Effect of intestinal flora on the formation of endometritis of sow

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Abstract

Background

Aberration of birth canal microbiota is one of the most important factors in the etiology of sow endometritis. Nevertheless, reports about the structure and composition of birth canal microbiota in endometritis sow and their relationship with intestinal microbes is limited. Therefore, understanding the relationship between birth canal microbiota and intestinal microbiota of the host has become exceedingly crucial.

Results

In this study, 4 healthy and 4 endometritis sows were selected basing on whether the sow had endometritis or not in a farm of China. The microflora of their birth canal secretions and fresh feces were analyzed via sequencing the V3 + V4 region of bacterial 16S rDNA gene. The results showed that the significant difference between endometritis and healthy sows birth canal flora in the composition and abundance. Sow endometritis was associated with increasing in the relative abundance of *Porphyromonas*, *Clostridium_sensu_stricto_1*, *Streptococcus*, *Ezakiella*, *Fusobacterium*, *Actinobacillus*, *Bacteroides*, and *Prevotella* as well as *Anaerococcus*. On the contrary, the majority of beneficial bacteria that belonging to *Firmicutes* phylum (e.g., *Lactobacillus* and *Enterococcus*) declined in endometritis sow. The increased relative abundance of *Porphyromonas* in the vaginal secretions might correlate with the decrease of *Lactobacillus* in the feces of endometritis sows. Moreover, the experimental result also found that some intestinal bacteria (such as *Escherichia-Shigella* and *Bacteroides*) may be bound up with the onset of sow endometritis.

Conclusion

Sow endometritis is closely related to the microbiota of birth canal, and that some intestinal bacteria may promote the onset of endometritis. The above results can supply a theoretical basis to research the pathogenesis of endometritis and the microbiota of sow's birth canal and gut.

Background

Endometritis is a common and frequent reproductive system disease in female domestic animal. It can lead to abnormal estrus, repeated infertility or miscarriage in female animals, which may bring enormous economic losses [1]. Although antibiotics have a certain therapeutic effect on livestock endometritis, that the long-term use of antibiotics has made problems of veterinary drug residues in animal products become increasingly prominent. Therefore, it is imperative to exploit a new therapy of curing endometritis. Many prevenient researches have shown that birth canals flora plays a vital role on the formation of biologic barriers that protect the health of the reproductive tract by the production of substances such as

lactic acid, hydrogen peroxide and bacteriocin [2]. Recent researches have shown that the intestinal microbiota is strongly associated with diseases such as metabolic syndrome, inflammatory bowel diseases (IBD) and colorectal cancer [3]. Hence, understanding the gut and the birth canal flora is significant for the prevention and treatment of livestock diseases.

In recent years, with the development of high-throughput sequencing technology of 16S rDNA gene, which is possible to analyze the diversity of bacterial community in different ecological niches. Growing evidence suggests that the intestinal microflora affects many important physiological functions of the host, such as immune system activation, metabolism, epithelial cell proliferation and anti-infection [4]. We found that the risk of endometritis was increased in the sows with constipation in clinical practice. Nevertheless, there are few reports on the association between birth canal secretions and intestinal microflora of sows. In this research, high-throughput sequencing of 16S rDNA gene was used to analyze the composition and differences in the vaginal secretions and intestinal bacterial communities of the sows in the health and endometritis. It is a new attempt to unveil the effect of intestinal flora on the pathogenesis of endometritis.

Results

Sequencing results and samples diversity

A total of 16 samples (healthy vaginal secretion (HV, N = 4), healthy feces (HF, N = 4), endometritis vaginal secretion (EV, N = 4), endometritis feces (EF, N = 4)) were collected from 8 sows in a farm. Samples total DNA were extracted and sequenced on Ion S5 XL platform. After cutting off the barcodes, primers and filtering low-quality reads, chimeras, a total of 1212768 high-quality sequences were acquired from all samples. These high-quality sequences were clustered into 7392 OTUs on the basis of 97% similarity. Each sample contained 75798 reads and 462 OTUs on average (see Additional file 1). In this study, six alpha diversity measures were calculated including observed-species (observed OTUs), Shannon, Simpson, Chao1, ACE and PD-whole-tree (see Additional file 2, Additional file 3, Additional file 4 and Additional file 5).

Analysis of the birth canal microbial community of endometritis sows and healthy sows

Under the condition that the similarity was 97%, a total of 1102 OTUs were observed in samples from HV and EV (Fig. 1A). The microbiota of HV and EV samples shared 219 OTUs, with 874 and 9 OTUs uniquely identified from EV and HV samples, respectively (Fig. 1A). Of which, among the 874 OTUs unique to the EV group include 301 bacterial genera, the 9 OTUs unique to the HV group contain 3 bacterial genera, the 219 OTUs shared by EV and HV contain 98 bacteria genera. Different from the analysis of other microfloras, the diversity of HV microfloras was significantly lower than that of EV. In the PCoA figure, both the unweighted UniFrac distance (Fig. 2A) and the weighted UniFrac distance (Fig. 2B) could distinguish the significantly difference in microbiota communities between EV and HV samples (Fig. 2).

Figure 3 showed the average relative abundance of the top 20 phylum and top 30 genus bacteria in the EV and HV samples. At the level of phylum, five predominant phyla were identified in the bacterial communities of EV and HV samples. On average, the relative abundance of these bacteria is over 1%. *Firmicutes* (41.26%) was the most predominant phyla in EV samples, followed by *Proteobacteria* (30.47%), *Bacteroidetes* (17.78%) and *Actinobacteria* (5.48%) (Fig. 3A). The most dominant bacteria in HV samples were *Firmicutes* (74.36%) and *Proteobacteria* (24.68%) (Fig. 3A). The relative abundance of *Firmicutes* in HV was significantly higher than that of in EV ($P < 0.05$). Compared with HV samples, the relative abundance of *Bacteroidetes*, *Actinobacteria* and *Fusobacteria* in EV samples were significantly increased ($P < 0.05$) (see Additional file 6).

A total of 337 genera were identified in the birth canal bacterial communities of endometritis sows compared to 100 genera in healthy sows. In EV samples, the most dominant bacterial genera included *Porphyromonas* (9.54%), *Clostridium_sensu_stricto_1* (6.66%), *Streptococcus* (6.26%), *Vulcaniibacterium* (5.88%), *Campylobacter* (5.24%), *Veillonella* (3.98%), *Escherichia-Shigella* (3.84%), *Ezakiella* (3.74%), *Schlegelella* (3.59%) and *Fusobacterium* (3.13%) (Fig. 3B). *Lactobacillus* (42.84%), *Enterococcus* (28.04%), *Pseudomonas* (21.27%), *Psychrobacter* (3.02%) and *Staphylococcus* (2.91%) were the dominant genera in HV samples (Fig. 3B). The relative abundance of *Clostridium-sensu-stricto-1*, *Streptococcus*, *Ezakiella*, *Fusobacterium*, *Actinobacillus*, *Bacteroides*, *Prevotella* and *Anaerococcus* were significantly higher in EV samples than that of HV sample ($P < 0.05$) (see Additional file 6). LEfSe (linear discriminant analysis effect size) analysis method was used to detect bacterial taxa of significant difference between EV and HV. The results showed that three bacterial species (*Actinobacillus_rossi*, *Streptococcus_gallolyticus_subsp_macedonicus*, and *Porphyromonas_somerae*) were the significant higher in EV samples compared with HV samples. *Lactobacillus_sakei* was the significant higher in HV samples compared with EV samples (Fig. 4A and Additional file 6).

The relationship between the birth canal and intestinal flora of endometritis sows

A total of 1115 OTUs were observed in samples from EV and EF (Fig. 1B). The microbiota of EV and EF samples shared 413 OTUs, with 680 and 22 OTUs uniquely identified from EV and EF samples, respectively (Fig. 1B). On the PCoA plot, the unweighted UniFrac distance (Fig. 2A) could completely separate the EV samples from EF samples. However, the weighted UniFrac distance does not completely separate the EV sample from the EF sample (Fig. 2B). This indicates that, to some extent, there is a certain similarity between the birth canal and intestinal flora of endometritis sows. At the levels of phylum, both *Proteobacteria* and *Firmicutes* have high relative abundance in EV and EF samples (see Additional file 7).

At the levels of genus, *Psychrobacter* (23.29%), *Pseudomonas* (18.38%), *Escherichia-Shigella* (15.91%), *Lactococcus* (4.91%), *Brochothrix* (3.84%), and *Bacteroides* (1.57%) were other six dominant genera in EF samples (Fig. 3B). In EV samples, *Porphyromonas* (9.54%), *Clostridium_sensu_stricto_1* (6.66%), *Streptococcus* (6.26%), *Vulcaniibacterium* (5.88%), *Campylobacter* (5.24%), *Veillonella* (3.98%),

Escherichia-Shigella (3.84%), *Ezakiella* (3.74%), *Schlegelella* (3.59%) and *Fusobacterium* (3.13%) were the predominant genera (Fig. 3B). It should be noted that both *Escherichia-Shigella* and *Bacteroides* were collaborative genera in EF and EV samples.

Difference of intestinal community of healthy sows and endometritis sows

In the study, a total of 1069 OTUs were observed in samples from HF and EF (Fig. 1C). The microbiota of HF and EF samples shared 251 OTUs, with 634 and 184 OTUs uniquely identified from HF and EF samples, respectively. The community richness index (Chao1 and ACE) and community diversity index (Shannon) were extremely significant higher in HF samples than those of EF samples ($P < 0.01$) (see Additional file 4), only the Simpson Index difference is not significant ($P < 0.05$), indicating that both community richness and community diversity were dramatically higher in HF samples than in EF samples. Next, the unweighted UniFrac distance showed remarkable segregations of microbiota between HF samples and EF samples (Fig. 2A). Similar discrimination was also observed, via weighted UniFrac distances, in the PCoA (Fig. 2B), suggesting that the Beta diversity of HF samples were also obvious higher than EF samples.

A total of 165 genera were identified in the intestines bacterial communities of endometritis sows compared to 211 genera in healthy sows. To identify the significant differences in gut bacteria between HF and EF samples, we compared the relative abundance of gut bacteria in HF and EF samples. The result indicated that the relative abundance of six genera (*Lactobacillus*, *Pseudomonas*, *Psychrobacter*, *Escherichia-Shigella*, *Brochothrix* and *Bacteroides*) exhibited obvious increased in the EF samples, although the difference is not significant (see Additional file 8). LEfSe analysis also revealed that *Brochothrix_thermosphacta*, *Lactococcus_raffinolactis*, *Psychrobacter_faecalis*, *Pseudomonas_fragi*, and *Psychrobacter_maritimus* were the significant higher in EF samples compared with HF samples (Fig. 4B). In brief, compared with HV samples, there were 874 (238 + 76 + 394 + 166) unique OTUs in EV samples, of which 242 (76 + 166) OTU were shared with EF; while among these 242 OTUs, 166 OTUs were shared with HF, and only 76 OTUs were shared with EF. 76 OTUs were the key to understanding the relationship between the occurrence of sow endometritis and its intestinal flora (Fig. 1D). It was found that there were 5 bacterial phylum, mainly including *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, and 46 bacterial genera in 76 OTUs. These bacterial genera including *Bacteroides*, *Peptoniphilus*, *Flavobacterium*, *Anaerococcus*, etc, among which *Bacteroides* was the most abundant genus.

Discussion

Differences between the birth canal microbiota of endometritis sows and healthy sows

Despite documented evidence indicating that birth canal flora has a key function in the etiology of endometritis, understanding for the structure and composition of the birth canal microbiota in

endometritis sows was still limited. The dramatically difference in the relative abundance of microbiota communities in endometritis and healthy sows' birth canal secretion supports the standpoint that endometritis of sows are associated with alterations in the interactions among microorganisms of the birth canal.

At the phylum level, the relative abundance of *Firmicutes* was the highest in the EV samples. *Bacteroidetes*, *Actinobacteria*, and *Fusobacteria* were only present in the EV samples, when compared with HV samples. At the genus level, the relative abundance of *Clostridium_sensu_stricto_1*, *Streptococcus*, *Fusobacterium*, *Escherichia-Shigella*, *Actinobacillus* and *Bacteroides* were remarkably higher in EV samples than those of HV samples ($P < 0.05$). Growing evidence suggests that *Clostridium_sensu_stricto_1*, *Streptococcus*, *Fusobacterium*, *Actinobacillus* and *Bacteroides* are closely correlated with diseases in animal. For instance, Correlation studies showed that the mRNA expression of IL-1 β and TNF- α were positively correlated with the enrichments in *Clostridium_sensu_stricto_1* in the colon mucosal of sheep, this enrichment eventually leads to inflammation of the colonic epithelium in sheep [5]. A study by Xiaojing Xia et al. reported that the pathogenic protein secreted by *Streptococcus* can escape host phagocytosis and complement-mediated immune destruction leading to the onset of the body [6]. Moreover, Wang et al. reported that *Clostridium_sensu_stricto_1*, *Fusobacterium* and *Bacteroides* are more abundant in the vagina of endometritis sows compared to healthy sows [7]. Similar results have been obtained in studies of human bacterial vaginosis, compared with healthy women, *Bacteroidetes*, *Actinobacteria* and *Fusobacteria* were more abundant in bacterial vaginosis women [8]. These investigations suggested that the onset of sow endometritis is inextricably linked to the increase relative abundance of these bacteria in the birth canal.

Another conspicuous difference in EV samples was the decreased relative abundance of *Firmicutes* members, including *Lactobacillus* and *Enterococcus*. While, we observed obvious statistically predominance of *Lactobacillus* in 9 OTUs unique to HV samples. *Firmicutes* was reported to have been the highest abundant phenotype in birth canals samples of the healthy sows [7], and a few members of this phylum are considered to adjust systemic immune responses [9]. Therefore, these beneficial bacteria may involve in regulating bacteria balance, inhibiting conditional pathogens, and preventing colonization of pathogenic microorganisms. For instance, *Lactobacillus* are generally studied as probiotic agents, which affect pathogenicity of opportunistic pathogens and host immune regulation [10]. *L. sakei* releases spherical membrane vesicles (MVs) through its cell wall components by activating host TLR2 signals, thereby enhancing the production of IgA, and then preventing the incursion of pathogenic microorganisms and regulating the composition of intestines microbiota [11]. In this study, *Lactobacillus* and *Enterococcus* were found at lower levels in EV samples, which are consistent with the previous studies. These data indicate that under the condition of endometritis, the environment of the birth canal maintains the competition and abundance of different bacteria, and the continuous reduction of these groups may affect the stability of bacterial balance and the immune regulation of the host.

Differences between the intestines microbiota of endometritis and healthy sows

The imbalances of microflora and abnormal immune responses to intestines bacteria can destroy intestinal homeostasis and host homeostasis [12]. Many research results indicated that the higher the diversity of intestinal flora, the stronger its ability to maintain the balance of intestinal flora [13]. In this study, we observed that the diversity of intestinal flora of sows with endometritis were significantly reduced. It may be related to the This may be related to the occurrence of endometritis.

In order to better understand the relationship between them, we conducted a comparative analysis of EF and HF samples. The results showed that: *Lactobacillus*, *Psychrobacter*, *Pseudomonas* and *Escherichia-Shigella* were the most dominated genera in EF samples, compared with HF samples. It is worth noting that there were 184 unique OTUs in EF samples. It is worth noting that there were 184 unique OTUs in EF samples, which were composed of 101 bacterial genera. *Bacteroides*, *Prophyromonas*, *Pseudomonas*, *Streptococcus*, etc. were the main bacterial genera. Many studies have shown that *Pseudomonas*, and *Psychrobacter* are associated with some diseases of the animal. For instance, some scholars have reported that *Pseudomonas* can be as an oral and tracheal pathogens in premature infants [14]. The members of genus *Psychrobacter* are considered to be opportunistic pathogens, as they are occasionally isolated from infected animals, as well as from human patients [15]. Specifically, the pathogenic mechanism of these bacteria needs further study.

Effect of sow birth canals and gastrointestinal flora on endometritis

The birth canal and gastrointestinal tract of mammals are extremely complex ecosystems that play an important role in animal health and disease. In this study, we found that *Firmicutes*, *Proteobacteria* and *Bacteroidetes* are the main bacterial phylum in the birth canals and gastrointestinal flora of endometritis sows, which is similar to the study by Koh [16]. At the genus level, *Escherichia-Shigella* and *Bacteroides* were bacterial genus shared in EF and EV samples. Both of their abundance were 0.02% in HV samples, and the abundance in HF samples is 0.50% and 0.63%, respectively. Neis et al. found that members of *Escherichia-Shigella* play a vital role in amino acid utilization in animals and prefer to live in the weakly alkaline environment [17]. In our study, the relative abundance of *Lactobacillus* was low in EV samples, creating a weakly alkaline environment, which may provide a favorable condition for the growth and reproduction of *Escherichia-Shigella* members. Remarkably, the relative abundance of *Bacteroides* was also high in EV samples. A study by Wang et al. reported that *Bacteroides* can lead to an endogenous infection when the immune system or intestinal microbiota is dysfunctional [18]. In addition, the high abundance of *Bacteroides* was found in cows with endometritis also indicated that *Bacteroides* were highly associated with uterine disease [19]. We speculate about that the intestinal microbiota (*Escherichia-Shigella* and *Bacteroides*) of the sow may be affected the balance of the flora of the birth canal, promote the growth and reproduction of opportunistic pathogens, which leads to endometritis. Specifically, how it affects requires further research to clarify.

In addition, some scholars have found that the first colonization flora of humans originates from maternal microorganisms [20]. In our previous study, the bacteria that *E. coli*, *Shigella* and *Clostridium*

existed in endometritis sows were also the main dominant bacteria in the intestines of a group of diarrhea piglets [21]. More interestingly, the *Lactobacillus*, which is more abundant in the birth canal of healthy sows, has been reported to have the effect of alleviating diarrhea in piglets [22]. The bacteriocin secreted by *Lactobacillus* can promote the absorption of intestinal fluid and reduce the secretion of intestinal fluid by activating phosphodiesterase activity and reducing cAMP and cGMP levels [23]. These indicate that the sow's birth canal microbiota may be related to the health of the piglets.

All in all, the imbalance of sow intestinal flora may affect the balance of the birth canal microbiota and lead to endometritis, while the vertical transmission of birth canal microbes will affect the health of piglets. Specifically, the way of the sow gut microbiota affects its birth canal and piglet microbiota (or the regulatory mechanism of the impact) needs further study to clarify.

Conclusion

In conclusion, our study unveiled differences in birth canals microbiota between endometritis and healthy sows and described the correlation between the birth canal and the gut microbiota of the endometritis sow. The results showed that *Clostridium_sensu_stricto_1*, *Streptococcus*, *Fusobacterium*, *Escherichia-Shigella*, *Actinobacillus* and *Bacteroides* may be related to the occurrence of sow endometritis. Of which, *Escherichia-Shigella* and *Bacteroides* may be from the intestinal tract of endometritis sows. Simultaneously, we have also found that a decrease in the abundance of *Lactobacillus* could lead to a diversity increase of the flora of the birth canal, which the latter has the risk of causing endometritis. These findings can provide a theoretical basis to research endometritis and the sow's birth canal and gut microbiota, and will be helpful to establish an effective strategy to reduce postpartum disease generating in sows.

Methods

Experimental design and sample collection

This research was approved via the Institutional Animal care and use committee of Jiangxi Agricultural University and performed according to its guidelines. According to the health status of the sows (Whether have endometritis), 8 fecal samples (from 4 healthy sows and 4 endometritis sows) and 8 vaginal secretions samples (from 4 healthy sows and 4 endometritis sows) were randomly collected from a farms in Jingdezhen, Jiangxi, China. During collecting samples, these animals were not disturbed. And there were no clinical abnormalities such as constipation and diarrhea in the intestines of sows with endometritis in this study. Fecal samples and vaginal secretions samples were kept at 4°C and transported to the laboratory, and then stored at -80°C until DNA extraction were performed.

DNA extraction and sequencing

Total bacterial genomic DNA from samples was extracted using CTAB/SDS method, and stored at -80 °C until further analysis. Sequencing was performed at the Novogen Bioinformatics Technology Co., Ltd,

Beijing, China. Briefly, the V3 + V4 region of the bacterial 16S rDNA gene was amplified from the total extracted DNA via using the 314F/806R primer set. All PCR reactions were carried out with Phusion® High Fidelity PCR Master Mix (New England Biolabs, USA) with the following programs: initial pre-denaturation 1 cycle of 94°C for 3 min, followed by 38 cycles of 94°C 45 s, 55°C 60 s, and 72°C 90 s, and a final extension step 1 cycle of 72°C 10 min. Using electrophoresis on 2% agarose gel and GeneJET™ Gel Extraction Kit (Thermo Scientific) to separate and purify the PCR products. Sequencing libraries were generated using Ion Plus Fragment Library Kit 48 rxns (ThermoFisher) following manufacturer's recommendations and were assessed on Qubit® 2.0 Fluorometer (ThermoFisher), and then sequenced on an Ion S5™ XL platform. 16S rDNA sequencing data was saved in the European Nucleotide Archive (ENA) under the Accession Number ERS3526284-ERS3526299.

Statistical analysis of microbial community

Low-quality partial of the reads were sheared by using Cutadapt (V1.9.1, <http://cutadapt.readthedocs.io/en/stable/>), then splited the sample reads from the obtained reads according to barcode, and the original reads was obtained by cutting off the initial quality control of barcode and primer sequences. Quality filtering on the original reads were performed under specific filtering conditions to obtain the high-quality clean reads on the basis of the Cutadapt (V1.9.1) quality controlled process.

The reads were compared with the reference database (Silva database, <https://www.arb-silva.de/>) by using UCHIME algorithm (UCHIME Algorithm, http://www.drive5.com/usearch/manual/uchime_algo.html) to detect chimera sequences and remove chimera sequences. Finally, we gained the high-quality clean reads. Using Uparse software(Uparse v7.0.1001, <http://drive5.com/uparse/>) to analyse these sequences and the sequences with $\geq 97\%$ similarity were assigned to the same operational taxonomic units (OTUs). Screen the representative sequences of each OTU and use the Silva Database (<https://www.arb-silva.de/>) based on Mothur algorithm to annotate taxonomic information.

Alpha and beta diversity analysis of the samples were performed with QIIME (Version 1.7.0) and display with R software (Version 2.15.3). Alpha diversity analysis included Observed-species, Chao1, Shannon, Simpson, ACE, PD-whole-tree. The result data was statistically analyzed by using SPSS 22.0. Beta diversity includeed Principal Co-ordinates Analysis. Principal Co-ordinates Analysis (PCoA) analysis of samples was performed based on Weighted Unifrac distance and Unweighted Unifrac distance. According to the results of OTUs clustering, the number of common and unique OTUs between different groups was analyzed using Novomagic cloud platform, and displayed with Venn diagram. According to the results of species annotations, the top 20 and top 30 species with the highest abundance of each group at the Phylum and Genus classification levels were selected to generate a columnar cumulative chart of relative abundance of species. The bacterial taxonomic differences represented between groups at the genus or higher taxonomy level was analyzed using LEfSe.

Abbreviations

IBD: inflammatory bowel diseases; HV: healthy vaginal secretion; HF: healthy feces;

EV: endometritis vaginal secretion; EF: endometritis feces; PCoA: Principal Co-ordinates Analysis

Declarations

Ethics approval and consent to participate

We contacted the owner of the farm and obtained verbal consent from the owner. And the Animal Protection and Utilization Committee of Jiangxi Agricultural University ruled that no formal ethics approval was required when we only collecting the waste of animals.

Consent for publication

Not applicable

Availability of data and materials

All data generated or analysed during this study are included in this published article [and its supplementary information files].

Competing interests

The authors declare that they have no competing interests

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Authors contribution

JZ and YD designed the study. LW, YW, and XZ collected the sows fecal and vaginal secretions samples. LW and YW performed the experiments. LW, JW, and XZ analyzed the data. LZ, LW, TT and JZ wrote and revised the manuscript. All authors read and approved the final manuscript.

Acknowledgments

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Figures

Figure 1

Compositions of the microbiota of the sows feces and vaginal secretions. (A) the number of OTUs shared in EV and HV samples are shown in Venn diagrams; (B) the number of OTUs shared in EV and EF samples are shown in Venn diagrams; (C) the number of OTUs shared in HF and EF samples are shown in Venn diagrams; (D) the number of OTUs shared in HF, HV, EF and EV samples are shown in Venn diagrams.

Figure 2

Principal coordinate analysis (PCoA) shows bacterial community structures based on Bray-Curtis distances. On the PCoA plot, each symbol represents one gut microbiome. (A) Unweighted UniFrac distance of the intestinal and vaginal sample microbiota; (B) Weighted UniFrac distance of the intestinal and vaginal sample microbiota. The numbers of PC1 and PC2 shows the percent variation explained by the PCoA plot.

Figure 3

The overall compositions of the microbiota of HF, HV, EF, EV. The overall compositions of the microbiota of the healthy feces (HF), healthy vaginal secretions (HV), endometritis feces (EF) and endometritis vaginal secretions (EV) were represented as bar plots at the phylum level (A) and the genus level (B). Each bar represents the average relative abundance of each bacterial taxon within a group. The phylum level shows the top 20 rich taxa, and the genus level shows the top 30 rich taxa.

Figure 4

Bacterial taxa significantly differentiated between samples groups identified by linear discriminant analysis coupled with effect size (LEfSe) using the default parameters. (A) show different taxa between EV and HV samples; (B) show the different taxa between HF and EF samples.

Supplementary Files

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