Mini Review

BIOMEDICAL Journal of Scientific & Technical Research

ISSN: 2574 -1241

DOI: 10.26717/BJSTR.2022.45.007243

Role Intestinal Microbiome in the Development of Osteoarthritis Sugar Diabetes

M Yu Gulneva* and EV Malafeeva

Yaroslavl State Medical University, Doctor of Medical Sciences, Russia

***Corresponding author:** M Yu Gulneva, Yaroslavl State Medical University, Doctor of Medical Sciences, Associate Professor, Russia

ARTICLE INFO

Received: August 02, 2022

Published: August 17, 2022

Citation: M Yu Gulneva and EV Malafeeva. Role Intestinal Microbiome in the Development of Osteoarthritis Sugar Diabetes. Biomed J Sci & Tech Res 45(4)-2022. BJSTR. MS.ID.007243.

SUMMARY

When studying of the intestinal microbiome in patients with osteoarthritis in combination with type 2 diabetes mellitus established change in the gut microbiome with pronounced intestinal colonization opportunistic pathogens of the family Enterobacteriaceae, PPE which may be an additional factor that has a pathogenic effect on OA. Normalization of the intestinal microbiome may be one of the directions for the complex treatment of OA andCD2.

ABSTRACT

When studying the intestinal microbiome in patients with osteoarthritis in combination with type 2 diabetes mellitus, a change in the intestinal microbiome with pronounced colonization of the intestine by opportunistic microorganisms of the Enter bactericide family, LPS may be an additional factor that has a pathogenic effect on OA, was found. Normalization of the intestinal microbiome can be one of the directions of complex treatment of OA and DM2.

Keywords: Osteoarthritis; Type 2 Diabetes Mellitus; Gut Microbiome; Intestinal Microbiome

Mini Review

Osteoarthritis (OA) and type 2 diabetes mellitus (DM2) were and remain one of the most important problems of medicine, having wide use and with an increased risk disability and reduced quality of life. The combination of this pathology is exacerbated by the fact that with diabetes mellitus - a metabolic disease that can have a direct systemic effect on the joints, provoking or aggravating joint damage [1]. Considering that about osteoarthritis, like other rheumatic autoimmune diseases, is caused by a complex interplay of environmental, genetic them, immune and sexual factors, the importance of study microbiome, because synanthropic microorganisms are one of major environmental factors. The study of the role of the microbiome in the development of patients with OA and T2DM is important as in understanding pathogenic processes, and in developing new therapies for these diseases.

The purpose of the study: to study the intestinal microbiome in patients with osteoarthritis in combination with type 2 diabetes mellitus. Conducted clinical and laboratory examination 65 patients with OA24 of which the disease was combined with type 2 diabetes. Microbiological study of the intestinal microflora was carried out by bacteriological method with the study of the total number of microorganisms, the number of individual representatives of the intestinal microflora in CFU / g of feces and the frequency of isolation of individual species microorganisms. Statistical analysis of the obtained results was carried out by programs is STATISTICA

10.0 (StatSoftInc. USA). Comparative study of microbial biocenosis of the large intestine in 24 patients with OAandT2DM and 41 OA patients who were not diagnosed with diabetes, showed that with a combination of OA and DM2, significant changes in the micro biocenosis of the large intestine are observed. The gut microbiome is characterized oval up to 75% increase in detection rate Gram-negative bacteria of the family Enterobacteriaceae, while in patients with OA these microorganisms were detected in 26.83% of cases (p<0,01).

Hos painter med type 2-diabetes mellitus OA in 25% of cases fungi of the genus were found Candida, which in patients with OA were isolated in 4.9% of cases (p<0,05) and an increased frequency of hemolytic microorganisms within 75%, in patients with OA they were isolated in 34.1% of cases (p<0,05). Quantitative composition of the intestinal microflora in patients with OA and DM2 did not differ significantly changes in the number of individual representatives of the intestinal microflora (p>0.05). In this case, the absolute values of the level bacteria of the family Enterobacteriaceae and Staphylococcus aureus were slightly higher in diabetic patients. Withing 6.40 ± 0.9 8 CFU/ml andlg4.00 ± 1.79 CFU/ml (in patients with OA, respectivelylg5.46 ± 1.35 8cfu/ml andlg3.68 ± 1.28 cfu /ml). Symbiotic structure relations of microorganisms in the micro biocenosis of the large intestine had some differences. In patients OA and DM2 there was a transition bacterium of the family Enterobacteriaceae, Clostridium and Staphylococcus aureus in the group of dominant species. Yeast-like fungi of the genus Candida in patients with diabetes mellitus belonged to additional species, while maintaining their position in the composition of transient species in patients with OA.

Patients with OA in combination with type 2 diabetes mellites formation of microbiological disorders of intestinal micro biocenosis in 100% of cases, while in OA these disorders of intestinal micro biocenosis were observed in 61% of patients (p<0,05). The presence of OA and CD2 characterized by the development microbiological disorders degrees in 8.3% of cases, in 16,7% of patients -III degrees, these indicators in patients with OA were respectively 24.4% and 2.4% (p>0,05). OA and CD2 were manifested by the formation microbiological disorders II degrees at 83.3% of cases while in patients with OA II degree microbiological disorders gut microbiome have been observed in 29,3% of cases (p<0,05). So Conducted studies have shown that in patients with OA in combination with type 2 diabetes mellitus there is a significant change in the intestinal microbiome with more frequent formation II the degree of microbiological disorders of the intestinal microflora, which confirms the value of the axis intestine–joint in the manifestation of joint health [2]. Patients with OA have CD2 leads to pronounced colonization of the organism by opportunistic pathogens of the family Enteron bactericide whose cell wall contains LPS endotoxin, what may contribute to the growth and intoxication and maintaining immune inflammation. Increase in the body of patients at CD2LPS levels may be an additional factor, providing pathogenic effect on OA along with oxidative stress and chronic inflammation through what degree of severity arising due to chronic hyperglycemia and insulin resistance [3]. Normalization of the intestinal microbiome may be one of the directions of complex treatment of OA and CD2.

Conflict of Interest

None.

References

1. Cannata F, Gianluca Vadalà, Ambrosio L, Nicola Napoli, Vincenzo Denaro, et al. (2020) Osteoarthritis and type 2diabetes: From pathogenic factors to therapeutic intervention. Diabetes Metab Res Rev 36(3): e3254.
2. Gleason B, Chisari E, Parvizi J (2022) Osteoarthritis Can Also Start in the Gut: The Gut-Joint Axis. Indian J Orthop 56(7): 1150-1155.
3. Veronese N, Cooper C, Jean Yves Reginster, Marc Hochberg, Roland Chapurlat, et al. (2019) Type2 diabetes mellitus and osteoarthritis. Semin Arthritis Rh`eum 49(1): 9-19.

ISSN: 2574-1241

DOI: 10.26717/BJSTR.2022.45.007243

M Yu Gulneva. Biomed J Sci & Tech Res