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Short Communication

Undiscovered Inhabitants of Hepatocytes in Healthy Rats' Liver Microbiomes

Xie Liang*

Department of Hepatology, University of Asahikawa, Asahikawa, Hokkaido, Japan

DESCRIPTION

The gut microbiota, which are found throughout the entire Gastrointestinal (GI) tract and contain a variety of microbial communities, could be identified with the aid of high-throughput nucleotide sequencing[1] .Numerous studies using human samples have further demonstrated the link between changes in the gut microbiome (primarily the fecal microbiome) and the occurrence of various diseases. These studies involved collecting feces and analyzing the composition of the intestinal microbiota and its metabolites in health and disease. These research and reviews made a solid case for the gut microbiota as a disease-causing factor.

According to recent findings, eating a high-fat diet can increase gut permeability and cause bacteria to move from the colon into tissues including adipose and liver tissues. In a recent study, it also discovered that feeding obese or post-fasting rats caused the small intestine's villi to create a channel, allowing for brief and functional unrestricted channel absorption (data not shown). These findings made it abundantly evident that the path by which the gut microbiota caused illnesses was gut permeability [2]. Studies have also shown bacteria in different tumor cells and offered the idea of intracellular bacteria that are specific to a certain type of tumor. Additionally, it has been reported by a number of studies that tissue microbiota occur in both mice and humans. The 16S rRNA gene signature has also been found in the blood of healthy persons, patients, and animals (particularly in the leukocyte and platelet fractions).

These crucial elements demonstrate how the gut and brain communicate. Microbiota, circulation, and tissues, i.e., the gut microbiota leak into the bloodstream, find their way into tissues, and transform into intracellular bacteria that are specific to the tissue and particular tumor types. They then lead to disease, while it is still unknown how tissue microbiota evolves [3]. The liver is unavoidably the frontier organ (the important gatekeeper) *via* which the gut microbiota enters the bloodstream based on this route. The "gut-liver axis" is the term used to characterize this link. Bacterial DNA was found in obese patients with Non-alcoholic Fatty Liver Disease (NAFLD), and immunohistochemistry was used to find Lipopolysaccharide in the portal system. Additionally, it can be inferred that the liver and mesenteric lymph nodes both play immunological functions similar to the spleen and acts as a transfer station for pathogens into the bloodstream.

Investigation of the liver bacteria in healthy persons and clarification of the link with the gut microbiota are of utmost importance in light of the complex etiology of diseases in visceral organs that are independent of gut and liver dysfunction [4]. This study's goal was to confirm the existence of the liver microbiome, as well as its composition, geographic distribution, and relationship to the gut microbiome. The study's justification is as follows:

The location of liver microbiota was validated by identifying Lipopolysaccharide(LPS) ,Laryngeal Tracheal Airway(LTA) or 16S rRNA gene in situ using immunofluorescence (IF), Fluorescence in Situ Hybridization (FISH), and western blotting.

Microbiota was discovered by high-throughput 16S rRNA gene sequencing.

By contrasting their diversity and composition, the liver and gut microbiomes' importance was established.

In this study, it can describe the presence of microorganisms in the healthy liver tissues and hepatocytes of rats, unaffected by diet or the onset of disease [5]. The "liver to gut" interaction of the microbiota can be inferred from the comparison of the liver and gut microbiota, which implies that hepatocytes are naturally home to the liver microbiome.

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Correspondence to: Xie Liang, Department of Hepatology, University of Asahikawa, Asahikawa, Hokkaido, Japan, E-mail: Xieliang@gmail.com

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