🏆 **BEST IN CATEGORY PRIZE: PREGNANCY AND PELVIC FLOOR DISORDERS**

CONTINENT PREGNANT WOMEN UROBIOME CHARACTERIZATION AND DYSBIOSIS INFLUENCE ON PREGNANCY-SPECIFIC URINARY INCONTINENCE: PRELIMINAR RESULTS

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HYPOTHESIS / AIMS OF STUDY

The human microbiome refers to a collection of microorganisms that reside in and interact symbiotically with various human organs and body systems at the genomic, metabolomic, transcriptomic, and proteomic [1]. The human microbiome has been studied in pregnant women, focusing on the behaviour of specific microbiota [2], such as urobiome which refers to microbiome from urinary tract. It has been proposed that changes in the maternal microbiota may be linked to a maternal metabolic profile, contributing to the development of pregnancy-related diseases [3]. The main objective of this research, therefore, was to characterize the urobiome of continent and urinary incontinent pregnant women, with the hypothesis that the compositions of the urobiome may be altered in the presence of pregnancy-specific urinary incontinence (PS-UI).

STUDY DESIGN, MATERIALS AND METHODS

The study was approved by the Research Ethics Committee (CAAE: 55033621.5.0000.5411). Participants were previously informed about the research and the destination of the material, and this was only collected and used with express consent in a specific form (Informed Consent Form – TCLE). Analysis was carried out in groups comparison. Continent Normoglicemic Group (C-NG), without presence of urinary incontinece, and Urinary Incontinence Normoglicemic Group (UI-NG), with occurrence of PS-UI, were composed of 10 volunteers each. To group composotion real-time PCR was performed on all urine samples to detect bacterial presence. Then, the samples characterized as “presence” were assimilated and others were excluded. Samples that did not meet the methodological criteria for 16s sequencing and analysis were also excluded. The volunteers initially took an anamnesis and answered the urinary incontinence questionnaires (ISI and ICIQ-SF), with an appropriate professional, to ascertain the presence or absence of PS-UI, and then the urine sample was collected. Other collection procedures were carried out through the hospital's internal procedures and were available in the database. Extraction of genomic DNA from urine samples was performed using spin columns from the QIAamp® Viral RNA mini kit, following the manufacturer's recommendations and protocols.

RESULTS

The genera most present in the samples were considered: Lactobacillus, Gardnerella, Ureaplasma, Haemophilus, Prevotella, Finegoldia, Bifidobacterium, Dialister, Veillonella, Atopobium, Corynebacterium, Staphylococcus, Fusobacterium, Clostridium*, Peptoniphilus and Anaerococcus. The raw results demonstrate that both groups demonstrate a high frequency of Lactobacillus, Gardnerella and Ureaplasma when compared to the frequency of other bacterial genera.

INTERPRETATION OF RESULTS

Abundance of Lactobacillus, Gardnerella and Ureaplasma was higher in the UI-NG group. It was also possible to note that the standard deviation in these bacterial genera was relatively high, even though it also shows greater volumes for the incontinent group. In relation to the other bacterial genera, haemophilus, prevotella and clostridium*, did not appear in the samples from the incontinent group, but they did appear in the continent group (C-NG), while Bifidobacterium was found only in the incontinent group (UI-NG).

CONCLUDING MESSAGE

From the results presented, it is possible to characterize the most frequent bacterial genera in normoglycemic pregnant women. Incontinent pregnant women appear to have a different abundance of bacterial genera when compared to the continent group, but other statistical analyses are necessary for the comparison analysis to be reliable.

FIGURE 1

	C-NG		UI-NG		
	Mean	SD	Mean	SD	Mean Difference
Bacterial Gender	n = 10		n = 10		
Lactobacillus	5,604.7	12,522.2	7,194	16,.510.7	-1,589.3
Gardnerella	2,896.6	5,851.8	4,220.7	8,091.4	-1,324.1
Ureaplasma	1,925.1	5,206.2	3,670.1	10,110.5	-1,745
Haemophilus	2,428.7	7,680.2	0	0	2,428.7
Prevotella	1.,8	46.8	0	0	14,8
Finegoldia	137.4	146.3	156.5	285.8	-19,1
Bifidobacterium	0	0	748.2	2,366.0	-748.2
Dialister	138.2	182.8	86.4	105.6	51.8
Veillonella	102.3	300.1	0.3	0.9	102
Atopobium	67.4	156.1	368.1	778.1	-300.7
Corynebacterium	197.1	600.3	4.4	13.9	192.7
Staphylococcus	75.2	73.9	39.4	53.5	35.8
Fusobacterium	9.9	19.2	25.6	34.6	-15.7
Clostridium*	67.9	154.3	0	0	67.9
Peptoniphilus	66.3	119.7	24.7	43.9	41.6
Anaerococcus	122.4	253.5	7.1	11.7	115.3

Characterization of the genera with the highest bacterial abundance and their respective bacterial frequency divided by groups. Mean and standard deviation of the two groups, C-NG: Continent - Normoglycemic; UI-NG: Urinary Incontinence – Normoglycemic.

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