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Cohort profile: Infant Gut Bacterial Study in Nigeria (INBUGS-NG)

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ABSTRACT

Purpose The Infant Gut Bacterial Study in Nigeria (INBUGS-NG) investigates how delivery mode, antibiotic exposure, feeding practices and environmental factors shape gut microbiome development and acquisition of antibiotic resistance genes (ARGs) during the first year of life in northern Nigeria.

Participants Between February and July 2024, 90 mother–infant dyads were enrolled at a tertiary hospital in Kano city, Nigeria. This was a prospective longitudinal cohort with follow-ups at 10 scheduled time points: days 0, 1, 3, 5, 7, 14, 28, 90, 180 and 365. We also intensified stool sampling after infant antibiotic administration, enabling dense early-life sampling. To date, the cohort has contributed 480 infant stool samples, 232 maternal rectal swabs, 254 breast milk samples and 806 environmental samples (total 1772). In parallel, socio-demographic, clinical and cultural data were collected using Research Electronic Data Capture (REDCap) and household visit diaries.

Findings to date Baseline data show that 84/90 mothers (93.3%) received postpartum antibiotics, and 26/90 infants (28.9%) received antibiotics within the first 3 months of life. Only 8% of infants were exclusively breastfed, with early water supplementation common. Caesarean deliveries accounted for 25% of births, and the mean gestational age was 38.5 weeks. Across the cohort, high retention was achieved, and the study has generated a unique long-read metagenomic resource from an African infant population, with analyses ongoing.

Future plans Shotgun long-read metagenomic sequencing (Oxford Nanopore) will enable strain-level and plasmid-level profiling of microbial communities and ARGs. Planned analyses include associations between early-life exposures and resistome dynamics, as well as cross-cohort comparisons with a parallel study in Pakistan. Follow-up will continue through 12 months.

STRENGTHS AND LIMITATIONS OF THIS STUDY

- ⇒ This study is one of the first prospective longitudinal African infant cohorts to integrate infant, maternal and environmental samples with long-read shotgun metagenomic sequencing, providing species-level and plasmid-level resolution of microbiome and resistome dynamics.
- ⇒ High-frequency longitudinal stool sampling at 10 time points in the first year and the inclusion of face-to-face data collection, household diaries and qualitative notes provide rich temporal, socio-demographic and cultural context rarely available in similar cohorts.
- ⇒ Our multidisciplinary UK and Nigerian teams ensured robust data collection; however, the hospital-enrolled cohort may not be fully generalisable to rural or exclusively home-birth populations in northern Nigeria.
- ⇒ Maternal health metrics (nutritional status, body mass index) were unavailable due to limitations in antenatal data collection, and cultural practice data (eg, uvulectomy, female genital mutilation) relied on voluntary self-reporting, potentially leading to under-representation.
- ⇒ A key limitation of the metagenomic approach is that transmission dynamics are difficult to infer solely from measures of genomic relatedness, and the reliance on self-reporting for all antibiotic exposure data introduces a risk of misclassification and confounding.

INTRODUCTION

The infant gut microbiome is critical for immune, nutritional and metabolic development,[1] with early-life disruptions linked to later risk of allergy, obesity and inflammatory disease.[2–4] Despite growing recognition of its importance, most microbiome data originate from high-income countries, limiting understanding of how exposures common in low- and middle-income countries (LMICs), including higher infection risk, widespread antibiotic use and differing cultural practices, shape microbial development and antimicrobial resistance trajectories.

Nigeria, the most populous country in Africa,[5] faces one of the highest burdens of neonatal sepsis and antibiotic consumption globally.[6–8] Household conditions in peri-urban Kano, where this study is based, are characterised by large multigenerational structures, limited sanitation infrastructure and frequent proximity to open dumpsites and stagnant water.[9] Yet, despite these enriched clinical, environmental and cultural exposures, microbiome-focused research in Nigerian infants remains extremely limited,[10] and virtually no longitudinal data exist to track microbial or resistome development in this context.

The resistome, the collection of antimicrobial resistance genes (ARGs) within a microbiome, is of public health concern, as ARGs can be transferred between commensal and pathogenic bacteria.[11 12] The Burden of Antibiotic Resistance in Neonates from Developing Societies (BARNARDS-I) project revealed unexpectedly high carriage of ARGs, including extended-spectrum β-lactamase and carbapenemase genes in neonatal stool compared with maternal samples across several LMIC sites, including Nigeria.[11] However, BARNARDS-I was cross-sectional, limiting insights into ARG acquisition dynamics, persistence and early-life exposure effects.

The Infant Gut Bacterial Study in Nigeria (INBUGS-NG) was designed to fill these gaps. It follows 90 mother–infant dyads in peri-urban Kano through their first year, with intensive stool sampling, paired maternal, breast milk and environmental collections and rigorous socio-demographic and cultural data capture. Unlike most similar cohorts, INBUGS-NG employs long-read shotgun metagenomic sequencing (Oxford Nanopore), often enabling species-level resolution of microbial communities and plasmid-level identification of ARGs.[13] This cohort profile describes the study's design, recruitment and baseline characteristics to inform future analyses of microbiome and resistome development in this unique population.

The primary objective of INBUGS-NG is to characterise the temporal development of the infant gut microbiome and resistome during the first year of life. Specific aims are to:

1. Describe the diversity and relative abundance of gut bacteria from birth through infancy.
2. Identify resistome signatures and their variation across defined time points.
3. Evaluate the influence of delivery mode, feeding practices and antibiotic exposure on microbial and resistome trajectories.
4. Explore the contribution of household environmental exposures (eg, sanitation, proximity to dumpsites) to microbial transmission and ARG acquisition.
5. Assess whether socio-demographic and socioeconomic factors influence microbiome composition and resistome development.

COHORT DESCRIPTION

Setting

INBUGS-NG was established at Murtala Muhammed Specialist Hospital (MMSH), a high-volume public tertiary hospital in Kano, northern Nigeria (>550 deliveries/month). Household follow-up was restricted to Kano city residents (straight-line distance from MMSH: median 6.5 km (IQR 3.7–8.7), range 0.3–27.5 km). Enrolled households were distributed across multiple local government areas, Kano Municipal, Gwale, Ungogo, Dala, Gezawa and Fagge, spanning informal urban settlements and peri-urban zones with large multigenerational households and limited sanitation (figure 1). This spatial diversity provides a relevant context for investigating environmental exposures and healthcare access in relation to infant microbiome and resistome development.

Recruitment and eligibility

Between February and July 2024, mothers were approached within 24 hours of delivery and invited to participate. Study information sheets were provided in English. For participants not literate in English, trained research assistants provided verbal explanations and interpretation in Hausa to ensure comprehension. Recruitment posters (online supplemental appendix A) and antenatal counselling sessions were used to raise awareness among mothers and hospital staff before they were approached for enrolment.

Inclusion criteria were: full-term delivery (37–42 weeks), residence within Kano city, absence of major congenital anomalies and no maternal antibiotic use in the preceding 6 months. Exclusion criteria were restrictive maternal diets (eg, vegan or medically prescribed) or residence outside Kano city.

Of 3287 deliveries recorded during the recruitment period, 90 mother–infant dyads were enrolled (~3% of all deliveries). Recruitment was capped at <10 dyads per week to ensure feasible follow-up. Enrolment was staggered across weekdays to reduce bias related to delivery timing or staffing. Three mothers withdrew prior to providing biological samples, leaving 87 infants with baseline data. By day 90, 79 dyads (91%) remained in active follow-up (figure 2), with most attrition occurring before day 14 due to relocation or voluntary withdrawal of consent. Families who withdrew consent permitted retention of samples already collected. This high retention rate shows the feasibility of longitudinal microbiome surveillance in low-resource, peri-urban settings when supported by consistent engagement and culturally sensitive field strategies.

INBUGS-NG was established as a substudy of the ongoing BARNARDS-II project,[14] which investigates neonatal sepsis and antibiotic resistance across multiple LMICs. Socio-demographic and clinical metadata were partly collected using the BARNARDS-II Research Electronic Data Capture (REDCap) case report forms and supplemented with INBUGS-NG-specific REDCap case report form and tools, including household event grids and qualitative field notes. This integration ensures consistency with the broader BARNARDS dataset while capturing additional contextual exposures relevant to microbiome and resistome development.

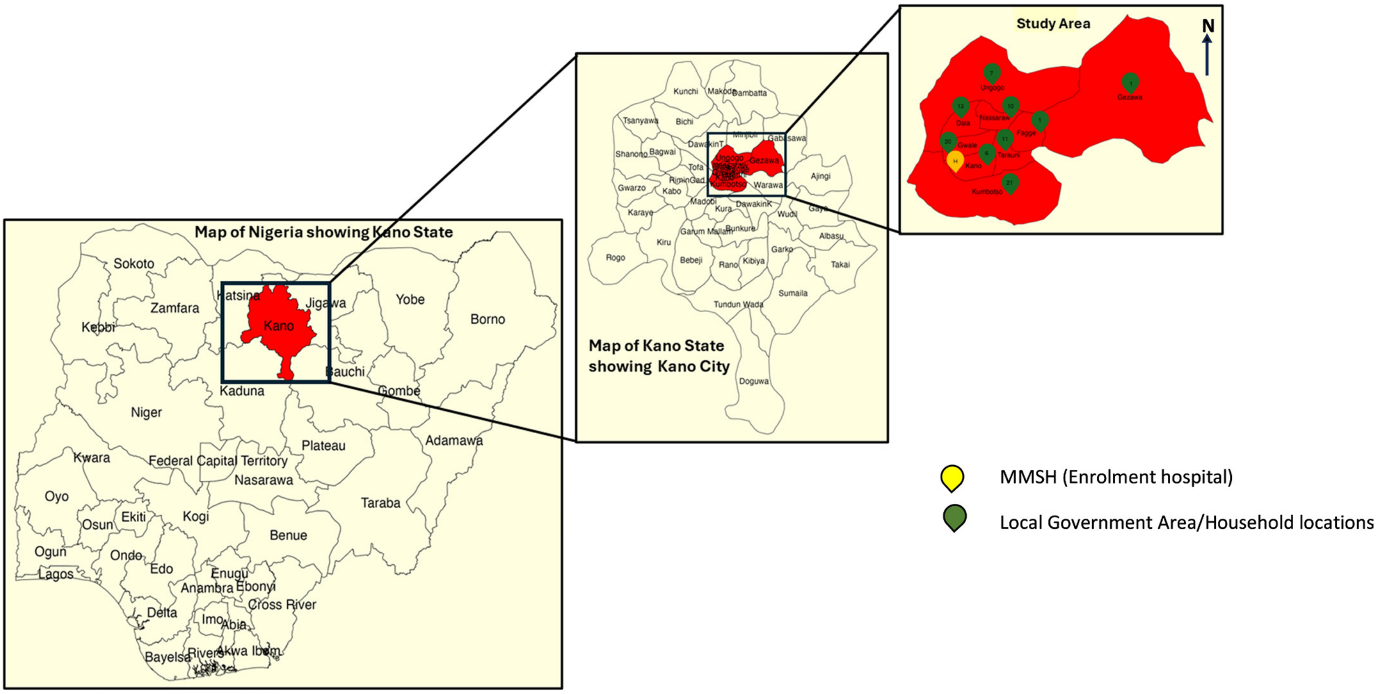

Figure 1 Study setting in Kano state, Nigeria. The left panel shows the location of Kano state within Nigeria (highlighted in red). The middle panel zooms to Kano state and indicates the Kano city area. The right panel shows the study area within Kano city, with labelled sampling locations/local government areas (points) and the approximate position of the recruitment hospital (MMSH). (Administrative boundary shapefiles were obtained from the Database of Global Administrative Areas and plotted in R (V.4.4.3). MMSH, Murtala Muhammed Specialist Hospital.

Engagement and participant support

To compensate participants for time and transport, mothers received small incentive packs containing baby care essentials (eg, diapers, wipes, baby romper) at enrolment and selected follow-up visits. Mobile airtime was also provided to facilitate communication. Mothers were given household 'event grids' (calendar-style diaries) to record infant illness, feeding and medication use (online supplemental appendix B). Retention was reinforced through reminder calls, culturally sensitive field engagement and collaboration with ward matrons and nurses.

DATA COLLECTION

Questionnaires

Maternal and household information was collected using structured REDCap questionnaires[15 16] with built-in validation checks. Variables included maternal age, education, household composition, income and healthcare access. To capture dynamic exposures, mothers completed calendar-style event grids to record infant illness episodes, feeding practices and medication use; mothers with limited literacy were supported by research assistants through verbal reporting.

Research assistants also documented qualitative observations during home visits on cultural and behavioural practices, including the use of herbal remedies; Qur'anic ink wash water (maḥw), water obtained by washing off written Qur'anic verses from a tablet or paper and administered orally or for bathing; uvulectomy; and female genital mutilation (FGM). Sensitive topics were recorded only when voluntarily shared and were handled with strict confidentiality.

Clinical data

Infant clinical characteristics were recorded within 24 hours of birth and included gestational age, birth weight, sex, mode of delivery and Apgar scores. Antibiotic administration was documented prospectively at the time of administration and verified against hospital records where applicable. Most exposures occurred outside formal healthcare settings, with antibiotics commonly purchased over the counter without prescription. Missing data were rare (<5%) and were followed-up at subsequent visits.

Biological sample collection

Samples were collected from infants, mothers, hospital and households across predefined hospital and home visits (figure 3).

- Infant stool: collected at 10 predefined time points (days 0, 1, 3, 5, 7, 14, 28, 90, 180, 365), with intensified collection at days 1, 3, 5 and 7 after infant antibiotic exposure. Stool was placed on ice, transported to the laboratory within 4 hours, processed immediately and DNA stored short-term at −20°C before shipment.
- Maternal samples: rectal swabs collected within 24 hours post partum, and on days 3 and 28. Breast milk collected on days 0, 3, 28 and 90 after handwashing, expressed into sterile tubes, aliquoted and stored at

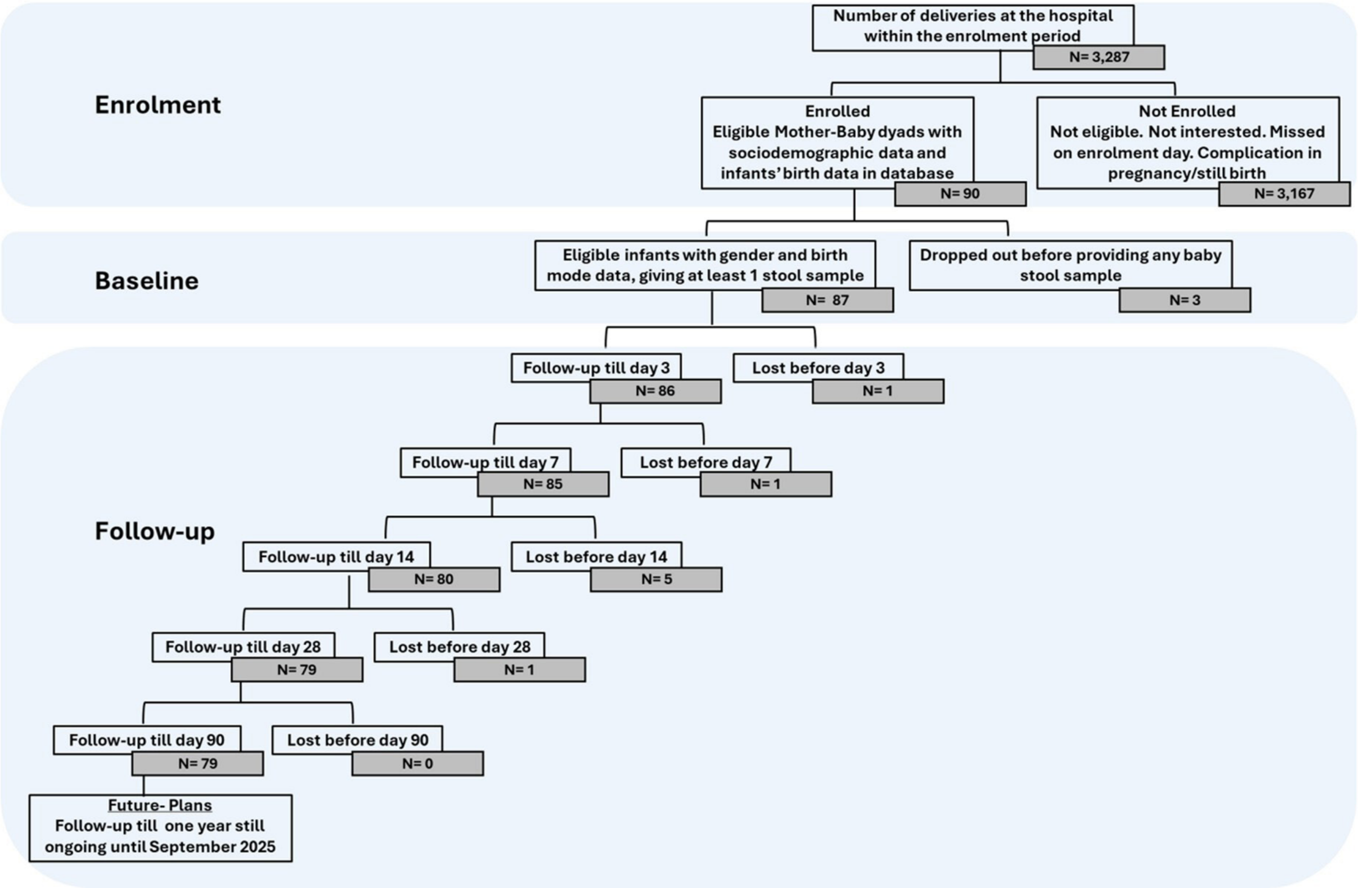

Figure 2 Participant enrolment and follow-up through day 90. Flow diagram showing the number of deliveries during the enrolment period (N=3287), mother–infant dyads enrolled (N=90) and not enrolled (N=3167; not eligible, not interested, missed on non-enrolment days or pregnancy complication/stillbirth). Of enrolled dyads, 87 infants contributed at least one stool sample at baseline (three withdrew before providing any infant stool sample). Retention across scheduled follow-up visits was: day 3 (N=86), day 7 (N=85), day 14 (N=80), day 28 (N=79) and day 90 (N=79).

−20°C. Rectal swabs were held at 4°C until processing, as per manufacturer guidance.

- Environmental samples: collected from 79 households on days 3, 7 and 28. High-contact sites included baby bedding, feeding surfaces, doorknobs, bathing areas, sewage outlets, drinking water and caregiver mobile phones. Swabs were stored at 4°C until processing.

Sample handling and sequencing

All samples were transported on ice immediately after collection. DNA was extracted using the DNeasy PowerSoil Pro Kit (QIAGEN), following a pilot comparison at MMSH to optimise local workflows.[17] Extracted DNA was shipped on dry ice to the University of Oxford, where long-read shotgun metagenomic sequencing was performed (Oxford Nanopore Rapid Barcoding Kit, sequenced on P2 Solo or GridION R V.10.4.1 flow cells). This approach enables strain-level microbiome profiling and plasmid-level detection of ARGs.

Sample size rationale

No prior large-scale infant microbiome studies have been conducted in low-resource African settings. Given the high variability of microbiome data and the lack of established power calculations,[18] the sample size was determined pragmatically, based on recruitment feasibility, anticipated attrition and reference to sample sizes in comparable high-income country cohorts.[19–21] This supports exploratory analysis and hypothesis generation. Small subgroup sizes (eg, caesarean deliveries, exclusive breastfeeding and antibiotic-exposed infants) will limit the feasibility and statistical power of planned stratified analyses. These subgroup analyses will therefore be considered exploratory and interpreted with caution.

Patient and public involvement

Patients and the public were not directly involved in the study design. However, early input was sought from local healthcare workers at the hospital to guide the recruitment approach, ensure cultural sensitivity of study materials and refine household data collection tools. Feedback from mothers during a pilot[17] informed modifications to the information sheet and event grid. Study findings will be disseminated to participants and local providers through lay summary reports.

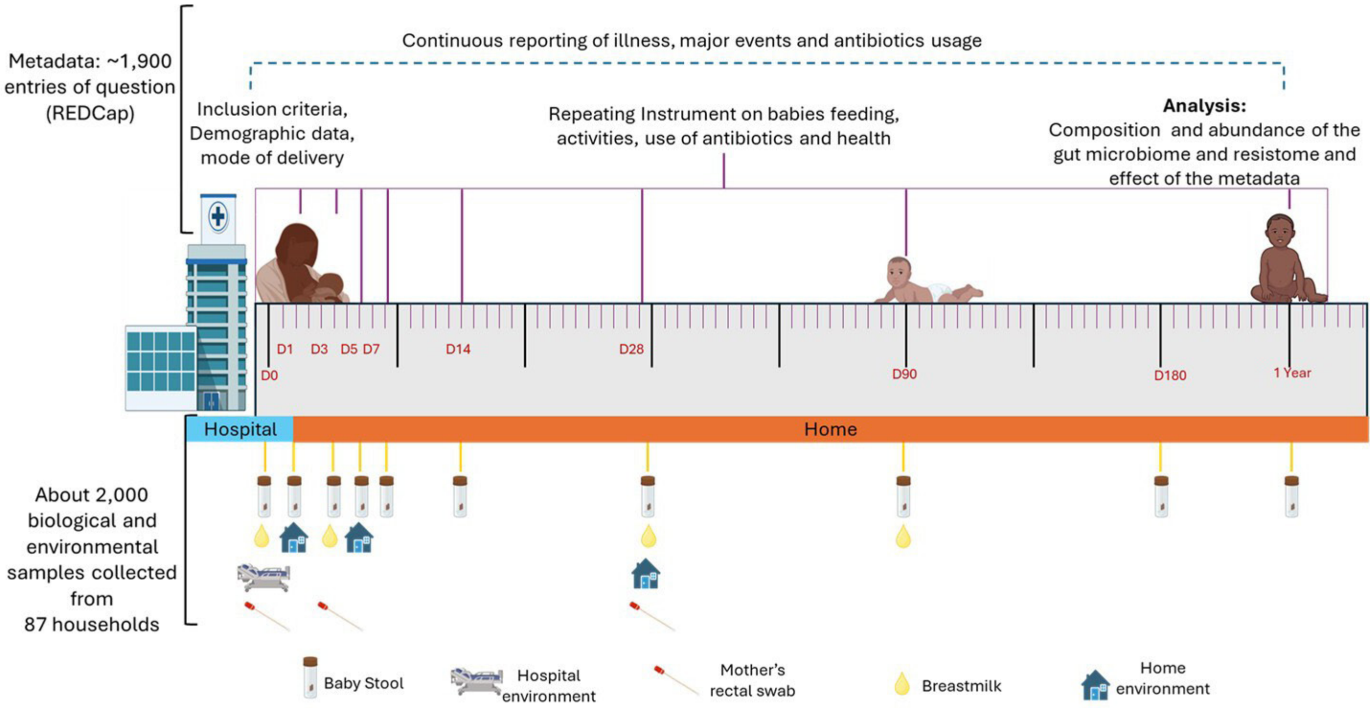

Figure 3 Infant Gut Bacterial Study in Nigeria longitudinal sampling schedule and follow-up timeline. Schematic of participant follow-up from birth (D0) through 1 year, indicating hospital-based sampling in the first few days and subsequent home follow-up visits. Icons denote the specimen types collected at each visit (eg, infant stool sampling, maternal/household sampling and associated clinical/metadata collection), with the transition from hospital to home-based follow-up highlighted. REDCap, Research Electronic Data Capture.

FINDINGS TO DATE

Maternal and household characteristics

Baseline characteristics are presented in table 1. Among the 87 mother–infant dyads contributing baseline biological samples (90 enrolled), maternal age ranged 17–42 years (mean 28.1±6.05), somewhat older than national/regional averages for age at first birth.[22 23] Parity was high (mean 3.2 pregnancies).

Table 1 Baseline maternal, birth and household characteristics of infants with baseline samples

Variable	Summary (N=87)
Maternal age (years)	28.13 (6.0)
Previous pregnancies	3.24 (2.5)
Monthly household income*	60 000 (40 000–100 000)
Gestation age (weeks)	38.48 (2)
Birth weight (grams)	2998.85 (352.2)
Apgar score†	8.8 (1.1)
Sex: female‡	43 (49.4)
Delivery: caesarean section‡	22 (25.3)
Insurance: government insurance‡	6 (6.9)
Insurance: private insurance‡	2 (2.3)

Summary statistics are expressed as mean (SD).
*Median (IQR).
†Three babies with missing Apgar score.
‡Number (%).

Maternal educational attainment varied: 14.5% had no formal education, 43.6% completed secondary school and 21.4% held higher education degrees. Although this cohort was more educated than women nationally,[24] likely reflecting hospital-based recruitment that favours those able to navigate research procedures and provide informed consent. Conversely, the most affluent and highly educated women in the city may preferentially attend private clinics or federal teaching hospitals with stronger infrastructure and specialist services. Our cohort is therefore more educated than the general population but may still under-represent the most socioeconomically advantaged.

Households were large (mean 7 members; many with multiple children <14 years, mean 4), consistent with peri-urban/urban-poor living conditions, limited sanitation, irregular electricity and proximity to informal dumpsites/stagnant water. Mean reported monthly income was 82 247 Nigerian naira (~US$52), which, assuming a seven-person household, equates to ~US$0.26 per person per day, well below the US$3.65 World Bank poverty threshold.[25] Only ~9.2% reported any form of health insurance.

Infant and birth characteristics

Sex distribution was balanced (~49% male, 51% female). Mean gestational age 38.5 weeks and mean birth weight 2999 g reflected term deliveries, and near the national mean of 2900 g.[22] Caesarean section

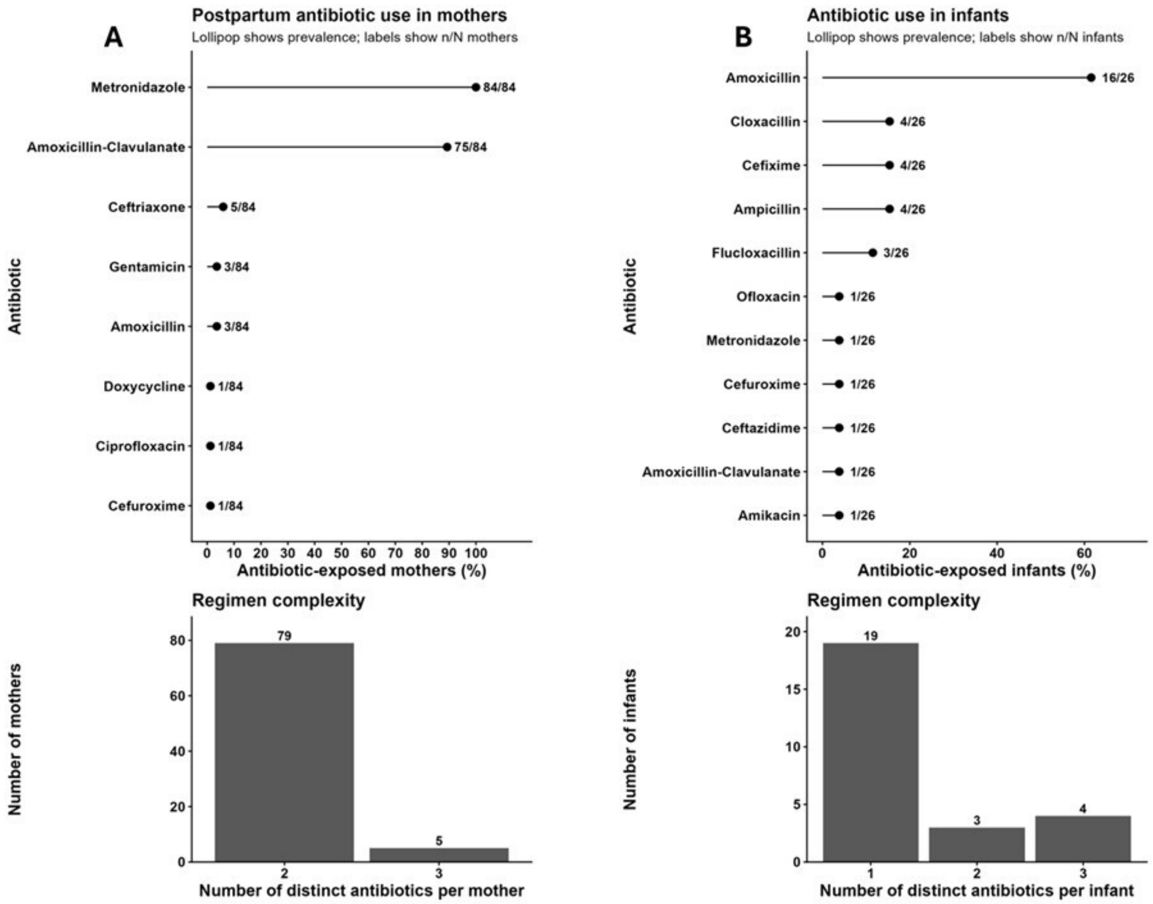

Figure 4 Postpartum antibiotic exposure in mothers and antibiotic exposure in infants. (A) Postpartum antibiotic use among mothers (N=84 exposed): lollipop plots show the prevalence of each antibiotic (percentage of exposed mothers receiving the drug), with labels indicating the number of mothers receiving that antibiotic (n/N exposed). The bar plot summarises regimen complexity as the number of distinct antibiotics received per mother. (B) Antibiotic use among infants (N=26 exposed): lollipop plots show the prevalence of each antibiotic among exposed infants with labels showing n/N exposed, and the bar plot summarises regimen complexity as the number of distinct antibiotics received per infant.

accounted for 25.3% of births (13.7% emergency). Premature rupture of membranes occurred in 23.9%, higher than national estimates[26 27] and relevant for early microbial exposures.

Feeding and cultural practices

By 3 months, exclusive breastfeeding (WHO definition)[28] was 8%. While ~83% received breastmilk as the primary feed, early water supplementation was common.

Cultural practices included traditionally done uvulectomy (7.5%), use of Qur'anic ink wash water (10.8%) and FGM among ~1.7% of female infants.

Antibiotic exposures (maternal and infant)

Intrapartum exposure was uncommon: 7/90 (7.8%) mothers received intravenous antibiotics during labour/caesarean, typically metronidazole, sometimes with ceftriaxone±gentamicin (perioperative prophylaxis).

Postpartum prescribing was very common (figure 4A): 84/90 (93.3%) mothers were prescribed antibiotics at discharge. Dual therapy predominated (79/84), almost always amoxicillin-clavulanate+metronidazole combination (74 mothers). Smaller numbers received amoxicillin+metronidazole combination (3); ceftriaxone+metronidazole±gentamicin combination(s) (3 and 2); amoxicillin-clavulanate+metronidazole+cefuroxime combination (1); or ciprofloxacin+metronidazole+doxycycline combination (1). Antibiotics were purchased out-of-pocket (not dispensed in-hospital), and cost was the usual reason for non-use among those who did not obtain postpartum antibiotics.

By 3 months, 26/90 (28.9%) infants received ≥1 antibiotic course (figure 4B); 4/26 (15%) had two distinct courses (30 courses total ≤90 days). Most were single-agent regimens, led by amoxicillin (n=16), cloxacillin (n=4), ampicillin (n=4), cefixime (n=4) and other less common courses as in figure 4B. Exposures were often empirical and frequently obtained over the counter without prescription.

Sampling and follow-up

Infant stool was the primary specimen with eight scheduled time points (D0, D1, D3, D5, D7, D14, D28, D90). 87/90 dyads contributed at least one stool sample (figure 5); retention at D90 was 79/87 (~91%) among infants providing a

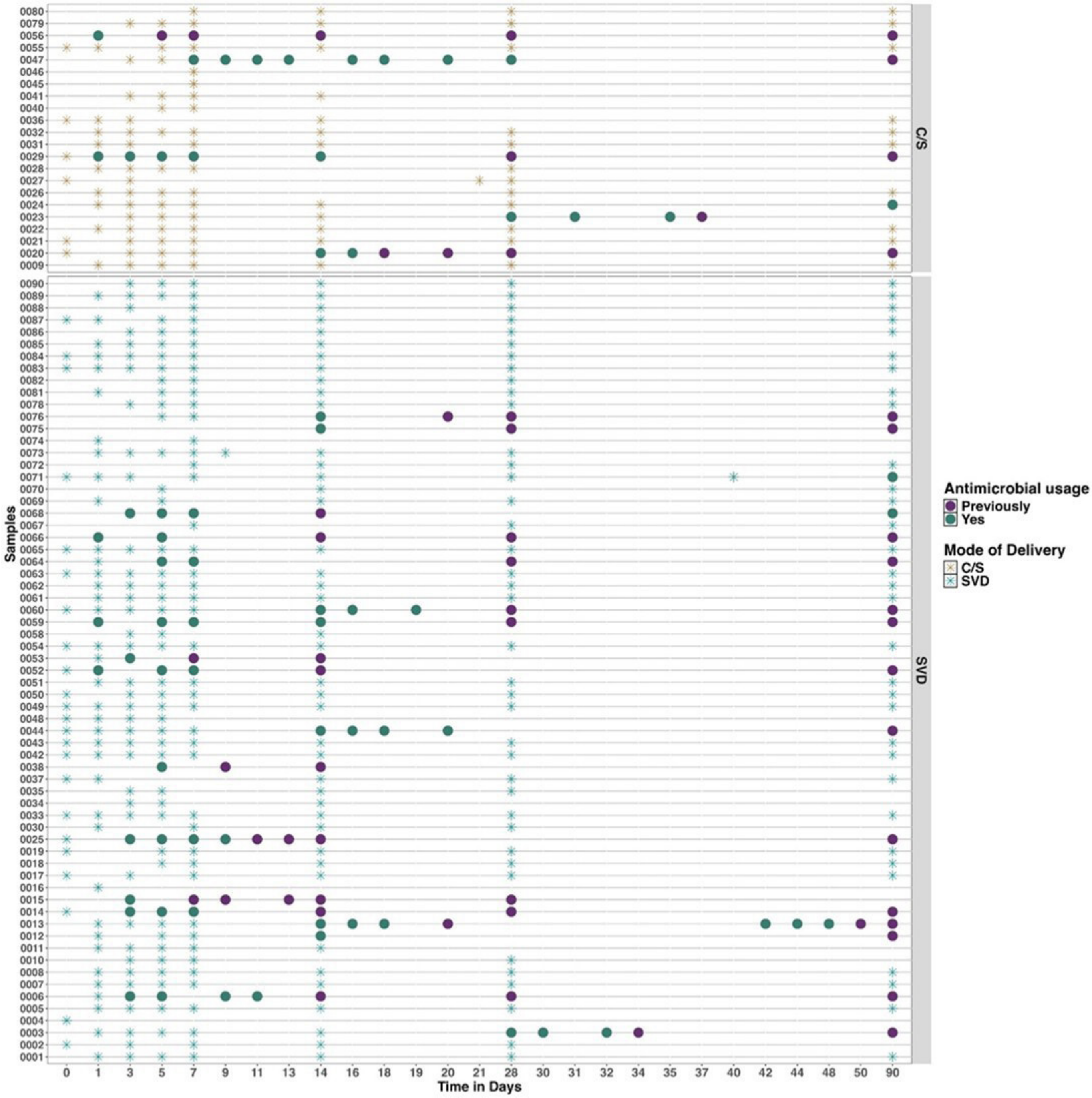

Figure 5 Longitudinal sampling coverage and antimicrobial exposure by mode of delivery. Each row represents an infant, and each point indicates a stool sample collected at the scheduled study visits (days 0, 1, 3, 5, 7, 14, 28 and 90). Samples collected outside the scheduled time points were increased sampling around the time of antibiotic exposure. Samples are stratified by mode of delivery (C/S; SVD). Asterisk (*) indicates that stool sample was collected, while point colour denotes sampling and also whether the infant had previously received antibiotics (previously) or was currently on antibiotics (yes) at the time of sampling. C/S, caesarean section; SVD, spontaneous vaginal delivery.

baseline sample. Most attrition occurred before D14; no participants were lost between D28 and D90.

Scheduled stool completeness ranged from 32% at D0 to 81% at D14, with 70% at D90 (total collected across scheduled visits=480 samples). For 26 infants exposed to antibiotics, additional (unscheduled) stools were collected in the days immediately following exposure (figure 5).

Maternal rectal swab completeness was 96% at day 0, 79% at day 3 and 83% at day 28 (~232 scheduled swabs). Breast milk completeness was 54% at day 0, 73% at day 3, 82% at day 28 and 72% at day 90 (~254 scheduled milk samples).

Hospital-context samples were collected during the first 48 hours (eg, delivery bed, hospital bed), and household sampling predominated from day 7 onward (eg, mothers phone swab, household drinking-water, doorknobs, baby bathing areas). High-touch surfaces and samples that would come into direct contact with the infant were prioritised.

Across days 0–28, we collected ~806 environmental swabs, with the highest returns from mothers' phones (~166), household drinking water (~156) and home doorknobs (~153). Exploratory subset analyses indicate that colonisation clustered on hospital-contact surfaces (eg, ward and delivery beds) and on maternal personal items (notably mothers' mobile phones), with lower yield from other household surfaces.

Follow-up to 12 months is ongoing; this report summarises data through day 90. Figure 5 visualises per-infant sampling across scheduled and post-antibiotic time points, with key metadata (antibiotic exposure and delivery mode). Comprehensive long-read metagenomic datasets have been generated; analyses are in progress.

STRENGTHS AND LIMITATIONS

Strengths

This study represents one of the first prospective longitudinal African infant cohorts to integrate infant, maternal and environmental sampling with long-read shotgun metagenomic sequencing. This advanced sequencing approach allows for unprecedented species- and plasmid-level resolution of microbiome and resistome dynamics within this specific geographic context. A significant strength of our methodology is the high-frequency longitudinal stool sampling; by collecting samples at 10 timepoints in the first year, including intensified sampling following antibiotic use, we provide a higher degree of temporal resolution than is currently available in most existing infant cohorts.

Furthermore, the integration of face-to-face data collection, household diaries and qualitative field notes adds a rich layer of sociodemographic and cultural context often missing from large-scale microbiome studies. The success of this data collection was bolstered by a multidisciplinary collaboration between UK and Nigerian teams, which ensured robust training, maintained researcher integrity and allowed us to capture important cultural nuances throughout the study duration.

Limitations

Despite these strengths, several limitations must be acknowledged. As a hospital-enrolled cohort primarily drawn from low-income, peri-urban households in Kano, our findings may not be fully generalisable to more affluent urban populations, remote rural communities or families who opt for homebirth settings. Additionally, certain maternal health metrics, such as nutritional status and body mass index, were unavailable due to existing constraints in antenatal data collection.

Regarding data accuracy, our reliance on self-reporting for infant antibiotic exposure, particularly for over-the-counter medications purchased without verification, introduces a potential risk of misclassification and confounding. Similarly, data on sensitive cultural practices, such as uvulectomy, Qur'anic ink wash and female genital mutilation, relied on voluntary reporting and may therefore be under-represented in our final dataset. Finally, while metagenomic approaches are powerful, a technical limitation remains: transmission dynamics are difficult to infer with total certainty based solely on genomic relatedness measures.

FUTURE PLANS

Follow-up will continue through 12 months, with scheduled sampling at days 180 and 365 and continued short-interval stool collections after infant antibiotic courses. Building on the long-read shotgun metagenomic datasets already generated from infant stools, we will extend profiling to maternal rectal swabs and household environmental samples (metagenomics and targeted culture), guided by infant findings, to identify shared microbial and ARG reservoirs and likely transmission pathways across mother–infant-environment.

Microbiome and resistome profiles will be stratified by key early-life exposures, including mode of delivery (vaginal vs caesarean), postpartum antibiotic use and breastfeeding practices, to assess their influence on microbial colonisation dynamics and resistance gene carriage. Longitudinal analyses will examine the temporal stability and persistence of ARGs across the first year of life, with a focus on infants exposed to antibiotics early or repeatedly.

To enhance generalisability, we will undertake a cross-site comparison with a harmonised cohort from Pakistan (INBUGS-P) to distinguish setting-specific from shared features of early-life microbiome and resistome development. De-identified sequence data and accompanying metadata will be deposited in public repositories at publication, and summary findings will be shared with participants and hospital stakeholders. Archived specimens (eg, breast milk, environmental swabs) will support targeted culture and genome-resolved follow-ups that complement metagenomic results. If funding permits, follow-up may be extended to 24 months to assess longer-term microbial maturation and ARG persistence.

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Collaborators We welcome collaboration with researchers interested in maternal–infant microbiome dynamics, antimicrobial resistance and early-life exposures in low-resource settings. Interested collaborators should contact the Ineos Oxford

Institute (https://www.ineosoxford.ox.ac.uk/contact-us), outlining their research objectives and proposed use of the data. Access will be granted for non-commercial academic purposes and will be subject to a data-sharing agreement. Restrictions may apply for sensitive variables or where limited by participant consent.

Contributors CA, KT, TRW and KS led protocol development, and CA led the field implementation and acts as the guarantor. CA, HMS, HA and HBI coordinated participant recruitment at MMSH, household follow-up, questionnaire administration and environmental sampling. JO and EO are responsible for the REDCap build and data management. AKL and LdN developed the bioinformatics approach and contributed to analysis. KI and AA act as the responsible study doctors. CRA, KI and AA provided site oversight, clinical governance and liaison with hospital services. KT, MS, TRW and KS supervised laboratory workflows and overall study conduct. CA drafted the manuscript, and all authors critically revised it and approved the final version. TRW contributed to funding acquisition and KT, MS, TRW and KS contributed to study supervision. CA is the guarantor.

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Competing interests None declared.

Patient and public involvement Patients and/or the public were not involved in the design, or conduct, or reporting, or dissemination plans of this research.

Patient consent for publication Not applicable.

Ethics approval This study involves human participants and was approved by (1) Oxford Tropical Research Ethics Committee (OxTREC reference: 36-22) and (2) Nigerian national ethical review approval number NHREC/17/03//2018. Participants gave informed consent to participate in the study before taking part.

Provenance and peer review Not commissioned; externally peer reviewed.

Data availability statement Data are available upon reasonable request. All microbiota and resistome data will be made publicly available upon publication of the results in scientific articles. Due to ethical constraints, questionnaire and registry data cannot be made freely accessible, even in de-identified form. Access to these datasets is subject to a formal application process, including the submission of a research plan for institutional evaluation.

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