Lactobacillus acidophilus alleviates Metabolic dysfunction–associated steatotic liver disease (MASLD)

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BACKGROUND & AIM

Metabolic dysfunction–associated steatotic liver disease (MASLD) is one of the most common chronic liver diseases globally. Gut probiotic depletion is associated with MASLD. This study aimed to elucidate the underlying mechanisms of High fat diet induced MASLD associated with the gut microbiome and explore the effects of Lactobacillus acidophilus from the gut microbiota profiles perspective.

MATERIAL & METHODS

A total of 127 stool sample divided into three groups (Healthy control; n=39, MAFLD patients; n=45, MASH patients; n=43). Five weeks old C57BL/6J mice were fed the High fat diet with/ without probiotics for 18 weeks. *L. acidophilus* was administered at a concentration of $3.91*10^9$ CFU/day. We compared liver/body weight ratio (L/B ratio), NAFLD activity score (NAS), Oral glucose tolerance test (OGTT) and performed liver function tests with serum. We also conducted the histopathological examination, fecal analysis, and markers for inflammation, lipogenesis, and β-oxidation in the liver.

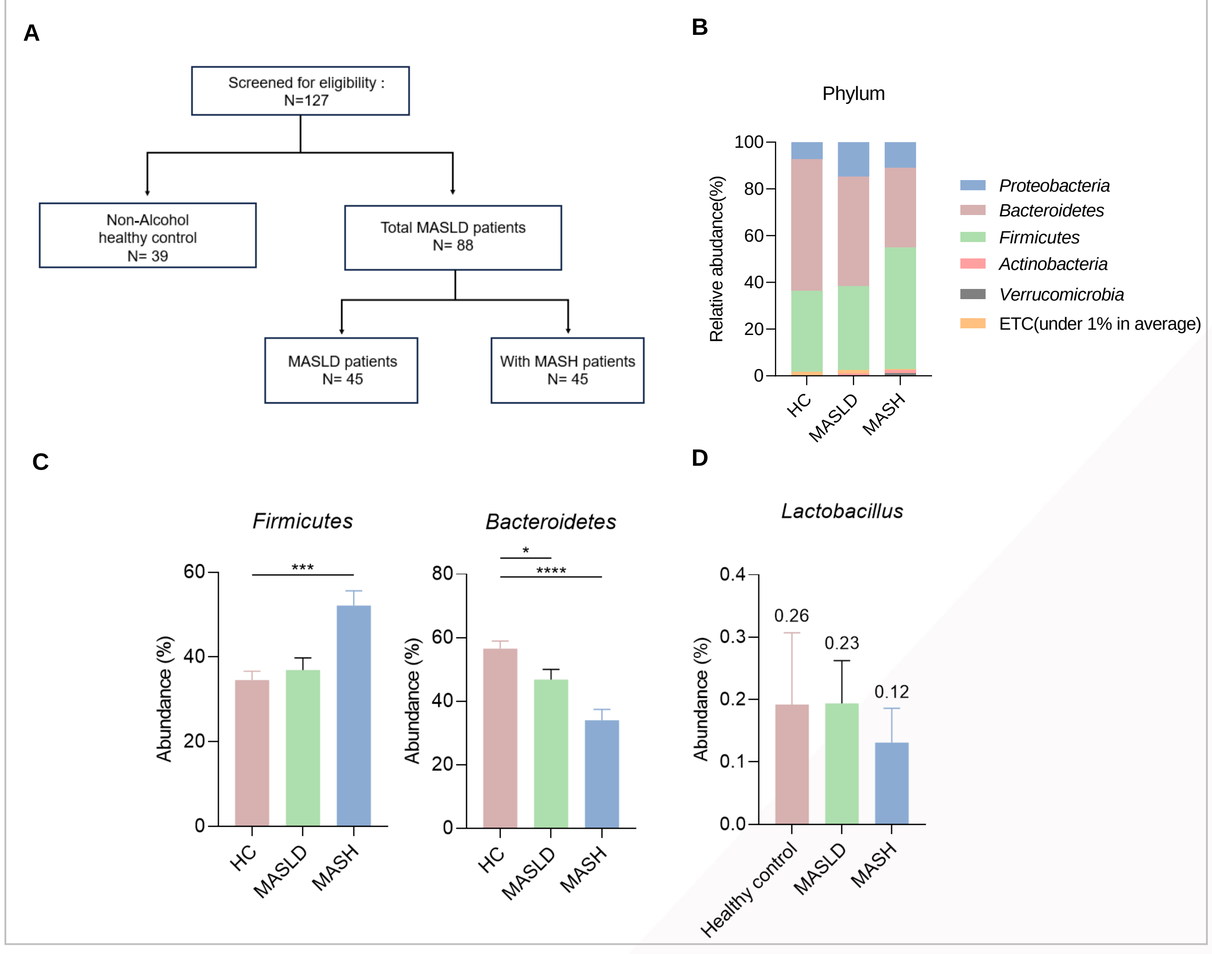
RESULTS

Lactobacillus genus was decreased according to the liver disease progression. *L. acidophilus* group shows significant results in liver enzymes (AST 86.10±21.1, P<0.05; ALT 66.44±37.20, P<0.05; TC 217.7±32.27, P<0.0001; LDL 61.29±13.20, P<0.05), L/B ratio (3.05±0.43, P<0.0001), Fasting glucose (173.33±31.85, P P<0.05) and improved NAS (1.44±1.47, P<0.0001) compared with the untreated group (AST 154.2±62.08; ALT 190.4±104; TC 293.8±25.11; LDL 84.65±13.27; L/B ratio 4.74±0.92; Fasting glucose 231.7±48.63; NAS 5.6±1.56).

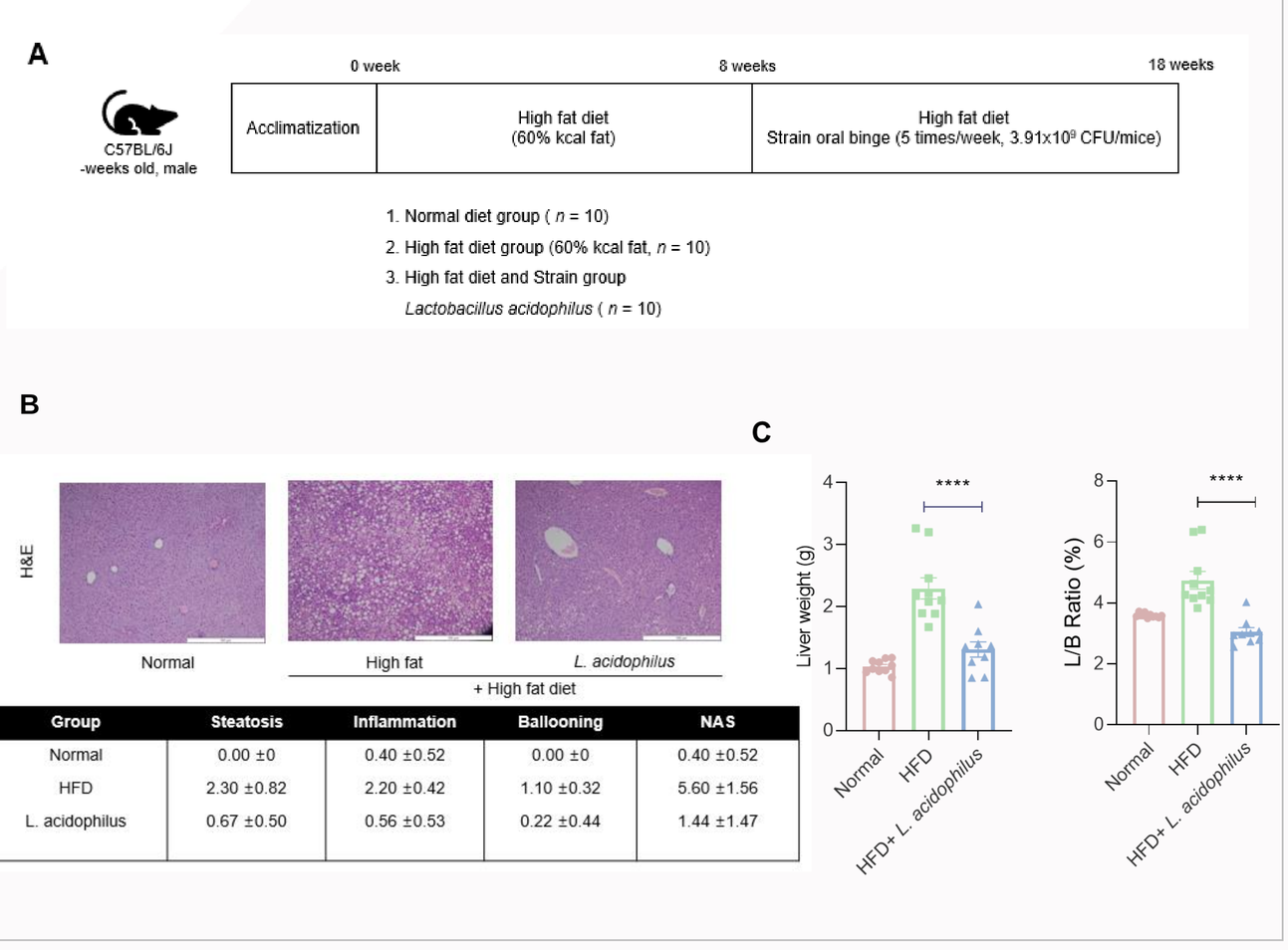
Moreover, *L. acidophilus* downregulated the expression of hepatic steatosis and inflammation biomarkers (TNF- α, P<0.05;). And upregulated the expression of oxidation (PPAR- α P<0.05) and tight junction gene (Occludin, P<0.05; Claudin, P<0.05). *L. acidophilus* ameliorates MASLD, dysbiosis, and gut microbiome metabolite through modulation of gut microbiota resulting in reduced hepatic inflammation, steatosis, and fatty acid synthesis.

RESULTS

Human gut microbiota for liver disease progression was analyzed by 16s rRNA sequencing.



L. acidophilus ameliorated high fat diet-induced hepatic steatosis.



Group	Steatosis	Inflammation	Ballooning	NAS
Normal	0.00 ±0	0.40 ±0.52	0.00 ±0	0.40 ±0.52
HFD	2.30 ±0.82	2.20 ±0.42	1.10 ±0.32	5.60 ±1.56
L. acidophilus	0.67 ±0.50	0.56 ±0.53	0.22 ±0.44	1.44 ±1.47

L. acidophilus ameliorated pathology and oral glucose tolerance test (OGTT) in high fat diet model.

Administration of *L. acidophilus* regulated expression levels of tight junction, inflammation, and lipid metabolism genes in mouse.

CONCLUSION

Our study highlighted role of the *L. acidophilus* on the MASLD and the importance of the gut-liver axis. *L. acidophilus* can alleviate MASLD by regulating glucose metabolism as well as reducing lipid accumulation and inflammation in the liver. Therefore, our study suggest that *L. acidophilus* will help design novel therapies

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