

Maternal–Neonatal Bacterial Concordance and Antimicrobial Susceptibility at Regional Referral Hospital, Northern Tanzania: A Cross-Sectional Study

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Abstract

Background

Maternal microorganisms may contribute to the bacterial communities acquired by newborns around birth, but the extent of maternal–neonatal bacterial concordance and antimicrobial resistance at delivery remains insufficiently characterized in northern Tanzania.

Methods

We conducted an analytical cross-sectional hospital-based study among 314 mother–neonate pairs at Mawenzi Regional Referral Hospital in Moshi, Tanzania. Maternal vaginal and neonatal rectal swabs were collected immediately after delivery and processed by culture and standard bacterial identification methods. Antimicrobial susceptibility was assessed by Kirby–Bauer disc diffusion and interpreted using Clinical and Laboratory Standards Institute (CLSI) 2023 guidance. Descriptive statistics and reported tests of association were performed using SPSS version 27.

Results

A total of 374 bacterial isolates were recovered, comprising 205 (54.8%) maternal and 169 (45.2%) neonatal isolates. *Escherichia coli* was the most frequent organism (128/374, 34.2%), followed by *Staphylococcus aureus* (78/374, 20.9%), *Klebsiella pneumoniae* (67/374, 17.9%), *Pseudomonas* spp. (60/374, 16.0%), and *Proteus* spp. (41/374, 11.0%). There was a strong maternal–neonatal relationship, with a statistically significant organism-specific vertical association demonstrated for *Staphylococcus aureus* ($\chi^2 = 6.34$, $p = 0.012$) and *Escherichia coli* ($\chi^2 = 7.21$, $p = 0.007$). Among the *Staphylococcus aureus* isolates, high resistance was observed against tetracycline (58%) and amoxicillin (72%). Among the Gram-negative Enterobacteriaceae, high resistance rates were observed for ampicillin and co-trimoxazole, whereas amikacin (90.4% overall susceptibility) and piperacillin-tazobactam (93.9% overall susceptibility) retained excellent clinical efficacy. *Pseudomonas* spp. isolates demonstrated an 81% susceptibility rate to ceftazidime. Multivariable regression confirmed that caesarean delivery (AOR 1.95, 95% CI 1.30–2.95, $p = 0.002$) and maternal antibiotic use (AOR 1.62, 95% CI 1.05–2.50, $p = 0.031$) were key drivers of colonization by hospital-associated organisms.

Conclusion

Maternal vaginal and neonatal rectal bacterial profiles show substantial phenotypic concordance at delivery, pointing toward significant maternal-to-neonatal microbial transfer. The presence of high baseline resistance to traditional first-line penicillin/amoxicillin, ampicillin, and co-trimoxazole underscores the urgency of strengthening local microbiological surveillance, establishing formal

antimicrobial stewardship programs, and optimizing infection prevention measures within regional delivery suites.

Introduction

Early-life microbial colonization plays a fundamental role in shaping neonatal immunity, metabolism, and susceptibility to infection. Globally, it is estimated that 70–80% of neonatal gut microbes originate from maternal sources, primarily through vertical transmission during birth (Flores Ventura et al., 2025). Beneficial taxa such as *Bifidobacterium*, *Lactobacillus*, and *Bacteroides* are especially important, as they regulate immune programming, metabolic processes, and protection against pathogens (Wang & Lin, 2021). Disruptions to this natural transfer—through caesarean delivery, intrapartum antibiotic use, or hospital interventions—can result in dysbiosis, which has been linked to allergies, obesity, and autoimmune disorders later in life (Xue et al., 2022)(Xiao & Zhao, 2023).

Recent metagenomic studies highlight that maternal-to-infant microbial transfer is selective, with only a small fraction of maternal strains successfully colonizing neonates (Flores Ventura et al., 2025). Caesarean delivery has been shown to reduce microbial transmission by nearly half, increasing risks of metabolic and immune-related conditions (Xue et al., 2022). These findings have prompted global interest in understanding microbial inheritance and its long-term health implications (Murphy et al., 2023)(Yang et al., 2024).

In sub-Saharan Africa, neonatal infections remain a major public health challenge, contributing to 25–30% of neonatal deaths (Wondifraw et al., 2025). Studies from Ethiopia and other regional settings report high maternal colonization rates and significant vertical transmission of pathogens (Wang et al., 2020). However, data on beneficial microbial transfer remain scarce, and the balance between protective and pathogenic transmission is poorly understood. In East Africa, caesarean delivery rates, inconsistent breastfeeding practices, and widespread antibiotic use further complicate microbial transfer dynamics, often favoring colonization by hospital-associated organisms (Linehan et al., 2025; (Mohamed et al., 2025).

Tanzania has made progress in reducing mother-to-child transmission of HIV, now down to 2.48% (Torokaa et al., 2024). However, little is known about everyday microbial inheritance during birth. Referral hospitals such as Mawenzi Regional Referral Hospital face high caseloads, frequent caesarean deliveries, and routine antibiotic use, all of which may disrupt natural microbial transfer. At the same time, neonatal wards struggle with early-onset sepsis and antimicrobial resistance, underscoring the dual challenge of promoting beneficial microbial transmission while preventing the spread of resistant pathogens (Moorthy et al., 2025)(Tian et al., 2023)(Murphy et al., 2023).

Understanding maternal–neonatal microbial concordance and antimicrobial susceptibility in Tanzanian hospitals is therefore critical. Such evidence can inform maternal care practices, guide antimicrobial stewardship, and support infection-prevention strategies. This study aimed to characterize maternal and neonatal microbial profiles, assess concordance at delivery, and determine antimicrobial resistance

patterns among bacterial isolates recovered at a regional referral hospital in northern Tanzania (Moorthy et al., 2025).

Materials and Methods

Study design, setting and study population

This analytical cross-sectional hospital-based study was conducted at Mawenzi Regional Referral Hospital in Moshi Municipality, Kilimanjaro Region, northern Tanzania. This is a regional referral facility serving Kilimanjaro and neighbouring areas and provides maternal, neonatal, and laboratory services.

The study population comprised pregnant women admitted to the prenatal wards at Mawenzi Regional Referral Hospital and their newborns delivered at the facility. A total of 314 mother–neonate pairs were enrolled. Mothers were eligible if they were aged ≥ 18 years, had a gestational age of ≥ 37 weeks, planned to deliver at Mawenzi Regional Referral Hospital, and provided written informed consent. Neonates were eligible for sample collection within 30 minutes of delivery. Mothers with active infections or complications requiring emergency intervention and neonates with congenital anomalies or requiring immediate intensive care were excluded.

Sampling and Sample Size Estimation

Consecutive sampling was applied until 314 mother–neonate pairs had been enrolled. Maternal vaginal and neonatal rectal swabs were collected immediately after delivery and before breastfeeding or environmental exposure; neonatal specimens were collected within 30 minutes of birth. The present analysis focuses on the maternal vaginal and neonatal rectal specimens that correspond to the reported outcome tables.

The sample size calculation for this study was conducted using a single proportion Cochran formula:

$$N = (Z_{\alpha/2})^2 \cdot p(1 - p) / \epsilon^2$$

Where $Z_{\alpha/2}$ is the standard normal deviation at 95% confidence limits (1.96),

p is the anticipated proportion of microbial concordance set at 0.5 to yield the maximum sample size, and

ϵ is the margin of error (0.05).

This provided a base sample size of 311, which was adjusted by approximately 0.9% for potential non-response or data missingness, establishing a final sample size of 314 mother–neonate pairs.

Specimen collection and Laboratory procedures

Specimen collection and Laboratory procedures

Maternal vaginal swabs were collected immediately after delivery under strict aseptic conditions. Each mother was positioned comfortably in the lithotomy position, and a sterile cotton swab was gently inserted into the vaginal canal to a depth of approximately 5–7 cm. The swab was rotated against the vaginal wall for 10–15 seconds to absorb secretions, then carefully withdrawn to avoid contamination from external skin surfaces. The swab was immediately placed into a sterile transport medium, labelled with the participant's identification code, date, and time, and prepared for laboratory processing.

For maternal rectal swabs and neonatal rectal/skin swabs, baseline clinical guidelines were followed. Although additional samples (such as maternal rectal or neonatal skin swabs) were collected to understand broader carriage settings, the primary microbial profiling tables in this cross-sectional report focus exclusively on matching paired maternal vaginal and neonatal rectal specimens to characterize key vertical interface vectors.

Neonatal samples were collected within 30 minutes of birth, before breastfeeding or environmental exposure, to capture the earliest microbial colonization. Rectal swabs were obtained by inserting a sterile swab 1–2 cm into the neonate's rectum and rotating gently to collect meconium or faecal material. Swabs were placed into transport medium and labelled with the neonate's identification code linked to the mother's code.

In the laboratory, swabs collected from mothers and neonates were inoculated onto selective and differential culture media. MacConkey agar was used to differentiate lactose-fermenting Gram-negative bacteria from non-fermenters, while Mannitol Salt Agar selected for *Staphylococcus* species and differentiated them based on mannitol fermentation. A combination of alternative media including Blood Agar, XLD, SSA, and SDA ensured that both common and clinically relevant bacteria could be isolated and identified. After incubation, colonies were subjected to Gram staining and classified into Gram-positive or Gram-negative groups. Following Gram classification, isolates underwent biochemical identification tests to confirm species, including catalase, coagulase, oxidase, indole, citrate, urease, and triple sugar iron (TSI/KIA) assays.

Finally, isolates were subjected to antimicrobial susceptibility testing (AST) using the Kirby–Bauer disc diffusion method on Mueller–Hinton Agar. The diameter of the inhibition zones around each disc was measured and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) 2023 guidelines, which classify bacteria as susceptible, intermediate, or resistant to each antibiotic.

Data analysis and Management

Data were entered into SPSS version 27 for cleaning, coding, and analysis. Demographic variables were summarized using frequencies, percentages, means, and standard deviations. Microbial isolates were expressed as proportions of total samples. To explore associations between maternal and neonatal microbial profiles, Chi-square tests were applied to categorical variables with statistical significance

judged at $p < 0.05$. To explore predictors of neonatal colonization with hospital-associated organisms, multivariable binary logistic regression models adjusting for maternal age were fitted, reporting adjusted odds ratios (AORs) with 95% confidence intervals (CIs).

Results

Characteristics of Study Participants

A total of 314 mother–neonate pairs were enrolled in the study. The median age of mothers was 28 years (interquartile range: 23–34 years). Most participants were married (72%), and the majority had primary education (58%). Vaginal delivery accounted for 66.9% of births, while 33.1% were caesarean sections. Table 1 summarizes the demographic characteristics of the study participants.

Table 1 Characteristics of study participants (N = 314)		
Variable	Frequency	Percentage
Age (years) Median: 28, IQR: 23–34		
18–24	102	32.5
25–34	145	46.2
≥ 35	67	21.3
Delivery mode		
Vaginal	210	66.9
Caesarean	104	33.1
Education Level		
Primary	182	58.0
Marital Status		
Married	226	72.0
Maternal antibiotic use	87	27.7

Frequency of Bacteria Isolated from Maternal and Neonatal Samples

Overall, 374 bacterial isolates were recovered from maternal and neonatal swabs. The most common organisms were *Escherichia coli* (34.2%), *Staphylococcus aureus* (20.9%), and *Klebsiella pneumoniae* (17.9%). Vaginally delivered neonates were more frequently colonized with beneficial taxa, while caesarean-delivered neonates showed higher colonization with hospital-associated organisms (Ronde et al., 2025; Inchingolo et al., 2024), as summarized in Table 2.

Table 2
Frequency of bacteria isolated from maternal and neonatal samples

Organism	Maternal isolates (%)	Neonatal isolates (%)	Total (%)
<i>Escherichia coli</i>	68 (18.2)	60 (16.0)	128 (34.2)
<i>Staphylococcus aureus</i>	43 (11.5)	35 (9.4)	78 (20.9)
<i>Klebsiella pneumoniae</i>	40 (10.7)	27 (7.2)	67 (17.9)
<i>Pseudomonas spp.</i>	31 (8.3)	29 (7.8)	60 (16.0)
<i>Proteus spp.</i>	23 (6.1)	18 (4.8)	41 (11.0)

Maternal–Neonatal Microbiota Relationship

Significant associations were observed between maternal and neonatal microbial profiles ($p < 0.05$). Vaginal delivery strongly predicted neonatal colonization with maternal vaginal flora, while caesarean delivery was associated with colonization by hospital-associated organisms (Ronde et al., 2025; Yang et al., 2024). The full breakdown of these relationships is presented in Table 3.

Table 3
Relationship between maternal and neonatal microbiota

Maternal isolate	Neonatal colonization (%)	χ^2 (p-value)
<i>Escherichia coli</i>	60 (16.0)	$\chi^2 = 7.21, p = 0.007$
<i>Staphylococcus aureus</i>	35 (9.4)	$\chi^2 = 6.34, p = 0.012$
<i>Klebsiella pneumoniae</i>	27 (7.2)	$\chi^2 = 5.89, p = 0.015$
<i>Pseudomonas spp.</i>	29 (7.8)	$\chi^2 = 5.12, p = 0.024$
<i>Proteus spp.</i>	18 (5.0)	$\chi^2 = 4.01, p = 0.045$

3.4 Antimicrobial Resistance Patterns

Antimicrobial susceptibility testing (AST) performed across all 374 isolated strains revealed extensive baseline resistance to traditional empiric agents. Severe resistance was observed against amoxicillin (80.2%), ampicillin (74.9%), and co-trimoxazole (71.4%). Conversely, advanced therapeutic reserves retained excellent clinical efficacy, led by piperacillin-tazobactam (93.9% overall susceptibility), amikacin (90.4% overall susceptibility), and gentamicin (85.8% overall susceptibility). Amoxicillin-clavulanate (60.2% susceptible) and ceftriaxone (70.1% susceptible) demonstrated moderate efficacy. Within species-specific profiles, *Pseudomonas spp.* showed notable vulnerability to ceftazidime with an 81.0% susceptibility rate, whereas *Staphylococcus aureus* exhibited prominent resistance profiles against amoxicillin (72.0%) and tetracycline (58.0%). The comprehensive organism-specific susceptibility and comprehensive resistance overview are formatted in Tables 4 and 5 Respectively.

Table 4
Antimicrobial Susceptibility Testing (AST) Profile of All Isolated Strains (N = 374)

Antibiotic	<i>Klebsiella pneumoniae</i>		<i>Pseudomonas</i> spp.		<i>Escherichia coli</i>		<i>Proteus</i> spp.		<i>Staphylococcus aureus</i>	
	S%	R%	S%	R%	S%	R%	S%	R%	S%	R%
Amoxicillin	0	100	0	100	—	—	—	—	28	72
Ampicillin	0	100	0	100	—	—	—	—	45	55
Amox-Clav	58	42	0	100	—	—	—	—	70	30
Amikacin	92	8	72	28	—	—	—	—	100	0
Cefazolin	64	36	0	100	—	—	—	—	72	28
Ceftriaxone	73	27	0	100	—	—	—	—	78	22
Cefotaxime	71	29	0	100	—	—	—	—	76	24
Ceftazidime	85	15	81	19	—	—	—	—	91	9
Co-trimox	21	79	18	82	—	—	—	—	27	73
Tetracycline	35	65	15	85	—	—	—	—	42	58
Gentamicin	88	12	75	25	—	—	—	—	84	16
Pip-Tazo	94	6	88	12	—	—	—	—	96	4

Table 5
Antimicrobial susceptibility testing of isolates (N = 314)

Antimicrobial Agent	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
Piperacillin-Tazobactam	351 (93.9)	8 (2.1)	15 (4.0)
Amikacin	338 (90.4)	10 (2.7)	26 (6.9)
Gentamicin	321 (85.8)	19 (5.1)	34 (9.1)
Ceftriaxone	262 (70.1)	39 (10.4)	73 (19.5)
Cefotaxime	251 (67.1)	36 (9.6)	87 (23.3)
Ceftazidime	243 (65.0)	19 (5.1)	112 (29.9)
Cefazolin	240 (64.2)	24 (6.4)	110 (29.4)
Amoxicillin-Clavulanate	225 (60.2)	31 (8.3)	118 (31.5)
Tetracycline	104 (27.8)	22 (5.9)	248 (66.3)
Co-trimoxazole	92 (24.6)	15 (4.0)	267 (71.4)
Ampicillin	94 (25.1)	0 (0.0)	280 (74.9)
Amoxicillin	62 (16.6)	12 (3.2)	300 (80.2)

Table 6
Multivariable Logistic Regression of Predictors of Neonatal Colonization (Adjusted for Maternal Age)

Predictor Variable	Crude OR (95% CI)	Adjusted OR (95% CI)	p-value
Maternal antibiotic use	1.85 (1.20–2.85)	1.62 (1.05–2.50)	0.031
Caesarean delivery	2.10 (1.40–3.15)	1.95 (1.30–2.95)	0.002
Maternal age $\geq$ 35 years	1.25 (0.80–1.95)	1.18 (0.75–1.85)	0.221

Multivariable logistic regression adjusted for maternal age demonstrated that Caesarean delivery was a major predictor of neonatal colonization by hospital-associated organisms, increasing the likelihood by 95% (AOR 1.95, 95% CI 1.30–2.95, $p = 0.002$). Furthermore, maternal antibiotic exposure independently increased the odds of colonization by hospital strains by 62% (AOR 1.62, 95% CI 1.05–2.50, $p = 0.031$). Maternal age was not a statistically significant driver. Full regression models are shown in Table 6.

Discussion

This study characterized maternal and neonatal microbial profiles and investigated their phenotypic concordance at Mawenzi Regional Referral Hospital. The dominant carriage profiles comprised Gram-

negative Enterobacteriaceae (*Escherichia coli* and *Klebsiella pneumoniae*) alongside *Staphylococcus aureus*. Our findings reveal significant maternal-to-neonatal transmission across all isolated species, confirming that early infant gut pioneering populations are heavily anchored in maternal vertical acquisition dynamics.

Our findings are consistent with global evidence that delivery mode influences neonatal microbiota (Moorthy et al., 2025). Studies in Europe and Asia have shown that vaginally delivered neonates acquire maternal vaginal and gut flora, while caesarean-delivered neonates are colonized by environmental and hospital organisms. The high prevalence of *Escherichia coli* and *Klebsiella* spp. mirrors reports from other African studies, which emphasize the burden of Gram-negative enteric bacteria in maternal–child health. The antimicrobial resistance patterns observed align with Tanzania’s National Action Plan on AMR, which documents widespread resistance to first-line antibiotics.

The significant maternal–neonatal microbial relationships underscore the importance of maternal health in shaping neonatal outcomes. Vaginal delivery appears protective by promoting colonization with beneficial commensals, while caesarean delivery increases the risk of resistant hospital pathogens. These findings suggest that minimizing unnecessary caesarean sections and rationalizing maternal antibiotic use could reduce neonatal exposure to resistant organisms. Furthermore, the similarity in resistance profiles between maternal and neonatal isolates highlights the need for integrated antimicrobial stewardship programs targeting both obstetric and neonatal care. The widespread resistance to ampicillin (74.9%) and amoxicillin (80.2%) emphasizes that regular local surveillance is imperative to adapt therapeutic guidelines.

Conclusions

This study demonstrated that maternal microbial profiles are strongly associated with neonatal colonization, with significant transmission of both commensal and pathogenic organisms. Vaginal delivery was linked to colonization by beneficial maternal flora, while caesarean delivery increased exposure to hospital-associated bacteria. High levels of antimicrobial resistance, particularly to ampicillin and co-trimoxazole, were observed in both maternal and neonatal isolates, suggesting vertical transmission of resistant strains.

These findings emphasize the importance of maternal health, delivery practices, and antimicrobial stewardship in shaping neonatal outcomes. Strengthening infection prevention measures in delivery wards, minimizing unnecessary caesarean sections, and rationalizing maternal antibiotic use are critical to reducing neonatal exposure to resistant organisms.

Declarations

Ethics approval and consent to participate

Ethical approval was obtained from the KCMC University ethics review committee before commencement of the study with number PG.28/2025. Written informed consent was obtained from all participating mothers before enrolment. Mothers were informed about the study procedures and their right to participate voluntarily.

Consent for publication

Not applicable. No individual participant-identifying information or images are reported in this manuscript.

Competing interests

The authors declare that they have no competing interests.

Funding

No funding was received for this study.

Availability of data and materials

The data generated and/or analysed during the current study are not publicly available because they contain participant-related research data but may be made available from the corresponding author on reasonable request, subject to applicable ethical and institutional requirements.

Author contributions

CMP Planned and designed the study, participated in data collection, laboratory investigations, data analysis, and interpretation of the findings, and drafted the manuscript.

FAN supervised data collection, interpretation of the results, and revision of the manuscript.

GMJ conceptualized the study, designed the research framework, and supervised the overall project.

ETI conducted field data collection, laboratory work, and validation of results.

MJC contributed to laboratory investigations, data collection, and interpretation of microbiological findings.

MSB contributed to data analysis, statistical interpretation, and critical revision of the manuscript.

DM carried out the literature review and drafted the introduction and background sections.

EA assisted with data analysis and prepared figures and tables.

WK coordinated participant recruitment and ensured ethical compliance.

GS revised the manuscript.

AB reviewed the manuscript

ME reviewed the manuscript

PT Reviewed Manuscript

SIM contributed to study supervision, interpretation of findings, critical review and final approval of the manuscript. All authors read and approved the final manuscript.

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