

THE SUCCESSION OF INTESTINAL MICROBIOTA IN CONDITIONS OF EXPERIMENTAL POST-CHOLECYSTECTOMY SYNDROME

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Abstract

Cholecystectomy is a frequently conducted surgical intervention that modifies the storage and secretion of bile acids, resulting in a continuous flow of bile and a disruption of the enterohepatic circulation. These changes may lead to increased exposure of the colon to bile acids and an imbalance in gut microbiota, potentially triggering intestinal inflammation, metabolic irregularities, and various long-term complications. Nevertheless, the precise mechanisms and clinical ramifications of these alterations remain inadequately elucidated. This review seeks to consolidate existing evidence regarding the effects of cholecystectomy on the composition of gut microbiota and its possible links to metabolic changes and clinical outcomes.

This study emphasizes the importance of regular bacteriological examinations in patients with fever persisting beyond seven days, as well as the identification of pathogenic serovars, their virulence factors, and antibiotic susceptibility profiles.

Keywords: *Cholecystectomy; gut microbiota; dysbiosis; bile acids.*

Objective

A total of 35 mice were selected for the experimental group and 35 for the control group, and the study was conducted at the Farmacology Institute's research laboratory. Bacteriological analyses were carried out at the bacteriology laboratory of the City Emergency Medical Assistance Clinical Hospital.

Materials and Methods

Stool samples and wound smears were collected and subjected to bacteriological culture according to standard microbiological protocols. A narrative review was conducted based on published clinical and *in vivo* studies evaluating microbiota changes after cholecystectomy. The associations between microbiota alterations and bile acid metabolism, intestinal inflammation, and metabolic outcomes were also examined.

Key Content and Findings: Cholecystectomy leads to a continuous secretion of bile acids into the intestine, which may modify the composition of bile acids and contribute to dysbiosis within the gut microbiome. Both clinical and preclinical investigations indicate that these changes are linked to intestinal inflammation. Such inflammation

has been correlated with post-cholecystectomy diarrhea, metabolic disruptions that could evolve into metabolic syndrome. Moreover, additional factors such as a high-fat diet and therapies that modulate bile acids may further impact microbial composition. Nonetheless, the findings across various studies remain inconsistent, and definitive causal relationships in human subjects have yet to be established.

Results

Following cholecystectomy, animal models showed an increase in bile acid-metabolizing bacteria. The following pathogens were identified: *Enterococcus* – 28.3%, *Staphylococcus epidermidis* – 12.3%, *Streptococcus* – 2.8%, *Escherichia/Shigella* – 10.9%, *Bacteroides*; – 4.2%, *Clostridium spp (E. coli)* – 8.7%, ↓*Lactobacillus*; – 8.4%, *Citrobacter spp.* – 2.6%, *Candida spp* – 1.8%. ↑*Proteobacteria*-2,3%

Antibiotic susceptibility testing revealed resistance among several isolates. Notably, resistance rates were as follows: Cefotaxime – 6.6%, Amikacin – 3.3%, Meropenem – 3.3%, Ceftriaxone – 6.6%, Levofloxacin – 3.3%, Ertapenem – 6.6%, Imipenem – 3.0%. Faster colonic transit might further reduce populations of slow-growing commensal bacteria, thereby exacerbating gut dysbiosis. In parallel, the reduction of *Lactococcus*, a beneficial genus within the *Lactobacillaceae* family, was associated with a decrease in lactic acid production through carbohydrate fermentation. ↓*Anaerotruncus*; ↓*Bilophila*; ↓*Enterococcus*; ↓*Harryflintia*; ↓*Lachnoclostridium*; ↓*Mucispirillum*; ↓*Parvibacter*; ↓*Rikenellaceae* RC9 gut group; ↓*Ruminiclostridium spp*; ↓*Streptococcus spp.*

Acetaltifactor; ↑*Escherichia/Shigella*; ↑*Eubacterium nodatum* group; ↑*Flavonifractor*; ↑*Muribaculum*; ↑*Negativibacillus*; ↑*Parabacteroides*; ↑*Parasutterella*. At the taxonomic level, the persistently primary bile acid-rich environment favored the enrichment of bile acid-metabolizing genera (*Bacteroides*, *Parabacteroides*, *Clostridium*), along with bile-resistant pathobionts (*Escherichia/Shigella*). In contrast, bacteria sensitive to elevated primary bile acids, including SCFA-producing genera (*Faecalibacterium*, *Roseburia*) and *Bifidobacterium*, were consistently reduced. *Prevotella*, however, showed inconsistent changes across studies. These findings indicated that cholecystectomy induced gradual remodeling of the gut microbial community over time in animal models, with patterns similar to those observed in clinical studies.

At the taxonomic level, the proportions of bile acid-metabolizing bacteria, including *Lactobacillus* (somespecies), *Clostridium*, *Ruminococcus*, and *Enterococcus*, were increased. In contrast, *Bifidobacterium* was decreased.

Conclusion

Cholecystectomy is associated with alterations in gut microbiota and bile acid metabolism that may affect intestinal and metabolic homeostasis. However, human evidence remains limited and heterogeneous, and causality has not been established. Clinical and animal studies support the gallbladder's role in maintaining microbial and metabolic balance. Cholecystectomy disrupts physiological bile acid flow, inducing gut dysbiosis characterized by enrichment of bile acid-metabolizing. Healthy controls had balanced communities, whereas gallstone patients exhibited pre-existing dysbiosis, which influenced the magnitude and timing of microbial adjustments.