NEONATUS
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Relationship between gestational age and mode of delivery on microbiota profile.

Anna Bartnicka, Monika Szewc,
Katarzyna Mielnik, Mirosława Gałęcka, Jan Mazela

Department of Neonatology and Infectious Diseases, Poznan University of Medical Sciences

Institute of Microecology, Poznan

INTRODUCTION

- First bacterial communities (seeding bacteria) are acquired from the mother (also intrauterinally) and the environment.
- Very crucial is initial priming of the neonatal digestive system with optimal microbiota.
- Microbiota composition is influenced by early life exposures
  - Mode of delivery (vaginal vs cesarean)
  - Breast milk vs formula feeding
  - Maternal microbiota (stress/diet/BMI during pregnancy)
  - Diet
  - Sanitation and level of cleanliness
  - Antibiotic therapy
- There is substantial new information on the role of first 1000 days of life on the development of optimal microbiome and human body programming.
- Gut dysbiosis can be responsible for many diseases such as NEC, celiac disease, obesity, chronic enetrocolitis, Crohn disease, irritable bowel syndrome, infantile colic, atopic dermatitis, allergy, autism, depression and autoimmune diseases, and finally non-comunicable diseases.

AIM

The goal of the study was to assess the impact of gestational age and mode of delivery on microbiota profile in term and preterm infants delivered vaginally or by C-section.

MATERIALS

GROUPS

- **Full-term newborns (n=32)**

Including criteria: gestation age >=37 weeks of pregnancy, body birth weight >=2,500 g

Excluding criteria: gastrointestinal disorders, congenital malformation

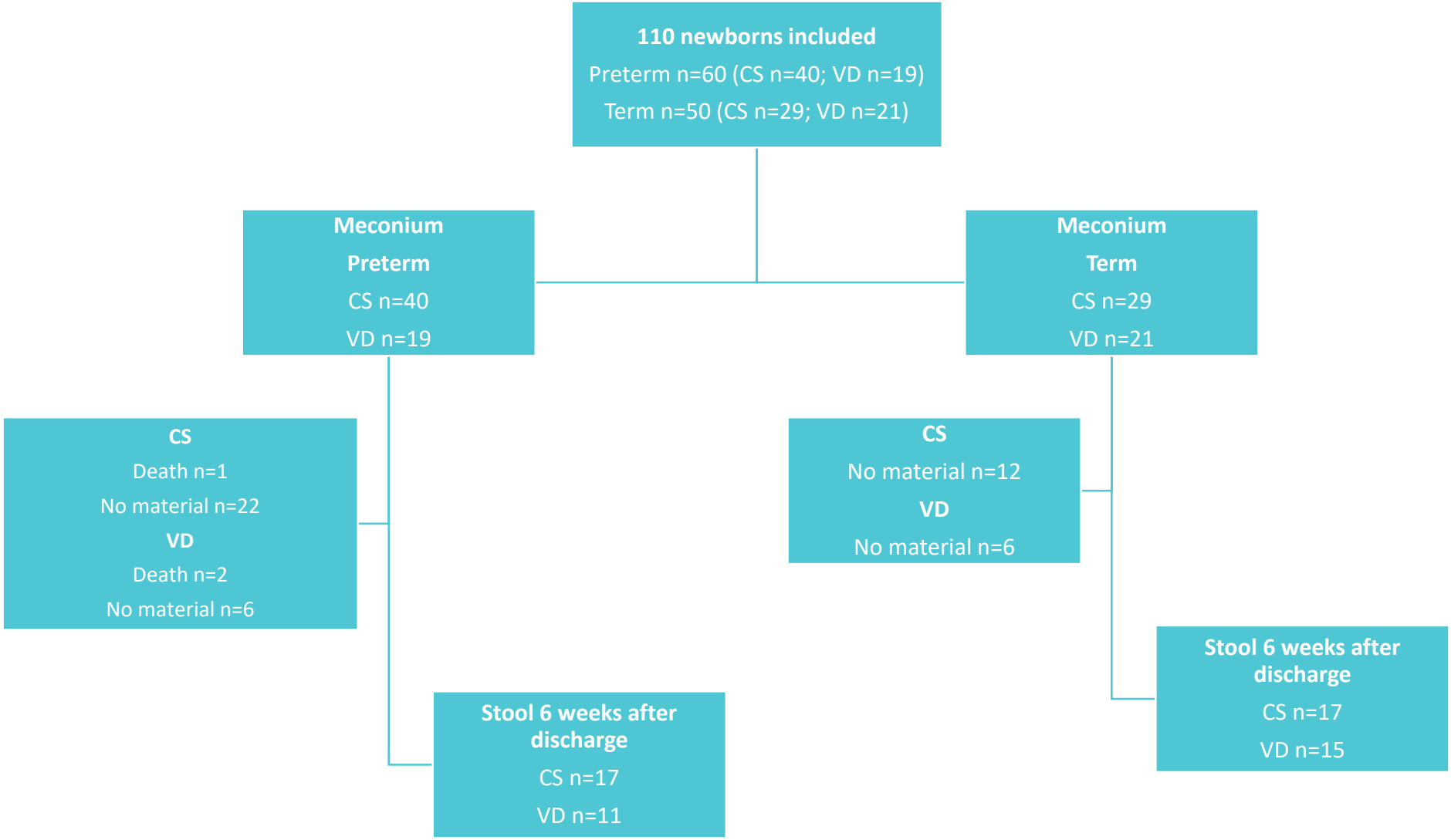
- **Preterm newborns (n=28)**

Including criteria: gestation age <32 weeks of pregnancy, body birth weight <2,500 g

Excluding criteria: gastrointestinal disorders, congenital malformation

MATERIALS

- **Meconium and stool 6 weeks after discharge from hospital**


110 newborns included
Preterm n=60 (CS n=40; VD n=19)
Term n=50 (CS n=29; VD n=21)
Meconium
Preterm
CS n=40
VD n=19
Meconium
Term
CS n=29
VD n=21
CS
Death n=1
No material n=22
VD
Death n=2
No material n=6
CS
No material n=12
VD
No material n=6
Stool 6 weeks after discharge
CS n=17
VD n=11
Stool 6 weeks after discharge
CS n=17
VD n=15

METHODS

- Determination of intestinal microbiota (qPCR and microbiological culture) in meconium and stool 6 weeks after discharge performed.
  - *Escherichia coli*
  - *Enterococcus* spp.
  - *Enterobacteriaceae*
  - *Lactobacillus* spp.
  - *Bifidobacterium* spp.
  - *Bacteroides* spp.
  - *Pseudomonas* spp.
  - *Proteus* spp.
  - *Clostridium* spp.
  - *Faecalibacterium prausnitzii*
  - *Akkermansia muciniphila*
  - Total bacterial count (TBC)
  - *Yeasts*
- The following statistical tests were utilized; non-parametric Mann Whitney, Kruskal-Wallis and Dunn test and correlations were tested with Fisher-Freeman and percentages with u-Gauss test.

RESULTS

Population

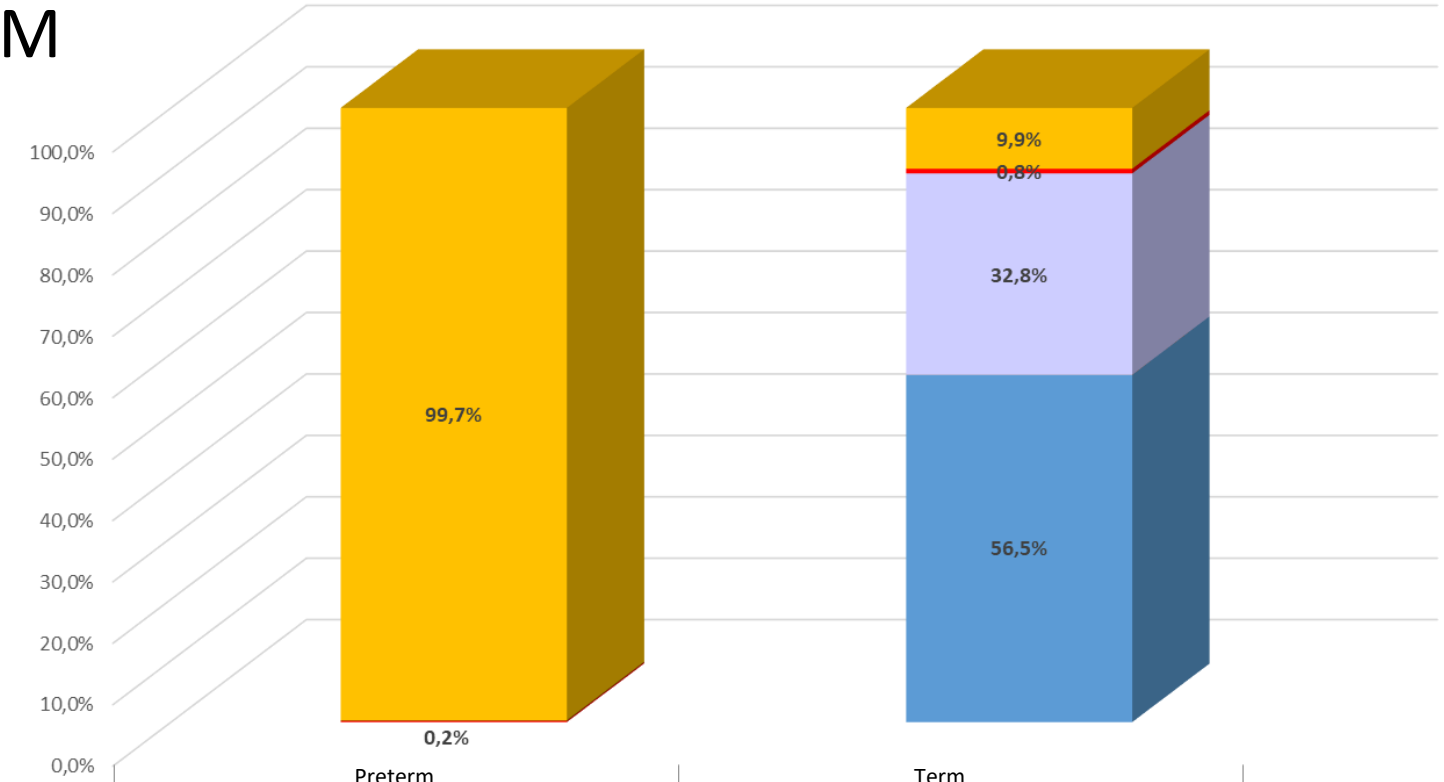
- ✓ Term

BW = 3536,3 g ± 517,4 (mean ± SD)
GA = 39,2 wks + 1,3 (mean ± SD)

- ✓ Preterm

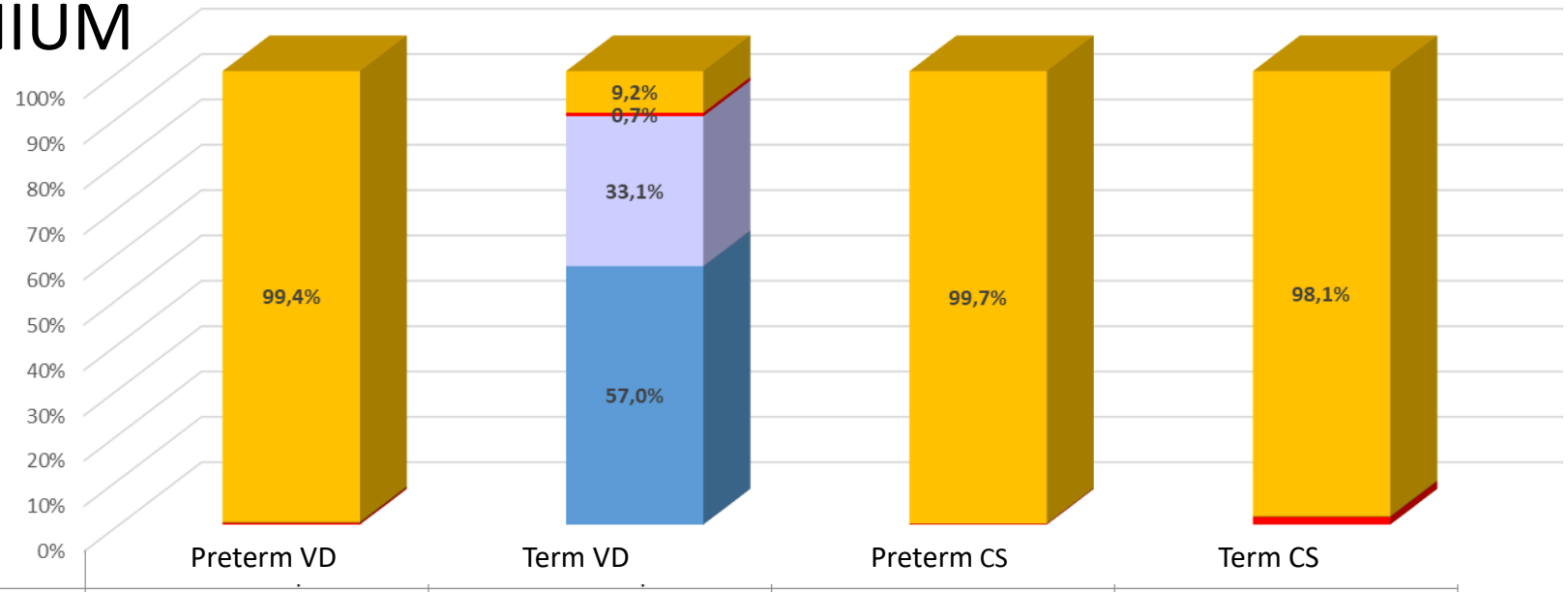
BW= 1586,7 g ± 350,9 (mean ± SD)
GA = 30,6 wks + 1,9 (mean ± SD)

MECONIUM



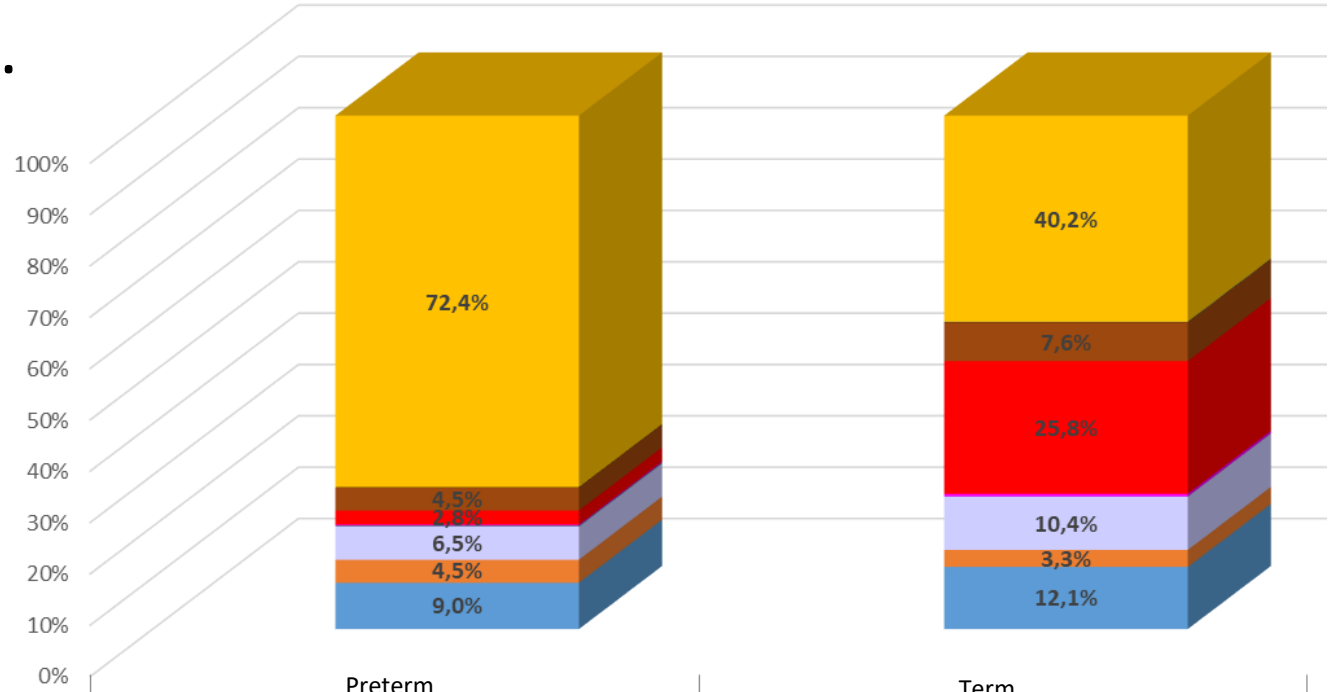
	Preterm	Term
Inne	99,7%	9,9%
Akkermansia muciniphila	0,0%	0,0%
Faecalibacterium prausnitzii	0,1%	0,0%
Clostridium	0,0%	0,0%
Bacteroides	0,0%	0,0%
Bifidobacterium	0,2%	0,8%
Lactobacillus	0,0%	0,0%
Pseudomonas	0,0%	0,0%
Proteus	0,0%	0,0%
Enterococcus	0,0%	32,8%
Enterobacteriaceae	0,0%	0,0%
E. coli	0,0%	56,5%

MECONIUM



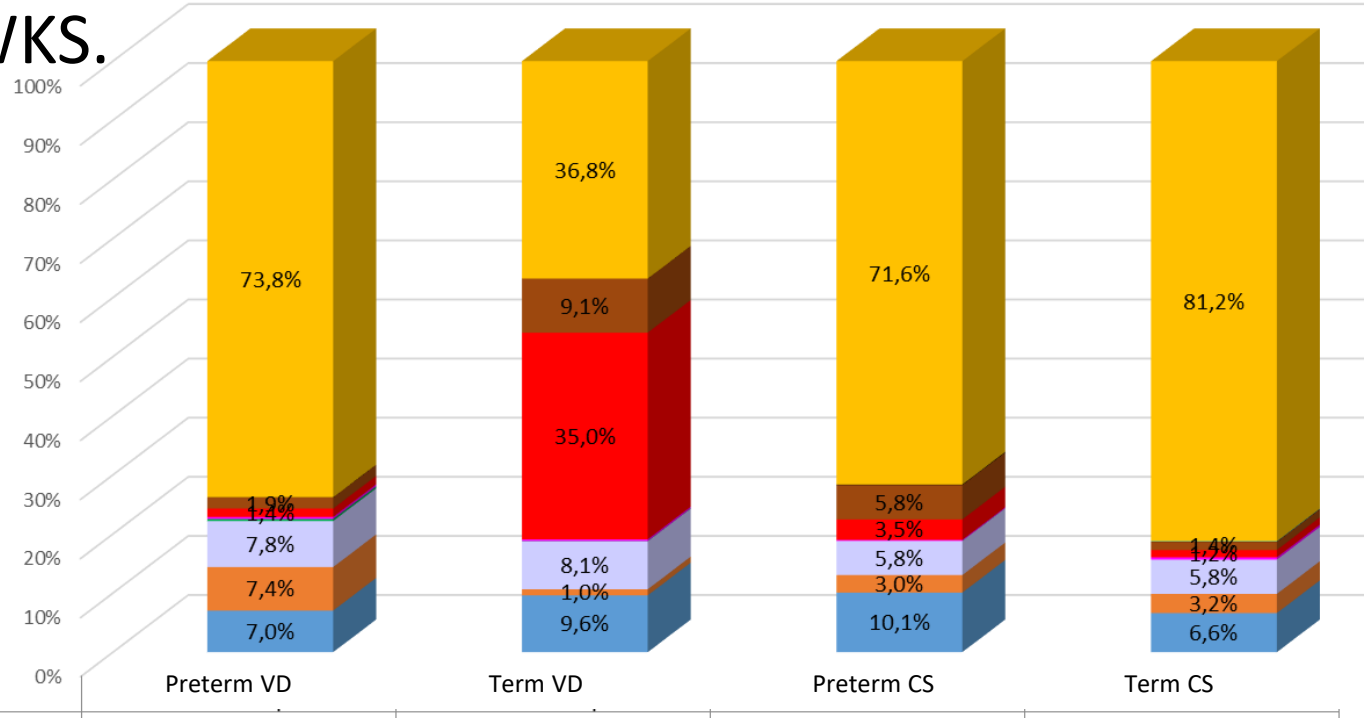
	Preterm VD	Term VD	Preterm CS	Term CS
Inne	99,4%	9,2%	99,7%	98,1%
Akkermansia muciniphila	0,0%	0,0%	0,0%	0,0%
Faecalibacterium prausnitzii	0,2%	0,0%	0,1%	0,2%
Clostridium	0,0%	0,0%	0,0%	0,0%
Bacteroides	0,0%	0,0%	0,0%	0,0%
Bifidobacterium	0,4%	0,7%	0,2%	1,7%
Lactobacillus	0,0%	0,0%	0,0%	0,0%
Pseudomonas	0,0%	0,0%	0,0%	0,0%
Proteus	0,0%	0,0%	0,0%	0,0%
Enterococcus	0,0%	33,1%	0,0%	0,0%
Enterobacteriaceae	0,0%	0,0%	0,0%	0,0%
E. coli	0,0%	57,0%	0,0%	0,0%

STOOL 6 WKS.



	Preterm	Term
Inne	72,4%	40,2%
Akkermansia muciniphila	0,0%	0,1%
Faecalibacterium prausnitzii	0,0%	0,0%
Clostridium	0,1%	0,0%
Bacteroides	4,5%	7,6%
Bifidobacterium	2,8%	25,8%
Lactobacillus	0,2%	0,5%
Pseudomonas	0,0%	0,0%
Proteus	0,1%	0,0%
Enterococcus	6,5%	10,4%
Enterobacteriaceae	4,5%	3,3%
E. coli	9,0%	12,1%

STOOL 6 WKS.



	Preterm VD	Term VD	Preterm CS	Term CS
Inne	73,8%	36,8%	71,6%	81,2%
Akkermansia muciniphila	0,0%	0,0%	0,0%	0,1%
Faecalibacterium prausnitzii	0,0%	0,0%	0,0%	0,0%
Clostridium	0,0%	0,0%	0,1%	0,0%
Bacteroides	1,9%	9,1%	5,8%	1,4%
Bifidobacterium	1,4%	35,0%	3,5%	1,2%
Lactobacillus	0,3%	0,3%	0,2%	0,4%
Pseudomonas	0,0%	0,0%	0,0%	0,0%
Proteus	0,3%	0,0%	0,0%	0,0%
Enterococcus	7,8%	8,1%	5,8%	5,8%
Enterobacteriaceae	7,4%	1,0%	3,0%	3,2%
E. coli	7,0%	9,6%	10,1%	6,6%

CONCLUSIONS

- Vaginal delivery is preferred mode of delivery assuring the most optimal microbiota priming for mature infants which can be observed in the stool profile at 6 weeks of being home.
- On the other hand impact of other factors negatively influencing gut microbiota of a preterm infant is so significant that vaginal delivery can not compensate its' negative impact on meconium and stool after 6 weeks being home.
- In summary, it can be speculated that infants born at the GPSK in Poznan can benefit by multistrain probiotic supplementation with *E. coli, Enterococcus, Bifidobacterium* and *Lactobacillus* if born prematurely. Further studies should establish safety and efficacy profile of such therapeutic approach.
- Further analysis of SCFA are ongoing.

Thank you for your attention