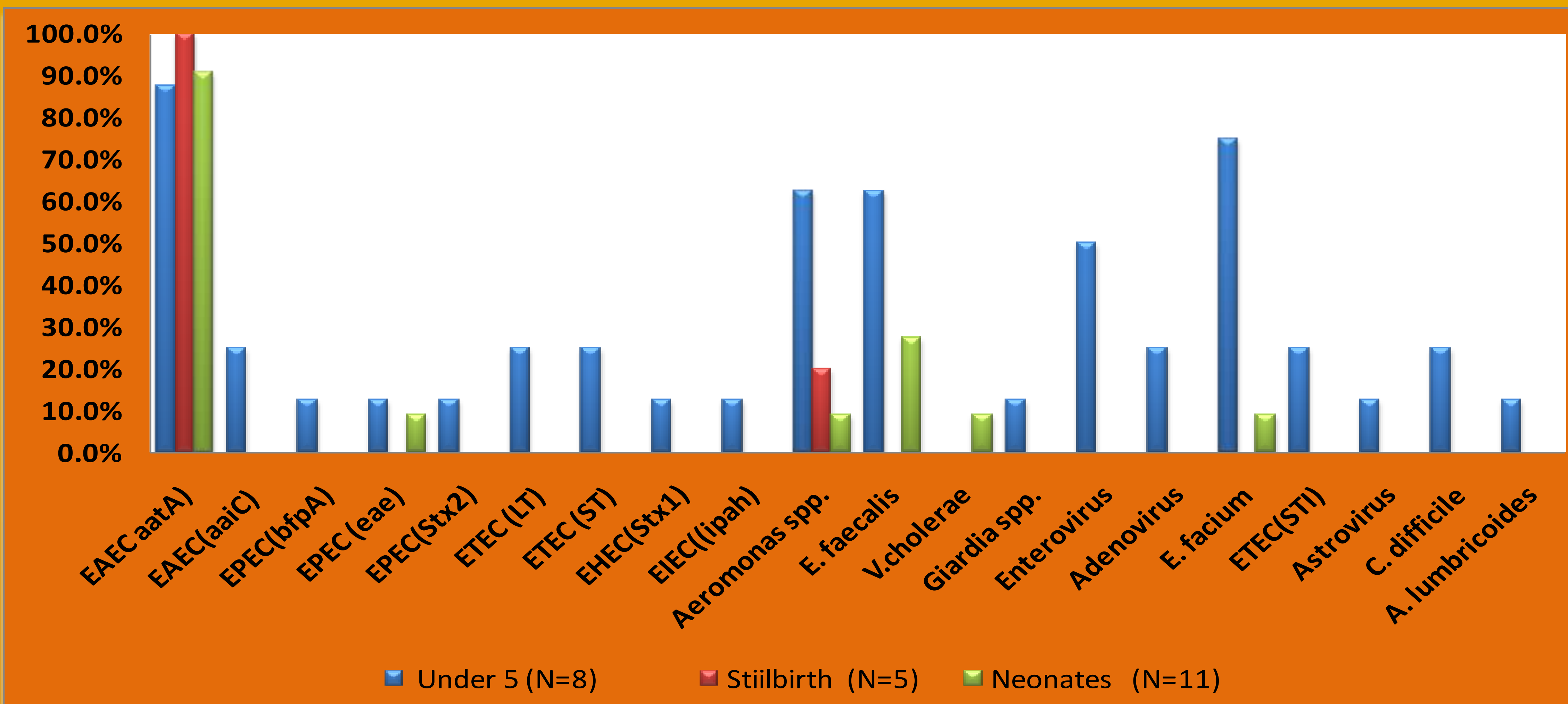


Table 2. Detection of diarrheagenic pathotypes stratified by age groups

Diarrheagenic <i>E. coli</i>		Under 5	Stillbirth	Neonates	Total
		n (%)	n (%)	n (%)	n (%)
EAEC	<i>aatA gene</i>	8/8 (100)	5/5 (100)	10/11 (90.9)	23/24 (95.8)
	<i>aaiC gene</i>	2/8 (25)	0	0	2/24 (8.3)
EPEC	<i>bfpA gene</i>	1/8 (12.5)	0	0	1/24 (4.2)
	<i>eae gene</i>	1/8 (12.5)	0	0	1/24 (4.2)
ETEC	<i>Stx2 gene</i>	1/8 (12.5)	0	0	1/24 (4.2)
	<i>LT gene</i>	2/8 (25)	0	0	2/24 (8.3)
EHEC	<i>ST gene</i>	4/8 (50)	0	0	4/24 (16.7)
	<i>Stx1 gene</i>	1/8 (12.5)	0	0	1/24 (4.2)
EIEC	<i>ipah gene</i>	1/8 (12.5)	0	0	1/24 (4.2)

- Only 8.3% (2/24) of tested samples were positive for both *aatA* and *aaiC*

