Patterned progression of gut microbiota in association with preterm infants to necrotizing enterocolitis and late onset sepsis: prospective pilot data from a non-Western population

Jiayi Liu[1], Jianhua Sun[2], Yuqing Li[3], Yi Feng[4], Liya Pan[5], Zhoulonglong Xie[6], Zhilong Yan[7], Jianhua Zhao[8], and Li Hong[9]

[1]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[2]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[3]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[4]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[5]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[6]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[7]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**
[8]**Shanghai Majorbio Bio-Pharm Technology Co., Ltd, Shanghai, China**
[9]**Department of Clinical Nutrition, Shanghai Children's Medical Center, School of Medicine Shanghai Jiao Tong University, Shanghai, China**

Corresponding author:

Li Hong[9]

Email address: hongli@scmc.com.cn

ABSTRACT

Background and Objectives

Recent studies associate intestinal microbiota dysbiosis with necrotizing enterocolitis(NEC) and late onset sepsis(LOS) preterm infants in western countries. To date, there is no report of similar studies performed among non-Western population. In this pilot study, we profiled gut microbiota of NEC and LOS patients from birth to deceased or discharged.

Methods

We enrolled preterm infants with gestational age less than 33 weeks and birth weight more than 950g, from July 2013 to December 2014. We began fecal sample collection from the meconium until death or discharge, whichever came first. Bacterial V3 V4 region of 16s rRNA genes from each stool sample were amplified and pyrosequenced. With the use of RM two-way ANOVA and Zero-Inflated Beta Random Effect models to account for repeated measures, we found out the development of NEC or LOS associated with gut bacterial communities.

Results

A total of 192 fecal samples from 24 patiens were studied, of whom four developed NEC, three LOS; the remaining 17 were used as controls. The microbial community struture in stool samples from both case groups differed significantly from those in controls stools. The divergence emerged after three days of life. In the random effect model, the time-by-onset interaction is posi[The post-partum gut microbiota colonization started to diverge among NEC, LOS and their matched control groups, from the second week after birth. Microbiota of the LOS infants was the least diversified (Shannon index=1.66), while that of the control group was the most diversified(Shannon index=0.88, p=0.01). Potentially pathogenic genus Enterococcus (20.86%) and Staphylococcus (8.67%) were prominent in NEC patients and Klebsiella (42.15%) in LOS group. Both two groups addressed lower proportion of Lactococcus (7.98% and 13.76% in NEC and LOS group, respectively) than the control group (3.66%)].

Conclusions

post-partum colonization pattern of gut microbiome might predispose preterm newborns to NEC or LOS, in which reduced diversity of the whole microbiota community and potentially pathogenic genus could have played an essential role in disease progression. Still, more studies are needed to identify etiological strains, underlying mechanisms and correspondent microbial patterns.

INTRODUCTION

Gut microbiota is a key contributor to human health and its dysbiosis has been proven to be associated with various diseases, such as atherosclerosis(Tang et al., 2017), obesity(Bouter et al., 2017), neuropathy(Sarkar et al., 2016), liver diseases(Tilg et al., 2016), etc. Temporal colonization pattern of the intestinal microbiota during early stages of life also provided evidence of its association with early life events, including Type 1 diabetes(Giongo et al., 2011; Vatanen et al., 2018), asthma(Stokholm et al., 2018) and allergy(Madan et al., 2012; Savage et al., 2018).

In preterm infants, perturbations in intestinal microbiota establishment during early stage of life, characterized by fewer observed species, less diversity, higher variability and more abundant potential pathogens such as *Escherichia coli*, *Enterococcus* sp., and *Klebsiella pneumoniae* (Schwiertz et al., 2003; Bezirtzoglou et al., 2011), are prevalent due to minimal contact with the birth canal microbes, high rates of broad-spectrum antibiotics usage, lack or delay in enteral feeding, being nursed inside a steril incubators where daily contact to human skin microbes is limited(Deweerdt, 2018). It may then initiate a cascade ????As as result, microbiota harboring abnormalities has been implicated as a key factor to the vulnerabilities to preterm-associated health consequences, such as necrotizing enterocolitis and late-onset sepsis.

Necrotizing enterocolitis, characterized by unpredictive, rapid progression, high morbidity and mortality, threatens mostly in preterm newborns; its etiologies remains elusive. Previous studies conducted in the US, Europe have suggested intestinal microbiota dysbiosis implicated in the condition. Several studies in Europe and the US have suggested that NEC is associated with both reduction in microbiota diversity and unusual microbial composition colonization(Jacquot et al., 2011; Warner et al., 2016). So far, there is no consensus as to the causative species in this condition. Studies reported phyla Proteobacteria increase and Firmicutes decrease before NEC onset(Mai et al., 2011; Zhou et al., 2015). Bloom of *Gammaproteobacteria* and under-representing in *Negativicutes* was in chronological association with the condition(Warner et al., 2016).

83 #% early pattern a/w LOS LOS is another major contributor to neonatal morbidity and mortality
84 among preterm infants.
85 However, no relevant studies have analysed sequences from non-western infants population. Hence, we
86 conducted this prospective study in Chinese preterm infants, with the aims to identify whether intestinal
87 microbiota dysbiosis precedes and therefore, may cause NEC or LOS.

METHODS

Ethics

90 This study was approved by the joint committee of ethics of Shanghai Children's Medical Center, School
91 of Medicine Shanghai Jiao Tong University (SCMCIRB-K2013022). Detailed written informed consent
92 was obtained from patients' parents before enrollment.

Patients

94 Newly born preterm infants with gestational age less than 33 weeks, birth weight over 950g were
95 enrolled from Neonatal Intensive Care Unit at Shanghai Children's Medical Center from July 2013 to
96 December 2014. The exclusion criteria were 1) diagnosed with early-onset sepsis, 2) hepatic diseases,
97 3) renal impairment (Cr >88 μM), 4) diagnosed with intestinal obstruction, 5) in foreseeable need of
98 cardiovascular or abdominal surgeries (except for male circumcision or PDA ligation), 6) estimated
99 parenteral support to supply over 50% of daily caloric intake for more than four days, 7) given intravenous
100 antibiotics administration (except prophylactic regimen of cefotaxime, piperacillin-tazobactam and/or
101 metronidazole), 8) history of oral antibiotics administration, 9) grossly bloody stools at admission, and
102 10) over five days old.
103 NEC cases were defined as infants who met the criteria for Stage II and Stage III NEC diagnosis(Bell
104 et al., 1978), including radiographic intestinal dilation, ileus, pneumatosis intestinalis, and/or absent bowel
105 sounds with or without abdominal tenderness, and/or mild metabolic acidosis and thrombocytopenia. LOS
106 cases was diagnosed if 1)an infant had a positive hemoculture or other suspicious loci of infection after
107 72 hours of life, with septic signs/symptoms reviewed independently by at least two neonatologists, and
108 had been treated with advanced antibiotics (e.g., Meropenem) after diagnosis. Infants with no infectious
109 complications or sepsis were regarded as controls.

Sample collection and handling

111 Fecal samples collection began from neonatal meconium till discharge. Although we intended to collect
112 fecal samples on a daily basis, due to working shifts and flexible clinical scheduling, we set seven days as
113 the maximum interval between two collections from every infant. Every sample was collected within 30
114 minutes of defecation from infants' diaper with a sterile spatula. The samples were immediately placed in
115 a cryogenic vial on dry ice and stored at 80°C within 30 minutes without additives. All samples were
116 collected and stored before knowing the diagnosis of respective patients.

DNA extraction and quality control amplification and 16s rRNA gene sequencing

118 Microbial genomic DNA was isolated from each fecal specimen using the E.Z.N.A.® Soil DNA Kit
119 (Omega Bio-Tek, Norcross, GA, U.S.) according to manufacturer's protocols. The concentration and
120 purity of the DNA were determined by NanoDrop 2000 UV-vis spectrophotometer (Thermo Scientific,
121 Wilmington, USA), and the DNA quality was checked by 1% agarose gel electrophoresis.

Broad-range PCR and High-throuput Sequencing of 16s rRNA gene amplicons

123 The V3-V4 hypervariable regions of the bacterial 16S rRNA gene were amplified from each sample using
124 bacterialarchaeal primers 338F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGG
125 GTWTCTAAT-3') using thermocycler PCR system (GeneAmp 9700, ABI, USA). The PCR reactions
126 were as follows: 3 min of denaturation at 95 °C, 27 cycles of 30 s at 95 °C, 30 s annealing at 55 °C and
127 45 s elongation at 72 °C, and a final extension at 72 °C for 10 min. The PCR reactions were performed in
128 triplicate, with each 20 μL mixture containing 4 μL 5X FastPfu Buffer, 2 μL 2.5 mM dNTPs, 0.8 μL
129 of each primer (5 μM), 0.4 μL FastPfu Polymerase and 10 ng template DNA. The PCR products were
130 extracted from a 2% agarose gel and further purified using the AxyPrep DNA Gel Extraction Kit (Axygen
131 Biosciences, Union City, CA, USA), and quantified using QuantiFluor™-ST (Promega, USA) according
132 to the manufacturer's protocols.

Equimolar amounts of purified amplicons were pooled and pairedend sequenced (2 x 300) on an Illumina MiSeq platform (Illumina, San Diego, USA) according to the standard protocols of Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai, China). The reads were de-multiplexed using the Illumina software and separate FASTQ files were generated for each specimen and deposited to the Sequence Read Archive NCBI under the BioProject accession PRJNA470548. Another public archive repository is available at figshare doi: 10.6084/m9.figshare.7205102

Raw Data Processing

Raw data was processed according to the standard protocols provided by Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai China) as previously described(Liu et al., 2018; Wang et al., 2018). In short, the protocols are as the followings: After pyrosequencing, de-multiplexed sequence reads were subjected to quality filtering utilizing Trimmomatic software(version????)(Bolger et al., 2014), and were truncated at any site with an Phred score <20 over a 50bp-sized window; barcode matching with the primer mismatch from 0 to 2 nucleotides was adopted and reads containing ambiguous characters were removed. After trimming, FLASh(Fast Length Adjustment of Short Read)(Magoč and Salzberg, 2011), a read pre-processing software, assembled and merged the paired-end reads from fragments and generated >10 bp overlapped, with the dead match ratio 0.2. Unassembled reads were discarded.

To fairly compare all the samples at the same sequencing depth, the "sub.sample" command of mothur program(version1.30.1)(Schloss et al., 2009) was used for normalization to the smallest sample size. UCHIME Algorithm detected chimeric sequences, removed chimera to obtain effective reads, which were then sorted by cluster size and processed using Operational Taxonomic Units(OTUs) with 97% similarity cutoff UPARSE-OTU algorithm (implementing "cluster_otus" command)(Edgar, 2013) in USEARCH(v10)(UPARSE version 7.1). The taxonomy of each 16S rRNA gene sequence was analyzed by RDP Classifier algorithm(Wang et al., 2007) against the Silva (SSU128)(Quast et al., 2012) 16S rRNA database using confidence threshold of 70%. Each sequence was assigned the taxonomy by QIIME(Caporaso et al., 2010). The representative sequences were allocated phylogenetically down to the domain, phylum, class, order, family, and genus levels. The relative abundance of a given taxonomic group was calculated as a percentage of the sequences number belonging to that group devided by the total number of obtained sequences.

Within-sample diversity(alpha diversity) analysis, including Shannon index and Observed species richness (sobs), were obtained using the "summary.single" command of mothur program(version1.30.1)(Schloss et al., 2009). Between-sample diversity(beta diversity) analysis was obtained estimating weighted UniFrac distances between samples.

Statistical and Bioinformatics Analysis

Demographics and Clinical Sample comparisons

Kruskal-Wallis test and Wilcoxon rank-sum test were used to identify statistically significant differences in continuous variables ,including gestational age, birth weight, age when the patients were diagnosed and length of hospitilization. The χ^2, or Fisher's exact test were used to identify differences in gender composition. α level was considered 0.05 for all statistical tests . All statistical test not involving microbiome 16s rRNA sequencing data was performed using *"stats"* package using R(v.3.5.1).

Microbiota and Bioinformatics Analyses

Disease-related Time Interval Definition   Under the circumstance that the sampling and disease onset timepoints for each patient were not perfectly universal, to illustrated the continuous longitudinal and repeated nature of the sampling and its relationship with onset and progression of diseases, we splitted the whole sampling span into 7 time intervals:

1. early post-partum(EPP): within 3 days afterbirth
2. early pre-onset(EPO): from the end of EPP to at least four days before disease onset
3. late pre-onset(LPO): from the end of EPO to the start of onset; for control group patients, the onset time is set at 16 days of life, as is the average diagnosis age of NEC and LOS groups.
4. early disease(ED): first third interval of whole disease span
5. middle disease(MD): second third interval of whole disease span
6. late disease(LD): last third interval of whole disease span
7. post disease(PD): from the end of disease to discharge time-point

Diversity Analyses The average of α diversity, if more than two were available within one analysis interval, of each patient was calculated. Kruskal Wallis tests were used to test shannon diversity differences either among groups within a time interval or among time intervals within a certain group. Repeated measures two-way ANOVA, with time intervals(EPP, EPO, LPO, ED, MD, LD, PD) as a within-subject factor and groups (NEC, LOS, control) as a between-subject factor) and Sidak's multiple comparisons test was used to test time-with-disease shannon diversity changes.

Modeling Strategies for Taxonomy Comparisons To compare the dynamics of microbiota diversity and relative taxonomic abundance preceding the disease, we took into account the EPP, EPO, LPO and ED interval among all patients and fit(Supplemantary matrix1). To compare the microbiome profile right after birth until disease alleviation, we selected EPP, EPO, LPO, ED, MD and LD interval of NEC and LOS patients(Supplementary matrix2 dataset). The average taxonomy relative abundances, if more than two were available within one analysis interval, of each patient was calculated. Zero-Inflated Beta Regression Model with Random Effects (ZIBR) and Linear Mixed-effects Model(LME) were used to test the association between OTU relative abundance and clinical covariates (diseases-related time intervals) for longitudinal microbiome data (Chen and Li, 2016). *ZIBR* and *nlme*(Pinheiro et al., 2018) R packages were utilized for each model.

Figures were generated with the *"ggpubr"*(Kassambara, 2017) and *"ggplot2"*(Wickham, 2016) packages using R(v.3.5.1). Scripts for modeling and figures plotting, input and output files, figures are available at our github repository.

Scripts and Figures Archiving

Figures were generated with the *"ggpubr"*(Kassambara, 2017) and *"ggplot2"*(Wickham, 2016) packages using R(v.3.5.1); Scripts for data analysis are available at our github repository

RESULTS

Overall 16s Sequencing Report and Coverage

A total of 7,472,400 optimized V3-V4 tags of 16s rRNA gene sequences were produced from 192 fecal samples, with an average read length of 448 bp (Table S1).

Patients characteristics

Totally 130 infants met the criteria of our study, and 1698 samples were collected from them in the neonatal intensive care unit (NICU) at Shanghai Children's Medical Center from July 2013 to December 2014. Among whom, we studied 192 fecal samples from 24 well-sampled preterm infants, including four subsequently diagnosed with NEC (2 in stage IIA and 2 in stage IIB), three with LOS, and 17 matched controls (Figure1 ,Supplemantary Table S2). Fecal samples were collected between days 1 and 69 of life. Sampling timepoints and numbers of samples varied among each infant.
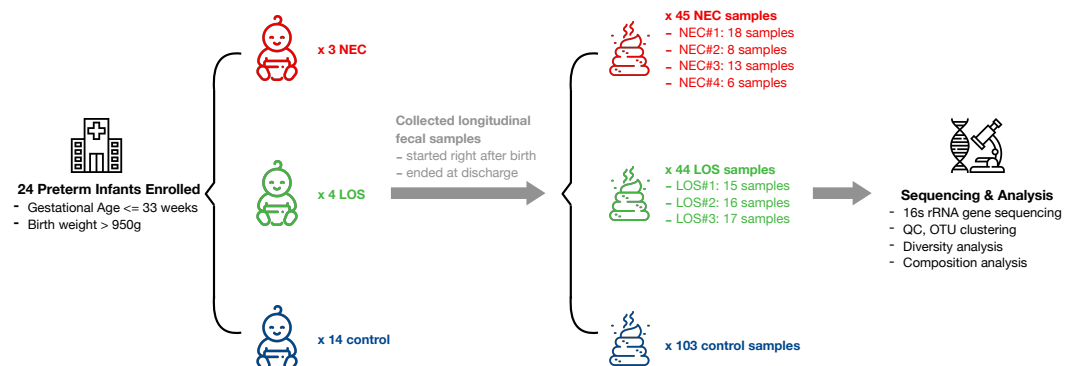

Figure 1. Flow of Study Design

All infants were delivered by cesarean section and fed on infant formula. No one was prescribed probiotics during hospitalization. Comparisons showed no significant difference in terms of gestational age, birth weight and gender proportions, diagnosed age among three groups (Table 1). Length of stay among three groups was significantly different however rational since NEC and LOS patients usually require longer period of healthcare because their worse health status often required longer health care time than the control group. All infants were delivered by cesarean section and fed on infant formula. No one was prescribed probiotics during hospitalization.

Table 1. Demographic characteristics of Preterm NEC, LOS and control groups.

	NEC (N=3)	LOS (N=4)	Control (N=17)	Statistical Test	*p value*
Gestational Age (weeks)	29(29-30)	30(29-31)	31(28-33)	Kruskal-Wallis test	0.074
Birth Weight(g)	1416.3 (773.4-2149.1)	1141.7 (633.4-1649.9)	1527.4 (1391.6-1663.1)	Kruskal-Wallis test	0.111
Gender				Fisher's exact test	0.82
Female	3(75%)	2(67%)	9(53%)		
male	1(25%)	1(33%)	8(47%)		
Diagnosis Age(days)	16(11-19)	16(10-22)	—	Wilcoxon rank-sum test	0.629
Length of Stay(d)	54.3 (13.5-95.0)	60.0 (24.8-95.2)	32.9 (26.3-39.5)	Kruskal-Wallis test	0.046
Number of Samples	46	42	103	—	—

Dynamics of Microbiome Diversity in diseases onset and progression

Mircobiome Richness Played Minor Roles

Overall, all three groups shared similar microbiota richness trend after birth, that the observed richness (Sobs) decreased significantly from post-partum period until the late disease stage (Fig2a. NEC group, p = 0.044; b. LOS group, p = 0.013; c. control group, p <0.01; supplemantary!!! rm-matrix1-sobs, two way RM ANOVA, p <0.0001). Nevertheless, the inter-time-interval comparison among groups (supplementary sobs-time-group!!!!!) didn't show any significant alterations and differences in sobs, indicating the minor effect of microbiota richness on the diseases acquisition.

Recession of Mircobiome Evenness Preceded NEC and LOS

Although, microbiota communities evenness among all patients, reflected by shannon diversity indices, tended to decrease after birth(Fig3, supplemantary!!!! rm_matrix1_shannon, p <¡0.0001), the shannon index of the NEC and LOS groups, from the early pre-onset interval to early disease decreased significantly (Fig3a.NEC group, early pre-onset = 1.92, early disease = 0.58, p = 0.04, b. LOS group, early pre-onset = 2.47, early disease = 0.47, p = 0.01), while the control group did not show the similar trend (Fig3c.control group, early pre-onset = 1.81, early disease =1.00, p = 0.05).
The inter-time-interval comparison among three groups showed signifant shannon index divergent during during early pre-onset interval (two way RM ANOVA, p = 0.0017 supplementary!!!) and the early disease stage(Fig4, p = 0.0037), implying the role of microbiota distortion in triggering NEC and LOS. As infants aged, two disease groups showed a non-significant difference in community evenness(Fig4 facet "middle disease", p = 0.034), indicating a similar community distribution pattern in both NEC and LOS development. Furthermore, alleviation of both diseases restored the microbiota evenness back to the level during early pre-onset interval (Fig3 a. NEC, early pre-onset vs. post disease, p = 0.79; b. LOS, early pre-onset vs. post disease, p = 0.16).

Kinetics of Microbiome Composition

To evaluate time-wise differences in beta-diversity between the microbiomes, we applied Principal Component Analysis (PCoA) to weighted UniFrac distance metric matrices, considered by timer intervals.
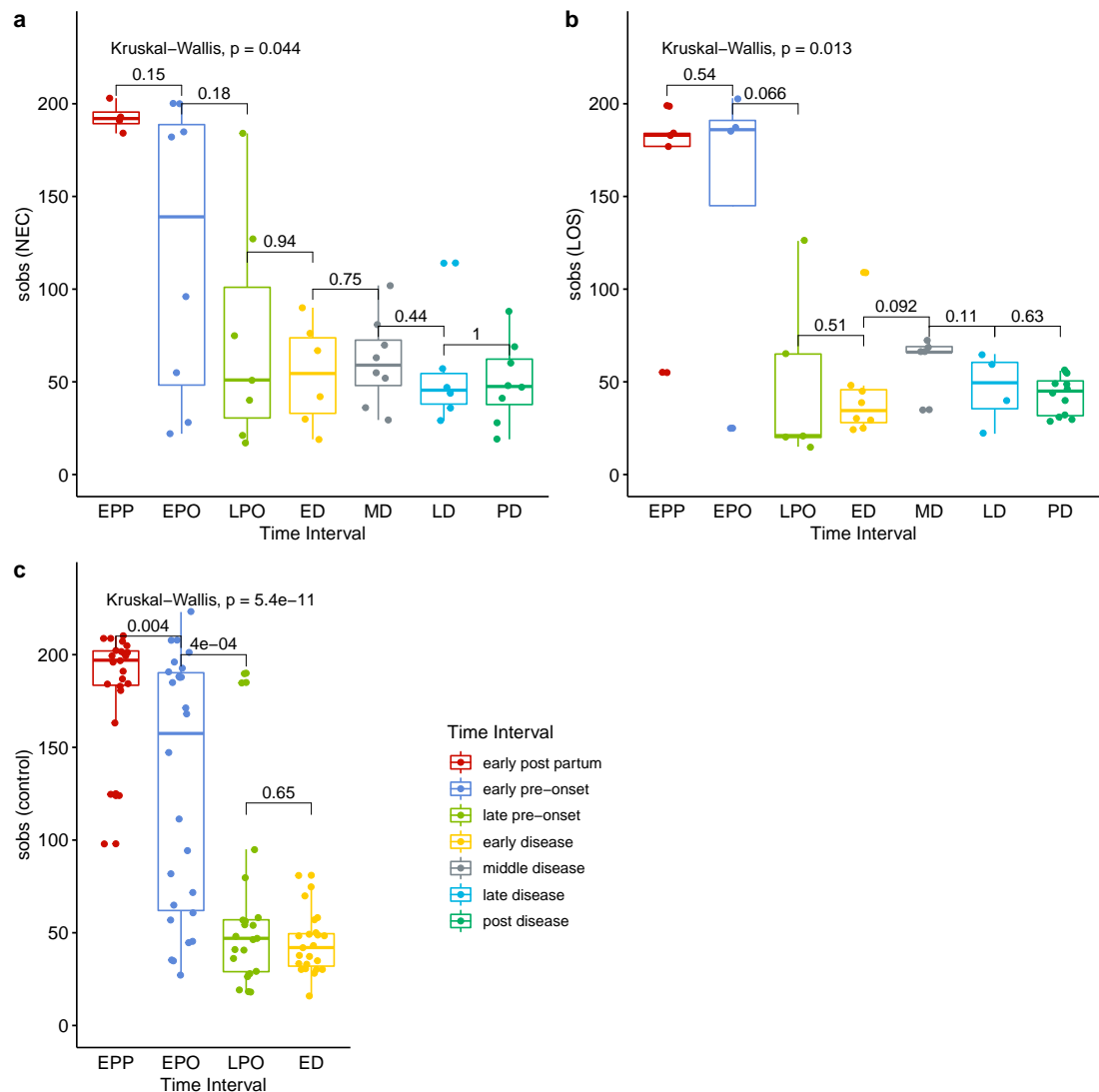
Figure 2. Post-partum microbiome richness (Sobs) trend in each group

During early post-partum interval, there appears to be no clear difference in beta-diversity among three groups, with the first principal coordinates accounted for 33.01%. In the process of entering diseases status, beta diversity continued drifting away, with the first principal coordinates accounted for 35.23% in early pre-onset phase, 38.36% in late pre-onset phase and 42.32% in early disease phase(Fig5). During the middle, late and post disease interval, samples from NEC and LOS groups clustered together respectively(). This phylogenetic dissimilarity indicated the different etiopathology and antibiotic regimes between NEC and LOS.

Potentially Pathogenic Genus Represented Both NEC and LOS Groups

To investigate specific genera that affect the course of diseases development, we filtered the genus of over 10% relative abundance among all samples and performed tests on a time-interval scale.

Before disease onset, ZIBR model showed significant time-by-NEC and time-by-LOS interaction factors for the progression over time of Bacillus and Solibacillus. Stools from both disease groups showed significantly higer Bacillus($p = 0.032$) and lower Solibacillus($p = 0.047$) relative to control samples(ZIBR table cited). Furthermore, both case groups experienced a rapid decline in Bacillus when approaching disease stages(NEC from 15.053% in early post-partum to 0.011% in early disease interval; LOS from 15.967% in in early post-partum to 0.002% in early disease interval).
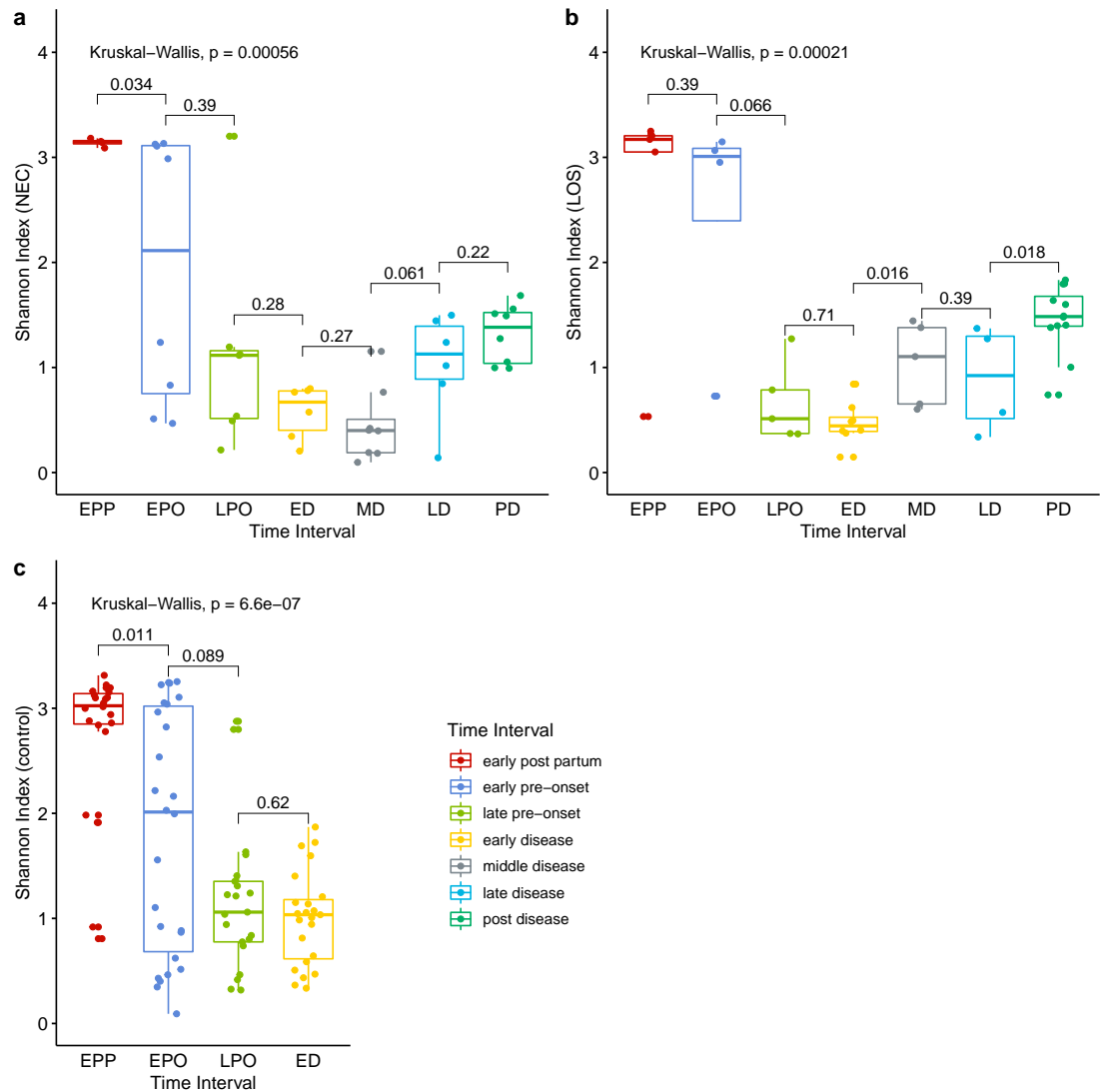
Figure 3. Post-partum microbiome evenness(shannon diversity index) trend in each group

For NEC samples, Enterococcus increased significantly from 0.009% in late pre-onset phase, to 28.801% in early disease and 58.959% in middle disease interval (p = 0.032). Meanwhile, after its transient boost in late pre-onset interval(27.231%), Staphylococcus had been constantly presented (12.571%) until late interval of NEC. Relative to control samples(6.010%), NEC samples showed higher Streptococcus(14.439%, p = 0.023) starting from late pre-onset stage to late disease stage. Peptoclostridium increased during late disease stage(#diarrhea!!)(Fig6a).

For LOS patients, a significant outburst of Klebsiella (EPP: 4.7%, EPO: 2.376%, LPO: 58.902%) with diminishment of other genus were characterized prior to the disease onset. Later on, Klebsiella aggressively dominated the intestine throughout the whole course of disease(ED: 73.529%, MD: 69.506%, LD: 45.333%). By contrast, Escherichia-Shigella, which might well be impacted by advanced antibiotics including Meropenem, was absent from late pre-onset to early disease interval(0.005%, p = 0.026 and 0.003%, p = 0.045, respectively), restored until middle disease interval(14.762%, p = 0.042) and became the second abundant genera dominating the intestine in late disease(48.336%, p = 0.262)(Fig6b)

DISCUSSION

This study investigated the microbiome diversity and composition over time, of the Chinese preterm infants who subsequently developed necrotizing enterocolitis or late-onset sepsis. The main findings

were that among case stools, the overall microbiota diversity was reduced and specific compositional characteristics of the microbiota was associated with potentially pathogenic genus, such as Enterococcus, Staphyloccus and Streptoccus.

Both case groups and control group showed decrease in richness and evenness after birth. In previous studies Several studies suggested a reduction in microbiota community diversity Community richness 1. alpha 1.1 evenness minor rols 1.2 richness dicrease during (corresponding 4 7 dol) may precede diseases, less diversified ¡-¿ s/s? # consistent with the hypothesis that dysbiosis precedes this severe event. 2. beta 3. over/underrepresenting of certain genus 4. Microbiome optimization – a novel strategy

Our study has its limitations. We acknowledge that the sample size is limited since this study is single-center-based and the incidence of both diseases are relatively low: among the 1148 preterm infants admitted within July 2013 to December 2014, only five developed NEC. The resultant overfitting possibility inevitably rose up, which became the pitfall in understanding the true microbiota patterns of NEC and LOS. Our results, however, showed the needs of an exceptionally larger, more heterogenous study population and longer follow ups, to draw a more meaningful and solid conclusion within the non-western population.

CONCLUSIONS

To our knowledge, our study is the first to report intestinal microbiota of preterm infants in Chinese population using 16s rRNA gene NGS data. Intestinal microbiota diversity reduction and phylogenetic dissimilarity away from healthy infants over time is associated with both NEC and LOS onset. Prevalence of potentially pathogenic genera over-growth were recognized, i.e. Enterococcus, Streptococcus and Peptoclostridium in NEC cases; Klebsiella in LOS cases. Our results is a starting point for further studying of microbial factors involved in preterm-associated complications within China range. A better understanding of microbial risk signatures in longitudinal microbial community assembly during early life, including its colonization mechanism and interaction with intestinal immunological responses, would assist in better understanding the etiology and assist in development of alternative biomarkers for early diagnosis and facilitate novel prevention and treatment strategies, to protect predisposed preterm infants in Chinese population.

ACKNOWLEDGMENTS

REFERENCES

Bell, M. J., Ternberg, J. L., Feigin, R. D., Keating, J. P., Marshall, R., Barton, L., and Brotherton, T. (1978). Neonatal necrotizing enterocolitis. therapeutic decisions based upon clinical staging. *Annals of surgery*, 187(1):1.

Bezirtzoglou, E., Tsiotsias, A., and Welling, G. W. (2011). Microbiota profile in feces of breast-and formula-fed newborns by using fluorescence in situ hybridization (fish). *Anaerobe*, 17(6):478–482.

Bolger, A. M., Lohse, M., and Usadel, B. (2014). Trimmomatic: a flexible trimmer for illumina sequence data. *Bioinformatics*, 30(15):2114–2120.

Bouter, K. E., van Raalte, D. H., Groen, A. K., and Nieuwdorp, M. (2017). Role of the gut microbiome in the pathogenesis of obesity and obesity-related metabolic dysfunction. *Gastroenterology*, 152(7):1671–1678.

Caporaso, J. G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F. D., Costello, E. K., Fierer, N., Pena, A. G., Goodrich, J. K., Gordon, J. I., et al. (2010). Qiime allows analysis of high-throughput community sequencing data. *Nature methods*, 7(5):335.

Chen, E. Z. and Li, H. (2016). A two-part mixed-effects model for analyzing longitudinal microbiome compositional data. *Bioinformatics*, 32(17):2611–2617.

Deweerdt, S. (2018). How baby's first microbes could be crucial to future health. *Nature*, 555(7695):S18–S19.

Edgar, R. C. (2013). Uparse: highly accurate otu sequences from microbial amplicon reads. *Nature methods*, 10(10):996.

333 Giongo, A., Gano, K. A., Crabb, D. B., Mukherjee, N., Novelo, L. L., Casella, G., Drew, J. C., Ilonen, J.,
334   Knip, M., Hyöty, H., et al. (2011). Toward defining the autoimmune microbiome for type 1 diabetes.
335   *The ISME journal*, 5(1):82.

336 Jacquot, A., Neveu, D., Aujoulat, F., Mercier, G., Marchandin, H., Jumas-Bilak, E., and Picaud, J.-C.
337   (2011). Dynamics and clinical evolution of bacterial gut microflora in extremely premature patients.
338   *The Journal of pediatrics*, 158(3):390–396.

339 Kassambara, A. (2017). ggpubr:"ggplot2" based publication ready plots. r package version 0.1. 6.

340 Liu, Y., Li, J., Jin, Y., Zhao, L., Zhao, F., Feng, J., Li, A., and Wei, Y. (2018). Splenectomy leads
341   to amelioration of altered gut microbiota and metabolome in liver cirrhosis patients. *Frontiers in
342   Microbiology*, 9.

343 Madan, J. C., Farzan, S. F., Hibberd, P. L., and Karagas, M. R. (2012). Normal neonatal microbiome
344   variation in relation to environmental factors, infection and allergy. *Current opinion in pediatrics*,
345   24(6):753.

346 Magoč, T. and Salzberg, S. L. (2011). Flash: fast length adjustment of short reads to improve genome
347   assemblies. *Bioinformatics*, 27(21):2957–2963.

348 Mai, V., Young, C. M., Ukhanova, M., Wang, X., Sun, Y., Casella, G., Theriaque, D., Li, N., Sharma, R.,
349   Hudak, M., et al. (2011). Fecal microbiota in premature infants prior to necrotizing enterocolitis. *PloS
350   one*, 6(6):e20647.

351 Pinheiro, J., Bates, D., DebRoy, S., Sarkar, D., and R Core Team (2018). *nlme: Linear and Nonlinear
352   Mixed Effects Models*. R package version 3.1-137.

353 Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., and Glöckner, F. O.
354   (2012). The silva ribosomal rna gene database project: improved data processing and web-based tools.
355   *Nucleic acids research*, 41(D1):D590–D596.

356 Sarkar, A., Lehto, S. M., Harty, S., Dinan, T. G., Cryan, J. F., and Burnet, P. W. (2016). Psychobiotics and
357   the manipulation of bacteria–gut–brain signals. *Trends in neurosciences*, 39(11):763–781.

358 Savage, J. H., Lee-Sarwar, K. A., Sordillo, J., Bunyavanich, S., Zhou, Y., O'connor, G., Sandel, M.,
359   Bacharier, L. B., Zeiger, R., Sodergren, E., et al. (2018). A prospective microbiome-wide association
360   study of food sensitization and food allergy in early childhood. *Allergy*, 73(1):145–152.

361 Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., Lesniewski, R. A.,
362   Oakley, B. B., Parks, D. H., Robinson, C. J., et al. (2009). Introducing mothur: open-source, platform-
363   independent, community-supported software for describing and comparing microbial communities.
364   *Applied and environmental microbiology*, 75(23):7537–7541.

365 Schwiertz, A., Gruhl, B., Löbnitz, M., Michel, P., Radke, M., and Blaut, M. (2003). Development of the
366   intestinal bacterial composition in hospitalized preterm infants in comparison with breast-fed, full-term
367   infants. *Pediatric research*, 54(3):393.

368 Stokholm, J., Blaser, M. J., Thorsen, J., Rasmussen, M. A., Waage, J., Vinding, R. K., Schoos, A.-M. M.,
369   Kunøe, A., Fink, N. R., Chawes, B. L., et al. (2018). Maturation of the gut microbiome and risk of
370   asthma in childhood. *Nature communications*, 9(1):141.

371 Tang, W. W., Kitai, T., and Hazen, S. L. (2017). Gut microbiota in cardiovascular health and disease.
372   *Circulation research*, 120(7):1183–1196.

373 Tilg, H., Cani, P. D., and Mayer, E. A. (2016). Gut microbiome and liver diseases. *Gut*, 65(12):2035–2044.

374 Vatanen, T., Franzosa, E. A., Schwager, R., Tripathi, S., Arthur, T. D., Vehik, K., Lernmark, Å., Hagopian,
375   W. A., Rewers, M. J., She, J.-X., et al. (2018). The human gut microbiome in early-onset type 1 diabetes
376   from the teddy study. *Nature*, 562(7728):589.

377 Wang, Q., Garrity, G. M., Tiedje, J. M., and Cole, J. R. (2007). Naive bayesian classifier for rapid
378   assignment of rrna sequences into the new bacterial taxonomy. *Applied and environmental microbiology*,
379   73(16):5261–5267.

380 Wang, R., Xiao, Y., Lv, F., Hu, L., Wei, L., Yuan, Z., and Lin, H. (2018). Bacterial community structure
381   and functional potential of rhizosphere soils as influenced by nitrogen addition and bacterial wilt disease
382   under continuous sesame cropping. *Applied Soil Ecology*, 125:117–127.

383 Warner, B. B., Deych, E., Zhou, Y., Hall-Moore, C., Weinstock, G. M., Sodergren, E., Shaikh, N.,
384   Hoffmann, J. A., Linneman, L. A., Hamvas, A., Khanna, G., Rouggly-Nickless, L. C., Ndao, I. M.,
385   Shands, B. A., Escobedo, M., Sullivan, J. E., Radmacher, P. G., Shannon, W. D., and Tarr, P. I. (2016).
386   Gut bacteria dysbiosis and necrotising enterocolitis in very low birthweight infants: A prospective
387   case-control study. *The Lancet*, 387(10031):1928–1936.

388 Wickham, H. (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York.

389 Zhou, Y., Shan, G., Sodergren, E., Weinstock, G., Walker, W. A., and Gregory, K. E. (2015). Longitudinal
390 analysis of the premature infant intestinal microbiome prior to necrotizing enterocolitis: a case-control
391 study. *PloS one*, 10(3):e0118632.

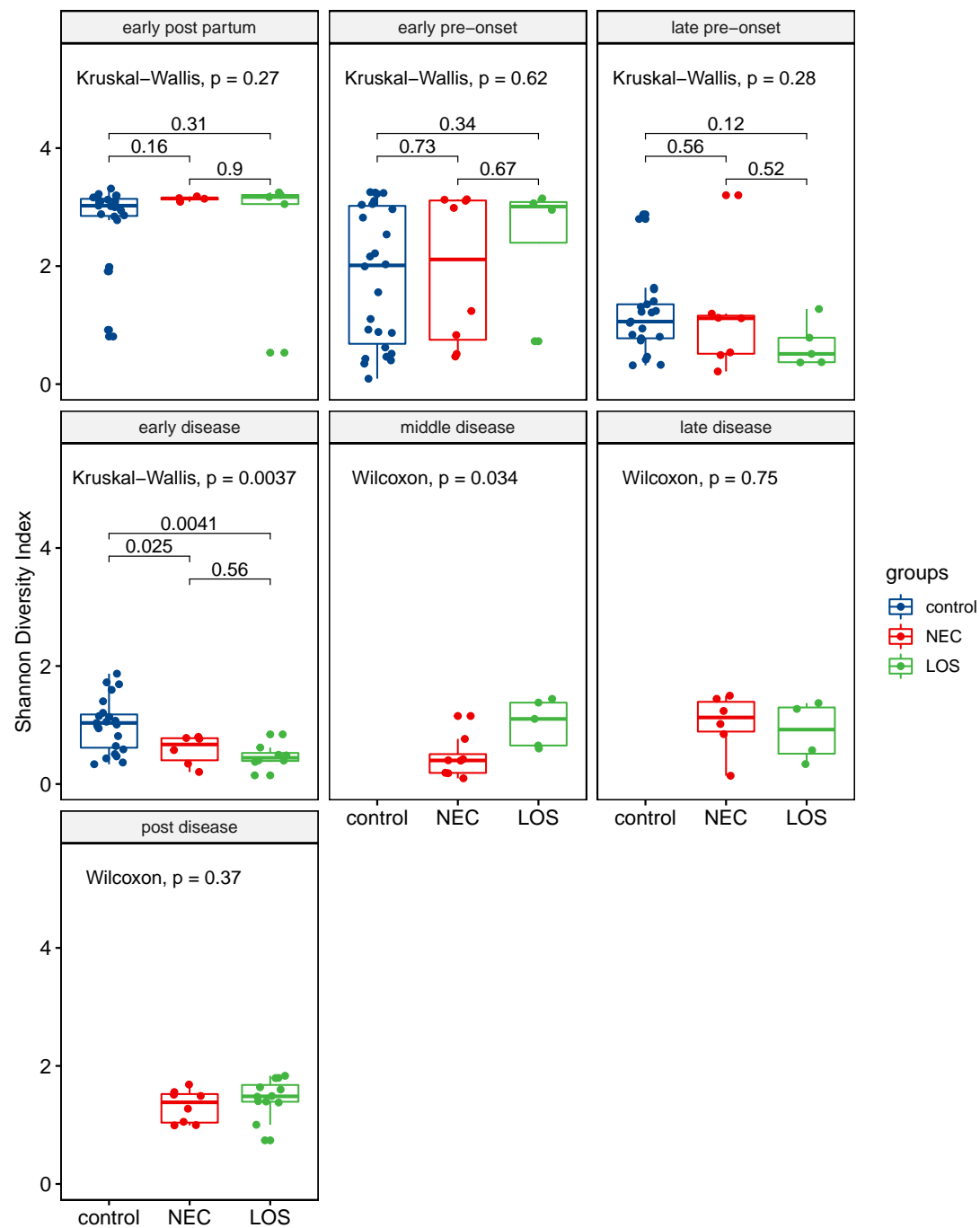**Figure 4.** Post-partum microbiome evenness(shannon diversity index) trend in each time interval
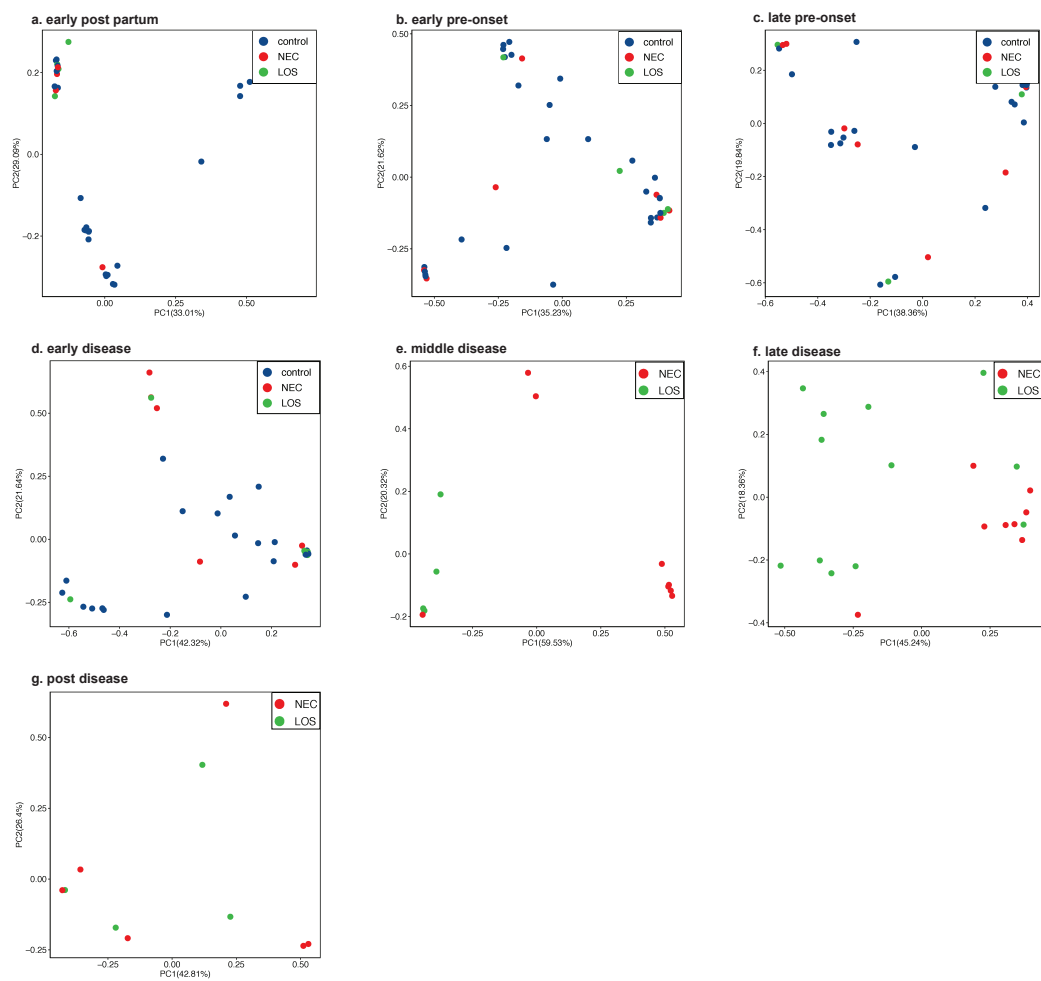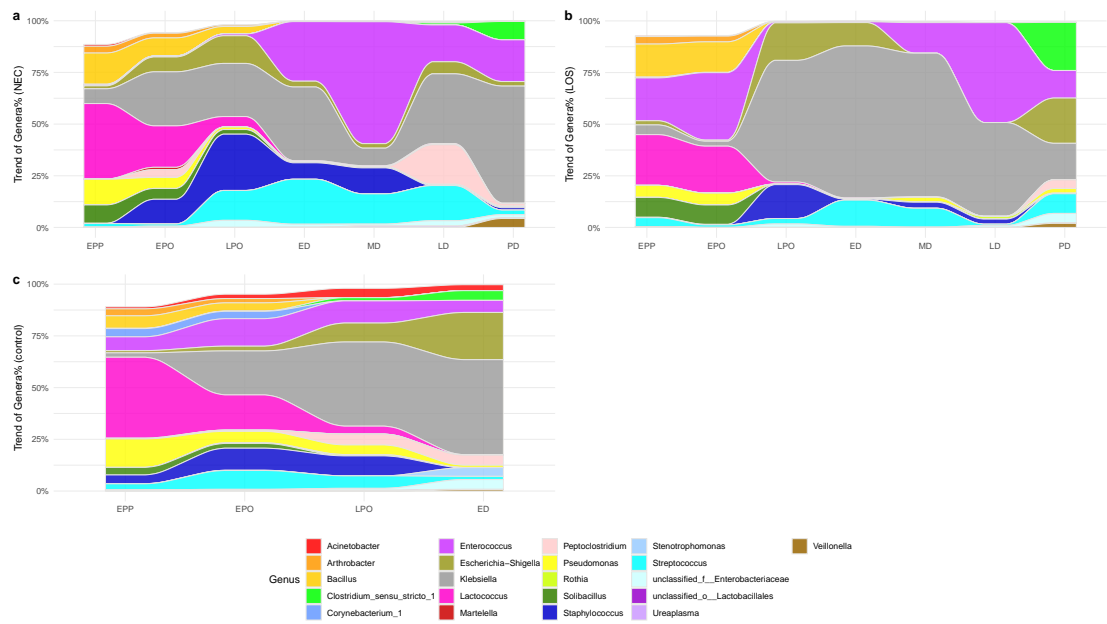
Figure 5. Beta Diversity

Figure 6. Kinetics of Genera Relative Abundance