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Neonatal diet alters fecal microbiota and metabolome profiles at different ages in infants fed breast milk or formula

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ABSTRACT

Background: Neonatal diet has a large influence on child health and might modulate changes in fecal microbiota and metabolites.

Objectives: The aim is to investigate fecal microbiota and metabolites at different ages in infants who were breastfed (BF), received dairy-based milk formula (MF), or received soy-based formula (SF).

Methods: Fecal samples were collected at 3 ($n = 16, 12,$ and $14,$ respectively), 6 ($n = 20, 19,$ and $15,$ respectively), 9 ($n = 12, 11,$ and $12,$ respectively), and 12 mo ($n = 14, 14,$ and $15,$ respectively) for BF, MF, and SF infants. Infants that breastfed until 9 mo and switched to formula were considered as no longer breastfeeding at 12 mo. Microbiota data were obtained using 16S ribosomal RNA sequencing. Untargeted metabolomics was conducted using a Q-Exactive Hybrid Quadrupole-Orbitrap mass spectrometer. The data were analyzed using R (version 3.6.0) within the RStudio (version 1.1.463) platform.

Results: At 3, 6, and 9 mo of age BF infants had the lowest α -diversity, SF infants had the highest diversity, and MF was intermediate. *Bifidobacterium* was 2.6- to 5-fold lower in SF relative to BF infants through 1 y of life. An unidentified genus from Ruminococcaceae higher in the SF (2%) than in the MF (0.4%) and BF (0.08%) infants at 3 mo of age was observed. In BF infants higher levels of butyric acid, D-sphingosine, kynurenic acid, indole-3-lactic acid, indole-3-acetic acid, and betaine were observed than in MF and SF infants. At 3 mo Ruminococcaceae was positively correlated to azelaic, gentisic, isocitric, sebacic, and syringic acids. At 6 mo *Oscillospira* was negatively correlated with 3-hydroxybutyric-acid, hydroxy-hydrocinnamic acid, and betaine whereas *Bifidobacterium* was negatively associated with 5-hydroxytryptamine. At 12 mo of age, Lachnospiraceae was negatively associated with hydroxyphenyllactic acid.

Conclusions: Infant diet has a large impact on the fecal microbiome and metabolome in the first year of life. This study was registered at clinicaltrials.gov as NCT00616395. *Am J Clin Nutr* 2020;111:1190–1202.

Keywords: breastfeeding, formula diets, microbiota, metabolites, immune system

Introduction

Exclusive breastfeeding is recommended by the WHO for the first 6 mo of life. There is no other period in life where nutrition comes from a sole source (breast milk or infant formula), and the health implications of early-life nutrition have been well described (1–4). For example, breastfeeding is associated with lower risks of infection during infancy, as well as a long-term decreased risk of atopy and obesity (1–4). Although the macro- and micronutrient composition of infant formula meets the requirements of a rapidly growing infant, there remain many bioactive components within human milk that have not been incorporated into the formula. Several of these components, such as proteins and oligosaccharides, remain partially undigested as they enter into the large intestine and thus influence the developing lower-gut microbiome (5, 6).

There is a growing body of literature describing the ability of the gut microbiome to modulate health (7). The infant's gut

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Supplemental Figures 1–10 and Supplemental Tables 1–9 are available from the “Supplementary data” link in the online posting of the article and from the same link in the online table of contents at <https://academic.oup.com/ajcn/>.

All the raw data will be available upon request.

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Abbreviations used: BF, breastfed; CLR, centered log ratio; ESI, electrospray ionization; FDR, false discovery rate; FF, formula-fed; FHWM, full width half maximum; MF, milk formula; NLB, no longer breastfeeding; OTU, operational taxonomic unit; PC, principal component; PCA, principal component analysis; PERMANOVA, permutational multivariate ANOVA; PICRUST, Phylogenetic Investigation of Communities by Reconstruction of Unobserved States; QC, quality control; rRNA, ribosomal RNA; SF, soy-based formula.

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microbiome is predominately seeded after birth (6). Breastfed (BF) infants have lower α -diversity and altered β -diversity measures compared with their formula-fed (FF) counterparts during the first year of life (8–10). Thus, the nutrition provided at this early age can significantly affect bacterial colonization and development. Whereas increased bacterial diversity is considered to be beneficial for adults (11), lower diversity displayed by BF infants is thought to be beneficial to the developing gut and immune system (12). In addition, breastfeeding is associated with increased abundances of specific bacteria, primarily *Bifidobacteria* and Bacteroidetes (6). Gut microbiota have been found to produce metabolites; specifically, SCFAs benefit to the colonic environment by improving barrier function, increase Treg cells to maintain homeostasis, and also protect from colonizing pathogenic bacteria (13, 14). These findings highlight that understanding the gut metabolite milieu is just as important as cataloging microbiome shifts, in terms of understanding microbe–host communication and physiology. It is increasingly appreciated that neonatal feeding and gut microbiota can influence the metabolites within urine, feces, and the sera (15, 16). Thus, an infant's microbiota and metabolite profile may be another link in the effect of early nutrition on healthy growth and development.

In this study, how early-life diet alters the lower-gut microbiome and host metabolism was examined. Toward this aim, we examined fecal samples from a clinical cohort that examined the effect of early infant diet on growth and body composition. Aside from examining BF compared with FF infants, this study contains 2 types of FF infants: those fed with a cow milk–based (MF) or a soy-based (SF) formula. To the best of our knowledge, an investigation into the fecal microbiome and metabolome of SF infants has not been carried out previously. The infant fecal microbiome and metabolome at 3, 6, 9, and 12 mo of age were determined.

Methods

Samples originated from a cross-sectional subset of a Central Arkansas cohort study, referred to as the Beginnings Study (NCT00616395). The study was approved by the institutional review board at the University of Arkansas for Medical Sciences and the study design has been reported previously (17). Inclusion criteria were that infants were born from healthy pregnancies and with no medical diagnosis (e.g., diabetes or pre-eclampsia) or had no medications that can affect fetal or infant growth (e.g., selective serotonin reuptake inhibitors or thyroid replacement). All women were nonsmokers, with no alcohol consumption and no usage of soy products or estrogenic compounds during pregnancy and lactation (if breastfeeding). An additional exclusion criterion was change of formula between 2 and 12 mo of age. Participants 1–2 mo of age were recruited between 2002 and 2010. Before enrollment, parents chose the diet to feed their infant with advice from their pediatricians. Infants were either BF or provided a milk (MF) (Similac Advance or Enfamil Lipil) or soy (SF) (Similac SoyIsomil or Enfamil Prosoabee) infant formula for the first 12 mo of life. Breastfeeding was encouraged until 12 mo of age. When this was not possible, infants were switched to MF and considered as no longer breastfeeding (NLB). In this study, a majority of the infants were switched to MF after 9 mo, thus only 12-mo

NLB samples were included in the analysis. The study visits presented in these analyses were conducted at ages 3 ($n = 16$, 12, and 14, respectively), 6 ($n = 20$, 19, and 15, respectively), 9 ($n = 12$, 11, and 12, respectively), and 12 mo ($n = 14$, 14, and 15, respectively) for BF, MF, and SF infants. NLB at 12 mo had 10 samples (Figure 1). Complementary food intake could start from 4 mo. Anthropometric measures were obtained at each study visit using standard methods that had been previously published (18). Briefly, weight was measured with the infant wearing only a diaper to the nearest 0.01 kg using a tared scale (model 727; SECA Corp.). Length was measured to the nearest 0.1 cm on a length board (Easy Glide Bearing Infantometer; Perspective Enterprises) (18). Sterile tubes were provided to families and fecal samples were collected either during the study visit or at home. If fecal samples were collected at home, the sample was frozen (-20°C) and delivered back to the research facility on ice. Samples were kept at -80°C until further analyses. Self-reported maternal prepregnancy weight and measured height at the 3-mo visit were used to compute maternal BMI (in kg/m^2). Infant race, gestational age, birth weight, and length at birth were also self-reported at the 3-mo visit.

16S ribosomal RNA amplicon sequencing

Fecal samples were homogenized and the PowerSoil® DNA Isolation Kit (MOBIO Laboratories, Inc.) was used for DNA extraction. The variable region 4 of bacterial 16S ribosomal RNA (rRNA) was amplified using 515F/806R forward and reverse primers (18). A $\sim 30\%$ PhiX DNA was added to pooled amplicons and paired-end sequences (2×250 bp) using Illumina MiSeq. Sequence reads were analyzed using QIIME 1.9.1 as described previously (19). Standard QIIME-based scripts were used for quality assessment of sequence reads, operational taxonomic unit (OTU) picking, and sequence alignment. A similarity threshold of 97% was used to cluster amplicon sequencing followed by taxonomic annotation of OTUs using the Greengenes 16S rRNA database at a confidence threshold of 80%.

Untargeted metabolomics analyses

Fecal samples were subjected to untargeted metabolomics analyses. Optima grade reagents and all equipment and instrumentation were obtained from Thermo Fisher Scientific unless otherwise noted. Fecal samples (100 mg) were dried overnight under a low-flow nitrogen stream to remove water (20), resuspended in 500 μL 50% aqueous methanol plus 100 μL recovery standard D4-glycocholic acid solution (2.1 mM), and homogenized using a Precellys 24 homogenizer (Bertin Corp) at 5300 rpm for two 30-s cycles. Homogenates were then extracted in 1 mL ice-cold acetonitrile. Experimental pools, used for quality control (QC) samples, were prepared by pooling equal volumes of each sample extract (10 μL). Samples and QC extracts were evaporated to dryness under a nitrogen stream and reconstituted in 300 μL 5% aqueous methanol containing an internal standard [Lorazepam (10 nM), (Sigma Aldrich)]. Chromatography was performed on a Dionex Ultimate 3000 UHPLC, using an XSelect CSH C18 reversed phase column (2.1×100 mm, 2.5 μm) kept at 49°C as previously described (21). Solvent A was 0.1% formic acid in water and solvent B was 0.1% formic acid in acetonitrile.

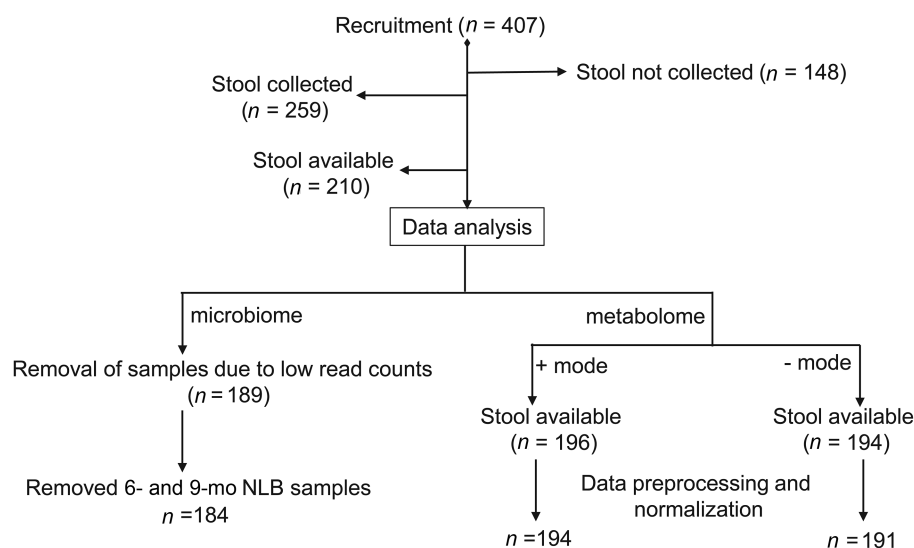


FIGURE 1 Flow diagram of the study participants showing enrollment, the number of stool samples collected, and the numbers of available samples for microbiota and metabolome data acquisition. The samples with low read counts and also the 6- and 9-mo NLB group for the microbiome data were excluded from analysis. After preprocessing and normalization of the metabolomics data, 2 samples in positive mode and 3 samples in negative mode were dropped. NLB, no longer breastfeeding.

Metabolites were eluted using the following gradient at a flow of 0.4 mL/min: 0–2 min, 0%–1% B; 2–6.5 min, 1%–20% B; 6.5–11.5 min, 20%–95% B; 11.5–13.5 min, 95%–99% B; 13.5–16.5 min, 99%–1% B; 16.5–20 min, 1% B; 20–21 min, 1%–0% B; 21–22 min, 0% B. Injection volumes were set to 5 μ L. Samples from all the groups were assayed in mixed and random order.

Detection was carried out on a Q-Exactive Hybrid Quadrupole-Orbitrap mass spectrometer with data acquisition executed using Xcalibur 4.0 software as previously described (21). All samples were analyzed by positive and negative electrospray ionization (ESI +/-) Full-MS scan mode. Nitrogen as sheath, auxiliary, and sweep gas was set at 50, 13, and 3 units, respectively. Other conditions were as follows: resolution, 70,000 full width half maximum (FWHM); automatic gain control (AGC) target, 3×10^6 ions; maximum injection time, 200 ms; scan range, 50–750 m/z ; capillary temperature, 320°C; source temperature, 425°C; and spray voltages, 2.7 and 3.6 kV for negative and positive modes, respectively. ESI +/- data-dependent MS² spectra were generated for QC pool samples using the following conditions: resolution, 17,500 FWHM; AGC target, 1×10^5 ions; maximum injection time, 50 ms; loop count, 5; isolation window, 4.0 m/z ; and normalized collision energy, 30.

The acquired data set, composed of full MS and data-dependent MS² raw files, was processed by Compound Discoverer 3.0 using an untargeted metabolomics workflow including retention time alignment, unknown compound detection, compound-grouping across all samples, gap filling, and metabolite identification using online and “in-house” data-dependent MS₂-fragmentation spectral databases (ddMS₂). The software parameters for alignment were as follows: adaptive curve model, 5 ppm mass tolerance, and 0.2-min maximum shift for alignment. The software parameters for detecting unknown compounds were as follows: mass tolerance for detection 10 ppm, intensity tolerance 30%, S/N threshold of 3, and minimum peak height 1×10^6 , and the parameters for compound groups were mass

tolerance 10 ppm and retention time tolerance 0.15 min. Gap filling was performed across all samples using the Real Peak detection method, a mass tolerance of 10 ppm, and S/N threshold of 1.5. Metabolites were identified by using MassList (accurate mass ± 5 ppm, retention time ± 15 s to a known standard), mzCloud (online ddMS₂ database), and mzVault (in-house ddMS₂ database). **Supplemental Table 1** lists the metabolite standards used to generate the MassList and mzVault databases. Metabolite identification confidence levels are as follows: level 1: accurate mass, retention time, and MS² spectra matching to mzVault or mzCloud; level 2: accurate mass, retention time matching to known standard, no ddMS₂ information.

Statistical analysis

All data preprocessing and analyses were conducted in R (version 3.6.0; R Development Core Team) within the RStudio (version 1.1.463) platform.

Microbiome

Total sampling depth was 3,192,176 sequencing reads. Mean sample depth per sample was 19,216 sequencing reads and sequences were not rarefied before analysis (22). Data were initially screened to remove samples with sequence reads < 1000 counts ($n = 21$). Low abundant OTUs were then removed if <20% of samples did not have ≥ 10 sequencing reads. OTUs in duplicated samples ($n = 16$) were analyzed for CV values and were removed if mean CV > 40%. For duplicated samples with mean CV < 40%, OTUs were averaged and rounded to the nearest whole number for subsequent data analysis. A total of 184 samples remained after preprocessing of the 16S rRNA sequencing data, with an average sampling depth of 11,414 reads. All data analysis was performed at the genus level. The phyloseq

package was used to merge, filter, and calculate α -diversity indexes and Bray–Curtis distance matrices (23). α -Diversity (within-sample diversity) was estimated for taxa richness (total number of taxa, Chao1 index), evenness (Shannon Index), and dominance (Simpson Index). These α -diversity estimates were analyzed with either a 2-factor or 1-factor ANOVA, depending on whether the main effect of age was included (i.e., 2-factor if all samples were analyzed together and 1-factor if assessing diet within age). β -Diversity (i.e., between-sample differences) was estimated using Bray–Curtis dissimilarities. Permutational multivariate ANOVA (PERMANOVA) was used to determine dietary and age differences of β -diversity in all samples, followed by pairwise assessment of diet within each age using PERMANOVA. These analyses were all adjusted for child sex and birth weight (kg) and conducted using the R vegan package (24). Only 22 of 98 infants had fecal samples at >2 ages; therefore, repeated measures were not conducted in these analyses. Post hoc analysis of α -diversity indexes was assessed using contrasts on estimated marginal means using the emmeans package (25). β -Diversity was visualized using principal coordinate analysis. Dietary differences in genera within age groups were assessed by identifying intersecting results by 2 statistical approaches: 1) Kruskal–Wallis and Dunn’s tests were assessed on percentage relative abundance data (full results in **Supplemental Table 2**), and 2) Wald’s test for pairwise comparisons (full results in **Supplemental Table 3**) on sequence counts as implemented in the DESeq2 package (22, 26). *P* values for all tests were adjusted for multiple comparisons using Benjamini and Hochberg’s false discovery rate (FDR) correction unless noted. Statistical significance was determined at $P_{\text{adj}} \leq 0.05$ (27).

Metabolomics

Data from the negative and positive modes were processed separately. Raw peak areas were first adjusted by dry fecal weights of samples. CVs of QC samples were then assessed and metabolites with CVs > 40% were removed. The overall and group variance of raw data were calculated and compared against variance estimates using several normalization procedures (e.g., vector sum, single internal standard, compensating multiple internal standards). Compensating multiple internal standards had lower overall and within-group variance than did the raw data and still maintained the metabolite distribution within samples; therefore, this normalization procedure was applied to the data using the crmn package (28). Sample outliers were visually assessed using principal component analysis (PCA) and removed if the sample PCA score was >3 SD along components 1 and/or 2 ($n = 7$). Univariate metabolite outliers were determined using an iterative assessment of Grubb’s test for outliers at $\alpha < 0.01$ ($n = 23$ and 29 in negative and positive modes, respectively). All missing samples were imputed using the K-Nearest Neighbor algorithm (29). Totals of 96 and 117 metabolites were used for statistical testing in the negative and positive modes, respectively. The effect of diet within each age group was then analyzed with the Kruskal–Wallis test followed by post hoc analysis by Dunn’s Multiple Comparison test (full results in **Supplemental Tables 4, 5**). *P* values derived from Kruskal–Wallis and Dunn’s Multiple Comparison tests were adjusted for FDR correction.

TABLE 1 Clinical cohort characteristics at 3, 6, 9, and 12 mo of age from either BF, MF, NLB, or SF infants¹

Parameters	3 Mo			6 Mo			9 Mo			12 Mo			
	BF	MF	SF	BF	MF	SF	BF	MF	SF	BF	MF	NLB	SF
Infants, <i>n</i>	16	12	14	20	19	15	12	11	12	14	14	10	15
Self-reported ethnicity, %													
White	100	83.3	64.3	100	84.2	80	100	100	75	92.9	78.6	100	86.7
African-American		16.7	21.4		15.8	20			25		21.4		13.3
>1 race			7.1							7.1			
Not reported			7.1										
Sex, % female	62.5	16.7	50	70	57.9	46.7	66.7	45.5	33.3	64.3	42.9	70	26.7
Maternal BMI, kg/m ²	24.9 ± 4.5	26.7 ± 4.3	27.0 ± 4.2	25.0 ± 4.7	26.5 ± 5.8	29.2 ± 8.2	24.1 ± 5.0	28.9 ± 6.2	23.3 ± 4.9	24.6 ± 3.2	27.9 ± 6.0	24.2 ± 2.7	26.6 ± 6.7
Birth length, cm	51.0 ± 2.0	50.6 ± 2.5	51.4 ± 2.1	50.7 ± 1.5	50.9 ± 2.3	50.6 ± 1.8	50.2 ± 2.5	51.3 ± 1.9	51.0 ± 2.8	51.2 ± 2.8	51.0 ± 1.9	50.8 ± 1.2	51.0 ± 2.6
Birth weight, kg	3.5 ± 0.3	3.3 ± 0.3	3.4 ± 0.4	3.4 ± 0.4	3.4 ± 0.3	3.4 ± 0.4	3.4 ± 0.3	3.4 ± 0.3	3.4 ± 0.4	3.5 ± 0.3	3.4 ± 0.3	3.4 ± 0.4	3.4 ± 0.4
Gestational age, wk	39.6 ± 0.6	39.2 ± 0.8	39.2 ± 0.8	39.5 ± 0.6	39.2 ± 1.0	39.0 ± 0.8	39.5 ± 0.6	39.6 ± 0.5	39.3 ± 0.8	39.5 ± 0.5	39.2 ± 0.9	39.6 ± 1.0	38.9 ± 0.8

¹*n* = 184. Values are percentages or means ± SDs unless otherwise indicated. BF, breastfed; MF, cow milk–based formula; NLB, no longer breastfeeding; SF, soy-based formula.

TABLE 2 Estimated marginal means (95% CIs) of fecal α -diversity indexes at 3, 6, 9, and 12 mo of age from either BF, MF, NLB, or SF infants¹

Age	Index	BF	<i>n</i>	MF	<i>n</i>	NLB	<i>n</i>	SF	<i>n</i>	Diet	Birth weight	Sex
3	Observed	22.0 (19.9, 24.1)	16	24.7 (22.1, 27.3)	12			23.7 (21.6, 25.9)	14	0.306	0.084	0.513
3	Chao1	24.1 (22.1, 26.1)		24.5 (22.0, 27.1)				25.1 (23.0, 27.2)		0.738	0.208	0.054
3	Shannon	1.3 (1.2, 1.5) ^a		1.8 (1.6, 2.0) ^b				2.0 (1.9, 2.2) ^c		<0.01	0.241	0.052
3	Simpson	0.6 (0.6, 0.7) ^a		0.8 (0.7, 0.8) ^b				0.8 (0.7, 0.9) ^c		<0.01	0.241	0.018
6	Observed	21.2 (19.6, 22.9) ^a	20	23.8 (22.2, 25.5) ^b	19			24.6 (22.8, 26.4) ^c	15	0.026	0.626	0.112
6	Chao1	22.2 (20.4, 24.0) ^a		25.1 (23.3, 26.8) ^b				25.1 (23.2, 27.1) ^c		0.048	0.992	0.241
6	Shannon	1.5 (1.3, 1.7) ^a		1.7 (1.6, 1.9) ^a				2.0 (1.8, 2.2) ^b		<0.01	0.958	0.571
6	Simpson	0.7 (0.6, 0.7)		0.7 (0.7, 0.8)				0.8 (0.7, 0.8)		0.066	0.94	0.778
9	Observed	22 (18.9, 25.0)	12	23.2 (19.8, 26.5)	11			25 (21.9, 28.1)	12	0.174	0.699	0.139
9	Chao1	22.6 (19.8, 25.4)		23.8 (20.8, 26.9)				25.4 (22.6, 28.2)		0.198	0.619	0.238
9	Shannon	1.5 (1.3, 1.7) ^a		1.8 (1.5, 2.0) ^a				1.9 (1.7, 2.2) ^b		0.032	0.707	0.534
9	Simpson	0.6 (0.6, 0.7)		0.7 (0.7, 0.8)				0.7 (0.7, 0.8)		0.069	0.715	0.726
12	Observed	24.9 (23.5, 26.2)	14	25.3 (24.0, 26.7)	14	26.0 (24.4, 27.5)	10	25.9 (24.6, 27.3)	15	0.765	0.026	0.783
12	Chao1	25.3 (24.0, 26.7)		25.8 (24.5, 27.2)		26.2 (24.6, 27.8)		26.2 (24.9, 27.5)		0.894	0.025	0.759
12	Shannon	1.7 (1.5, 1.9)		1.7 (1.5, 1.9)		1.8 (1.6, 2.1)		1.9 (1.7, 2.1)		0.470	0.144	0.085
12	Simpson	0.7 (0.6, 0.8)		0.7 (0.6, 0.7)		0.7 (0.6, 0.8)		0.7 (0.7, 0.8)		0.615	0.373	0.059

¹Differences in dietary intake assessed by ANCOVA, blocked for gender and birth weight as covariate. Estimated marginal means in the same row without a common letter differ. *P* value provided for main effect (diet), covariate (birth weight), and blocking variable (sex). Post hoc pairwise assessment performed by contrast analysis. Sample sizes range from 10 to 20 per diet group at 3, 6, 9, and 12 mo of age. BF, breastfed; MF, cow milk-based formula; NLB, no longer breastfeeding; SF, soy-based formula.

Functional gene prediction of gut microbiota of infants fed with either breast-milk or formula diets

The functional gene prediction of the gut microbiota of the BF, MF, and SF infants was carried out using Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt) (30). A closed-reference OTU was generated in QIIME and taxonomy assignment was made with the Greengenes database with a 97% similarity. To obtain the functional prediction of the metagenome, the OTU data were normalized with the PICRUSt at level 3 pathways. Statistical analysis was conducted using the STAMP version 2.1.3 (Statistical Analysis of Metagenomic Profiles) software package (31) with the nonparametric Welch test to investigate and illustrate alterations in microbial functions between groups.

Correlation analysis of 16S rRNA sequencing and metabolomics data

16S rRNA data were adjusted for correlation-based analyses (e.g., PCA and Pearson's correlations) using a centered log ratio (CLR) transformation (32). Zeros were imputed using the geometric Bayesian multiplicative methods using the zCompositional package (33). Metabolomics and adjusted 16S rRNA data were separately assessed by PCA for dimension reduction and visualization. Components from each PCA were correlated and plotted. Correlations between metabolites altered by diet and CLR-transformed genera were assessed using Pearson's correlations, and correlations with FDR-adjusted *P* values < 0.05 were visualized using heat maps.

Results

The cohort was 19.1% African American, 88.0% Caucasian, and 7.1% reporting >1 race. Girls made up 50.2% of the infants. **Table 1** shows gestational age, birth weight, and length, as well as maternal BMI.

BF infants have lower α -diversity through the first 9 mo of life than FF infants

To determine if infant diet, age, sex, or birth weight influence microbiota richness and diversity, a 2-factor ANCOVA was performed on all samples with covariate adjustments for child sex, and birth weight (**Supplemental Table 6**) at genus level. After covariate adjustment, a significant effect of diet was noted for all α -diversity indexes (**Supplemental Table 6**). Furthermore, a significant effect of age was seen with Observed (*P* < 0.01) measures. Child sex was also statistically significant in the Shannon (*P* < 0.05) and Simpson (*P* < 0.05) indexes.

Investigation of dietary differences within age showed differences in α -diversity measures between the diet groups at 3, 6, and 9 mo of age (**Table 2**). At 3 mo of age the BF group showed significantly lower Shannon and Simpson diversity measures than the MF and SF groups (**Table 2**). At 6 mo of age, the BF group had lower Observed and Chao1 measures than did the 2 formula groups. Interestingly, the Shannon and Simpson indexes were significantly different between BF and SF at 6 mo of age. At 9 mo of age only the Shannon index was significantly lower in the BF than in the SF group. At 3, 6, and 9 mo, the SF infants showed higher diversity than MF infants (**Table 2**). No differences were observed between diet groups at 12 mo of age (**Table 2**).

BF infants have distinct microbiota through the first 9 mo of life compared with FF infants

When comparing the effect of diet and age, PERMANOVA results showed diet (*P* < 0.05) and age (*P* < 0.05) effects with no interaction, and child sex was a significant confounder (*P* = 0.05) (**Supplemental Table 7**). Next, the diet effect on community structure at genus level within time was determined. **Figure 2** displays the first 2 components from PCA ordinations of genus data at 3, 6, 9, and 12 mo of age. Based on Bray-Curtis dissimilarities, in comparison with BF infants, SF infants had an altered microbial profile at all ages (**Figure 2A–D**). The

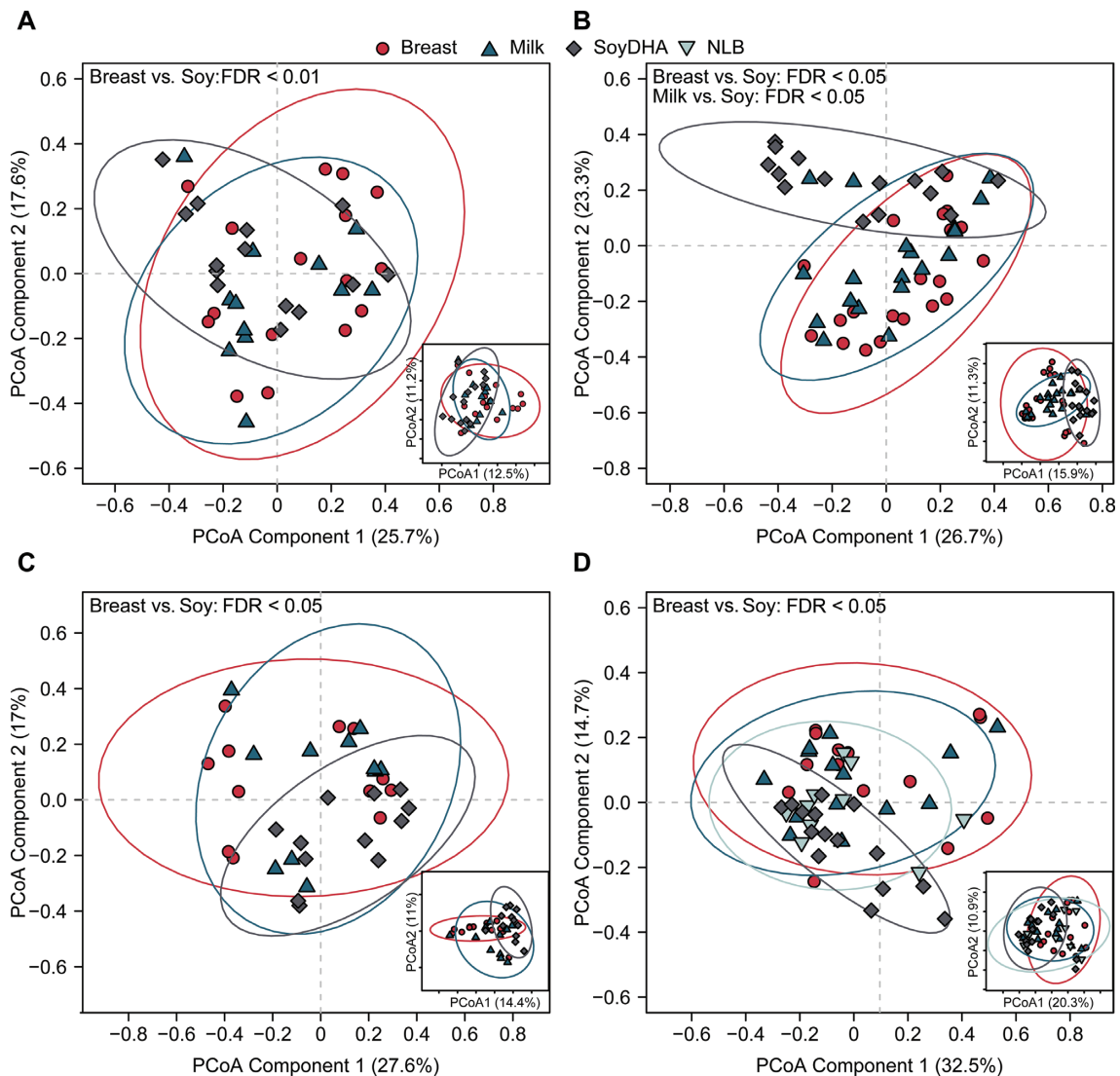


FIGURE 2 Visualization of β -diversity (between-sample diversity) by PCoA in infants consuming differential diets at 3 (A), 6 (B), 9 (C), and 12 (D) mo of age. Data generated from 16S ribosomal RNA amplicon sequencing on fecal samples. β -Diversity estimated by Bray–Curtis dissimilarities at both genus and OTU levels. The first 2 components of PCoA scores (i.e., individual samples) are displayed for genera (large plots) and OTUs (inserts). Confidence regions of group clusters are presented as 95% confidence ellipses based on Hotelling’s T2 statistic. Red circles indicate breastfed infants, dark blue triangles indicate cow milk formula-fed infants, grey diamonds indicate soy-formula-fed infants, and light blue upside-down triangles indicate infants that were no longer breastfeeding. Statistical difference in diet within an age group was assessed by pairwise comparison of diets by permutational multivariate ANOVA. P values were adjusted by FDR to control for the family-wise error rate. Sample numbers were $n = 10$ –20 per group and age. FDR, false discovery rate; OTU, operational taxonomic unit; PCoA, principal coordinate analysis.

distinguishing of SF infants was most apparent at 6 mo of age, where the microbial profile of SF infants was also altered when compared with MF infants (Figure 2B). There were no statistical differences between BF and MF infants at any ages. In addition, BF and MF were both different from SF at 3, 6, and 9 mo of age, whereas only BF was different from SF at 12 mo of age at OTU level (Figure 2).

Microbiota relative abundance is significantly altered in BF in comparison with FF infants

The significant differences in relative abundances of genera due to infant diet were determined with both

Kruskal–Wallis with post hoc Dunn’s test and Wald test from Deseq2 (Supplemental Tables 2, 3). *Bacteroides* and *Bifidobacterium* were the most abundant genera observed in all 3 diet groups at all ages (Supplemental Tables 2, 3). Table 3 presents the statistically significant differences obtained from both analyses. Diet-associated differences were consistent across multiple ages. *Bifidobacterium* was significantly different by diet at 3, 6, 9, and 12 mo of age. BF infants had a higher relative abundance of *Bifidobacterium* than did the SF infants. At 3 and 6 mo of age BF infants had lower abundance of unidentified genera from the Clostridiaceae family than did SF infants. An unidentified genus belonging to the Peptostreptococcaceae family was significantly lower in the BF than in the SF infants

TABLE 3 Median [IQR] percentage relative abundances of sequencing counts representing fecal bacterial genera at 3, 6, 9, and 12 mo of age from either BF, MF, NLB, or SF infants¹

Age	Genus	BF	NLB	MF	SF	FDR
3	<i>Bifidobacterium</i>	13.791 [10–33] ^a		24.195 [14–35] ^a	7.919 [2–12] ^b	0.021
3	f__Clostridiaceae	0.026 [0–0] ^a		0.279 [0–1] ^b	0.672 [0–3] ^b	0.002
3	f__Peptostreptococcaceae	0.053 [0–0] ^a		0.219 [0–1] ^a	2.225 [1–4] ^b	<0.001
3	f__Ruminococcaceae	0.087 [0–1] ^a		0.448 [0–1] ^b	2.081 [1–4] ^c	<0.001
3	<i>SMB53</i>	0.015 [0–0] ^a		0.057 [0–0] ^a	0.373 [0–1] ^b	<0.001
6	<i>Bifidobacterium</i>	23.625 [15–39] ^a		27.52 [12–34] ^a	3.361 [0–7] ^b	<0.001
6	<i>Coprococcus</i>	0.021 [0–0] ^a		0.293 [0–1] ^b	0.481 [0–2] ^b	<0.001
6	<i>Enterococcus</i>	0.044 [0–0] ^a		0.04 [0–0] ^a	0 [0–0] ^b	0.017
6	f__Clostridiaceae	0.024 [0–0] ^a		0.158 [0–1] ^{ab}	0.571 [0–5] ^b	0.007
6	f__Lachnospiraceae	0.115 [0–1] ^a		0.901 [0–2] ^b	4.17 [2–7] ^c	<0.001
6	o__Clostridiales	0 [0–0] ^a		0 [0–0] ^a	0.226 [0–0] ^b	<0.001
6	<i>Roseburia</i>	0 [0–0] ^a		0 [0–0] ^a	0.088 [0–2] ^b	0.013
6	<i>SMB53</i>	0.007 [0–0] ^a		0.071 [0–0] ^a	0.616 [0–1] ^b	<0.001
9	<i>Akkermansia</i>	0 [0–0] ^a		0.017 [0–0] ^b	0.107 [0–2] ^b	0.038
9	<i>Bifidobacterium</i>	17.951 [11–37] ^a		11.847 [10–30] ^a	6.065 [3–17] ^b	0.038
9	<i>Clostridium</i>	1.096 [0–4] ^a		0.047 [0–0] ^b	0.032 [0–0] ^b	0.026
9	f__Peptostreptococcaceae	0.064 [0–1] ^a		0.282 [0–1] ^a	2.447 [1–7] ^b	0.005
9	f__Veillonellaceae	0.027 [0–2] ^a		7.207 [1–18] ^b	0 [0–0] ^a	0.01
9	o__Clostridiales	0 [0–0] ^a		0 [0–0] ^a	0.228 [0–0] ^b	<0.001
9	<i>SMB53</i>	0 [0–0] ^a		0.076 [0–0] ^a	1.227 [1–2] ^b	<0.001
12	<i>Bifidobacterium</i>	14.202 [13–19] ^a	8.631 [4–12] ^{ab}	15.18 [6–22] ^a	4.604 [2–6] ^b	0.008
12	f__Lachnospiraceae	1.267 [1–2] ^a	1.473 [1–3] ^{ab}	2.894 [2–5] ^{bc}	3.836 [2–6] ^c	0.012
12	<i>Veillonella</i>	0.836 [0–4] ^a	0.415 [0–1] ^{ab}	0.36 [0–1] ^{ab}	0.25 [0–0] ^b	0.047

¹Featured genera were found to be significantly altered by diet by both Kruskal–Wallis and DESeq2 Wald assessments. Zeros indicate abundances of genera lower than the quartiles. See Supplemental Tables 4 and 5 for full assessments of each statistical output. Only the FDRs for the Kruskal–Wallis tests are provided. Groups with different letters differ according to Dunn’s test. Sample sizes range from 10 to 20 per diet group at 3, 6, 9, and 12 mo of age. BF, breastfed; FDR, false discovery rate; MF, cow milk–based formula; NLB, no longer breastfeeding; SF, soy-based formula.

at 3 and 9 mo of age. Another unidentified genus belonging to the *Clostridiales* order was of lower abundance in the BF and MF infants than in the SF infants at 6 and 9 mo of age. *SMB53* was significantly lower in the BF and MF infants at 3, 6, and 9 mo of age than in the SF infants. In addition, at 3 mo of age, in comparison with BF and MF, an unidentified genus in the Ruminococcaceae family was significantly enriched in the SF infants. At 6 mo of age, relative to the BF or MF infants, an unidentified genus in the Lachnospiraceae family, unidentified genera from the order Clostridiales, *Coprococcus*, and *Roseburia* were all higher in the SF infants. At 9 mo of age, an unidentified genus in the Veillonellaceae family was higher in MF infants than in the BF or SF infants. In addition, *Clostridium* was significantly higher in BF infants than in the MF or SF infants. Finally, at 12 mo of age in the BF, *Veillonella* was significantly higher whereas an unidentified genus in the Lachnospiraceae family was lower than in SF infants.

Breastfeeding alters the metabolite profile relative to formula feeding in infants through 1 y of life

Effects of dietary changes on the fecal metabolome within each time point were investigated using PCA. **Figure 3** displays the first 2 components within each age group. There was a significant effect of diet at 3, 6, and 9 mo within both principal component (PC) 1 and PC2 (**Supplemental Table 8**). The SF group is different than the BF and the MF infants at 3, 6, and 9 mo of age ($P < 0.001$). In order to determine differences due to diet within each age group, a Kruskal–Wallis test followed by post hoc (Dunn

test) analysis with the metabolites detected in negative or positive mode was performed. A large number of metabolites across all ages were found to be significantly affected by infant diet (**Supplemental Tables 4, 5**). **Table 4** provides a select number of these metabolites categorized by functional category determined by descriptions found in the Human Metabolome Database (34). Butyric acid is significantly higher in BF than in MF and SF infants. Tryptophan metabolism also appears to be affected by infant diet with significantly increased kynurenic acid in the BF compared with the MF and SF infants. Fecal dopamine and sphingosine were increased in the BF relative to the MF and SF infants. Not surprisingly, relative to BF or MF infants higher abundance of plant-based metabolites (jasmonic acid and genistein) were observed in SF infants. For the complete list of metabolites altered by early infant diet, please see Supplemental Tables 4 and 5, which display the negative and positive mode metabolite results, respectively.

The predictive metagenome analysis shows significant differences between BF and FF infants

Several microbial metabolic pathways were predicted to be differentially abundant in BF and FF infants across all the ages (**Supplemental Figures 1–7**). Relative to BF, porphyrin and chlorophyll metabolism of microbiota was higher in SF across all the ages, suggesting gut bacterial activity due to the soy diet. Glutathione metabolism was higher in BF microbiota than in FF infant microbiota at all ages. PICRUSt analysis provided predictive information of microbial metabolism but did not

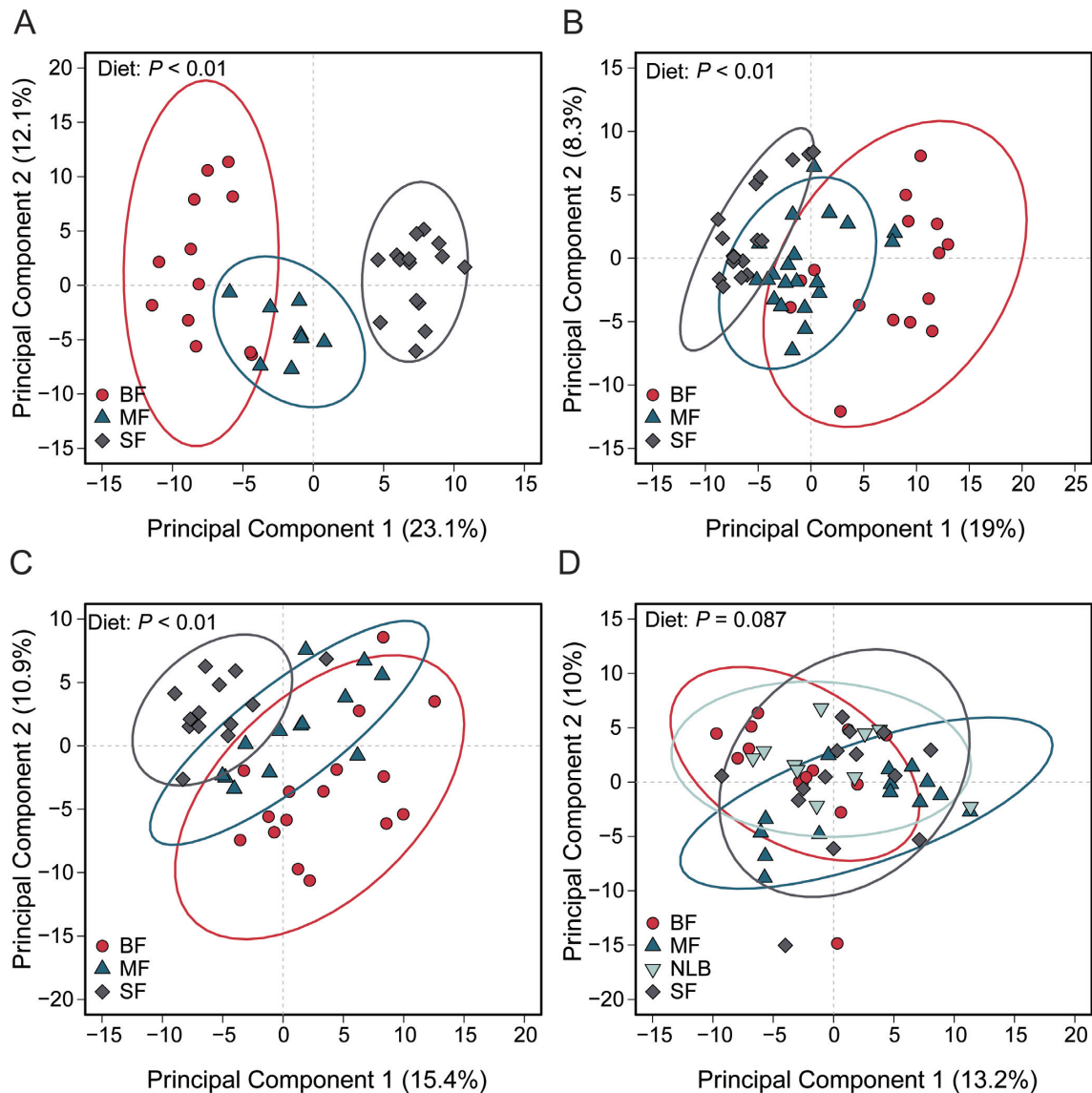


FIGURE 3 Visualization of variance associated with infant diet in fecal metabolomics data from infants consuming differential diets at 3 (A), 6 (B), 9 (C), and 12 (D) mo of age. Fecal metabolomics data were generated from LC-MS. Results from positive and negative modes were combined, log transformed, and scaled to unit variance before assessment by PCA. PCA scores (i.e., individual samples) for PCA components 1 and 2 are displayed. Confidence regions of group clusters are presented as 95% confidence ellipses based on Hotelling's T2 statistic. Red circles indicate BF infants, dark blue triangles indicate MF infants, grey diamonds indicate SF infants, and light blue upside-down triangles indicate NLB infants. Scores from PCA component 1 were assessed for differences in diet group by 1-factor ANOVA. Sample numbers were $n = 10\text{--}20$ per group and age. BF, breastfed; MF, cow milk formula fed; NLB, no longer breastfeeding; PCA, principal component analysis; SF, soy-based formula fed.

necessarily integrate the metabolite data, thus correlation analysis was conducted.

Fecal metabolites show significant association with microbiota in infants fed either breast-milk or formula diets

In order to examine global differences in fecal metabolites and their associations with the microbiota, PCA on metabolite data was performed across all age groups and correlated with CLR-transformed microbiome PCA data. A strong correlation was observed between the taxa in PC1 and the metabolites within PC1 (coeff. = -0.582 ; $P < 0.001$) (Figure 4). Some of the metabolites within PC1 that separated on the positive end included isovaleric

acid, valeric acid, indole-3-acetic acid, indole-3-propionic acid, and dopamine, whereas kynurenic acid and betaine appeared to separate out on the negative end (Supplemental Figure 8). Some of the bacteria that separated within PC1 on the positive side included *Bifidobacterium*, *Clostridium*, *Bacteroides*, *Streptococcus*, *Ruminococcus*, and an unspecified genus in the Enterobacteriaceae family, whereas on the negative end *SMB53* and unspecified genera in the Lachnospiraceae and Ruminococcaceae families and also genera in the Clostridiales order were observed (Supplemental Figure 9).

Next we performed an examination within each age group by correlating the metabolites found to be significant from the aforementioned Kruskal–Wallis and Dunn's tests to the

TABLE 4 Fecal metabolites and their associated functional metabolic categories at 3, 6, 9, and 12 mo of age from either BF, MF, or SF infants¹

Metabolite	Functional category	Diet effect	Month
Butyric acid	SCFA	BF > MF; BF > SF	3, 6, 9; 3, 6
Propionic acid	SCFA	BF < FF	3, 6
Isovaleric acid	SCFA	BF > FF	3, 6
Isobutyric acid	SCFA	BF < FF	3, 6
Dopamine	Neurotransmitter	BF > MF; BF > SF	3, 6, 9; 3, 6
D-sphingosine	Involved in immune cell trafficking	BF > FF	3, 6, 9
Kyneuric acid	Tryptophan metabolism	BF > FF	3, 6, 9
Indole-3-lactic acid	Tryptophan metabolism	BF > SF	3, 6
Indole-3-acetic acid	Tryptophan metabolism	BF > SF	3
Betaine	Helps reduce Th17 cells, IL-6 production	BF > FF	3, 6, 9
Genistein	Soy-derived isoflavone	BF, MF < SF	3, 6, 9
Jasmonic acid	Plant stress hormone	BF, MF < SF	3, 6, 9
3,5-Dihydroxybenzoic acid	Phenyl alanine metabolism in bacteria	BF > FF	9, 12
1-Methyluric acid	Microbial metabolite of methylxanthines	BF > FF	3, 6, 9
Azelaic acid	Plant product	BF, MF < SF	3, 6, 9, 12

¹See Supplemental Tables 6 (metabolites detected in positive ion mode) and 7 (metabolites detected in negative ion mode) for a complete list of the metabolites affected by diet. Statistical differences were assessed by Kruskal–Wallis test followed by correction for multiple comparisons using Benjamini and Hochberg's false discovery rate adjustment. The functional categories of the metabolites were obtained from the Human Metabolome Database. BF, breastfed; MF, cow milk-based formula; SF, soy-based formula.

CLR-transformed taxa. At 3 mo, genera from the family Clostridiaceae were positively correlated to dihydroferulic acid. In addition, genera from the family Ruminococcaceae were positively correlated to azelaic acid, gentisic acid, isocitric acid, sebacic acid, and syringic acid (Figure 5). Figure 6 displays the significant correlations at 6 mo of age at a cutoff of $P < 0.01$. Supplemental Figure 10 shows the full list of significant correlations. At 6 mo of age, there were multiple correlations between metabolites and bacteria that are also affected by diet. At 6 mo *Oscillospira* was negatively correlated with 3-hydroxybutyric-acid, hydroxy-hydrocinnamic acid (lower in SF than in MF and BF), and betaine (higher in BF than in MF and SF). Interestingly, at 6 mo of age *Oscillospira* was enriched owing to the formula diets (Supplemental Table 3). All 3 diet groups were different from each other and the *Oscillospira* abundance was highest in the SF and lowest in the BF infants (Supplemental Tables 2, 3). *Bifidobacterium*, which was found to be significantly less abundant in the SF than in the MF and BF infants, but not different between the MF and BF infants (Supplemental Table 2), was negatively associated with 5-hydroxytryptamine and inosine at 6 mo. These metabolites were higher in the SF than in the MF or BF infants (Supplemental Tables 4, 5). An unspecified genus in the Clostridiales order that was enriched in the SF group was positively associated with azelaic acid (higher in SF than in MF and BF at all ages).

At 9 mo of age *Ruminococcus* and genera in the Lachnospiraceae family were negatively associated with hexadecanoic acid (data not shown). Interestingly, only Lachnospiraceae was significantly higher in SF than in BF or MF infants (Table 3). At 12 mo of age, genera in the Lachnospiraceae family were negatively associated with hydroxyphenyllactic acid (Figure 7). See Supplemental Table 9 for all the quantitative data on correlations.

Discussion

This study investigated the role of neonatal diet on fecal microbiota and metabolite profile during the first year of life.

The novel aspect of our study includes 1) fecal metabolite assessment from infant groups fed 3 neonatal diets through the first year of life and 2) association of metabolites to microbiota profiles to determine the host–microbiota crosstalk with different neonatal diets. Significant differences in bacterial diversity and abundance due to infant diets were observed at multiple ages, similar to previous publications (8, 35). Specifically, BF infants showed the lowest α -diversity measurements in comparison with both groups of FF infants. Previously, a study by Baumann-Dudenhoefter et al. (36) investigated microbiota differences between breast milk, cow milk formula, and soy formula from 0 through 8 mo of age and found similar results in which the SF group had the highest α -diversity. In the same line, the current study showed that the SF group has higher bacterial diversity and a greater number of altered metabolic pathways than have the BF and MF groups, suggesting that the components of neonates' diet uniquely promote microbiota growth and development. At 3, 6, and 9 mo of age, a large proportion of the total genera consisted of *Bacteroides* and *Bifidobacterium*. Interestingly, higher abundance of *Bifidobacterium* at 5–16 wk of age showed a positive association to bacille Calmette–Guérin, tetanus toxoid, and polio vaccine-specific response at 2 y of age (37). At 12 mo of age the proportion of *Bacteroides* increased and *Bifidobacterium* decreased in this study. Studies from different cohorts across the world have reported that some BF infants tend to have higher *Bacteroides* than *Bifidobacterium* (8, 38–43). Interestingly, *Bacteroides* spp. utilize human milk oligosaccharides (44). These shifts in microbiome correspond to what has previously been described in the literature, in which large changes are in part due to the human milk oligosaccharides used by *Bacteroides* and also the introduction of solid food (44–47).

Our group has published studies on the effect of infant formulas, both soy and dairy based, on the microbiota and immune system within a piglet model (48). The soy group was found to have higher relative abundances of *Bilophila*, *Ruminococcus*, and *Clostridium*. However, how SF affects microbiota development in infants has not been thoroughly

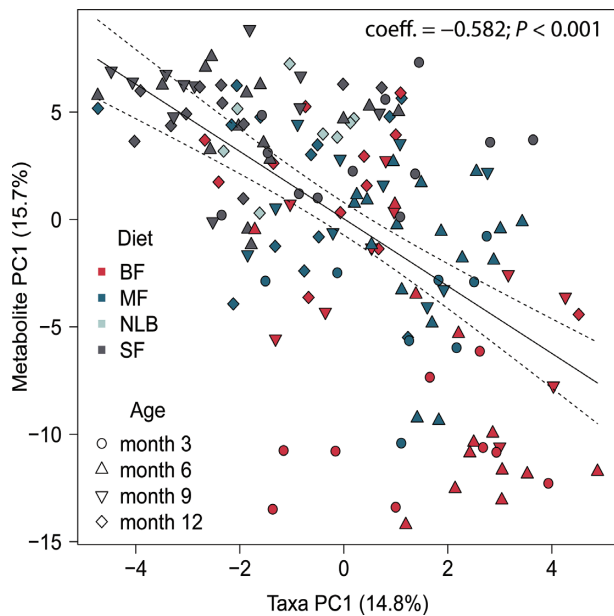


FIGURE 4 Correlation between fecal microbiota and metabolome in infants consuming differential diets at 3, 6, 9, and 12 mo of age. Genus-level microbial sequencing data and metabolomics data were assessed separately by PCA. Before PCA, sequencing data were transformed by center-log ratio to ensure the data were linearly related, whereas metabolomics data were log transformed and scaled to unit variance. PCA scores (individual samples) were plotted along components 1 and 2 and variation associated with diet was determined along the first components in both PCAs. The percentage explained variance for each component is provided in parentheses. The shapes of the PCA scores represent age (3 mo: circle; 6 mo: triangle; 9 mo: upside down triangle; 12 mo: diamond) and colors represent diet (red: BF; blue: MF; light blue: NLB; grey: SF). The linear relation between the first components for the microbial and metabolomics PCA is shown. The solid line is the best-fit line whereas the dotted lines represent 95% CIs. Pearson's r coefficient and P value are provided in the figure. Sample numbers were $n = 10$ – 20 per group and age. BF, breastfed; MF, cow milk formula fed; NLB, no longer breastfeeding; PC, principal component; PCA, principal component analysis; SF, soy-based formula fed.

investigated. In the current study, an unidentified genus from Ruminococcaceae was enriched in the SF group compared with the MF and BF groups at 3 mo of age. In addition, unidentified genera in the *Clostridiales* order were higher in the SF group than in the MF or BF groups at 6 and 9 mo of age, supporting previously observed data from the animal model. Thus, both the neonatal piglet model and the data from this study suggest that the components of soy formula may differentially affect gut microbiota and metabolism.

Infant nutrition strongly influences the gut environment during infancy, which in turn modulates the developing immune system. Indeed, human milk oligosaccharides have been shown to improve epithelial barrier function and alter microbiota profile and SCFA production in vitro (49). In our study, the levels of butyric acid present in feces of BF infants were higher than in FF infants. Butyric acid has been shown to increase Treg cell production in the colon and periphery (50–52) and reduced levels of butyrate increase salmonella infection in the gut (14). In addition, D-sphingosine, the precursor of sphingosine 1-phosphate (which regulates immune cell trafficking) (53) and related microbial metabolic pathways such as the glycosphingolipid biosynthesis series, was significantly higher in BF infants than in both

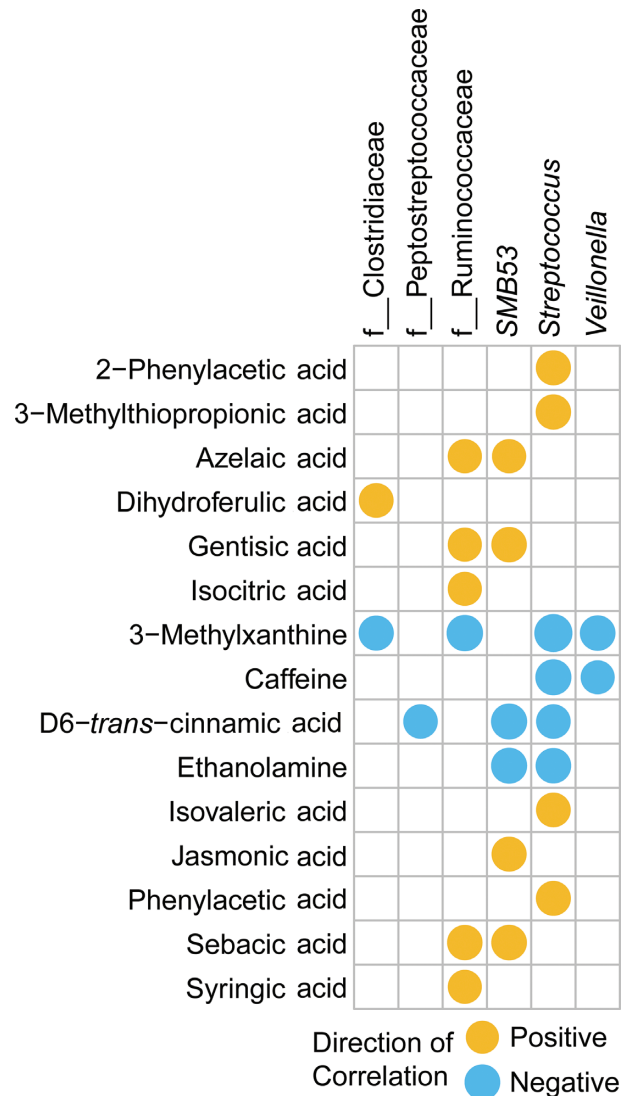


FIGURE 5 Correlation heatmap of genera and metabolites from infants fed either breast milk, milk-based formula, or soy-based formula at 3 mo of age ($n = 161$). Circles represent significant Pearson's correlations (FDR-adjusted P values < 0.05). Orange circles indicate positive relations and blue circles indicate negative relations. Supplemental Table 9 gives Pearson's r coefficients, raw P values, and FDR-corrected P values of significant correlations. FDR, false discovery rate.

FF groups, suggesting an advantage to BF infants in fighting infections during the infancy period. Furthermore, in the current study betaine was significantly higher in BF than in both groups of FF infants. This is an important observation because betaine has been shown to inhibit dendritic cell inflammatory cytokine production (IL-6) and Th17 differentiation (54), suggesting a role for T cell function in BF relative to FF infants. In our study, *Bifidobacterium* was significantly higher in BF than in SF infants. A high prevalence of *Bifidobacterium* has been shown to be negatively correlated with the acquisition of antimicrobial-resistant genes (55). The microbiota of infants has been shown to influence sensitization to atopy. Fujimura et al., study grouped infants by risk of atopy (3). Infants grouped into the highest risk of atopy had lower abundances of *Bifidobacterium*, *Akkermansia*, and *Faecalibacterium*. When adult-population of T-cells were

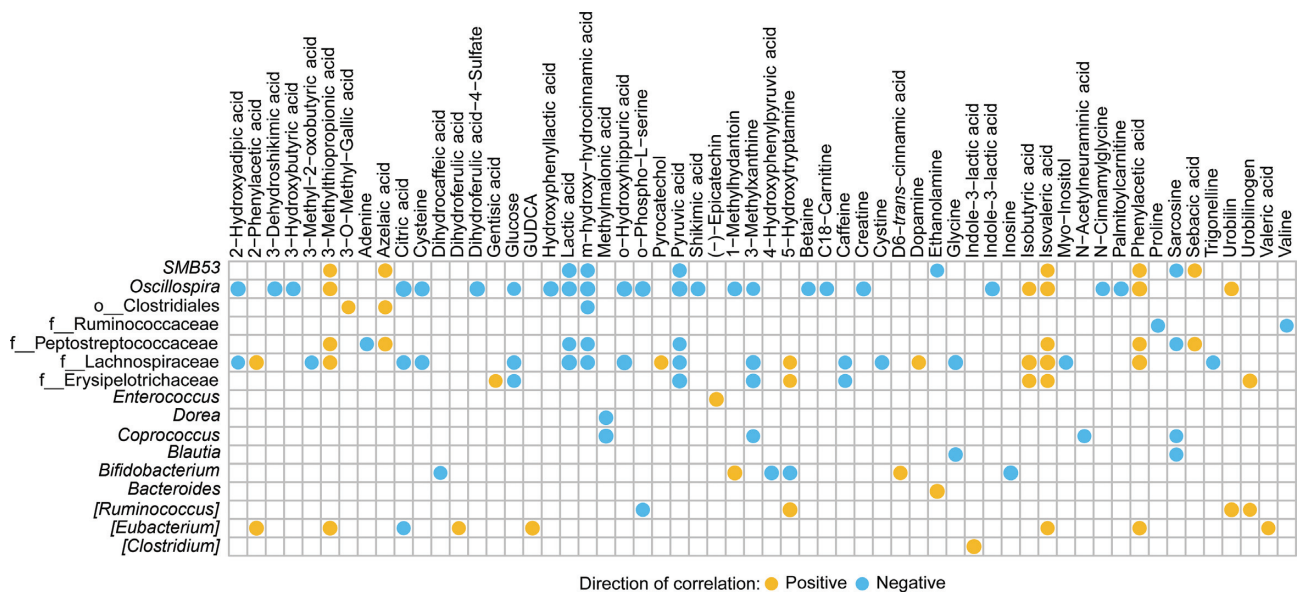


FIGURE 6 Correlation heatmap of genera and metabolites from infants fed either breast milk, milk-based formula, or soy-based formula at 6 mo of age ($n = 160$). Circles represent significant Pearson's correlations (FDR-adjusted P values < 0.05). Orange circles indicate positive relations and blue circles indicate negative relations. Supplemental Table 9 gives Pearson's r coefficients, raw P values, and FDR-corrected P values of significant correlations. FDR, false discovery rate; GUDCA, glycoursoxycholeic acid.

cultured with fecal water containing the fecal material from this high-risk group, the cells displayed higher concentrations of IL-4 (implicated in inflammation) expression and lower differentiation into the T regulatory (CD25+ FOXP3+) phenotype (3), suggesting again benefits of *Bifidobacterium* in BF infants. Serum and urine metabolites after breastfeeding or formula feeding in rhesus macaques have been previously investigated (15). In this

model, microbiota and metabolites were altered as seen using PCA plots, and separation by feeding method was observed at 2 wk. FF monkeys had higher urine and serum galactose and amino acid levels (15). In support of this notion, our results highlighted that breastfeeding induced greater numbers of microbial genes related to D-glutamine and D-glutamate metabolism; cysteine and methionine metabolism; valine, leucine, and isoleucine biosynthesis; tyrosine metabolism; and tryptophan metabolism. These results highlight that gut microbiota and metabolites produced by bacteria can play a role in the developing immune system.

The kynurenine pathway for tryptophan metabolism has been implicated in developing tolerance within the immune system (56). Along with kynurenic acid, changes in tryptophan-related metabolites were observed that were due to the infant diet. Kynurenic acid, indole-3-lactic acid, and indole-3-acetic acid were increased in BF compared with FF infants. In vitro models have shown that both kynurenic acid and synthetic analogs influence the expression of inflammatory and noninflammatory cytokines, albeit differently depending on the type of infection investigated (56). When monocyte cells were infected with heat-inactivated *Staphylococcus aureus*, there was attenuated TNF- α (inflammatory) secretion and increased tumor necrosis factor-stimulated gene-6 (TSG-6) mRNA (anti-inflammatory) expression. A similar phenotype was seen in *Chlamydia pneumoniae*-infected cells with kynurenic acid, but not the synthetic analog (57). Thus, differences in these metabolites may have functional consequences for the developing immune system and, further, allergy outcomes (56). Within this study, multiple metabolites were altered by neonatal diet, suggesting metabolite-mediated communication with the microbiota and the immune system possibly affecting cellular mechanisms in the gut and other organs.

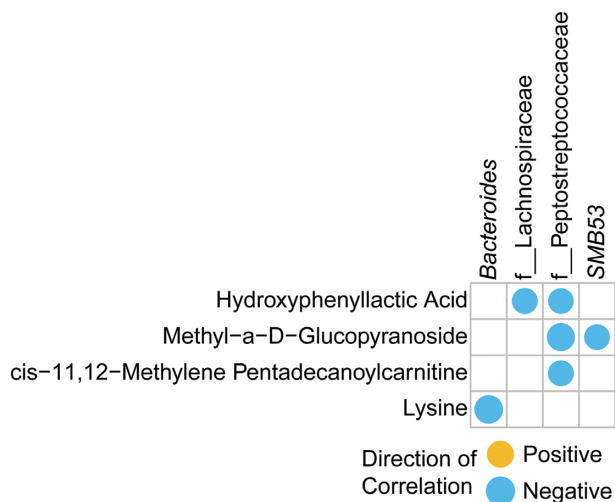


FIGURE 7 Correlation heatmap of genera and metabolites from infants fed either breast milk, milk-based formula, or soy-based formula at 12 mo of age ($n = 72$). Circles represent significant Pearson's correlations (FDR-adjusted P values < 0.05). Orange circles indicate positive relations and blue circles indicate negative relations. Supplemental Table 9 gives Pearson's r coefficients, raw P values, and FDR-corrected P values of significant correlations. FDR, false discovery rate.

Limitations

It is important to note that different species of *Bifidobacterium* and *Bacteroides* colonize the guts of BF and FF infants. Within this study, the relative abundance of *Bifidobacterium* between the BF and MF infants was not different and no significant effect of diet was observed on *Bacteroides* abundance. However, the species-level differences were not captured due to the limitations of 16S rRNA sequencing. The other limitations include lack of data on mode of delivery, weight gain, and perinatal consumption of probiotics/antibiotics. These factors can influence the microbiota composition. These data are a secondary analysis of a clinical cohort, and the same subjects were not available at all the time points to enable longitudinal assessments of microbiota and metabolites. Furthermore, the absence of breast-milk samples limited our ability to determine mothers' secretor or nonsecretor status, as well as the possible association of secretor status with microbiota composition. Nonetheless, this work further demonstrates the large influence infant diet has on the developing microbiota and metabolome through the first year of life.

Future mechanistic studies are needed to determine the role of components of breast milk, microbiota, and specific gut-derived metabolites on regulating the developing infant's immune and other physiological systems.

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The authors' responsibilities were as follows—LY: designed the research; LRB, BDP, and AE: conducted the data analysis; LB and LY: wrote the manuscript; AKB and KSM: conducted technical aspects of the research; SVC and KS: acquired the microbiota data; LP, SHA, and KEM: generated the metabolomics data; TMB and AA: were principal investigators of the Beginnings cohort; LY: had primary responsibility for the final content and for editing the manuscript; and all authors: read and approved the final manuscript. The authors report no conflicts of interest.

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