Aims & Methods: We aimed to establish the first stool bank in an Eastern European country - Bulgaria. A multidisciplinary team of gastroenterologists, medical microbiologists, infectious diseases specialist and geneticists was set up. We used a questionnaire based on the First European FMT Consensus (1) in order to recruit possible stool donors. Microbiota analysis was performed on all selected donors.
Results: Between October 2018 and April 2019, 112 donor volunteers completed a questionnaire; 70 (62.5%) were excluded, mainly because age above 50, an unhealthy BMI and risk behavior. Fourty-two (37.5%) donor candidates were invited for laboratory testing of blood and feces of which 12 (28.6%) passed this screening. Presence of Helicobacter pylori fecal antigen and Multi Drug Resistant Organisms were the most observed exclusion criteria. Of 12 donors, 4 (33%) failed at a following screening test, which is performed every three months. Finally, 8 (7.14%) active donors were enrolled.
Conclusion: Even though we found many healthy volunteers, only a low percentage (7.14%) of them are suitable to become feces donors. Establishing of a stool bank in a country with lower HDI is important for making FMT saver and more popular as a treatment method, finding further implementation and regulation of FMT and supporting physicians offering this treatment to their patients.
References: 1. Cammarota G, Ianiro G, Tilg H, et al. European consensus conference on faecal microbiota transplantation in clinical practice. Gut. 2017 Apr;66(4):569-580.
Disclosure: Nothing to disclose

P1841 DYNAMIC CHANGES OF OXALATE-DEGRADING ACTIVITY OF FECAL MICROBIOTA IN RATS AFTER CEFTRIAXONE TREATMENT

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Introduction: An urgent problem of modern urology is the increase in the number and rejuvenation of the age of patients suffering from urolithiasis. It has been established that from 70 to 80% of stones excreted during urolithiasis are calcium oxalate, and the level of oxaluria depends in a certain way on the composition and functional activity of intestinal microbiota, in particular on the ability to degrade oxalates. Except for *Oxalobacter formigenes*, a number of normobiote representatives are capable to metabolize oxalate salts (e.g. *Lactobacillus spp., Bifidobacterium spp., Eubacterium lentum, Bacillus spp, Enterococcus faecalis,).* The anbibiotics decreased the quantity of oxalate-degrading bacteria (ODB) but there is no available data and approaches to evaluate the total oxalate-degrading activity (ODA) of fecal microbiota (without isolation of pure culture).
Aims & Methods: The aim of the present study was to develop approach for evaluation of total ODA of fecal microbiota and to assess the dynamics changes in the ODA of fecal microbiota after broad-spectrum antibiotic ceftriaxone treatment in rats. The object of the study was fecal microbiota of male Wistar rats (200-300 g, n = 6). Ceftriaxone (300 mg/kg, CJSC "Darnitsa", Ukraine) was injected intramuscularly for 7 days. Faeces were collected before antibiotic treatment and on the 1st, 14th and 56th days after antibiotic withdrawal. The quantity of ODB was determined by culture method on a highly selective *Oxalate Medium* (g/L): K_2HPO_4 - 0.25; KH_2PO_4 - 0.25; $(NH_4)_2SO_4$ - 0.5; $MgSO_4 \cdot 7H_2O$ - 0.025; CH_3COON - 0.82; yeast extract - 1.0; rezazurin - 0.001; Na_2CO_3 - 4; L-cysteine-HCl - 0.5; *Trace element solution SL-10* - 1 ml with the following composition per L: HCl (25%; 7.7 M) - 10.00 ml, $FeCl_2 \times 4H_2O$ - 1.50 g, $ZnCl_2$ - 70.00 mg, $MnCl_2 \times 4H_2O$ - 100.00 mg, H_3BO_3 - 6.00 mg, $CoCl_2 \times 6H_2O$ - 190.00 mg, $CuCl_2 \times 2H_2O$ - 2.00 mg, $NiCl_2 \times 6H_2O$ - 24.00 mg, $Na_2MoO_4 \times 2H_2O$ - 36.00 mg; та $Na_2C_2O_4$ - 5 mg (cultivated anaerobically at 37°C for 48 hours). The redoximetric titration (with KMnO4) was adopted to evaluate the total ODA of faecal microbiota. The results were expressed in % degradation of oxalate for 0.01 g of feces.
Results: At the 1st day after ceftriaxone withdrawal, we observed increase a number of ODB from lg 8.02±0.25 CFU/g to lg 9.47±0.17 CFU/g ($p< 0.05$) and fecal microbiota ODA from 9.50±1.78 % to 11.67±2.99 %. At the 14th day there was a significant decrease a number of ODB by more than 2 orders of magnitude (from lg 8.02±0.25 CFU/g to lg 5.72±0.48 CFU/g, $p< 0.05$), that was accompanied diminish the fecal ODA - from 9.50±1.78 % to 6.3±1.46 %. By the 56th day, a number of ODB was almost unchanged *vs.* 14th day of experiment (lg 5.28±0,45 CFU/g, $p< 0.05$), but fecal ODA continued decrease (from 9.50±1.78 % to 4.67 ± 1.87%, $p< 0.05$).
Conclusion: 1) The redoximetric titration (with KMnO4) is the reliable method for evaluation of total ODA of the fecal microbiota without isolation of pure culture and might have clinical application. 2) Ceftriaxone treatment reduced the total oxalate-degrading activity of fecal microbiota independently on number of ODB.
Disclosure: Nothing to disclose

P1842 THE DYNAMICS OF MUCOSA-ASSOCIATE BACTERIA IN IRRITABLE BOWEL DISEASE

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Introduction: The gut microbiota between individuals varies greatly, while the composition of gut microbiota within individual slightly changes over time. Fecal samples can be easily collected and are often used to analyzing gut microbiota.
On the other hand, the composition of mucosal bacteria differs from that of luminal bacteria. Though mucosal bacteria are considered to be important in the pathophysiology of intestinal disease including irritable bowel disease (IBS), there are small numbers of study investigating the dynamic analysis of mucosa-associated bacteria because of the difficulty of collecting the sample comparing to fecal samples.
Aims & Methods: The purpose of this study is to analysis the dynamics of mucosa-associated bacteria over time in patient with IBS. The mucus samples including mucosal bacteria were collected from terminal ileum, cecum, transverse colon, sigmoid colon and rectum in same patient with IBS three times at the examination with lower endoscopy using cytology blush. After extracting DNA from mucus samples, 16S metagenome were performed by Miseq platform(Illumina). Sequence data were quality filtered and microbial composition, alpha and beta diversities were analyzed using QIIME open-source software.
Results: The microbial composition of mucosal samples collected by blush were comparable to that of mucosal samples collected by mucosal biopsy and microbial DNA amount in the mucus samples collected by blush were more than 1000 times larger than that of from biopsy samples. Though the microbial composition of mucosal bacteria were different from that of fecal samples, there were not big different change when comparing between each mucosal samples collected from terminal ileum, cecum, transverse colon, sigmoid colon and rectum.
Compared to luminal bacteria, the proportion of Sutterella, Enterobacteriaceae, Delftia and Pseudomonas were increased in the mucus samples on the other hands Phascolarctobacterium, Blautia, Lachnospiraceae, Parabacteroides were decreased. Interestingly PCoA analysis revealed that the microbial composition of mucosa-associate bacteria had slightly changed over time as with the fecal microbial composition.
Conclusion: In this study there are small dynamic changes of mucosa-associate bacteria as with luminal bacteria within the individuals in IBS patient over time and may constantly contribute to the pathophysiology of IBS.
Disclosure: Nothing to disclose

P1843 PEOPLE'S MOTIVATION THROUGH SOCIAL NETWORKS COULD INCREASE PARTICIPATION IN COLORECTAL CANCER SCREENING CAMPAIGNS

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Introduction: Colorectal cancer (CRC) screening using fecal occult blood testing results in reduced CRC mortality. However participation rates in organized campaign remains low and rarely exceed 50% in most French departments. The Colorectal Cancer Screening Association in Seine-Saint-