

Questioning the fetal microbiome and pitfalls of low-biomass microbial studies

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Whether the human fetus and the prenatal intrauterine environment (amniotic fluid and placenta) are stably colonized by microbial communities in a healthy pregnancy remains a subject of debate. Here we evaluate recent studies that characterized microbial populations in human fetuses from the perspectives of reproductive biology, microbial ecology, bioinformatics, immunology, clinical microbiology and gnotobiology, and assess possible mechanisms by which the fetus might interact with microorganisms. Our analysis indicates that the detected microbial signals are likely to be the result of contamination during the clinical procedures to obtain fetal samples, or during DNA extraction and DNA sequencing. Furthermore, the existence of live and replicating microbial populations in healthy fetal tissues is not compatible with fundamental concepts of immunology, clinical microbiology and the derivation of germ-free mammals. These conclusions are important to our understanding of human immune development and illustrate common pitfalls in the microbial analyses of many other low-biomass environments. The pursuit of a fetal microbiome serves as a cautionary example of the challenges of sequence-based microbiome studies when biomass is low or absent, and emphasizes the need for a trans-disciplinary approach that goes beyond contamination controls by also incorporating biological, ecological and mechanistic concepts.

Fetal immune development prepares the neonate for life in a microbial world and underpins lifelong health^{1–4}. Neonates born at term are not immunologically naive and are specifically adapted to cope with abrupt exposure to microbial, dietary and environmental stimuli^{5,6}. Several research groups have characterized immune cell development in human fetal tissues^{7–9}. However, our mechanistic understanding of how and when immune priming by microorganisms occurs, and the factors that drive it, is incomplete. The long-held view that the prenatal intrauterine environment (placenta, amniotic fluid and fetus) is protected from live microorganisms¹⁰ has been recently challenged^{11–15}, leading to the hypothesis that fetal immune development may be driven by the presence of live microorganisms at intrauterine sites^{16–20}. Some groups have reported the presence of a microbiota¹³, defined as a community of microorganisms in a defined habitat, or a microbiome¹⁵, referring to a microbiota as well as their constituent genes and metabolites, which form a dynamic and interactive micro-ecosystem

that is integrated within environments including eukaryotic hosts²¹. However, these interpretations have been debated^{22–28} because several concurrent studies^{29–35} suggest that contaminating microbial DNA in sequencing data from sites of low microbial biomass^{36–38} is likely to be the only source of microbial DNA detected in the intrauterine environment. Since 2020, four studies have characterized the microbiology of the human fetus directly, and these studies have come to opposing and irreconcilable conclusions. Two reports described viable low-density microbial populations in human fetal intestines³⁹ and organs⁴⁰, and linked these microorganisms to fetal immune development. By contrast, two other research groups, which include several of the authors of this perspective, reported no detectable microorganisms in the fetal meconium and intestines^{30,41}.

Such disagreement over a fundamental aspect of human biology poses a challenge for scientific progress. The notion of a fetal microbiome, if proven correct, has implications for clinical medicine and

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would call for a comprehensive reappraisal of previous concepts and research. It would require a radical revision of our understanding of the development of the immune system and other systems in early life and the anatomical and immunological mechanisms that mediate host–microbe interactions within fetal tissues. Failure to resolve this issue risks diverting finite resources into research that results in no advancement for fetal and maternal health, and misguided attempts to therapeutically modify a non-existent fetal microbiome. The dilemma has further relevance for the characterization of the microbiota in other low-biomass samples, such as those derived from blood, the brain, other internal organs and cancer tissues. Therefore, we assembled a trans-disciplinary group of scientists and clinician scientists to examine experimental evidence relating to how and when the fetus becomes prepared for life with microorganisms, to identify research pitfalls and mitigation strategies, and to propose specific directions for future research.

Claims and counterclaims

Although disagreement over the presence of microorganisms in prenatal intrauterine locations (placenta and amniotic fluid) spans dozens of studies with contradictory findings^{12,14,15,23,29,31–34,37,42–44}, we focused our analysis on four recent studies, because they provide a direct assessment of the fetus itself^{30,39–41}. Collecting human fetal samples is difficult and can only occur after the termination of a pregnancy, or immediately before birth by C-section. Three of the studies used samples collected after vaginally delivered, elective, second-trimester pregnancy terminations^{39–41}, and one collected samples from breech C-section deliveries immediately at birth³⁰.

Rackaityte et al.³⁹ reported that 18 bacterial taxa were enriched in the intestinal contents of vaginally delivered fetuses from second-trimester terminations compared to negative controls using 16S rRNA gene amplicon-sequencing (V4 region). To account for contamination, the authors removed operational taxonomic units (OTUs) that were detected in more than 50% of procedural controls, and then identified remaining contaminants in silico (using the decontam R package). They found that most fetal samples were microbiologically similar to negative controls (labelled as ‘other meconium’; $n = 25$), but that some samples, dominated by *Lactobacillus* (six samples) or Micrococcaceae (nine samples), had distinct bacterial profiles. The authors also detected low amounts of total bacteria by quantitative PCR (qPCR), fluorescent in situ hybridization (FISH), scanning electron microscopy (SEM) and culture (as discussed below).

Several of the study’s conclusions have been challenged by de Goffau et al.⁴⁵, who reanalysed the publicly available data and found no evidence for a distinct bacterial profile in the subset of samples with matched procedural controls, and concluded that the positive findings were caused by a sequencing batch effect (indicative of contamination) and further contamination during culture⁴⁵. In addition, the suggestion that particles detected in SEM micrographs constitute micrococci³⁹ was disputed, as their size exceeded that of known Micrococcaceae⁴⁵. Furthermore, the 16S rRNA gene sequence of the *Micrococcus luteus* cultured from the fetal samples differed from that detected by sequencing, further supporting contamination during culture (*M. luteus* is a common contaminant of clean rooms and surgical instruments^{46,47}).

Mishra et al.⁴⁰ detected a low but consistent microbial signal across tissues of vaginally delivered fetuses from second-trimester terminations by 16S rRNA gene amplicon sequencing (V4–V5 region), with seven genera enriched in fetal samples (*Lactobacillus*, *Staphylococcus*, *Pseudomonas*, *Flavobacterium*, *Afiplia*, *Bradyrhizobium* and *Brevundimonas*). The 16S rRNA gene-sequencing data were accompanied by SEM, RNA-in situ hybridization (RNA-ISH) and culture. In recognition of the high risk of contamination, all samples were processed in isolation with negative controls collected during sample processing. In contrast to Rackaityte et al., Mishra et al. found that *Micrococcus* was enriched

in phosphate-buffered saline (PBS) reagent controls, and reported it as a contaminant, with the *M. luteus* cells detected by culture being consistent with the size and morphology of the coccoid structures that were found by SEM⁴⁰.

Both Rackaityte et al. and Mishra et al. included assays of fetal immune development and concluded that the microorganisms detected could contribute to immune maturation. In Rackaityte et al.³⁹, this conclusion was based on differences in T cell composition and epithelial transcription between fetal intestines in which Micrococcaceae was observed to be dominant and those in which this taxa was absent, leading to the suggestion that bacterial antigens contribute to T cell activation and immunological memory in utero. Mishra et al.⁴⁰ used flow cytometry to expand on previous findings of effector (TNF- and IFN γ -producing) memory (CD45RO⁺) T cells in fetal tissues, including gut tissue and mesenteric lymph nodes. Bacterial isolates cultured from the fetal samples, including *Staphylococcus* and *Lactobacillus* strains, induced in vitro activation of memory T cells isolated from fetal mesenteric lymph nodes.

In contrast to these reports, Li et al.⁴¹, who also investigated fetal intestinal tissue from second-trimester terminations, did not detect bacterial DNA by PCR (V4 region of the 16S rRNA gene, 35 cycles) on the basis of a visual inspection of agarose gels in any of the 101 samples tested. The authors detected a diverse set of microbially derived metabolites that were present and enriched in the fetal intestinal samples, and hypothesized that these microbiota-derived metabolites are passed via the mother’s blood through the placenta to ‘educate’ the fetal immune system. This conclusion is supported by research in mice that showed that fetal immune education can be driven in the absence of direct microbial exposure by trans-placental passage of microbial metabolites originating from the maternal gut^{48,49}.

Kennedy et al.³⁰ used a different approach and collected samples using rectal swabs during elective C-section for breech presentation at term gestation³⁰. Comparisons with environmental and reagent-negative controls from two independent sequencing runs were included to account for contamination and stochastic noise. No microbial signal distinct from negative controls was detected, and aerobic and anaerobic bacteria (*Staphylococcus epidermidis* and *Cutibacterium acnes* (formerly *Propionibacterium acnes*)) detected by culture of fetal samples were identified by the authors as skin contaminants.

To compare these reports, we reanalysed the publicly available unfiltered relative abundance data associated with the three publications that reported sequence data and determined the relative abundance of each detected genus. Although there was good agreement between the two studies using second-trimester vaginally delivered fetuses^{39,40}, the bacterial taxa that were detected in fetuses from C-sections³⁰ were significantly different (Fig. 1). The number of genera was much lower in C-section-derived fetuses, and entire groups of microorganisms—especially those usually found in the vagina—were absent. Most importantly, in the studies that claimed fetal microbial colonization^{39,40}, every genus detected in fetal samples was also detected in most of the control samples.

Reproductive biology and obstetrics perspectives

The embryo and fetus develop within the uterus but not in the uterine cavity per se. The early embryo invades the maternal decidua and is completely embedded by ten days after fertilization. The fetus grows within the amniotic cavity, which originates between the trophoblast and inner cell mass in the second week after fertilization, surrounded by two layers of reproductive membranes and bathed in amniotic fluid. Hence, even if microorganisms were present in the uterine cavity⁵⁰, they would have to pass through to the amniotic cavity and enter the amniotic fluid to colonize the fetus. Amniotic fluid has antimicrobial properties, being enriched for example in lysozyme⁵¹, human β -defensin 2

Q10

(ref.⁵²) and GP340 (DMBT1)⁵³, which binds and agglutinates diverse Gram-negative and Gram-positive bacteria.

The placenta mediates communication between the fetus and the mother and is a potent immune organ that protects the fetus. Historically, the placenta has been considered sterile (defined here as free from living microorganisms), but in 2014 a complex but low-biomass placental microbiome was detected by DNA sequencing. The proposed placental microbiome showed some similarity with sequencing data of microbial communities of the oral cavity¹⁵. Contamination controls were not included in this study, and subsequent evaluation of the work found that most of the genera detected were also common contaminants^{26,36,38,54}. Several detected taxa, such as *Gloeobacter*, a genus of photosynthetic cyanobacteria, appeared biologically implausible as a component of a putative placental microbiome^{24,55}. Since this early report, dozens of studies have conducted a sequence-based microbial analysis of placenta tissues, with opposing conclusions (as reviewed by Bolte et al.²⁰).

Regardless of whether placental samples are collected by biopsy via the vagina, clinically by chorionic villus sampling or after delivery, it is always necessary to control for contamination, particularly from the tissues through which a placenta must pass before sampling. Accordingly, de Goffau et al.²⁹ performed a comprehensive study of the possible placental microbiome, using samples from uncomplicated and complicated (pre-eclampsia and small for gestational age) pregnancies that were delivered both at term and preterm either vaginally or by C-section. Sampling was confined to the placental terminal villi (fetal tissue), as this represents the site of exchange (across the vasculosyncytial membrane) between the fetus and the mother's blood and tissues. The authors detected a range of species that are known to dominate the vaginal microbiota⁵⁶, such as *Lactobacillus iners*, *Lactobacillus jensenii*, *Lactobacillus crispatus*, *Lactobacillus gasseri* and *Gardnerella vaginalis*. When the presence of vaginal microorganisms and those in the laboratory reagents (the 'kitome') were accounted for, there was no evidence for a placental microbiome, which is in agreement with several additional recent studies^{23,29,31–34,37}.

Pathogenic infection of the placenta by viral or bacterial pathogens is a well-recognized clinical phenomenon that contributes to preterm birth and neonatal sepsis⁵⁷. de Goffau et al. detected *Streptococcus agalactiae* in around 5% of cases as the only verifiable bacterial signal in placentas obtained by C-section deliveries that were conducted before the rupture of the fetal membranes and the onset of labour²⁹. The presence of this species is plausible as it colonizes the genital tract of about 20% of women and has invasive potential, being an important cause of maternal and neonatal sepsis⁵⁸. However, the ability of specific pathogens to colonize and/or infect the placenta is distinct from the presence of an indigenous microbiota—that is, a prevalently stable, non-pathogenic, complex microbial community that is metabolically active²¹.

Research claiming that viable low-density microbial communities are present in the fetal intestine³⁹ and fetal organs⁴⁰ likewise calls for an evaluation of the sampling process. Mishra et al. obtained fetal tissues after medical termination of pregnancy in the second trimester with prostaglandins⁴⁰. This procedure typically involves the individual going through hours of labour and often leads to the rupture of the fetal membranes hours before vaginal delivery. Even with a standardized approach, labour may be prolonged and may be accompanied by infection and fever, which are common with second-trimester terminations^{59,60}. Both Li et al.⁴¹ and Rackaityte et al.³⁹ also used second-trimester terminations but obtained the fetal tissues from core facilities. The tissues used by Li et al. were from surgical terminations (14–23 weeks) performed with mechanical dilation. Rackaityte et al.⁶¹ did not provide sufficient information to determine whether fetuses were obtained through surgical procedures or medical inductions. Although the latter increases the risk of the fetus being exposed to vaginal microorganisms during labour, both procedures involve vaginal delivery of the fetus.

As outlined below, the reported microbiology of these fetuses mainly reflects the sources of microorganisms to which they are exposed during these procedures.

Microbial ecology perspectives

Host–microbe relationships range from mutualism (a prolonged symbiotic association from which both benefit), to commensalism (the host is unaffected), to pathogenesis, in which the microorganism harms the host. Although claims for fetal microbial exposure^{39,40} have not established the nature of the host–microbe interaction, and the duration of exposure or colonization, they have suggested that live organisms have a beneficial role in fetal immune development, thereby implying a symbiosis. The microbiological approaches applied by Rackaityte et al.³⁹ and Mishra et al.⁴⁰ are, in large part, robust, and well suited to studying symbiotic microbial populations. The combination of 16S rRNA gene sequencing, qPCR, microscopy, FISH and culture is laudable, as the approaches are complementary. Next-generation sequencing of 16S rRNA gene amplicons provides a broad community overview and can detect microorganisms that escape cultivation, whereas qPCR, microscopy and bacterial cultures have a high dynamic range, low detection limits and reasonable specificity. The DNA-sequence-based microbiota composition data in both studies are quite consistent (Fig. 1), which suggests that several of the bacterial taxa detected were present in the samples and not artefacts derived from laboratory reagents or DNA-isolation-kit contamination. However, although the microbiological analyses of samples were sound, the sampling procedures allowed the introduction of contaminant species, and critical controls to determine whether contamination occurred were missing.

In agreement with the unavoidable vaginal exposure of fetuses obtained by second-trimester abortions (see above), both Rackaityte et al.³⁹ and Mishra et al.⁴⁰ found that the genera *Lactobacillus* and *Gardnerella*, which dominate the vaginal microbiota⁵⁶, were among their most consistent findings (Fig. 1). The species cultured by Mishra et al.—*G. vaginalis*, *L. iners* and *L. jensenii*—are largely restricted to the human vagina⁶². Other microorganisms detected, such as *Staphylococcus* species and *Cutibacterium acnes*, are skin commensals. As shown in Fig. 1, the abundances of *Lactobacillus*, *Gardnerella* and *Staphylococcus* that were found by Mishra et al. showed gradients with high population levels in fetal samples exposed to sources of contaminants (placenta and skin) and lower levels in internal samples (gut, lung, spleen and thymus). The omission of vaginal controls by both Rackaityte et al. and Mishra et al. to determine the microbiota of vaginally delivered fetuses is a considerable limitation that casts doubt on the authors' conclusion that the microorganisms originate from the womb. Indeed, Li et al.⁴¹ obtained samples from second-trimester surgical terminations using mechanical dilatation, which reduces the risk of bacterial exposure to the fetus during sampling. In this study, positive bacterial PCR results were not reported, which raises the possibility that sampling contamination may be a serious confounder in both of the other studies that claimed the presence of microorganisms at these sites.

Although vaginal controls were not included by Rackaityte et al.³⁹ and Mishra et al.⁴⁰, direct comparisons of their findings with those of Kennedy et al.³⁰ also provide evidence for vaginal contamination of terminated fetuses (Fig. 1). The C-section-derived fetal samples in Kennedy et al., which were not exposed to the vagina, carried no *Gardnerella* or *Lactobacillus*, but instead contained skin and reagent contaminants^{30,54}. Despite attempts to reduce contamination, C-section-derived fetal meconium had at least one positive culture³⁰. Kennedy et al. did not consider these microorganisms to be of fetal origin, as they were skin commensals, and half of the samples, as well as many culture replicates, did not show growth. The authors concluded that such inconsistencies point to stochastic contamination and not colonization by a stable functional microbial community.

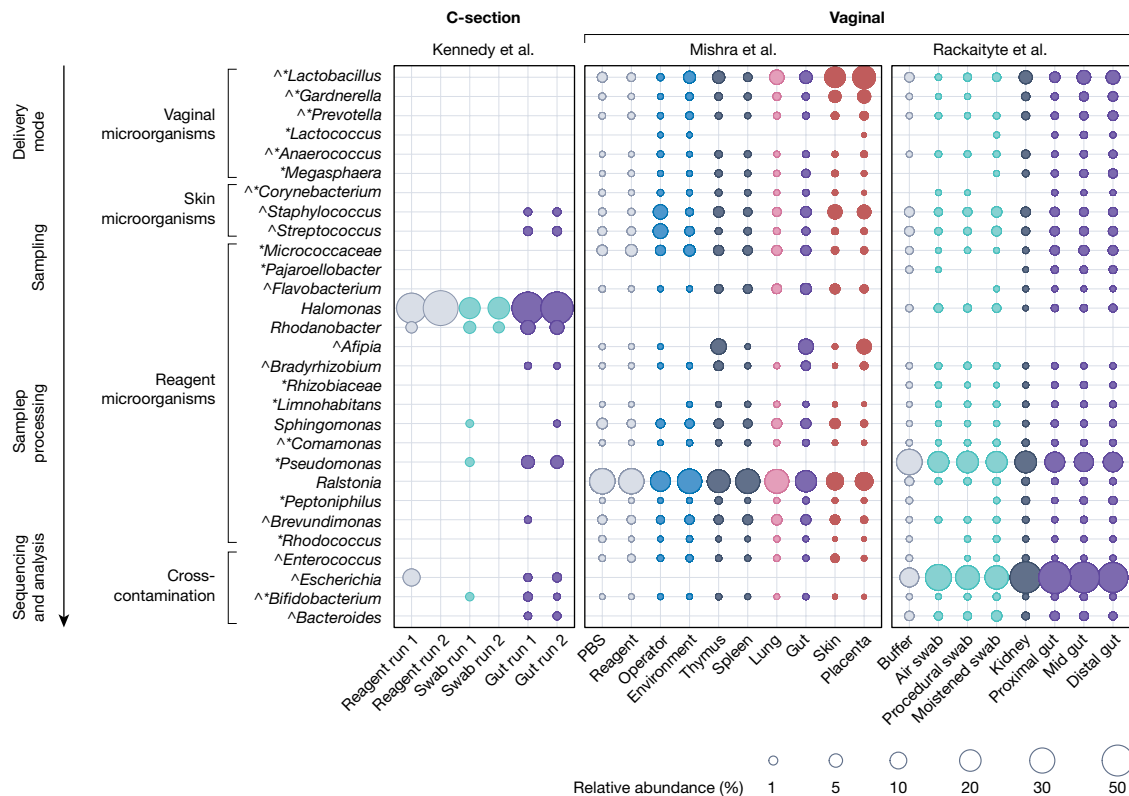


Fig. 1 | Relative abundance of bacterial taxa from three recent fetal studies. Distribution and mean relative abundance (%) of taxa present in fetal samples from three recent studies^{30,39,40} investigating the fetal microbiome and their corresponding abundance in control samples. Taxa were selected on the basis of the following criteria: genera that were cultured from or detected as enriched in fetal samples as described by Mishra et al.⁴⁰ (indicated by *) or by Rackaityte et al.³⁹ (indicated by *, including the family Micrococcaceae); all genera detected in fetal samples from Kennedy et al.³⁰ and the PBS-enriched genus *Ralstonia*⁴⁰. Taxa were grouped by potential source of contamination (see illustrations on the left) in agreement with the likely origin of genera (for skin microorganisms) and previous studies that characterized sources of contamination^{36–38}. Publicly available unfiltered relative abundance data associated with each publication were merged into a single phyloseq object (RRID:SCR_01380). Amplicon sequence variants (ASVs) were grouped at the

genus or family level (for Micrococcaceae). The mean relative abundance of each taxon was calculated for each sample type within each study and plotted in R (tidyverse, ggplot2; RRID:SCR_014601). Dot size corresponds to the mean relative abundance by sample type and study (mean relative abundances of less than 0.0001% were excluded). Dots are coloured by sample type: reagent controls in lightest blue (Mishra: PBS *n* = 42, reagent *n* = 23; Rackaityte: buffer *n* = 11; Kennedy: reagent *n* = 2), sampling negatives in light blue (Kennedy: swab *n* = 1; Rackaityte: air swab *n* = 19; procedural swab *n* = 16; moistened swab *n* = 17) and environmental negatives in sky blue (Mishra: environment *n* = 47, operator *n* = 12), internal controls in dark blue (Mishra: thymus *n* = 27, spleen *n* = 12; Rackaityte: kidney *n* = 16), fetal lung in pink (Mishra: *n* = 25), fetal gut in purple (Kennedy: *n* = 20; Mishra: *n* = 44; Rackaityte: proximal *n* = 41, mid *n* = 45, distal *n* = 42), and external tissues in red (Mishra: skin *n* = 35, placenta *n* = 16). Parts of this figure were created with BioRender.com.

In addition to the potential detection of contaminants, the bacterial load found in terminated fetuses was extremely low^{39,40}. Signals derived from qPCR experiments were only marginally higher than those of controls, with Mishra et al. reporting cycle thresholds (Ct) of more than 30 cycles, with Ct values for negative controls being around 31–32 cycles. Cell counts as detected by both microscopy and culture were also low. Mishra et al. reported fewer than 100 colonies on average per entire fetus, with high inconsistencies among individual fetuses and tissues (see Table S6 in the original publication⁴⁰). Such findings are more likely to be a result of contamination than colonization. Neonatal meconium samples have been studied for a century by culture-based methods, and, more recently, by DNA sequencing. Evaluations of such samples are also associated with contradictory findings^{11,43,44,63}, probably owing to contamination⁶⁴ and because postnatal colonization may occur before the first passage of meconium²⁶. However, when meconium is passed soon after birth, culturable bacteria are seldom detected (as reviewed by Perez-Muñoz et al.²⁶). In agreement with this, an analysis of meconium samples collected from extremely premature infants⁶⁵ showed that taxa regularly identified as contaminants^{36,38} make up a large proportion of sequences that are collected within the first three days after delivery and which drop to levels below 1% of the total microbiota profile in most samples at days 4–6 (Fig. 2).

This indicated that bacterial sequences that cannot be assigned to contamination are initially rare in early meconium, which is consistent with a recent study that applied strict controls for sequencing and culture and did not detect a meconium microbiota⁶⁴. Members of an authentic fetal microbiota should be, in theory, detectable in early-life faecal samples independent of birth mode. There is, indeed, some overlap between the reported fetal microbial taxa in vaginal versus C-section deliveries^{39,40}, for example, staphylococci, enterococci, lactobacilli and enterobacteria, and the microbiota detected in infant faecal samples in the first week of life^{66–68}. However, there have been few attempts to track species and strains to confirm fetal origin. One study investigated gastric aspirates of newborn infants immediately after birth⁶⁹; this should in theory detect in-utero bacterial exposure as the fetus swallows amniotic fluid (as demonstrated by the detection of pathogenic *Ureaplasma* species⁷⁰). However, aspirates from vaginally born infants contained the specific *Lactobacillus* species (*L. iners* and *L. crispatus*) that also dominate the microbiota of the vagina, whereas most samples from C-section deliveries contained low microbial loads near the detection limit and clustered with negative controls⁶⁹. This finding is consistent with vaginal transfer of microorganisms to a sterile fetus during delivery. In addition, many of the genuine bacterial signals that were detected in early meconium⁶⁵

were typical maternal skin representatives (*Staphylococcus* spp. and *Corynebacterium* spp.) and were strongly associated with C-section, or in the case of vaginal deliveries, species that are common in the maternal faecal microbiota (*Escherichia coli* and *Bacteroides fragilis*) (Fig. 2), indicating that these genuine signals were derived from microorganisms acquired ex utero.

Research is beginning to determine the origin of post-partum neonatal microbial colonizers and has shown a delay in the appearance of bacterial species that are presumed to originate from the mother's gut (for example, *Bifidobacterium* and *Bacteroides* species) in early faecal samples of infants born by C-section^{66,67,71–73}. A substantial proportion of strains acquired by infants postnatally can be traced back to their mother's faecal samples^{73–75}, and faecal microbiota transplant from the mother restores the microbiome in infants delivered by C-section⁷⁶. Thus, the published evidence, although incomplete, suggests that the early-life microbiota in humans is acquired through the vertical and horizontal transfer of microorganisms whose origin is faecal or environmental (from outside) rather than fetal (from inside).

Bioinformatic and data science perspectives

Characterizing low-biomass samples by 16S rRNA gene amplicon sequencing is challenging as DNA contamination can occur from the microbial DNA present in reagents, labware, tools, instruments and DNA-isolation kits^{36–38}, and through cross-contamination between PCR tubes or wells, sequencing runs or sequencing lanes³⁷. A common misconception in the field of low-microbial-biomass samples is that the use of negative controls is sufficient to account for all kinds of contaminants. Commonly, imperfect negative controls are used that account for only a limited number of the sample-processing steps or are not spread evenly amongst all batches (thus not accounting for processing days, reagent batches and different sequencing runs), leading to batch effects that may be mistaken for genuine signals⁴⁵. Overreliance on or under-analysis of such negative controls, in combination with the misapplication of contamination-removal programs like decontam⁷⁷, specifically by not having negative controls in all batches, frequently results in false positive signals owing to the detection of contaminants⁴⁵. Even with appropriate controls, it is challenging to separate genuine signals from low abundance contaminants as signals may appear sporadically in samples and negative controls⁷⁸. Thus, suboptimal processing of sequencing control samples may not reveal the full spectrum of contaminants because only the most abundant species of contaminants are consistently detected. On the other hand, potentially genuine sample-associated signals sometimes also erroneously appear in negative-control samples through cross-contamination during the PCR or sequencing steps (machine contamination)³⁷.

In the case of both Rackaityte et al.³⁹ and Mishra et al.⁴⁰, many of the taxa reported are common contaminants (Fig. 1). The most obvious case is *Bradyrhizobium*, which is one of the most dominant and consistent contaminants found in sequencing studies^{38,79}. Rackaityte et al. interpreted the presence of *Micrococcus* and *Lactobacillus* as genuine fetal inhabitants, but a reanalysis of the data suggested that these findings were a result of batch effects (indicative of contamination⁴⁵). Although the authors rejected this interpretation⁶¹, this batch effect is clearly visible if the findings of the different batches are plotted together (Fig. 3). Furthermore, in the study by Mishra et al., the authors concluded that *Micrococcus* was likely to be a contaminant⁴⁰, whereas the genera *Afipia*, *Flavobacterium*, *Pseudomonas* and *Brevundimonas* were reported as part of the fetal microbiota⁴⁰, although these taxa are also commonly detected as kit or laboratory reagent contaminants^{36,38}.

Mishra et al. and Rackaityte et al. also reported a marginally higher total bacterial load in fetal samples, as compared to controls, using qPCR^{39,40}. However, nucleic acids (DNA, RNA and tRNA) in tissue samples (which are absent in negative controls) might have a DNA carrier effect⁸⁰, leading to a more efficient DNA precipitation of prokaryotic

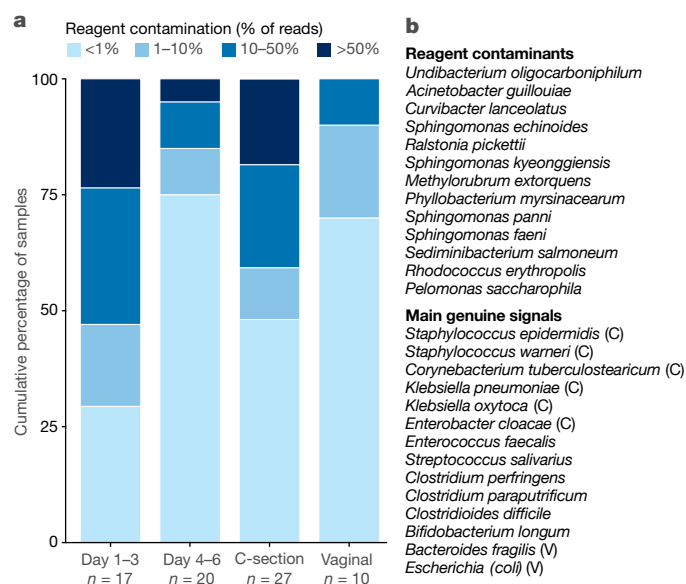


Fig. 2 | Reagent contamination in meconium samples from extremely premature infants. **a**, Representation of the percentage of reagent contamination in the first meconium of extremely premature infants collected in a previous study⁶⁵ in relation to the day of procurement of said samples (day 1–3 or day 4–6) or in regard to the mode of delivery (C-section or vaginal). Colours indicate the percentage of reagent contamination reads (legend on top). The day of procurement is significantly correlated with the percentage of reagent contamination reads ($P = 0.005$ by Mann–Whitney U test or $P = 0.01$ by Spearman rho test) and the mode of delivery shows a trend ($P = 0.07$ by Mann–Whitney U test). The number of samples (n) is noted below each category. **b**, Top, list of reagent contaminants shown together in **a**. Bottom, list of the most abundant sample-associated signals and their association (or lack thereof owing to limited size of cohort) with vaginal (V) or C-section (C) delivery.

material. In addition, bacterial PCR primers that target the 16S rRNA gene can also amplify mitochondrial DNA⁸¹, which is evolutionarily of bacterial origin. Together, these factors offer alternative explanations for a higher microbial burden in samples from low-biomass sites compared to controls. Rackaityte et al. removed human mitochondrial DNA (mtDNA) from their 16S rRNA gene-sequence-based results that co-amplified in the PCR, but neither study accounted for mtDNA in their qPCR analysis, although their qPCR primers targeted the 16S rRNA gene and were therefore potentially susceptible to cross-reactivity^{39,40}.

Immunological perspective

The enteric microbiota is a potent driver of adaptive mucosal immune maturation and priming in the adult host^{82–85}. Besides their intrinsic immunogenic nature, microorganisms also generate metabolites that promote and shape immune maturation and priming^{86–88}. Although the early fetal immune system is immature, recent research shows the migration of fetal dendritic cells (DCs) to the mesenteric lymph nodes; somatic hypermutation in fetal B cells; and an expansion of T cell receptor repertoire diversity, evenness and activation during late fetal development^{7,89,90}.

The existence of metabolically active microorganisms in the fetus could, in principle, provide one possible explanation for these findings. Mishra et al.⁴⁰ used an autologous T cell expansion assay to show that fetal DCs loaded with antigen from bacteria that had been isolated from fetal tissues stimulated the proliferation of CD45RO⁺ and CD69⁺ T cells. T cell proliferation was reduced but still detectable in the absence of DC-derived cytokine release, suggesting an activated memory response⁴⁰. Evidence that the fetal T cell memory response is specific for the bacteria present in one individual fetus would be necessary

Q15

Q13

Q14

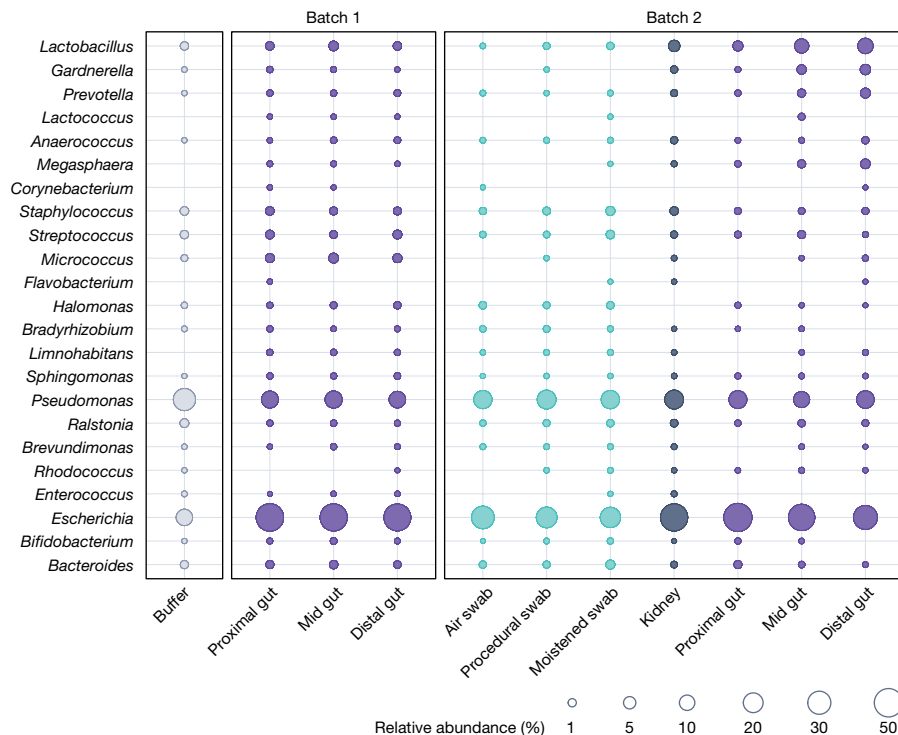


Fig. 3 | Relative abundance of bacterial taxa in samples from Rackaityte et al. Distribution and mean relative abundance (%) of taxa present in fetal and control samples from Rackaityte et al.³⁹ by batch as defined by Rackaityte et al.⁶¹. Dominant taxa were selected as described in Fig. 1. Publicly available unfiltered relative abundance data associated with each publication were merged into a single phyloseq object (RRID:SCR_01380). ASVs were grouped at the genus or

family (for Micrococcaceae) level. The mean relative abundance of each taxon was calculated for each sample type within each batch and plotted in R (tidyverse, ggplot2; RRID:SCR_014601). Dot size corresponds to the mean relative abundance by sample type and batch. Dots are coloured by sample type: reagent controls in lightest blue (buffer), sampling negative controls in light blue, internal controls in dark blue (kidney) and fetal gut samples in purple.

to strengthen the interpretation that specific immune responses are routinely driven by fetal bacterial colonization.

There are alternative explanations for fetal immune responses apart from bona fide microbial colonization. Maternal antigen–IgG complexes have been detected in cord blood, and trans-placental immune priming of the fetal immune system in early gestation has been demonstrated^{91,92}. Cross-reactivity, as observed for microbiota reactive enteric secretory immunoglobulin A, would support fetal priming by maternal microbial antigens⁸⁷. Similarly, maternal-microbiota-derived molecules partly bound to IgG stimulated innate immune maturation of the fetal gut in mice⁴⁸, and maternal intestinal carriage of *Prevotella* has been reported to protect the offspring from food allergy in humans⁹³. Thus, antigens and metabolites derived from the maternal microbiota can pass the placental filter directly or bound to IgG, and offer an alternative explanation for the observed fetal immune responses⁹⁴.

The hypothesis of a low-biomass fetal microbiome requires the identification of host mechanisms that control and tolerate bacterial populations and prevent overt inflammation and tissue destruction in the presence of viable microorganisms, many of which are opportunistic pathogens (see below). Alongside this, mechanisms by which the commensal or symbiotic microorganisms survive the immune response and antimicrobial effector molecules would also have to be identified, and it is unclear how the fetal immune system would differentiate between pathogens and symbionts once protective barriers are breached⁵⁷. Given that such immunological and anatomical mechanisms have not been identified or even proposed²⁸, the observed immune maturation and priming during fetal development is probably not induced through colonization of the fetus with live microorganisms. Instead, fetal immune development might be driven through maternal immune components or microbial fragments and metabolites crossing

the placenta, which protects the sterile fetus from live microorganisms through multiple layers of immunological defence⁵⁷.

Clinical microbiology perspective

No part of the human body is impregnable to bacterial invasion. Transient bloodstream bacteraemia can result from innocuous activities such as brushing the teeth⁹⁵, and most host tissues can tolerate occasional ingress by microorganisms. However, to avoid serious pathology, bacteraemia must be rapidly cleared by innate immune mechanisms and inflammation. Some pathogens establish persistent infections that may be asymptomatic either by evading the immune system or by forming persister cells in response to antibiotic treatment⁹⁶. The claims for non-pathogenic fetal microbial exposure^{39,40} have not established whether host–microbe interactions reflect small-scale translocation, asymptomatic infection, persistent symbiosis or mutualism.

The ‘fetal-enriched taxa’ reported include *Micrococcus*, *Lactobacillus*, *Flavobacterium*, *Staphylococcus*, *Escherichia*, *Enterococcus*, *Afipia*, *Pseudomonas*, *Bradyrhizobium* and *Brevundimonas*^{39,40}. Mishra et al. also report successful culturing of lactobacilli and staphylococci from fetal tissue⁴⁰, but the lack of unambiguous species-level taxonomic identification of the cultured organisms is a major technical limitation. Bacteria such as *Micrococcus*, which were detected in fetal intestines by Rackaityte et al.⁶¹, rarely cause invasive infection in humans. Their prolonged presence within healthy tissues and transmission through the placenta would require bacterial mechanisms of resistance against antimicrobial effector molecules of the host innate immune system⁵⁷. Such mechanisms have not been described for the genus *Micrococcus*, which is an environmental organism found in water, dust and soil, and is also a common contaminant^{46,47}. Lactobacilli are usually of

low pathogenic potential; they inhabit external mucosal surfaces of healthy humans, including the nose⁹⁷ and the vagina⁵⁶, and are often used as probiotics⁹⁸. However, some strains and species of lactobacilli do express potential virulence factors^{99–101}, resist oxidative stress¹⁰² and grow in the absence of iron¹⁰³, which allows them to cause serious infections such as endocarditis when provided with the opportunity to access the bloodstream^{104,105}. This raises potential problems with the interpretation of lactobacilli as asymptomatic colonizers of fetal tissue rather than contaminants that are picked up during vaginal delivery.

An even greater challenge arises when species of the genus *Staphylococcus* are considered, particularly strains that were cultured from fetal tissue and that exhibit high-level 16S rRNA gene-sequence identity (99–100%) to *Staphylococcus aureus* and several closely related coagulase-negative *Staphylococcus* species (CoNS)⁴⁰. These organisms can be long-term colonizers of external mucosal surfaces of humans^{106,107} and do not typically cause disease unless the mucosal barrier is breached. However, once they bypass mucosal barriers, they can deploy a more extensive repertoire of virulence factors to invade tissues by degrading connective tissues and, in the case of *S. aureus*, a repertoire of over a dozen cytolytic toxins that kill human cells^{108,109}. CoNS, on the other hand, are ubiquitous skin colonizers. Their detection in clinical diagnostic laboratories is so common that it is considered a major diagnostic challenge^{110,111} and is usually assumed to reflect contamination from the patient and occasionally the healthcare worker, in the absence of other reasons to suspect a CoNS infection^{77–79}. There are, however, distinct clinical scenarios in which the presence of CoNS and their pathogenic capacity are considered critical: for example, in patients with indwelling medical devices and in preterm neonates, they are the most common cause of late-onset neonatal sepsis¹¹². Therefore, given that they are either contaminants or overt pathogens, the detection of staphylococci, no matter whether *S. aureus* or CoNS, is difficult to reconcile with in-utero colonization of a healthy fetus.

Other bacteria identified as part of a notional ‘fetal microbiome’, such as *Enterococcus faecalis* and *Klebsiella pneumoniae*, are equally problematic. These belong to a group known as ‘ESKAPE pathogens’, which include *Enterococcus faecium*, *S. aureus*, *K. pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* species. The lethality of tissue colonization with ESKAPE pathogens is well documented, and these microorganisms are leading causes of healthcare-acquired infections worldwide, with considerable mortality and morbidity, even when treated with antibiotics¹¹³. Several ESKAPE pathogens readily survive in adverse conditions outside of vertebrate hosts, including drying, oxidative stress and exposure to heat or sanitation chemicals¹¹⁴. They are likely to persist on inanimate surfaces including utensils or clinical fabrics^{115,116}, thereby increasing their likelihood of being contaminants. Although these microorganisms were not reported at the species level⁴⁰, it is noteworthy that closely related organisms can also cause neonatal sepsis^{117–119}, which makes them unlikely to be colonizers of a healthy fetus.

A consideration prompted by a notional fetal microbiome is the possibility that the fetus might cope better with nosocomial pathogens than neonates or even adults. However, there is ample evidence to show that amniotic fluid, the placenta and fetal tissues are highly susceptible to bacterial infection, and the outcomes of infections with *S. agalactiae* or *Listeria monocytogenes* are often catastrophic^{120,121}. Notably, in *L. monocytogenes* infections that occur during the third trimester of pregnancy, fetal infection progresses, whereas the mother’s infection can be cleared, indicating that the fetus does not have greater resistance to infection than an adult human. Therefore, from a clinical perspective, most interpretations brought forward in recent publications^{39,40} with regard to the presence of microorganisms in fetuses seem to be biologically difficult to reconcile, as it is highly plausible that they would result in harm to or death of the fetus. In agreement with this conclusion, in a series of well-controlled studies in various clinical settings, DiGiulio

and co-workers found no evidence for microorganisms in amniotic fluid except when associated with neonatal morbidity and mortality^{122–125}.

Gnotobiology perspective

The traditional assumption that the human fetus is free from other life forms in utero is based mainly on the observation that, with few exceptions, bacterial and viral pathogens that infect the mother are incapable of crossing the placental barrier to infect the fetus^{126–128}. In addition, the amnio-chorionic membranes that enclose the fetus in the uterine cavity, as well as the cervical mucus plug, protect the fetus from external microorganisms. Sterility of the fetus is the basis for the derivation by hysterectomy of germ-free mammals (mainly mice and rats, but also pigs and other species²⁶), which have long been used to study the biochemical, metabolic and immunological influences of microorganisms on their mammalian hosts^{129–131}. The primary consideration is whether germ-free animals are truly ‘free of all demonstrable forms of microbial life’¹³². If they lack microbial associates, there cannot be a fetal microbiome. Testing germ-free animals for contaminating microorganisms uses microscopic observation of stained faecal smears, culture of faeces in nutrient media under various conditions of temperature and gaseous atmosphere^{127,132–134}, PCR using ‘universal bacterial’ primers^{133,135}, and serological assays for viral infections¹³⁶. These tests consistently demonstrate an absence of microbial associates. Therefore, gnotobiology provides strong evidence that the fetus in utero is sterile.

A healthy human fetus is sterile

Through multiple angles of explanatory considerations, we conclude that the evidence is strongly in favour of the ‘sterile womb’ hypothesis. Although it is impossible to disprove the occasional presence of live microorganisms in a healthy human fetus, the available data do not support stable, abundant colonizers under normal, non-pathogenic circumstances. We are aware that our position conflicts with dozens of publications that claim evidence for in-utero microbial populations²⁰, but we are confident in the validity of our multi-layered approach.

The processes by which the fetus matures and becomes immunologically equipped for life in a microbial world have lifelong implications. Aside from the caution and safeguards recommended in this perspective, our aim here is not to dissuade scientists from investigating the microbial drivers of fetal immune development. We agree with proposals that there is a need to better understand microbial interactions at the maternal–fetal interface²⁰, but do not think that symbiotic microbial populations in the placenta or fetus play a role in this. Paradoxically, we contend that sterile tissues are both immunologically and microbiologically fascinating, but require an adjustment of the methodological approaches used. How does the fetus mature and become immunologically equipped for life in a microbial world in the absence of direct exposure to live microorganisms? Are maternal-derived microbial metabolites sufficient for fetal immune education? Future research could include explorations of how maternal microbial-derived metabolites and small molecules, as well as maternal immune components, prepare the fetus for the microbial challenges of postnatal life⁹⁴.

Lessons for low-biomass research

Contamination is always a potential confounder in microbiology but is of particular concern for those studying low- or no-biomass samples^{36,38}. The issue has been highlighted by recent reports of human tissues, such as blood, brain and cancers (Box 1), which were previously thought to contain no, or very little, bacterial biomass, but apparently contain diverse microbial communities. As with the intrauterine studies

Q16

Q17

Box 1

Experimental considerations for low-biomass research

High-biomass samples

Examples: Faeces, dental plaque, wastewater, soil.

Impact of contamination: Very low: The high microbial biomass derived from the sample dominates the signal from background contamination, meaning that most observations are robust.

Mitigations: Experimental design seldom needs to be substantially adjusted to account for contamination. Inclusion of 'blank' negative sequencing controls and removing samples with significant levels of contamination using basic post-sequencing analysis is nevertheless prudent.

Low-biomass samples

Examples: Skin swabs, nasal tract swabs, breastmilk, most respiratory tract samples, tissue biopsies and mucosal samples, including intestinal crypts.

Impact of contamination: Low to high: Contaminated samples are progressively affected with reducing input microbial biomass³⁸.

Mitigations: Inclusion of multiple controls for recognition of contamination. Ideally, samples should be concentrated before processing to increase input biomass. Consideration of potential sources of contamination during the sample acquisition stage is always recommended. After sample collection, processing should be carried out in a clean-room environment, preferably with all surfaces bleached and UV-treated. DNA extraction may benefit from the use of non-kit-based methods (for example, phenol-chloroform extractions) in which plastic-ware and reagents can be UV-treated before use. Contamination from DNA-isolation and PCR kits is usually identifiable, particularly if well-defined batches are created⁶⁴ and controlled using different lot numbers of kits. Regardless of the method of DNA extraction, the presence of contaminants should be monitored by including 'blank' negative controls. Inclusion of controls generated by serial dilution of DNA of known composition (for example, mock community) will indicate the biomass level at which contamination becomes a dominant feature of sequencing results. Contamination may also be estimated before sequencing

by qPCR using serially diluted known quantities of spiked input DNA. Post-sequencing analyses, using programs like decontam, and analysis steps described by de Goffau et al.³⁶ and used by Heida et al.⁶⁵, will usually identify contaminants.

Samples in which the existence of microorganisms is not established (potential 'no (zero) biomass' samples)

Examples: Placental and fetal tissues, amniotic fluid, meconium, brain tissue and cerebrospinal fluid, blood, bone and internal cancer tissues, healthy middle ear samples.

Impact of contamination: High and potentially up to 100% unless infection or injury is present.

Mitigations: Experimental design should be directed specifically against contamination. Initial assessment using quantitative methods (for example, qPCR) with low detection limit and microscopic visualization (for example, Gram staining or labelling by FISH) is required to determine whether microorganisms are present, before embarking on sequencing approaches. Such techniques are still susceptible to sample contamination and other artefacts (for example, non-specific staining or auto-fluorescence from mucins can sometimes appear 'microbe-like' in size and shape)^{45,144}. All mitigations outlined for 'low biomass' samples above should be adopted. Repeating sample processing with different DNA extraction kits or methods³² and/or at different days can be informative¹⁴⁵. These will track the presence of species in sequencing profiles associated with specific kits, reagents or environment. Species that are repeatedly detected regardless of the technical approach are more likely to be genuine signals, unless they were introduced during sample collection. Binary statistics (absence–presence) are recommended. The presence of microorganisms identified by sequencing should be verified with a different technique such as cultivation, another sequencing technique with sufficient taxonomic resolution, and/or species-specific qPCR or FISH using high magnification to visualize the size and morphology of individual microbial cells.

described above, these microbial populations are often discussed considering their perceived importance for human diseases and health.

In studies on low-biomass samples, it is challenging to identify relevant signals from among contaminating noise. In instances of contamination, a tissue may be misjudged as non-sterile, whereas in others, a real microbiological signal may be obfuscated by contamination. The removal of all sequences present in negative-control samples or that have been previously identified as contaminants in the literature may result in a loss of authentic signals. Post-sequencing contamination removal using software packages such as decontam⁷⁷ or other statistical approaches^{36,137} have been developed to remove the more abundant contaminants, leading to microbiome profiles that are more likely to reflect the real community. Practical examples of contamination removal in 16S rRNA gene-sequence data is provided by Heida et al.⁶⁵, Saffarian et al.¹³⁸, and Jorissen et al.¹³⁹, and we expand on these examples in Box 1.

We draw attention to the distinction between 'low biomass' and 'no (zero) biomass' samples. This has practical significance; true 'low (microbial) biomass' samples are amenable to contamination-removal approaches but 'no (microbial) biomass' samples require a different approach (Box 1). For credible assertions of the presence of microorganisms, multiple layers of evidence are required, first with quantitative, sensitive (lower detection limit) approaches such as qPCR, with strict controls, before contamination-sensitive sequencing approaches are

applied. Because contamination removal will provide data regardless of whether microorganisms are present or absent, the starting proposition should be the null hypothesis to avoid confirmation bias, particularly when results are inconsistent and at the outer technical limits for detection, or if results defy mechanistic plausibility.

Given the limitation of sequencing approaches, confirmation by alternative methods, such as FISH and culture, is required. However, as shown by recent studies of fetal samples, even a combination of approaches has the potential to produce false findings, because contamination during sampling is a considerable challenge. We posit that studies on all low-biomass samples could benefit from a similar trans-disciplinary assessment to that applied above for fetal samples, to interpret findings considering biological and mechanistic explanations²⁸. When obligately photosynthetic, psychrophilic, thermophilic, halophilic or chemolithoautotrophic bacteria are found in human tissues that do not provide the growth conditions for such organisms^{24,140}, or if the detected genera are known contaminants of laboratory kits or reagents (such as readily culturable Proteobacteria like *Pseudomonas* and *E. coli*, for example)^{141–143}, the authenticity of such signals should be questioned.

Q18

Q19

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Q14	Please check that the full name of <i>C. tuberculo</i> stearicum added in Fig. 2b is correct.
Q15	Please check that the minor changes to the sentence beginning 'Although the authors rejected this interpretation...' are okay; this sentence was revised by the editor.
Q16	Please check that the minor changes to the sentence beginning 'There are, however, distinct clinical scenarios...' are okay.
Q17	Please check that the minor changes to the sentence beginning 'The issue has been highlighted by...' are okay.
Q18	Please check that the minor changes to the sentence beginning 'For credible assertions of the presence of microorganisms...' are okay. It was not clear whether the 'with strict controls' referred to the qPCR ('qPCR with strict controls') or whether it was a caveat to the next part of the sentence ('...with strict controls before contamination-sensitive sequencing approaches are applied'). Please adjust the punctuation if appropriate.
Q19	Please check that the minor changes to the sentence beginning 'We posit that studies on all low-biomass samples...' are okay.
Q20	Please check that the Acknowledgements section is correct. Note that this section may have been edited for style and brevity. We do not include titles or affiliations and only include the surname and the initial(s) of the first name(s) of colleagues mentioned here; please check that any shortenings are correct.
Q21	Please check that the Author contributions and Competing interests sections are correct.

Author Queries

Journal: **Nature**
Paper: **s41586-022-05546-8**
Title: **Questioning the fetal microbiome and pitfalls of low-biomass microbial studies**

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