

MICROBIOTA AND THE GUT-PLACENTA AXIS IN NON-HUMAN PRIMATES (*PAPIO SPP.*)

Natalia Schlabritz-Loutsevitch¹, Xuan Ji Li², Christopher Rensing², Bill Taylor³, Caitlin Costelle³, Gene Hubbard⁴, Gary Ventolini¹ and Edward Dick⁵

¹Department of Obstetrics and Gynecology, College of Medicine, Texas Tech University Health Sciences Center1 Texas Tech University Health Sciences Center at the Permian Basin, Odessa, TX, USA

²University of Copenhagen, Denmark

³University of Tennessee Health Sciences Center, Memphis, TN, USA

⁴University of Texas health Sciences Center at San Antonio, TX, USA

⁵Texas, Biomedical Research Institute, San Antonio, TX, USA



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 (*Papio spp.*).

Method

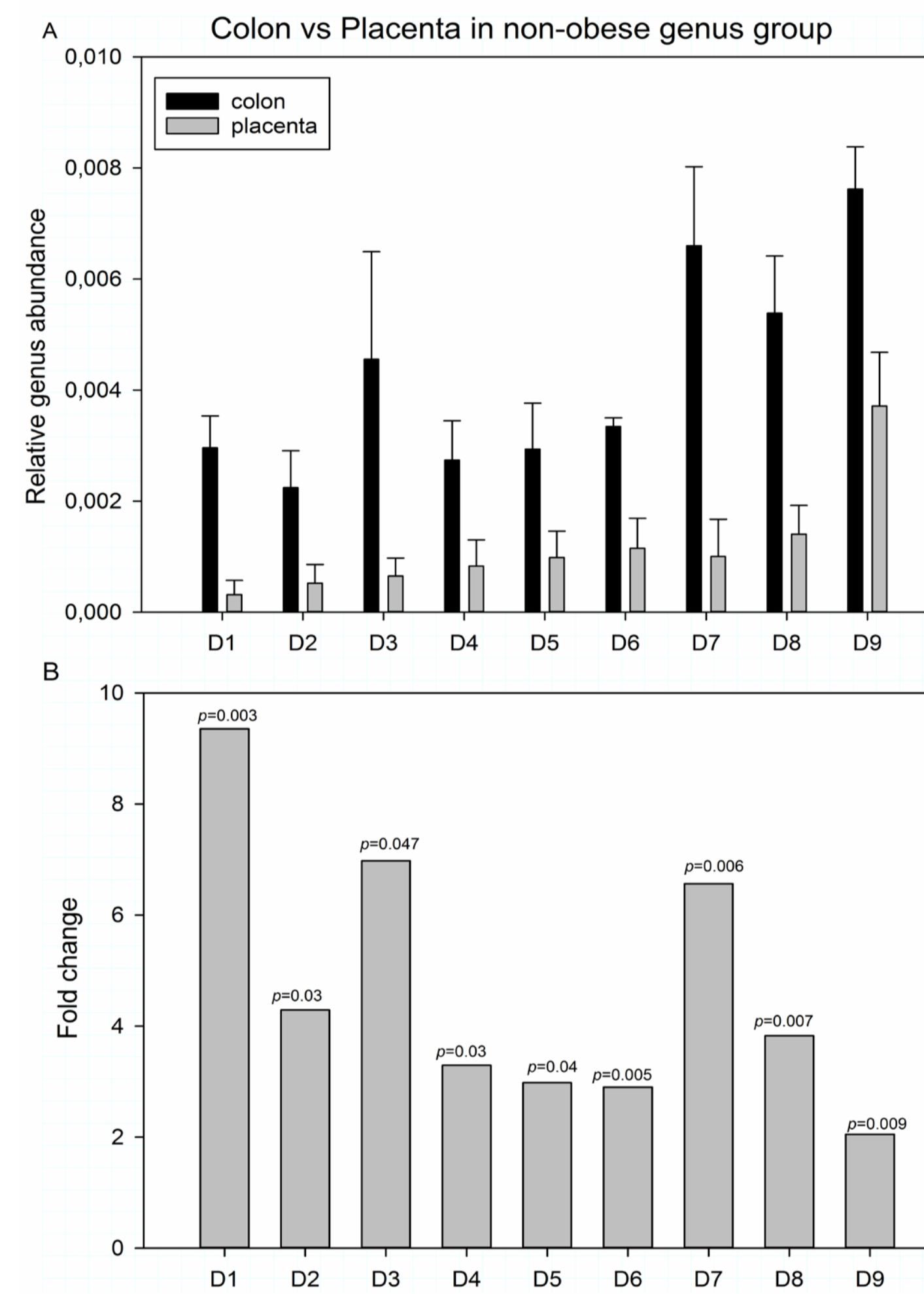
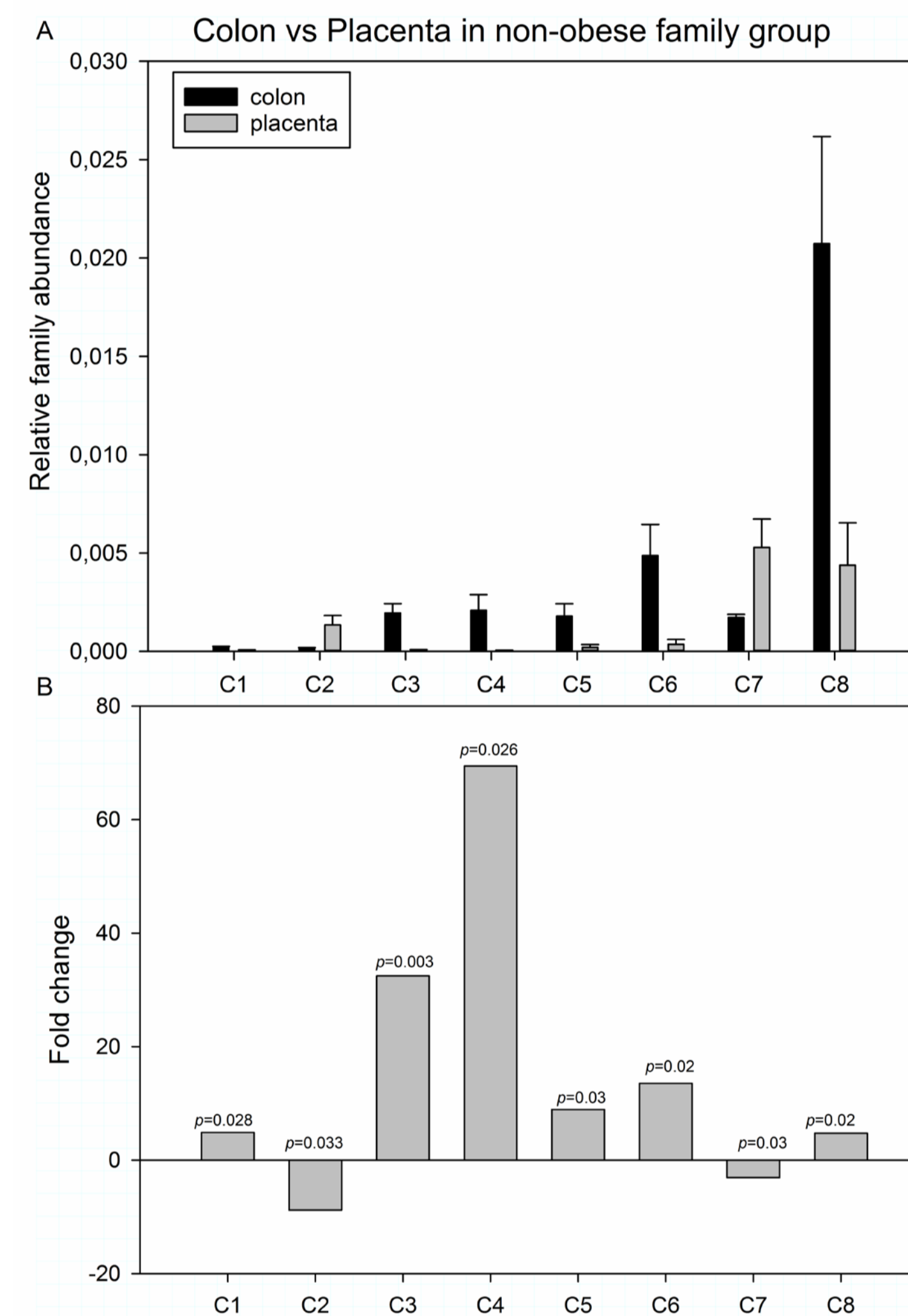
Samples were collected under sterile conditions during necropsy from three non-obese pregnant baboons (165 days of gestation), described in detail previously (Placenta .Nov; 32(11)). Two paired samples from each animal (colon and placenta) were flash-frozen in liquid nitrogen and stored at -80C. The 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). Sigmaplot 13.0 was used for drawing figures.

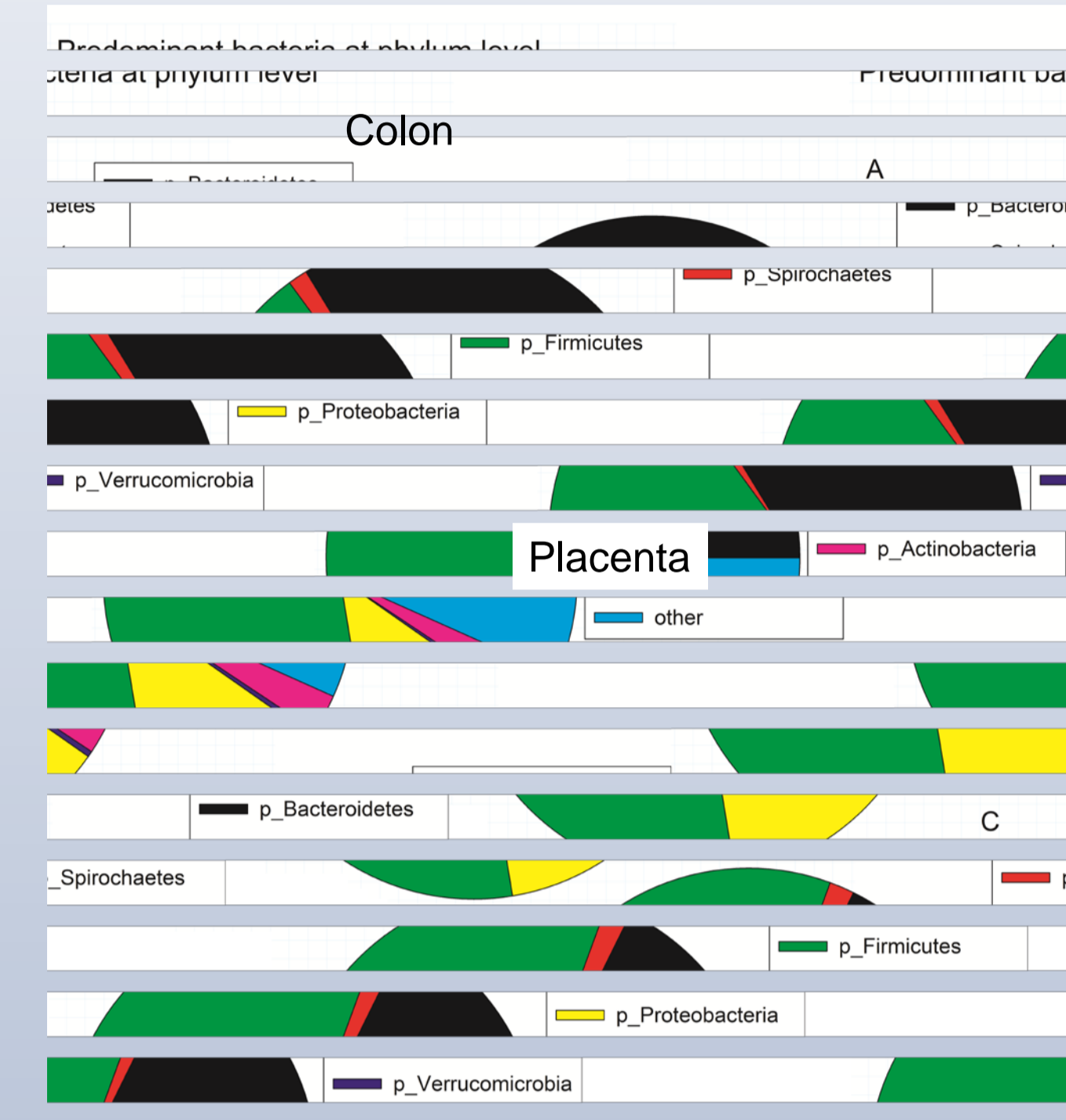
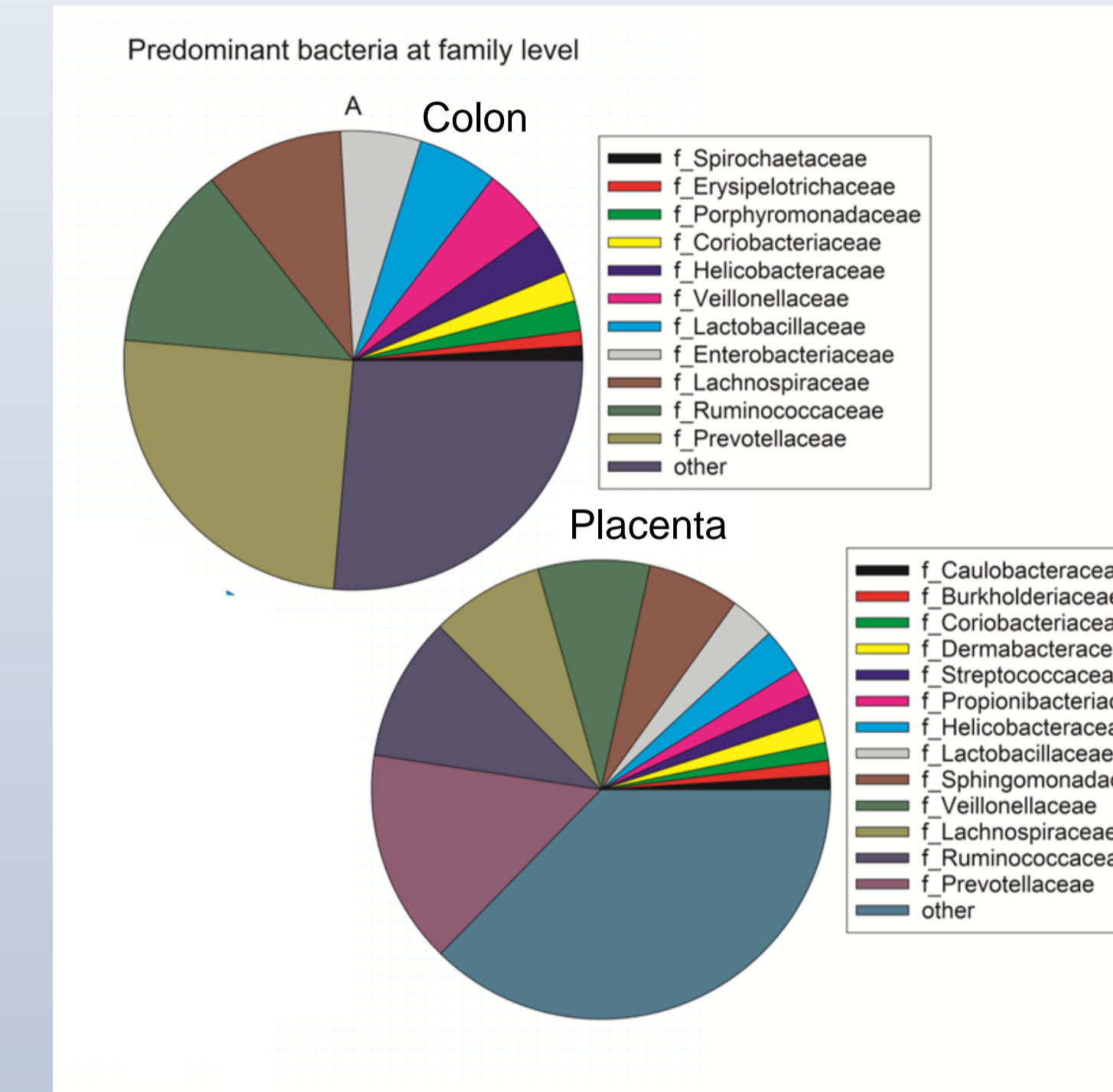
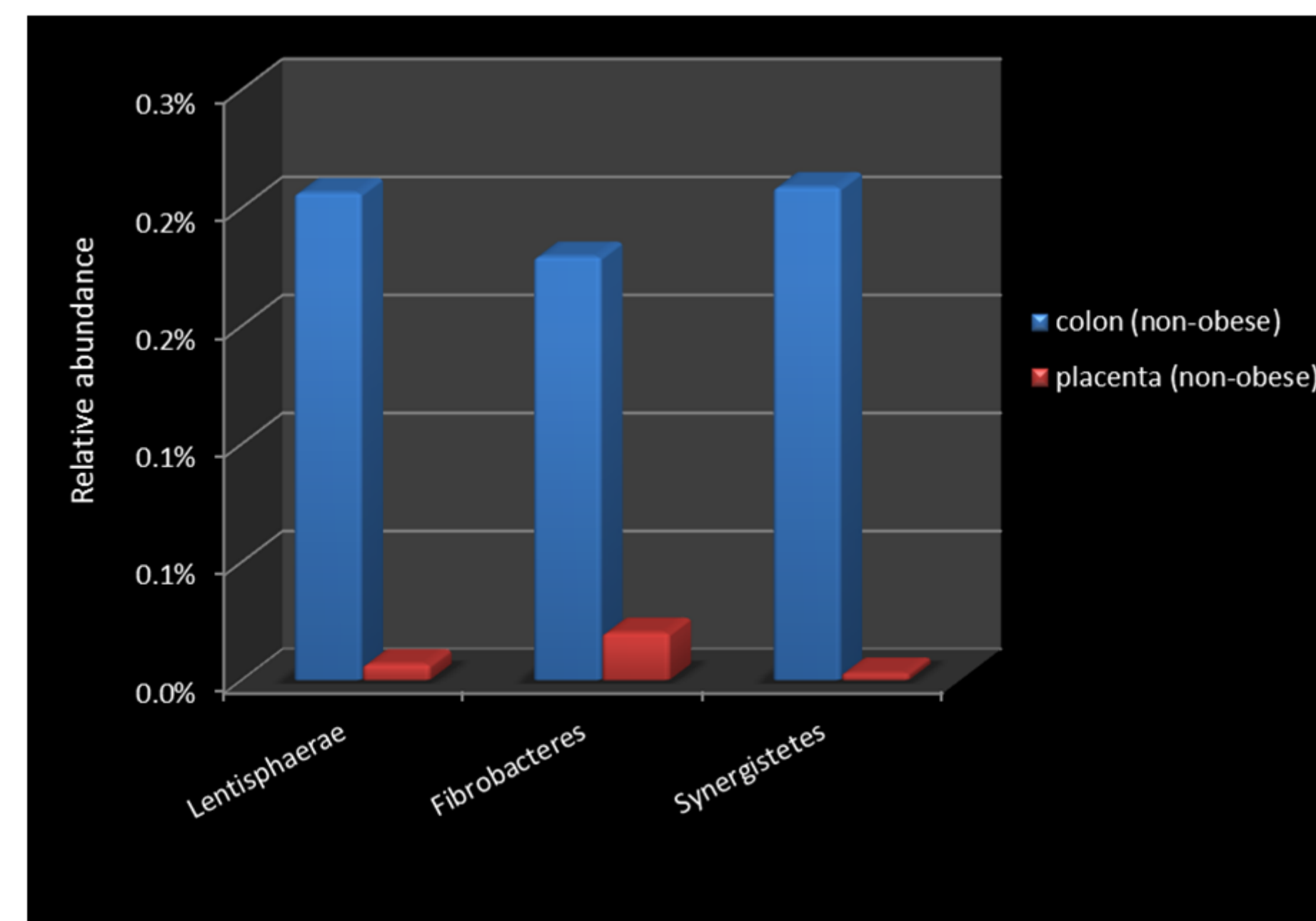
Results

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, Pedicoccus and Robinsoniella were more represented in placenta compared to colon.



Root_k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptococcaceae.1	C1	Root_k_Bacteria.p_Lentisphaerae.c_Oligosphaeria.o_Oligosphaerales.f_Oligosphaeraeae.g_Oligosphaera.D1
Root_k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Carrobacteriaceae	C2	Root_k_Bacteria.p_Fibrobacteres.c_Fibrobacteria.o_Fibrobacterales.f_Fibrobacteraceae.g_Fibrobacter.D2
Root_k_Bacteria.p_Lentisphaerae.c_Oligosphaeria.o_Oligosphaerales.f_Oligosphaeraeae	C3	Root_k_Bacteria.p_Firmicutes.c_Erysipelotrichia.o_Erysipelotrichiales.f_Erysipelotrichaceae.other
Root_k_Bacteria.p_Synergistetes.c_Synergistales.o_Synergistales.f_Synergistaceae	C4	Root_k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Butyrvibrio.D4
Root_k_Bacteria.p_Fibrobacteres.c_Fibrobacteria.o_Fibrobacterales.f_Fibrobacteraceae	C5	Root_k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae
Root_k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae	C6	g_Parabacteroides
Root_k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae	C7	Root_k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae
Root_k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae	C8	g_Hallella
		Root_k_Bacteria.p_Verrucomicrobia.c_Subdivision5.g_Subdivision5_genera_incertae_sedis
		g_Pseudobutyrvibrio
		Root_k_Bacteria.p_Actinobacteria.c_Actinobacteria.s_Corrobacteriaceae.o_Corrobacteriales.s_Corrobacteriaceae.f_Corrobacteriaceae.other

The phylum with changes under non-obese group by statistical analysis



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

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