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Conference Abstract A12

Colonic Microbiota Profile in Patients with Polycythemia Vera

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Background

Polycythemia vera (erythremia) is a chronic myeloproliferative neoplasm frequently accompanied by the development of ulcers in various parts of the gastrointestinal tract. This is associated with thrombosis of small vessels and trophic disturbances in the mucosa, leading to reduced strength of the mucosal barrier, translocation of Helicobacter pylori and fungi, disruption of the normal microbiota, and the development of systemic inflammation [1,2]. Several authors have demonstrated that the gut microbiota of patients with chronic myeloproliferative neoplasms differs from that of healthy individuals and is characterized by a reduced relative abundance of Firmicutes [3,4]. Therefore, the study of the composition of the colonic microbiota may make it possible to modulate the qualitative and quantitative parameters of bacterial associations and thereby improve the quality of life of patients with polycythemia vera.

Aim

To investigate the qualitative and quantitative composition of the colonic microbiota in patients with polycythemia vera.

Materials and Methods

The state of the colonic microbiota was assessed by real-time polymerase chain reaction using the "Kolonoflor-16" reagent kit (Alfalab, Russia) in 41 patients with polycythemia vera (Group 1) and 20 healthy donors (Group 2). Statistical analysis was performed using Microsoft Excel 2010 and IBM SPSS Statistics version 26.0. Results were considered statistically significant at $p < 0.05$ (Spearman's rank correlation coefficient).

Results

The composition of the colonic microbiota differed markedly between Groups 1 and 2 (Table 1).

Table 1. Comparison of quantitative indicators in patients with polycythemia vera and healthy donors.

Components	**Group 1**	**Group 2**	**p**
Total bacterial mass	3*10^8	1*10^13	0,084
Lactobacillus spp.	< 10^3	1*10^8	0,026
Bifidobacterium spp.	1*10^6	2*10^9	0,119
Escherichia coli	7*10^5	2*10^8	0,046
Bacteroides spp.	5*10^9	4*10^12	0,080
Faecalibacterium prausnitzii	2*10^6	7*10^10	0,031
Bacteroides thetaomicron	3*10^7	5*10^9	0,078
Akkermansia muciniphila	Not detected	4*10^9	0,108
Enterococcus spp.	4*10^10	2*10^6	0,022
Escherichia coli enteropathogenic	Not detected	4*10^3	0,047
Klebsiella pneumoniae	2*10^3	1*10^2	0,027
Klebsiella oxytoca	Not detected	2*10^3	
Candida spp.	5*10^7	1*10^2	0,046
Staphylococcus aureus	3*10^4	1*10^2	0,064
Clostridium difficile	1*10^2	Not detected	
Clostridium perfringens	Not detected	Not detected	
Proteus vulgaris/mirabilis	2*10^5	1*10^2	0,0424
Citrobacter spp.	4*10^3	Not detected	
Enterobacter spp.	3*10^5	2*10^2	0,173
Fusobacterium nucleatum	1*10^3	Not detected	
Parvimonas micra	Not detected	Not detected	
Salmonella spp.	Not detected	Not detected	
Shigella spp.	7*10^5	1*10^2	0,0416
Proportion of Bacteroides spp. And Faecalibacterium prausnitzii (Bfr/Fprau)	3300	0,01–100	0,0247

Note: p — statistical significance of differences in the analyzed parameters between patients with polycythemia vera and healthy donors.

Conclusion

Alteration of the normal colonic microbiota was identified in 84.6% of the examined patients. This was characterized by a decrease in the abundance of commensal microorganisms such as Lactobacillus spp., Bifidobacterium spp., and Faecalibacterium prausnitzii, and by an increase in Enterobacter spp., Candida spp., Staphylococcus aureus, and Clostridium difficile. An increase in the ratio of Bacteroides spp. to Faecalibacterium prausnitzii was observed, reflecting the anaerobic imbalance index and confirming chronic inflammation and immunodeficiency in patients with polycythemia vera during therapy.