with functional constipation will possible to significantly reduce the incidence of SIBO.

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P3.33 | Nitrofurans in correction of gut microbiota disorders

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Background: Choice of effective method for correction of moderate and severe disorders of gut microbiota is an actual question for many scientists. Nitrofurans are the antimicrobial drugs that often use for gut microbiota correction. The aim: To estimate drug resistance of opportunistic bacteria to two common used nitrofurans: nifuratel and nifuroxazide.

Methods: 62 patients with high risk of gut dysbiosis were observed. We perform bacteriological analysis and real time PCR in stool with detection of opportunistic bacteria level for all patients. If level of these bacteria was high, we estimated them resistance to nifuratel and nifuroxazide.

Results: We saw that more than half of investigated bacteria were sensitive to nifuratel and most of them were resistant to nifuroxazide (Table).

Conclusion: We recommend using nifuratel as an more effective of nitrofurans for correction of moderate and severe gut microbiota disorders especially in case of dysbiosis associated with Enterobacter spp. (widely prevalence and highly sensitive to nifuratel).

TABLE - Drug resistance of opportunistic bacteria to nitrofurans

Type of microorganism	% of patient with high level of microorganism	% of microorganisms sensitive to nifuratel	% of microorganisms sensitive to nifuroxazide
Enterobacter spp.	35.5 (n = 22)	100	0
Citrobacter spp.	4.8 (n = 3)	100	0
Klebsiella spp.	4.8 (n = 3)	0	0
St. aureus	9.7 (n = 6)	100	0
Candida spp.	3.2 (n = 2)	0	0
Proteus spp.	3.2 (n = 2)	0	0
E.coli with hemolytic features	19.4 (n = 12)	75	8.3
E. coli lac (-)	6.5 (n = 4)	75	0

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P3.34 | Circulating blood microbiome signatures in patients with liver cirrhosis and portal hypertension

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Aim of the study: To detect changes in circulating blood microbiom in patients with portal hypertension(PH).

Introduction: Studies from recent years have shown that intestin microbiome is linked to the development of liver cirrhosis and di ease related complications. In the last two years, studies have shov changes in circulating microbiome in patients with liver diseas however, circulating microbiome in patients with PH has not be assessed yet.

Methods: Study was conducted in Department of Gastroenterolo of Lithuanian University of Health Sciences, Kaunas Clinics and i cluded a cohort of 58 patients with liver cirrhosis and 46 healt control (HC) subjects. 16S rRNA gene sequencing of V1-V2 va able regions was used to determine bacterial composition of blo plasma samples.

Results: Taxonomic composition analysis at the phylum level r vealed that blood microbiome in both PH patients and HC subjec was predominated by *Proteobacteria*, *Bacteroidetes*, *Actinobacte* and *Firmicutes*. α-diversity was not significantly different betwe HC and PH patients, nor between different blood compartmen of PH patients. Bacterial community structure did show significa clustering between HC and PH patients. Differential abundan analysis revealed several differently abundant genera between H and PH patient. Subgroup analysis of PH patients with different d gree of PH revealed no significant differences in composition at ph lum level, α-diversity or β-diversity.

Conclusions: Circulating blood microbiota comprises of four ma phyla - *Proteobacteria*, *Bacteroidetes*, *Actinobacteria* and *Firmicut* Several genera were differently abundant between PH patients a HC subjects.

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