Microbiota and the Gut-Placenta Axis in Non-Human Primates (Papio spp.)

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Introduction.

Microbial participation is critical for host functions such as defense, metabolism, and reproduction. Perturbations in the placental microbial communities have been associated with preterm deliveries. Fecal microbiome has been recently recognized as an important part of pregnancy maintenance. The fecal microbiome is connected to the tissues microbiomes through the mechanism of commensal bacteria translocation. There are no data available regarding microbial gut-placental interaction in non-human primates (NHP). This data would be essential for the translational interpretation and analyses of experimental studies in NHP.

Aim

The goal of this study was to compare placental and colon microbiomes of non-obese pregnant baboons as defense, metabolism, and reproduction. Microbial participation is critical for host functions such as defense, metabolism, and reproduction.

Method

Samples were collected under sterile conditions during necropsy from three non-obese pregnant baboons (165 days of gestation), described in detail previously (Placenta; Nov; 32(11)). Two paired samples from each animal (colon and placenta) were flash-frozen in liquid nitrogen and stored at - 80C. The genomic DNA extraction was performed using conventional methodology, followed by massive parallel sequencing of partial 16S rRNA gene amplicons (Ion Torrent proton®). Trimming the raw fastq files were trimmed using CLC Genomics workbench. For quality trimming, the Phred quality score (Q) was converted to an base-calling error probability (p) and the default parameters including the limit p value and maximal number of ambiguous nucleotides for quality trimming were maintained. For length trimming, the reads with length below 80bp were discarded. Taxonomy identification

The Ribosomal Database Project (RDP) classifier (http://rdp.cme.msu.edu) was used to arrange taxonomic identification with a confidence threshold of 50%, which was recommended by RDP for fragments shorter than 250bp. (After trimming, the average length of reads in every group is around 200bp). Signaplot 13.0 was used for drawing figures.

Results

Three phylum groups (Lentisphaerae, Fibrobacteres, Synergistetes) were present in both placenta and colon samples with 30 to 70 times higher levels in colon, compared to placenta (p<0.05). When analyzed by the family members, Brachyspiraceae and Veillonellaceae (former Acidaminococcaceae) were more abundant in placenta, while Porphyromonadaceae and unclassified Bacteroidales were more abundant in colon. When classified by genus, Brachyspira, Pediococcus and Robinsoniella were more represented in placenta compared to colon.

Conclusions

Veillonellaceae has been detected in the oral and nasopharyngeal cavities in NHP. Robinsoniella – an anaerobic spore-forming bacteria - has been recently isolated from the feces of preterm infants. Our data suggests that these bacteria, shared between gut and placenta, might be essential for placental and fetal development.

Acknowledgments

We acknowledge the help and dedication of J.J. Gunter, S. Chmielewski, and the many excellent animal caretakers, technicians, and veterinarians of the Southwest National Primate Center. This investigation used resources which were supported by the Southwest National Primate Research Center grant ROI P50 ROI P50 AI113102-11 from the National Centers for Research Resources, National Institutes of Health, and P51 OD011133. This investigation was conducted in facilities constructed with support from the Office of Research Infrastructure Programs, NIH, and which are currently supported by the Office of Research Infrastructure Programs, NIH through Grant Number 1P51 OD011133. This investigation was conducted in facilities constructed with support from the Office of Research Infrastructure Programs, NIH, through Grant Number 1P51 OD011133 and 1RO1 LM046176. The research was also supported by New Investigator 5T32DK007662 and UT Health San Antonio T32 training grant to Dr. Peter Nathaniel (5T32DK007662-San Antonio).