



جامعة بنها
BENHA UNIVERSITY
Learn Today ... Achieve Tomorrow
www.bu.edu.eg



أكاديمية البحث العلمي والتكنولوجيا
Academy of Scientific
Research & Technology



July 10 - 12, 2023
Malcolm Hotel, Canmore, AB, Canada

A study whether the status of the generated mRNA - ncRNA network (related to gut microbiota derived mediators) is involved in the potential improvement due to the microbiota treatment.

Reda Albadawy 1,* , Amany Helmy Hasanin², Maha Saad³, Mohamed Othman⁴, Marwa Matboli⁵

1-Department of Gastroenterology, Hepatology & Infectious Disease, Faculty of Medicine, Benha University, Benha 13518, Egypt; reda.albadawy@fmed.bu.edu.eg

2-Clinical pharmacology department, Faculty of medicine, Ain Shams University, Cairo, Egypt; amany_hasanin@med.asu.edu.eg & rehamhoussein@med.asu.edu.eg

3-Biochemistry Department, Faculty of medicine, Modern University for Technology and Information, Cairo 11382, Egypt; mahasaad9292@gmail.com

4-Gastroenterology and Hepatology Section, Baylor College of Medicine, Houston, TX77030, US; Mohamed.Othman@bcm.edu

5-Medical biochemistry and molecular biology department, Faculty of medicine, Ain Shams University, Cairo 11566, Egypt; DrMarwa_Matboly@med.asu.edu.eg

Correspondence: DrMarwa_Matboly@med.asu.edu.eg (M.M.) & reda.albadawy@fmed.bu.edu.eg *

Aknowldegment to Academy of Scientific Research and Technology, Cairo, Egypt

Abstarct: Microbiome is a novel issue in health and diseases. Non Alcoholic Fatty Liver Disease (NAFLD) is the most health problem world wide. Not yet there is no drugs for Non Alcoholic steatohepaitis (NASH).

Aim: of the study to explore gut microbiome mediators in NAFLD diagnostic , therapeutic.

Methodology: An experimental study was done on 60 mice after feeding high fat diet for 14 weeks. Blood and stool sample taken for microbiome studies Analysis done by 16 sRNA sequencing.

Results: At the phylum level, the NASH mice had significantly increased relative abundance of Verrucomicrobia and unclassified colistridiae and decreased relative abundance of Bacteroidetes compared to the Naive mice, which were partially restored by Rosavin treatment. At the genus level, the NASH mice had a significantly higher abundance of Ruminococcus, Eubacterium, and Clostridium, Bacteroides and lower abundance of Cronobacter, Streptococcus, and Alistipes, which were also partially restored by Rosavin treatment.

Discussion: Since a large dose of Rosavin (30mg/kg) treatment had better efficiency as demonstrated above, 16S rRNA gene sequencing on the mice gut microbiota among naive, NASH model, and HFHD-Roavin (30 mg/kg) groups was performed to analyze the gut microbial community structure, indicating gut microbiota composition among the groups was different from each other. The HFHD diet led to an increased abundance of Firmicutes and decreased abundance of Bacteroidetes, which were considered as "fat bacteria" and "lean bacteria" respectively, and such dysbiosis was reversed after Rosavin treatment, Rosavin treatment might, at least in part, explain the improved hepatic inflammation of NASH without diet alteration. As Alistipes is an acetate producer, which is a type of short-chain fatty acids that have anti-inflammatory actions, it can be suggested that improvement of hepatic inflammatory after Rosavin treatment in the present study might be due to the restoration of Alistipes and its products.

Conclusion: the generated mRNA-ncRNA network (related to gut microbiota derived mediators) has involved in the potential improvement due to the microbiota treatment.