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Gut Microbiota Changes After Cholecystectomy: Unraveling the Microbial Mysteries - A Systematic Review

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Gut Microbiota Changes After Cholecystectomy: Unraveling the Microbial Mysteries - A Systematic Review.

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Abstract

Aims: This review aims to expand upon previous research examining change in gastrointestinal microbiota before and after cholecystectomy.

Methods: A systematic review, combined with a pooled analysis, was conducted to assess gut microbiota dysbiosis post-cholecystectomy, utilizing 71 articles retrieved from 3 databases, with 13 undergoing full-text appraisal. The publication dates ranged from 2018 to 2023.

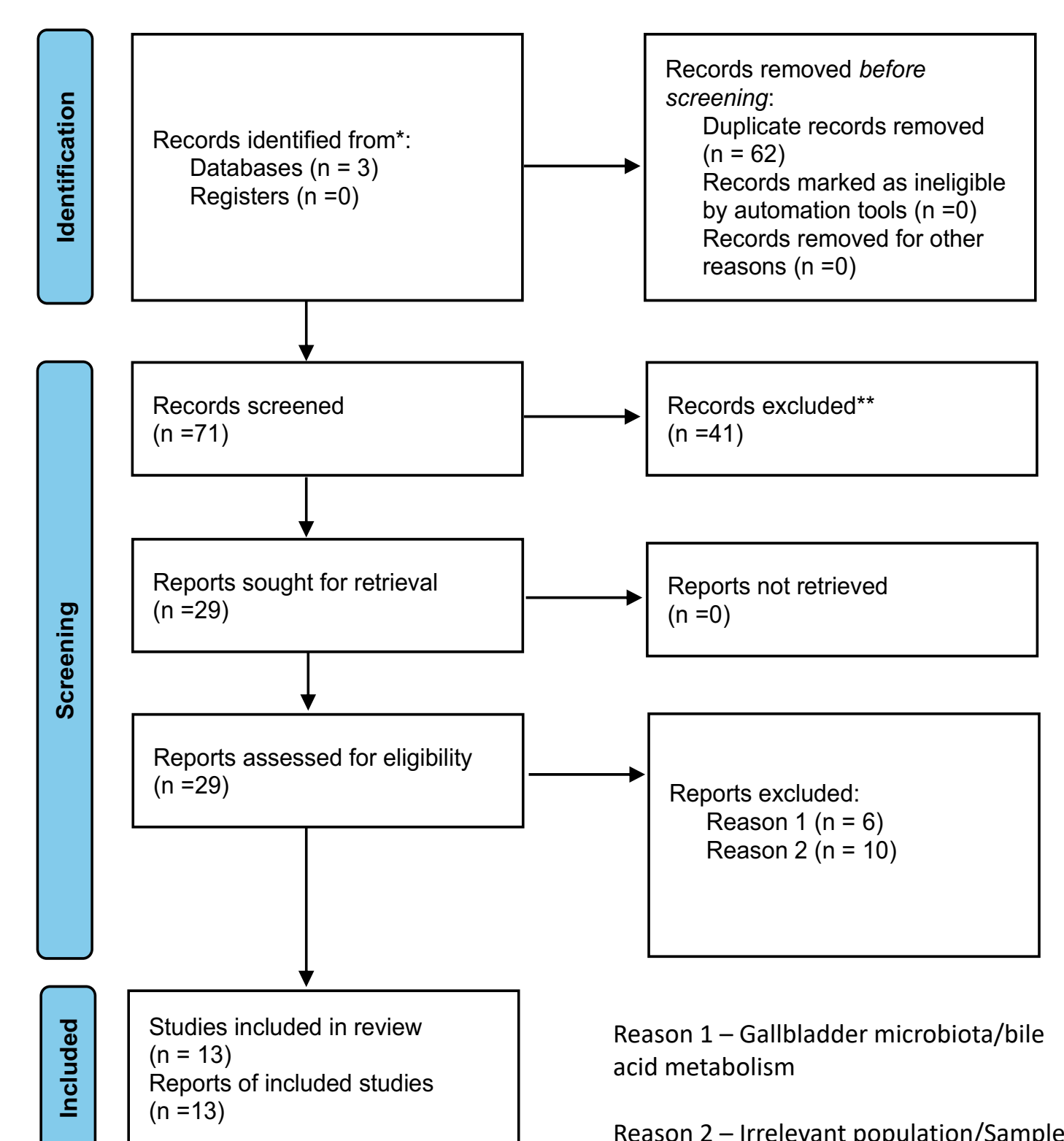
Results: Results suggested a greater degree of microbiota alteration in symptomatic post-cholecystectomy patients, characterized by a decrease in the *Firmicutes/Bacteroidetes* ratio, *Bifidobacterium* and *Lactococcus*, alongside increased levels of harmful microbiota such as *Prevotella*, *Sutterella*, *Proteobacteria*, *Verrucomicrobia*, *Blautia obeum*, and *Veillonella* species. Interestingly, an increase in *Firmicutes* and *Bacteroidetes* was observed in two different studies.

Conclusion: the research consistently shows dysbiosis in gut microbiota following cholecystectomy with potential implications for gastrointestinal and overall health. These findings emphasize the need for future research in maintaining a balanced gut microbiota when managing post-cholecystectomy patients with dysbiosis.

Background

The gallbladder is a digestive organ that stores and concentrates bile. This organ facilitates the digestion of lipids. When the gallbladder is surgically removed, the procedure is called a cholecystectomy. In the United States, cholecystectomies are one of the most common surgical procedures. Indications for a cholecystectomy include gallstones, cholecystitis, and gallbladder tumors¹. With regards to the digestive system, the human gut microbiota has been a recent topic of interest. The gut microbiome is a collection of microorganisms that inhabit a person's digestive tract. Each individual's gut flora is highly diverse and has the potential to elicit their overall digestive health. The human gut microbiota has ties to an individual's physiologic balance and metabolism². Previous research has revealed a potential link between cholecystectomies and the human gut microbiota. This study seeks to discuss the composition of patients' gut microbiota who have undergone a cholecystectomy procedure, as well as confirm a correlation between a cholecystectomy and the changes in gut microbiota composition³.

Methods



Results

| Authors/Year | Title of Paper | Subjects/Methodology | Results |
|--|--|---|---|
| W W, J W, J L, et al. (2018) | Cholecystectomy Damages Aging-Associated Intestinal Microbiota Construction. | Male and female subjects 16S rRNA sequencing of fecal sample Study done in China | ↑ <i>Firmicutes</i> , ↑ <i>Bacteroidetes</i> ↑ <i>Proteobacteria</i> ↑ <i>Verrucomicrobia</i> ↑ <i>Actinobacteria</i> ↑ <i>Fusobacteria</i> ↑ <i>Synergistetes</i> ↓ <i>Anaerotruncus</i> ↓ <i>Parabacteroides</i> ↓ <i>Paraprevotella</i> |
| Z K, M L, M J, D Z, H H. (2019) | Proteobacteria Acts as a Pathogenic Risk-Factor for Chronic Abdominal Pain and Diarrhea in Post-Cholecystectomy Syndrome Patients: A Gut Microbiome Metabolomics Study | Male and female subjects DNA analysis of fecal sample Participants from 2 nd Affiliated Hospital, Kunming Medical University (China) | ↑ <i>Proteobacteria</i> ↑ <i>Verrucomicrobia</i> ↑ <i>Proteobacteria</i> ↓ <i>Bacteroidetes</i> ↓ <i>Firmicutes</i> |
| Yoon W, Kim H, Park E, et al. (2019) | The Impact of Cholecystectomy on the Gut Microbiota: A Case-Control Study. | Male and female subjects DNA analysis of fecal sample Participants from Kangbuk Samsung Cohort Study of Korea | ↓ <i>Bacteroidetes</i> ↑ <i>Lactobacillaceae</i> ↑ <i>Ruminococcus</i> ↑ <i>Bifidobacterium adolescentis</i> |
| Ren X, Xu J, Zhang Y, et al. (2020) | Bacterial Alterations in Post-Cholecystectomy Patients Are Associated with Colorectal Cancer. | Male and female subjects 16s rRNA gene sequencing of fecal sample Study done in China | ↑ <i>Bacteroides ovatus</i> ↑ <i>Parabacteroides distasonis</i> ↑ <i>Prevotella copri</i> ↑ <i>Fusobacterium varium</i> ↓ <i>Faecalibacterium prausnitzii</i> ↓ <i>Roseburia faecis</i> ↓ <i>Bifidobacterium adolescentis</i> ↓ <i>Eubacterium rectale</i> |
| YD L, BN L, SH Z, YL Z, L B, EQ L. (2021) | Changes in gut microbiota composition and diversity associated with post-cholecystectomy diarrhea | Male and female subjects DNA analysis of fecal sample Participants from 1 st Affiliated Hospital of Xi'an Medical University (China) | ↓ <i>Firmicutes/Bacteroidetes</i> ratio ↓ <i>Bifidobacterium</i> ↓ <i>Lactococcus</i> ↑ <i>Prevotella and Sutterella</i> |
| Wang Q, Lu Q, Shao W, Jiang Z, Hu H. (2021) | Dysbiosis of gut microbiota after cholecystectomy is associated with non-alcoholic fatty liver disease in mice | Mouse models 16s rRNA sequencing of fecal sample Study done in China | ↑ <i>Verrucomicrobia</i> ↑ <i>Allobaculum</i> ↓ <i>Firmicutes</i> ↓ <i>Parabacteroides</i> |
| Grigor'eva I, Romanova T, Naumova N, Alikina T, Kuznetsov A, Kabilov M. (2021) | Gut microbiome in a Russian cohort of pre- and post-cholecystectomy female patients. | Female subjects 16s rRNA gene sequencing of fecal sample Study done in Russia | ↑ <i>Firmicutes</i> ↑ <i>Bacteroidetes</i> ↑ <i>Actinobacteria</i> ↑ <i>Proteobacteria phyla</i> |
| Frost F, Kacprowski T, Rühlemann M, et al. (2021) | Carrying asymptomatic gallstones is not associated with changes in intestinal microbiota composition and diversity but cholecystectomy with significant dysbiosis. | Female subjects 16s rRNA gene sequencing of fecal sample Study done in Germany | ↓ <i>Faecalibacterium</i> ↓ <i>Haemophilus</i> ↑ <i>Escherichia/Shigella</i> ↑ <i>Flavonifractor</i> ↑ <i>Mogibacterium</i> |
| Georgescu D, Caraba A, Ionita I, et al. (2022) | Dyspepsia and Gut Microbiota in Female Patients with Postcholecystectomy Syndrome | A cross-sectional study consisting of female subjects Next-generation sequencing of fecal sample Study done in Romania | ↑ <i>Firmicutes</i> ↑ <i>Bacteroidetes</i> ↑ <i>Proteobacteria</i> ↑ <i>Actinobacteria</i> ↑ <i>Verrucomicrobia</i> |
| Y M, R Q, Y Z, C J, Z Z, W F. (2022) | Progress in the Study of Colorectal Cancer Caused by Altered Gut Microbiota After Cholecystectomy | Review of Epidemiological studies Study done in China | ↑ <i>Fusobacteria</i> ↑ <i>Escherichia</i> ↓ <i>Proteobacteria</i> ↓ <i>Faecalibacterium</i> |
| Xu Y, Wang J, Wu X, et al. (2023) | Gut microbiota alteration after cholecystectomy contributes to post-cholecystectomy diarrhea via bile acids stimulating colonic serotonin | 8-weeks-old C57BL/6 mice 16S rRNA sequencing of fecal sample Study done in China | ↑ <i>Firmicutes</i> ↑ <i>Verrucomicrobiota</i> ↑ <i>Proteobacteria</i> ↓ <i>Bacteroidota</i> |
| Xu F, Chen R, Zhang C, et al (2023) | Cholecystectomy Significantly Alters Gut Microbiota Homeostasis and Metabolic Profiles: A Cross-Sectional Study | Cross-sectional study 16s rRNA sequencing of fecal sample Study done in China | ↑ <i>Akkermansia</i> ↑ <i>Erysipelatoclostridium</i> ↑ <i>Lachnospirillum</i> ↑ <i>Lactobacillus</i> ↑ <i>Megamonas</i> ↓ <i>Collinsella</i> ↓ <i>Faecalibacterium</i> |
| Noh CK, Jung W, Yang MJ, Kim WH, Hwang JC. (2023) | Alteration of the fecal microbiome in patients with cholecystectomy: potential relationship with postcholecystectomy diarrhea - before and after study | Male and female subjects 16s rRNA sequencing of fecal sample Study done in Korea | ↑ <i>Bacteroidetes</i> ↑ <i>Proteobacteria</i> ↓ <i>Firmicutes</i> ↓ <i>Actinobacteria</i> |

Discussion

Cholecystectomy, the surgical removal of the gallbladder, can lead to significant alterations in gut microbiota composition, which may impact gastrointestinal health. Studies have shown that individuals, post-cholecystectomy exhibit reduced microbial diversity, altered *Firmicutes/Bacteroidetes* ratios, and changes in specific bacterial populations. For example, post-cholecystectomy diarrhea (PCD) patients often show lower levels of probiotic bacteria such as *Bifidobacterium* and elevated levels of harmful bacteria like *Prevotella* and *Sutterella*. Similarly, post-cholecystectomy patients demonstrate higher abundances of *Proteobacteria* and *Verrucomicrobia* and lower levels of *Bacteroidetes* and *Firmicutes*. These microbiota changes may contribute to digestive issues such as diarrhea, bloating, and abdominal discomfort, particularly in PCD. Imbalances in gut microbiota can also lead to increased gut inflammation, nutrient absorption issues, and a higher risk of infections.

Conclusion

Alterations in gut microbiota following cholecystectomy are evident. There are overall decreases in healthy bacteria with an overgrowth of harmful bacteria. The ratios of healthy to harmful are unbalanced and the diversity of bacterial species is lacking. This has adverse effects on gut health as well as overall health. Gastrointestinal dysbiosis leads to abdominal discomfort, nutritional deficiencies, inflammation and a compromised immune barrier. Limitations of the paper include a high variability in population, not accounting for lifestyle factors as potential confounders. Further research is needed to conclude a link between inflammatory bacteria and the incidence of colorectal cancer. As well as control for confounders to isolate a direct effect. This research may be taken in the direction of the proper management of patients post-cholecystectomy to avoid adverse effects.

Limitations/Future Directions

In reviewing these studies, several limitations emerge. The studies were conducted across various countries and populations, potentially leading to variations in gut microbiota composition due to factors such as diet, lifestyle, and genetic differences. Moreover, the results often fail to account for potential confounders, such as body mass index, and underlying health conditions, all of which can independently influence gut microbiota composition. Addressing these limitations would bolster the conclusions drawn from the studies. To better understand and address the reviewed studies' limitations, future research should aim to encompass more diverse geographical regions to control for potential confounding factors, such as body mass index, and underlying health conditions. This approach would improve the generalizability of the findings, enabling a deeper exploration of the impact of cholecystectomy on gut microbiota across different cultural and dietary contexts.

Reference

