Supplementary

Table S1 Impact of cholecystectomy on gut microbiota composition associated with colorectal cancer: evidence from in vivo studies

Animal models	Sample/ methods	Interventions	Major findings of gut microbiota					Interpretation	Ref.
			Alpha (α) diversity	Beta (β) diversity	Taxa increased	Taxa decreased	Other findings		
Male wild-typed C57BL/6 mice with post-CS	Fecal samples/16S rRNA gene sequence	AOM/DSS; $APC^{min/+}$	↓ (Shannon index) ↔ (Shannon index)	NS NS	Species: ↑Ruminococcus gnavus Species: ↑Ruminococcus gnavus	Species: ↓Bifidobacterium breve Species: ↓Bifidobacterium breve	↑Serum total BAs Fecal BAs profiles: ↑conjugated/unconjugated ratio; ↑α-MCA; ↑DCA; ↑UDCA; ↑TUDCA; ↑TCDCA Ileal BAs profiles: ↑total BAs; ↑conjugated/ unconjugated ratio Fecal BAs profiles: ↑conjugated/unconjugated ratio; ↑TUDCA	Cholecystectomy mice with CRC induced by AOM/DSS and $APC^{min/+}$ mutation had altered gut microbiota composition, which correlated with fecal BAs levels particularly TUDCA	(27)

a-MCA, alpha-muricholic acid; AOM/DSS, azoxymethane/dextran sulfate sodium; APCmin/+, adenomatous polyposis coli multant; BAs, bile acids; CRC, colorectal cancer; CS, cholecystectomy; DCA, deoxycholic acid; NS, non-significant; rRNA, ribosomal ribonucleic acid; TCDCA, taurochenodeoxycholic acid; TUDCA, tauroursodeoxycholic acid; UDCA, ursodeoxycholic acid.

Table S2 Impact of cholecystectomy on gut microbiota composition associated with post-cholecystectomy diarrhea: evidence from in vivo studies

Animal models	Sample/ methods	Interventions	Major Findings of Gut microbiota					Interpretation	Ref
			Alpha (α) diversity	Beta (β) diversity	Taxa increased	Taxa decreased	Other findings		
Adult C57BL/6 mice with post-CS	Fecal samples/ V3-V4 region of the 16S rRNA gene sequence	PCD *vs.* non-PCD	↓ (Faith's PD, Simpson index) ↔ (ACE, Shannon index)	S	Phylum: ↑Firmicutes; ↑Verrucomicrobiota; ↑Proteobacteria	Phylum: ↓Bacteroidota	Predicted metabolomic pathways: ↑tryptophan metabolism; ↑quorum sensing; 5-HT biosynthesis; ↑serum 5-HT; ↑colon 5-HT; ↑TpH1 in colon; ↑5-HT3R in colon; ↑cAMP in colon; ↓SERT in colon 5-HT associated with PCD: DCA, LCA, HDCA α 5-HT *vs.* TpH1 in colonic; expression of BAs receptor; ↑TGR5 in colon; ↑TRPA1 in colon Microbiota associated 2° BAs in Post-CS + PCD: family: ↑unidentified Lachnospiraceae; genus: ↑Clostridium spp.	Cholecystectomy with PCD altered gut microbiota composition and modulated bile acid metabolism, leading to enhanced 5-HT biosynthesis	(17)

2° BAs, secondary bile acids; 5-HT, serotonin; 5-HT3R, serotonin receptor subtype 3; ACE, Abundance-based Coverage Estimator; BAs, bile acids; cAMP, cyclic adenosine monophosphate; DCA, deoxycholic acid; HDCA, hyodeoxycholic acid; LCA, lithocholic acid; PCD, post-cholecystectomy diarrhea; PD, phylogenetic diversity index; Post-CS, post-cholecystectomy; rRNA, ribosomal ribonucleic acid; S, significant; SERT, serotonin selective reuptake transporter; TGR5, Takeda G-protein-coupled receptor 5; TpH1, tryptophan hydroxylase 1; TRPA1, transient receptor potential ankyrin 1.

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