Shahid Bahonar University of Kerman
Agricultural Biotechnology Journal
Iranian Biotechnology Society
Print ISSN: 2228-6705 Online ISSN: 2228-6500

Association of genetic expression of the ACE and GHRL genes with chronic fatty liver disease: clinical and metabolic insights

Tariq Hussein Mgheer

Department of Chemistry and Biochemistry, College of Medicine, University of Babylon, Iraq.
E-mail: tariq-almgheer@yahoo.com

Abstract

Objective

Fatty liver disease (FLD), or hepatic steatosis, is a pathological condition described by excessive lipid accumulation surpassing 5–10% of liver weight. Given its multifactorial etiology, involving both metabolic dysfunction and genetic predisposition, this investigation aimed to investigate the relationship between biochemical parameters, expression of the ACE and GHRL genes, and demographic variables like age and body mass index (BMI) in patients with FLD compared with healthy controls.

Materials and methods

The investigation enrolled 200 individuals, comprising 100 patients with ultrasonographically affirmed FLD (G2) and 100 age- and ethnicity-matched healthy controls of Iraqi descent (G1). All participants were non-smoking adults between 20 and 60 years recruited from Diwaniyah Teaching Hospital, Iraq. Standardized biochemical assays were carried out to calculate creatinine, blood urea, insulin, fasting blood sugar (FBS), glycated hemoglobin (HbA1c), total cholesterol (TC), triglycerides (TG), high-density lipoprotein (HDL), very-low-density lipoprotein (VLDL), alanine aminotransferase (ALT), aspartate aminotransferase (AST), AST/ALT ratio, and alkaline phosphatase (ALP). In parallel, quantitative gene expression analysis of ACE and GHRL was conducted, and expression levels were validated for clinical relevance to metabolic disturbances in FLD.

Results

Patients with FLD showed meaningfully higher BMI, creatinine, blood urea, insulin, FBS, HbA1c, TC, TG, VLDL, ALT, AST, and ALP levels compared to controls, along with markedly lower HDL levels ($P < 0.05$). Importantly, expression levels of both ACE and GHRL genes were meaningfully upregulated in the FLD group, correlating with the biochemical abnormalities observed. These results reinforce the interaction between altered gene expression and metabolic derangements in FLD pathophysiology.

Conclusion

The consistently low P-values ($P < 0.05$) affirm the robustness of the associations observed. Altered expression of ACE and GHRL genes may serve as reliable molecular biomarkers for identifying individuals at higher risk of FLD progression. Furthermore, wide evaluation of BMI, renal function markers, glycemic indices, lipid profiles, and liver enzyme activities supplies worth clinical discernment, supporting an integrative approach to early diagnosis and management of FLD.

Keywords: Fatty liver disease, hepatic steatosis, ACE gene, GHRL gene, biomarkers.

Paper Type: Research Paper.

Citation: Mgheer, T. H. (2025). Association of genetic expression of the ACE and GHRL genes with chronic fatty liver disease: clinical and metabolic insights. *Agricultural Biotechnology Journal,* 17(4), 285-304.

Agricultural Biotechnology Journal, 17(4), 285-304. DOI: 10.22103/jab.2025.25933.1769

Received: July 18, 2025. Received in revised form: September 25, 2025.

Accepted: September 26, 2025. Published online: November 30, 2025.

Publisher: Shahid Bahonar University of Kerman & Iranian Biotechnology Society.

Introduction

Fatty liver disease (FLD), or hepatic steatosis, is a metabolic disorder described by excessive lipid accumulation within hepatocytes. It is generally classified into two categories: alcoholic fatty liver disease (AFLD) and non-alcoholic fatty liver disease (NAFLD) (Sveinbjornsson et al., 2022). AFLD expands as a consequence of chronic and excessive alcohol intake, often progressing to alcoholic hepatitis, fibrosis, or cirrhosis. In contrast, NAFLD arises in individuals who consume little to no alcohol and is strongly related to obesity, type 2 diabetes, dyslipidemia, and metabolic syndrome (Shiha et al., 2021). In the early stages, fatty liver disease is typically asymptomatic, which complicates timely diagnosis and intervention (Rinella et al., 2023). Nevertheless, some patients report nonspecific manifestations like persistent fatigue, unintended weight loss, or discomfort in the upper right abdominal quadrant. Without appropriate management, NAFLD can evolve into more severe conditions, containing non-alcoholic steatohepatitis (NASH), progressive fibrosis, cirrhosis, hepatocellular carcinoma, or ultimately liver failure (Teng et al., 2022). Diagnosis relies on a combination of biochemical assays, imaging modalities like ultrasonography and magnetic resonance imaging, and in some cases, liver biopsy,

which remains the gold standard for staging disease progression (Eslam et al., 2020). Genetic and molecular mechanisms play critical roles in the initiation and progression of NAFLD. Dysregulation of genes involved in lipid metabolism leads to hepatic steatosis. Specifically, reduced expression of peroxisome proliferator-activated receptor alpha (PPAR-α) and improved expression of sterol regulatory element-binding protein-1c (SREBP-1c) contribute to excessive lipid accumulation within hepatocytes (Buchynskyi et al., 2024). Furthermore, aberrant regulation of pro-inflammatory cytokines and insulin signaling pathways—like tumor necrosis factor alpha (TNF-α) and forkhead box protein O1 (FOXO1)—exacerbates inflammation and impairs insulin sensitivity (Yang et al., 2022). As disease severity escalates toward NASH, oxidative stress-related genes, containing nuclear factor erythroid 2–related factor 2 (Nrf2), and pro-fibrogenic markers like transforming growth factor beta 1 (TGF-β1) and collagen type I alpha 1 (COL1A1), show improved activity. Genetic polymorphisms further influence susceptibility to NAFLD. Variants like patatin-like phospholipase domain-containing protein 3 (PNPLA3) and transmembrane 6 superfamily member 2 (TM6SF2) improve lipid metabolism pathways, meaningfully elevating disease risk and affecting progression (Li et al., 2023). These results highlight the importance of incorporating genetic profiling into the investigation of NAFLD pathogenesis and therapeutic development. The renin-angiotensin system (RAS), regulated largely by the angiotensin-converting enzyme (ACE) gene, is another pathway implicated in NAFLD. ACE overexpression elevates angiotensin II levels, promoting oxidative stress, pro-inflammatory cytokine release, hepatic lipid accumulation, and insulin resistance (Yang et al., 2023; Liu et al., 2021). With continued progression, these alterations can precipitate fibrosis, NASH, and cirrhosis (Kong et al., 2021). Notably, the D allele of the ACE insertion/deletion (I/D) polymorphism has been linked to heightened ACE activity and a greater risk of NAFLD progression (Rajapaksha et al., 2022). Another key regulator of metabolic balance is ghrelin, a hormone encoded by the GHRL gene. Ghrelin influences appetite regulation, lipid metabolism, insulin sensitivity, and energy homeostasis. In NAFLD, altered expression of the GHRL gene contributes to impaired lipid handling and metabolic dysfunction (Rezamand et al., 2021). Reduced ghrelin activity may diminish its protective roles, containing attenuation of inflammation, regulation of fibrotic pathways, and enhancement of insulin responsiveness (Tabaeian et al., 2021). Consequently, oxidative stress and excessive lipid deposition in hepatocytes can accelerate the transition from simple steatosis to NASH (Tuero et al., 2023). Interestingly, elevated ghrelin levels and improved GHRL gene expression have been related to milder forms of NAFLD, proposing that this pathway may serve as a worth biomarker for disease severity as well as a potential therapeutic target (Choochuay et al., 2024). Furthermore, the epigenome, which comprises various mechanisms such as DNA methylation, chromatin

remodeling, histone tail modifications, microRNAs, and long non-coding RNAs, interacts with environmental factors like nutrition, pathogens, and climate to influence gene expression profiles and the emergence of specific phenotypes (Shahsavari et al., 2023; Mohammadabadi et al., 2023). These interactions are complex and occur across multiple levels, involving dynamic crosstalk between the genome, epigenome, and environmental stimuli (Amiri Roudbar et al., 2020). Increasing evidence suggests that epigenomic variation plays a crucial role in determining health outcomes and production traits (Alavi et al., 2022; Safaei et al., 2022). The expression of eukaryotic genes is temporally and spatially regulated through multidimensional control mechanisms (Hajalizadeh et al., 2021). Only a limited subset of the entire genome is actively expressed in each tissue type, and gene expression is closely tied to developmental stages (Heidarpour et al., 2011; Khabiri et al., 2023). Consequently, gene expression patterns in eukaryotes are tissue-specific (Mohammadabadi & Asadollahpour Nanaei, 2021; Mohammadabadi et al., 2024). Additionally, the levels of gene products synthesized within a given tissue, as well as those contributed by other tissues, collectively regulate gene expression (Shokri et al., 2023). Epigenetic modifications serve as a critical mechanism by which environmental factors leave a lasting imprint on the genome (Mohammadabadi et al., 2022a). These modifications can be heritable, influencing successive generations without altering the DNA sequence itself (Mohammadabadi et al., 2025). For instance, maternal nutrition during pregnancy has been shown to induce epigenetic changes that affect offspring metabolism, growth, and disease susceptibility (Safaei et al., 2024). Similarly, environmental stressors such as exposure to toxins or pathogens can trigger epigenetic responses that modify gene expression and cellular function (Noori et al., 2017). Understanding epigenetic mechanisms can improve breeding strategies, enhance productivity, and promote disease resistance (Roudbar et al., 2015). Additionally, epigenetic markers are increasingly used to predict performance and health outcomes, providing a valuable tool for precision (Mohamadinejad et al., 2024). A fundamental aspect of genetic research involves the investigation of genes and proteins associated with specific traits, examined at both cellular and chromosomal levels (Khabiri et al., 2023). Advancing our understanding of these regulatory processes holds significant potential for improving biological insights and practical applications in health and production (Arabpour et al., 2021). Further research into epigenetic biomarkers and their role in gene regulation will contribute to more effective therapeutic strategies and enhanced understanding of complex biological systems (Mohammadabadi et al., 2022b). Overall, the interplay between lipid metabolism, inflammatory signaling, oxidative stress, and genetic susceptibility underlies the pathogenesis and progression of NAFLD. Identifying the contributions of genes like ACE and GHRL, in combination with established genetic variants like PNPLA3 and TM6SF2, supplies new chances for refining risk

evaluation and expanding aimed interventions. Understanding these molecular and genetic mechanisms is essential for designing preventive strategies and personalized therapies aimed at reducing the global burden of NAFLD.

Materials and Methods

This investigation enrolled a total of 200 participants, divided equally into two groups. Group 2 (G2) consisted of 100 patients diagnosed with fatty liver disease (FLD), while Group 1 (G1) included 100 apparently healthy individuals who served as controls. Recruitment was carried out sequentially at Diwaniyah Teaching Hospital, Diwaniyah, Iraq, and all samples were gathered up to June 28, 2025. Eligible participants were between 20 and 60 years of age, were nonsmokers, and had no history of chronic illness unrelated to fatty liver disease. Exclusion criteria included excessive alcohol consumption, viral hepatitis, autoimmune disorders, malignancies, and recent application of hepatotoxic medications. The investigation was managed in accordance with the Declaration of Helsinki, and informed consent was derived from all participants prior to enrollment.

Sample collection and preparation: For each subject, 5 mL of venous blood was drawn under aseptic conditions applying sterile vacutainer tubes. Samples were permited to clot at room temperature and then centrifuged at 4000 × g for 10 minutes to separate serum from the cellular fraction. The serum was carefully aliquoted and stored at −20 °C until biochemical analysis. Whole blood samples intended for RNA extraction were also stored at −20 °C until processing.

Biochemical assays: Biochemical and clinical parameters were evaluated to evaluate metabolic and hepatic task. The calculated variables included creatinine, blood urea nitrogen (BUN), fasting blood sugar (FBS), glycated hemoglobin (HbA1c), serum insulin, total cholesterol (TC), triglycerides (TG), high-density lipoprotein cholesterol (HDL-C), very low-density lipoprotein cholesterol (VLDL-C), alanine aminotransferase (ALT), aspartate aminotransferase (AST), the AST/ALT ratio, and alkaline phosphatase (ALP). All measurements were carried out applying the Beckman Coulter AU 480 automated analyzer (Beckman Coulter, USA) based on the manufacturer's instructions. Internal quality controls were included in each run to ensure accuracy and reproducibility.

RNA extraction and quantification: The second phase of the investigation investigated gene expression of angiotensin-converting enzyme (ACE) and ghrelin (GHRL). Total RNA was extracted from 5 mL of whole blood applying a commercial RNA Extraction Kit (ADDBio, Korea). RNA concentration and purity were evaluated by spectrophotometry at 260/280 nm applying a NanoDrop instrument (Thermo Fisher Scientific, USA). Samples with purity ratios between 1.7 and 1.9 were attended acceptable. Additional quantification was carried out applying

a Quantus™ Fluorometer (Promega, USA), yielding RNA concentrations ranging from 10 to 65 ng/μL.

cDNA synthesis and real-time PCR: Complementary DNA (cDNA) was synthesized from purified RNA applying the cDNA synthesis kit (ADDBio, Korea), subsequent the manufacturer's protocol. The cDNA served as the template for quantitative real-time polymerase chain reaction (RT-qPCR), which was carried out applying a Bio-Rad real-time PCR diagnosis system (Bio-Rad, USA). Specific primers were designed for the target and reference genes as follows:

GAPDH (housekeeping control): Forward 5′-GTCTCCTCTGACTTCAACAGCG-3′; Reverse 5′-ACCACCCTGTTGCTGTAGCCAA-3′

ACE: Forward 5′-CATCACCACAGAGACCAGCAAG-3′; Reverse 5′-CCGCTTGATAGTGGTGTTCTGC-3′

GHRL: Forward 5′-GAAGCCACCAGCTAAACTGCAG-3′; Reverse 5′-CTGACAGCTTGATGCCAACATCG-3′

Thermal cycling parameters included an initial denaturation step, followed by 40 amplification cycles consisting of denaturation, annealing, and extension, in accordance with Bio-Rad system guidelines. Negative controls were included in each batch to exclude contamination, and each sample was analyzed in triplicate to ensure reliability.

Gene expression analysis: Relative expression of ACE and GHRL was calculated applying the comparative cycle threshold (ΔΔCt) method, with GAPDH as the internal reference gene. The formulas applied were:

ΔCt (test) = Ct (target, test) − Ct (reference, test)

ΔCt (control) = Ct (target, control) − Ct (reference, control)

ΔΔCt = ΔCt (test) − ΔCt (control)

Relative expression = 2^−ΔΔCt

Amplification efficiency (E%) was calculated from the slope of the standard curve applying the equation:

$$E\% = 10^{(-1/\text{slope})} - 1$$

Only assays with amplification efficiencies close to 100% were included in the analysis.

Statistical analysis: All data are presented as mean ± standard deviation (SD) for continuous variables or as percentages for categorical variables. Comparisons between G1 (controls) and G2 (patients) were carried out applying the independent Student's t-test for normally distributed data. Statistical significance was defined as a p-value < 0.05 at the 95% confidence interval. Statistical analyses were managed applying SPSS version 27 (IBM SPSS, Chicago, IL, USA). Graphical data representations and supplementary analyses were carried out with GraphPad Prism version

9 (GraphPad Software, San Diego, CA, USA). All experiments and assays were independently replicated three times to affirm reproducibility.

Results

Demographic characteristics and clinical features of study groups: The demographic characteristics and clinical features of the control group (G1) and patients with fatty liver disease (G2) are summarized in Table 1. A total of 200 participants were included, with 100 individuals in each group. No statistically meaningful difference was observed in age between groups (36.18 ± 11.31 years in G1 vs. 38.96 ± 11.81 years in G2; p = 0.0907), affirming appropriate age matching. In contrast, body mass index (BMI) was meaningfully higher in FLD patients compared with controls (p = 0.0018). Renal function indicators showed clear differences. Serum creatinine and blood urea were both elevated in the patient group, reflecting possible early renal impairment related to metabolic dysfunction. Marked metabolic alterations were also found. Insulin levels were meaningfully lower in FLD patients compared with controls, whereas fasting blood sugar (FBS) and HbA1c were both substantially elevated, in line with impaired glucose metabolism and insulin resistance. The lipid profile demonstrated a dysregulated pattern. Patients showed meaningfully reduced total cholesterol (TC) and HDL, but higher triglycerides (TG) and very low-density lipoprotein (VLDL), reflecting an atherogenic lipid imbalance. Liver enzyme markers were notably improved in the FLD group, with alanine aminotransferase (ALT), aspartate aminotransferase (AST), and alkaline phosphatase (ALP) all meaningfully elevated compared with controls. However, the AST/ALT ratio did not differ meaningfully, proposing proportional improves in transaminases. These results highlight the broad systemic alterations present in FLD patients, involving metabolic, renal, and hepatic pathways.

Gene expression of ACE and GHRL compared with GAPDH: The expression of ACE and GHRL genes was evaluated relative to the housekeeping gene GAPDH. As shown in **Table 2**, ACE expression was meaningfully improved in patients compared with controls (p = 0.0018). GHRL expression was also markedly elevated in FLD patients (p < 0.0001).

Relative quantification of gene expression: Relative quantification applying the 2^-ΔΔCt method supplied further discernment into expression alters (Table 3). ACE and GHRL expression levels were substantially altered in patients, with reduced normalized expression efficiency compared to controls.

Table 1. Comparison of the demographic parameters and clinical aspects of the study groups (G1 and G2)

Parameters	Groups	T-test	P-value
	G1-control Mean ± SD	G2-FLD Mean ± SD	
Age (Year)	36.18 ± 11.31	38.96 ± 11.81	1.7
BMI (Kg/m²)	22.37 ± 3.819	24.01 ± 3.508	3.157
Creatinine (mg/dl)	0.7880 ± 0.3560	1.042 ± 0.6007	3.638
B. Urea (mg/dl)	26.36 ± 13.19	33.60 ± 20.68	2.952
Insulin levels (U/mL)	31.31 ± 6.800	17.70 ± 5.268	15.82
FBS (mg/dl)	100.4 ± 13.64	248.5 ± 69.81	20.83
HbA1c (mmole/mol)	4.668 ± 0.4501	8.894 ± 1.415	28.47
TC (mg/dl)	187.8 ± 3.741	145.7 ± 13.46	30.16
TG (mg/dl)	128.0 ± 2.776	194.1 ± 19.47	33.59
HDL (mg/dl)	48.78 ± 2.870	29.53 ± 3.556	42.13
VLDL (mg/dl)	25.61 ± 0.5552	38.82 ± 3.894	33.59
ALT (IU/L)	26.52 ± 5.771	51.20 ± 10.71	20.28
AST (IU/L)	23.61 ± 5.158	45.98 ± 9.772	20.24
AST/ALT Ratio	0.9388 ± 0.3193	0.9333 ± 0.2640	0.1339
ALP (IU/L)	94.63 ± 21.25	193.1 ± 23.79	30.87

Abbreviations: TC, total cholesterol; TG, triglycerides; BMI, body mass index; FBS, fasting blood sugar; HbA1c, hemoglobin A1c; HDL, high-density lipoprotein; VLDL, very low-density lipoprotein; ALP, alkaline phosphatase; ALT, alanine aminotransferase; AST, aspartate aminotransferase. Data are presented as mean ± SD. *Meaningful at $p < 0.05$.

Table 2. Comparison between gene expression of ACE and GHRL relative to GAPDH in study groups

Genes	Groups	T-test	P-value
	G1-control (Mean ± SD)	G2-FLD (Mean ± SD)	
ACE	22.37 ± 3.819	24.01 ± 3.508	3.157
GHRL	4.764 ± 2.679	8.926 ± 5.108	7.216

Abbreviations: ACE, angiotensin-converting enzyme; GHRL, ghrelin; GAPDH, glyceraldehyde-3-phosphate dehydrogenase. *Meaningful at $p < 0.05$.

Table 3. Relative quantification of ACE and GHRL genes compared with GAPDH in study groups

Gene (ref GAPDH)	Average Ct	Average ΔCt	Average ΔΔCt	Average 2^-ΔΔCt	Efficiency %
	G1-control	G2-FLD	G1-control	G2-FLD	G1-control
ACE	28.73	35.74	3.06	12.60	3.2
GHRL	25.90	34.40	3.22	10.74	7.70

Figures 1-8 show amplification curves, dissociation analyses, and comparative 2^-ΔΔCt outcomes. Amplification curves for GAPDH, ACE, and GHRL clearly differentiated between patients and controls, while dissociation curves affirmed specificity of the reactions. The bar plots (Figures 3 and 6) affirmed meaningful differences in gene expression ratios between groups.

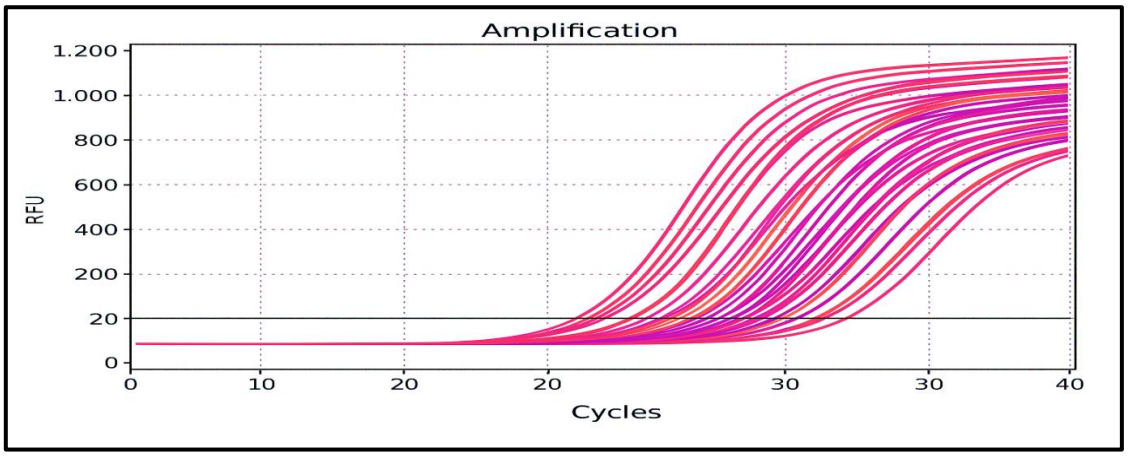

Figure 1. Amplification curve of housekeeping gene (GAPDH) in FLD patients (G2, red line) and control individuals (G1, purple line)

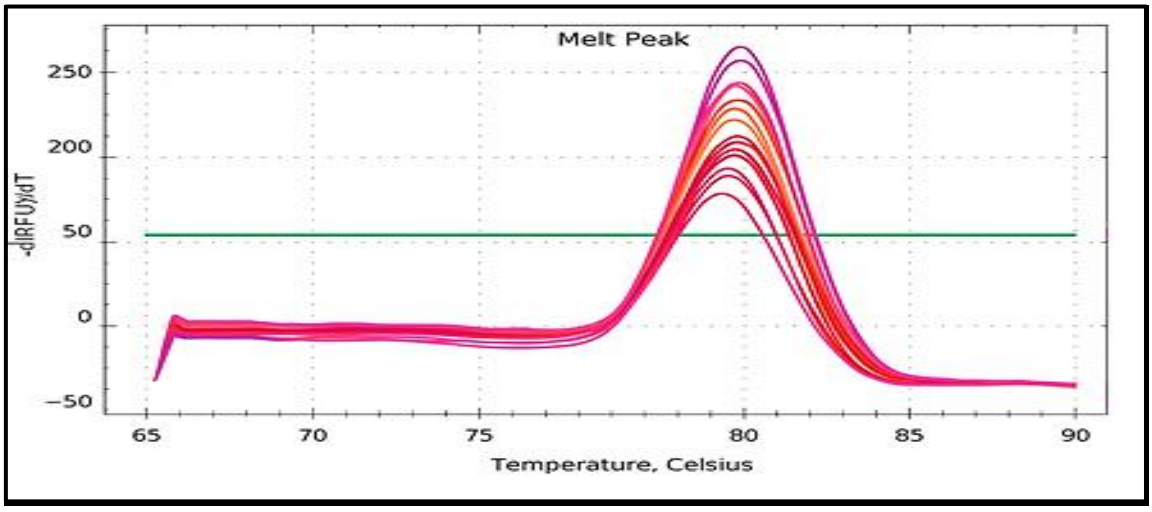

Figure 2. Dissociation (melting) curve analysis of GAPDH gene expression in FLD patients (G2, red line) and controls (G1, purple line)

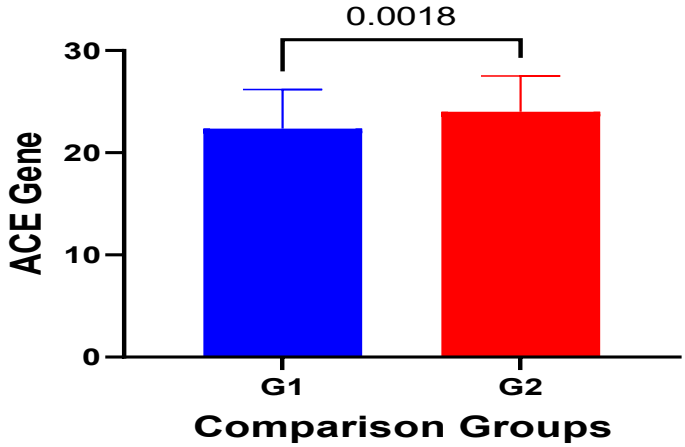

Figure 3. Relative quantification (2^-ΔΔCt) comparison of ACE gene expression between FLD patients (G2) and control group (G1)

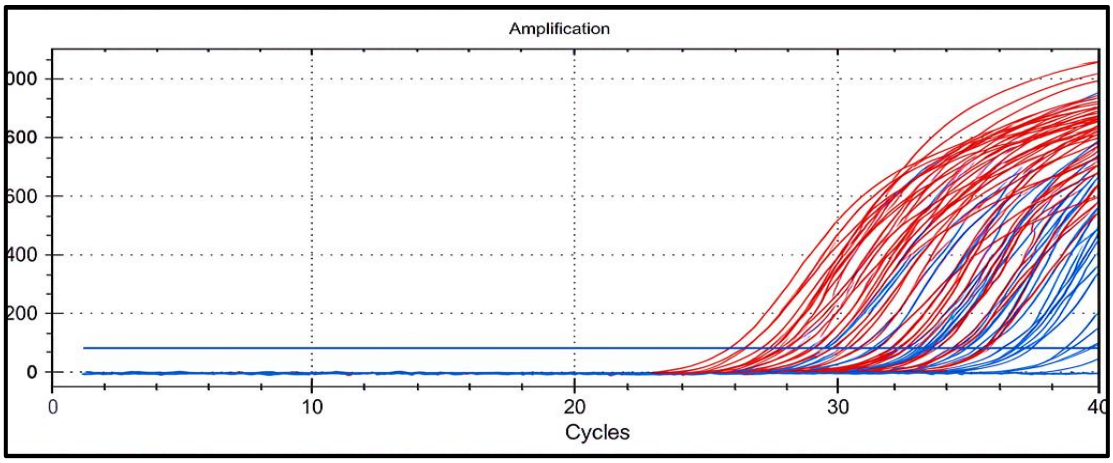

Figure 4. Amplification curve of ACE gene expression in FLD patients (G2, red line) and controls (G1, blue line)

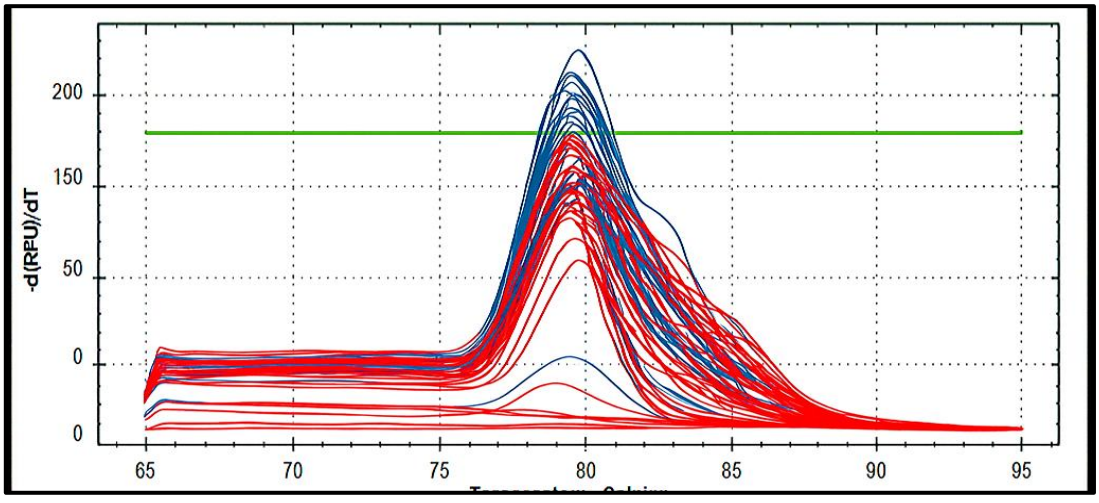

Figure 5. Dissociation (melting) curve analysis of ACE gene expression in FLD patients (G2, red line) and controls (G1, blue line)

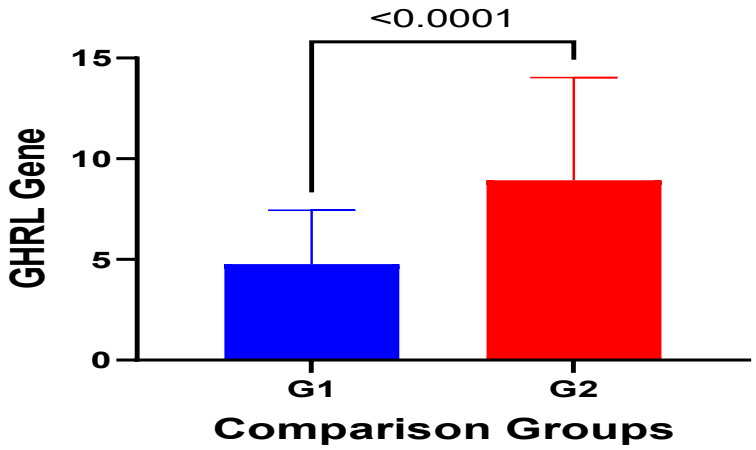

Figure 6. Relative quantification (2^-ΔΔCt) comparison of GHRL gene expression between FLD patients (G2) and control group (G1)

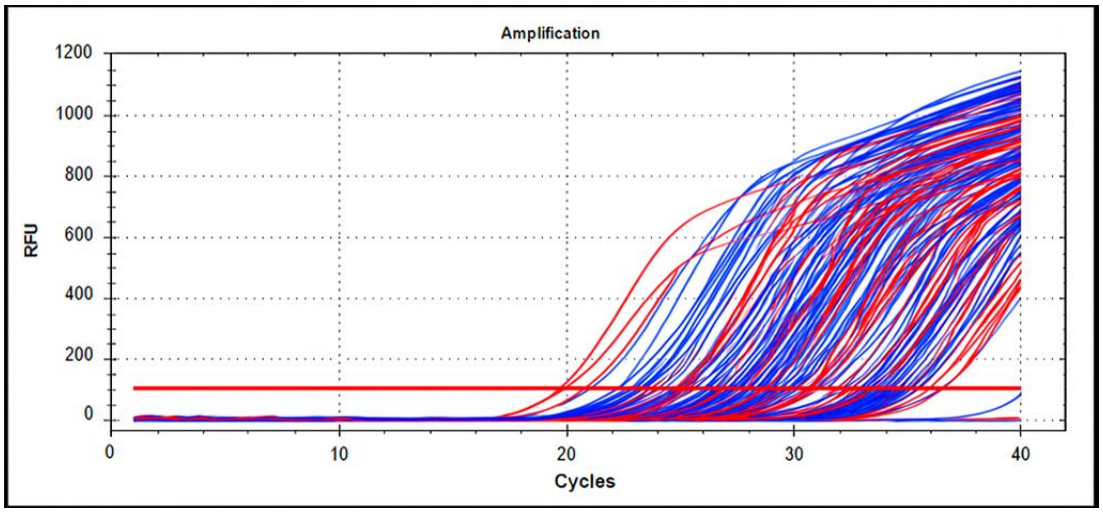

Figure 7. Amplification curve of GHRL gene expression in FLD patients (G2, blue line) and controls (G1, red line)

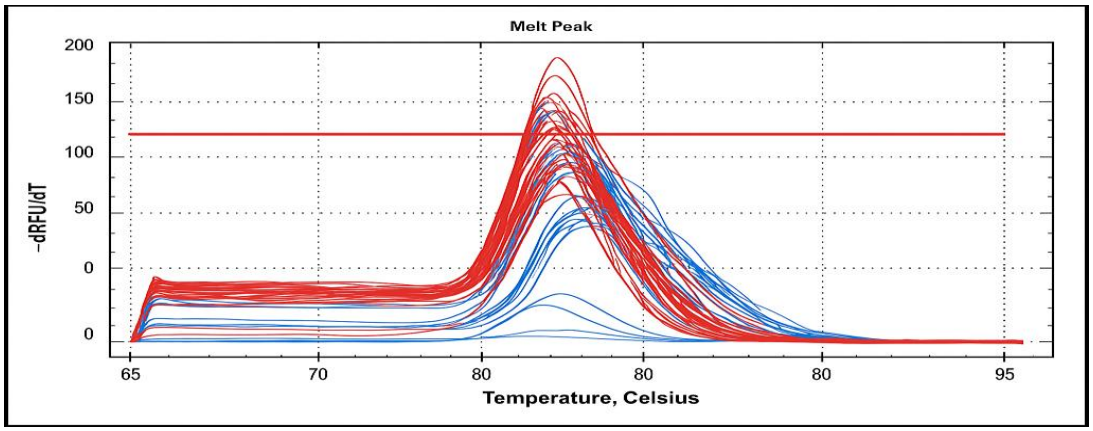

Figure 8. Dissociation (melting) curve analysis of GHRL gene expression in FLD patients (G2, blue line) and controls (G1, red line)

Overall, patients with FLD exhibited meaningful differences from controls in demographic, metabolic, biochemical, and molecular calculates. Alterations in glucose and lipid metabolism, elevated liver enzymes, and impaired renal parameters underscore the systemic impact of fatty liver disease. At the genetic level, upregulation of ACE and GHRL was observed, further supporting their involvement in disease progression and potential as biomarkers or therapeutic targets.

Discussion

Table 1 presents the mean ± SD values for FLD patients (G2) and healthy controls (G1). The analysis disclosed meaningful differences in different clinical and biochemical parameters, containing BMI, creatinine, blood urea, insulin levels, fasting blood sugar (FBS), HbA1c, total cholesterol (TC), triglycerides (TG), HDL, VLDL, ALT, AST, and ALP, between the FLD group (G2) and the control group (G1). The differences were statistically meaningful ($P < 0.05$). In contrast, age and the AST/ALT ratio were not meaningfully different ($P > 0.05$), denoting effective age-matching and the early-stage liver disease profile in the studied population. Lin et al. (2023) announced that individuals with fatty liver disease exhibit higher age-related metabolic burden, persistent systemic inflammation, oxidative stress, and mitochondrial dysfunction, all of which contribute to premature cellular ageing and reduced life expectancy. Telomere attrition and cellular senescence, exemplified by cirrhosis or fibrosis, further impair hepatic task and quality of life. In line with our results, Quek et al. (2023) demonstrated that patients with FLD have higher BMI than healthy controls. Insulin resistance, a hallmark of NAFLD, contributes to impaired lipid oxidation and increased lipogenesis, promoting fat accumulation in hepatocytes. Excess visceral fat releases free fatty acids into the liver, exacerbating inflammation and disease progression. Creatinine levels were meaningfully elevated in FLD patients, in line with Liu et al. (2023), who announced that systemic inflammation, oxidative stress, and insulin resistance in FLD impair renal task, leading to improved creatinine levels. Similarly, Imamura et al. (2021) found elevated blood urea nitrogen (BUN) in FLD, reflecting compromised renal filtration due to shared metabolic pathways between the liver and kidneys. These results underscore the importance of monitoring renal task in patients with liver disease. Insulin resistance and hyperinsulinemia are closely related to FLD pathophysiology. Smith et al. (2020) announced that elevated fasting insulin levels reflect impaired glucose metabolism and exacerbated hepatic lipid accumulation, increasing oxidative stress, inflammation, and the risk of NASH and fibrosis. Fasting blood glucose and HbA1c were also meaningfully higher in FLD patients (Wang et al., 2023; Chen et al., 2020), in line with our results. Elevated HbA1c signifies chronic hyperglycemia, ongoing insulin resistance, and progression toward cardiometabolic complications. Regarding lipid

profiles, FLD patients exhibited lower TC and HDL and higher TG and VLDL levels compared to controls, in line with investigations by Lu et al. (2023), Hou et al. (2021), Mocciaro et al. (2023), and Carlier et al. (2020). Dysregulated lipid metabolism in FLD, driven by insulin resistance, promotes hepatic steatosis, oxidative stress, and inflammatory signaling, accelerating progression to NASH and fibrosis. Low HDL and elevated VLDL are key markers of atherogenic dyslipidemia, increasing cardiovascular risk in FLD patients. Liver enzymes ALT, AST, and ALP were meaningfully elevated in FLD patients, in line with Ma et al. (2020), Huang et al. (2021), and Ali et al. (2021). ALT elevation reflects hepatocyte injury and early steatosis, while improved AST illustrates mitochondrial dysfunction and progressive disease stages. ALP elevation may result from cholestasis, bile ductular proliferation, or fibrosis-induced hepatobiliary injury. The AST/ALT ratio remained within normal limits, proposing early-stage NAFLD rather than progressive fibrosis or cirrhosis (Zhang et al., 2024). Gene expression analysis demonstrated meaningful upregulation of ACE and GHRL in FLD patients (G2) compared to controls (G1). The GAPDH amplification and dissociation curves affirmed the accuracy and reliability of the RT-qPCR outcomes (Figures 1–2). ACE expression was meaningfully elevated in G2 ($P = 0.0018$), reflecting activation of the renin-angiotensin system, which contributes to oxidative stress, inflammation, and insulin resistance in FLD. Amplification efficiency varied from 85–96%, affirming assay reliability (Figures 3–5, Table 3). Similarly, GHRL gene expression was meaningfully higher in FLD patients ($P = 0.0001$), with amplification efficiency of 94–98% (Figures 6–8, Table 3). These results propose that GHRL plays a role in appetite regulation, insulin sensitivity, and lipid metabolism. Dysregulation of GHRL may exacerbate hepatic fat accumulation and inflammation, emphasizing its potential as a diagnostic biomarker and therapeutic target for FLD. Dissociation curves illustrated single, sharp peaks, affirming the specificity and accuracy of the gene expression measurements.

Conclusion: The study demonstrates that BMI, creatinine, blood urea, insulin, FBS, HbA1c, TC, TG, HDL, VLDL, ALT, AST, ALP, and the expression of ACE and GHRL genes are reliable indicators for identifying and evaluating the severity of fatty liver disease. ACE and GHRL in special may serve as worth molecular markers for diagnostic and therapeutic purposes.

Author contributions

Tariq Hussein Mgheer: Conceptualization and methodology, software and validation, formal analysis and investigation, resources, data curation, writing-original draft preparation, writing-review, visualization, and funding acquisition.

Data availability statement

Data are available from the authors upon reasonable request.

Acknowledgements

The author thanks all the subjects who participated in this research.

Ethical Considerations

The study was carried out with integrity, with no fabrication, falsification, plagiarism, or scientific misconduct.

Funding

No external funding was received for this study from public, commercial, or charitable organizations.

References

Alavi, M., Mozafari, M. R., Ghaemi, S., Ashengroph, M., Hasanzadeh Davarani, F., & Mohammadabadi, M. (2022). Interaction of epigallocatechin gallate and quercetin with spike glycoprotein (S-glycoprotein) of SARS-CoV-2: In silico study. *Biomedicines, 10*(12), e3074. https://doi.org/10.3390/biomedicines10123074

Ali, A. H., Petroski, G. F., Diaz-Arias, A. A., Al Juboori, A., Wheeler, A. A., Ganga, R. R., Pitt, J. B., Spencer, N. M., Hammoud, G. M., Rector, R. S., Parks, E. J., & Ibdah, J. A. (2021). A model incorporating serum alkaline phosphatase for prediction of liver fibrosis in adults with obesity and nonalcoholic fatty liver disease. *Journal of Clinical Medicine, 10*(15), 3311. https://doi.org/10.3390/jcm10153311

Amiri Roudbar, M., Mohammadabadi, M. R., Ayatollahi Mehrgardi, A., Abdollahi-Arpanahi, R., Momen, M., Morota, G., Brito Lopes, F., Gianola, D., & Rosa, G. J. M. (2020). Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. *Heredity, 124*(5), 658-674. https://doi.org/10.1038/s41437-020-0301-4

Arabpour, Z., Mohammadabadi, M., & Khezri, A. (2021). The expression pattern of p32 gene in femur, humeral muscle, back muscle and back fat tissues of Kermani lambs. *Agricultural Biotechnology Journal*, *13*(4), 183-200. https://doi.org/10.22103/jab.2022.18782.1371

Buchynskyi, M., Oksenych, V., Kamyshna, I., Vorobets, I., Halabitska, I., & Kamyshnyi, O. (2024). Modulatory roles of AHR, FFAR2, FXR, and TGR5 gene expression in metabolic-associated fatty liver disease and COVID-19 outcomes. *Viruses, 16*(6), 985. https://doi.org/10.3390/v16060985

Carlier, A., Phan, F., Szpigel, A., Hajduch, E., Salem, J. E., Gautheron, J., Le Goff, W., Guérin, M., Lachkar, F., Ratziu, V., Hartemann, A., Ferré, P., Foufelle, F., & Bourron, O. (2020). Dihydroceramides in triglyceride-enriched VLDL are associated with nonalcoholic fatty liver disease severity in type 2 diabetes. *Cell Reports Medicine, 1*(9), 100154. https://doi.org/10.1016/j.xcrm.2020.100154

Chen, C., Zhu, Z., Mao, Y., Xu, Y., Du, J., Tang, X., & Cao, H. (2020). HbA1c may contribute to the development of non-alcoholic fatty liver disease even at normal-range levels. *Bioscience Reports, 40*(1), BSR20193996. https://doi.org/10.1042/BSR20193996

Choochuay, K., Kunhapan, P., Puangpetch, A., Tongsima, S., Srisawasdi, P., Sobhonslidsuk, A., Sungkanuparph, S., Biswas, M., & Sukasem, C. (2024). Associations of PNPLA3 and LEP genetic polymorphisms with metabolic-associated fatty liver disease in Thai people living with human immunodeficiency virus. *World Journal of Hepatology, 16*(3), 366–378. https://doi.org/10.4254/wjh.v16.i3.366

Eslam, M., Sanyal, A. J., George, J., & International Consensus Panel. (2020). MAFLD: A consensus-driven proposed nomenclature for metabolic associated fatty liver disease. *Gastroenterology, 158*(7), 1999–2014.e1. https://doi.org/10.1053/j.gastro.2019.11.312

Hajalizadeh, Z., Dayani, O., Khezri, A., Tahmasbi, R., Mohammadabadi, M., Solodka, T., Kalashnyk, O., Afanasenko, V., & Babenko, O. (2021). Expression of calpastatin gene in Kermani sheep using real-time PCR. *Journal of Livestock Science and Technologies*, *9*(2), 51-57. https://doi.org/10.22103/jlst.2021.18165.1381

Heidarpour, F., Mohammadabadi, M. R., Zaidul, I. S. M., Maherani, B., & Saari, N. (2011). Use of prebiotics in oral delivery of bioactive compounds: A nanotechnology perspective. *Pharmazie, 66*(5), 319-324. https://pubmed.ncbi.nlm.nih.gov/21699064/

Hou, X., Guan, Y., Tang, Y., Song, A., Zhao, J., Ren, L., Chen, S., Wei, L., Ma, H., & Song, G. (2021). A correlation study of the relationships between nonalcoholic fatty liver disease and serum triglyceride concentration after an oral fat tolerance test. *Lipids in Health and Disease, 20*(1), 54. https://doi.org/10.1186/s12944-021-01483-z

Huang, C., Seah, J. J., Tan, C. K., Kam, J. W., Tan, J., Teo, E. K., Kwek, A., Wong, Y. J., Tan, M., Ang, T. L., & Kumar, R. (2021). Modified AST to platelet ratio index improves APRI and better predicts advanced fibrosis and liver cirrhosis in patients with non-alcoholic fatty liver disease. *Clinical Research in Hepatology and Gastroenterology, 45*(4), 101528. https://doi.org/10.1016/j.clinre.2020.08.006

Imamura, Y., Mawatari, S., Oda, K., Kumagai, K., Hiramine, Y., Saishoji, A., Kakihara, A., Nakahara, M., Oku, M., Hosoyamada, K., Kanmura, S., Moriuchi, A., Miyahara, H., & Ido, A. (2021). Changes in body composition and low blood urea nitrogen level related to an increase in the prevalence of fatty liver over 20 years: A cross-sectional study. *Hepatology Research, 51*(5), 570–579. https://doi.org/10.1111/hepr.13631

Khabiri, A., Toroghi, R., Mohammadabadi, M., & Tabatabaeizadeh, S. E. (2023). Introduction of a Newcastle disease virus challenge strain (sub-genotype VII.1.1) isolated in Iran. *Veterinary Research Forum, 14*(4), 221. https://doi.org/10.30466/vrf.2022.548152.3373

Kong, L., Chen, J., Ji, X., Qin, Q., Yang, H., Liu, D., Li, D., & Sun, M. (2021). Alcoholic fatty liver disease inhibited the co-expression of Fmo5 and PPARα to activate the NF-κB signaling pathway, thereby reducing liver injury via inducing gut microbiota disturbance. *Journal of Experimental & Clinical Cancer Research, 40*(1), 18. https://doi.org/10.1186/s13046-020-01782-w

Li, Z., Zhang, B., Liu, Q., Tao, Z., Ding, L., Guo, B., Zhang, E., Zhang, H., Meng, Z., Guo, S., Chen, Y., Peng, J., Li, J., Wang, C., Huang, Y., Xu, H., & Wu, Y. (2023). Genetic association of lipids and lipid-lowering drug target genes with non-alcoholic fatty liver disease. *EBioMedicine, 90,* 104543. https://doi.org/10.1016/j.ebiom.2023.104543

Lin, H., Yip, T. C., Zhang, X., Li, G., Tse, Y. K., Hui, V. W., Liang, L. Y., Lai, J. C., Chan, S. L., Chan, H. L., Wong, G. L., & Wong, V. W. (2023). Age and the relative importance of liver-related deaths in nonalcoholic fatty liver disease. *Hepatology, 77*(2), 573–584. https://doi.org/10.1002/hep.32633

Liu, H., He, B., Hu, W., Liu, K., Dai, Y., Zhang, D., & Wang, H. (2021). Prenatal dexamethasone exposure induces nonalcoholic fatty liver disease in male rat offspring via the miR-122/YY1/ACE2-MAS1 pathway. *Biochemical Pharmacology, 185,* 114420. https://doi.org/10.1016/j.bcp.2021.114420

Liu, J., Peng, H., Wang, C., Wang, Y., Wang, R., Liu, J., Zhou, T., & Yao, S. (2023). Correlation between the severity of metabolic dysfunction-associated fatty liver disease and serum uric acid to serum creatinine ratio. *International Journal of Endocrinology, 2023,* 6928117. https://doi.org/10.1155/2023/6928117

Lu, S., Xie, Q., Kuang, M., Hu, C., Li, X., Yang, H., Sheng, G., Xie, G., & Zou, Y. (2023). Lipid metabolism, BMI and the risk of nonalcoholic fatty liver disease in the general population: Evidence from a mediation analysis. *Journal of Translational Medicine, 21*(1), 192. https://doi.org/10.1186/s12967-023-04047-0

Ma, X., Liu, S., Zhang, J., Dong, M., Wang, Y., Wang, M., & Xin, Y. (2020). Proportion of NAFLD patients with normal ALT value in overall NAFLD patients: A systematic review and meta-analysis. *BMC Gastroenterology, 20*(1), 10. https://doi.org/10.1186/s12876-020-1165-z

Mocciaro, G., Allison, M., Jenkins, B., Azzu, V., Huang-Doran, I., Herrera-Marcos, L. V., Hall, Z., Murgia, A., Susan, D., Frontini, M., Vidal-Puig, A., Koulman, A., Griffin, J. L., & Vacca, M. (2023). Non-alcoholic fatty liver disease is characterised by a reduced polyunsaturated fatty acid transport via free fatty acids and high-density lipoproteins (HDL). *Molecular Metabolism, 73,* 101728. https://doi.org/10.1016/j.molmet.2023.101728

Mohamadinejad, F., Mohammadabadi, M., Roudbari, Z., Eskandarynasab Siahkouhi, S., Babenko, O., Klopenko, N., Borshch, O., Starostenko, I., Kalashnyk, O., & Assadi Soumeh, E. (2024). Analysis of liver transcriptome data to identify the genes affecting lipid metabolism during the embryonic and hatching periods in ROSS breeder broilers. *Journal of Livestock Science and Technologies*, *12*(2), 61-67. https://doi.org/10.22103/jlst.2024.23814.1554

Mohammadabadi, M., & Asadollahpour Nanaei, H. (2021). Leptin gene expression in Raini Cashmere goat using Real Time PCR. *Agricultural Biotechnology Journal*, *13*(1), 197-214. https://doi.org/10.22103/jab.2021.17334.1305

Mohammadabadi, M., Afsharmanesh, M., Khezri, A., Kheyrodin, H., Babenko, O. I., Borshch, O., Kalashnyk, O., Nechyporenko, O., Afanasenko, V., Slynko, V., & Usenko, S. (2025). Effect of mealworm on GBP4L gene expression in the spleen tissue of Ross broiler chickens. Agricultural Biotechnology Journal, 17(2), 343–360. https://doi.org/10.22103/jab.2025.25277.1714

Mohammadabadi, M., Babenko, I., Borshch, O., Kalashnyk, O., Ievstafiieva, Y., & Buchkovska, V. (2024). Measuring the relative expression pattern of the *UCP2* gene in different tissues of the Raini Cashmere goat. *Agricultural Biotechnology Journal, 16*(3), 317-332. https://doi.org/10.22103/jab.2024.24337.1627

Mohammadabadi, M., Golkar, A., & Askari Hesni, M. (2023). The effect of fennel (*Foeniculum vulgare*) on insulin-like growth factor 1 gene expression in the rumen tissue of Kermani sheep. *Agricultural Biotechnology Journal, 15*(4), 239-256. https://doi.org/10.22103/jab.2023.22647.1530

Mohammadabadi, M., Kheyrodin, H., Latifi, A., & Babenko Ivanivna, O. (2022a). mRNA expression profile of DNAH1 gene in testis tissue of Raini Cashmere goat. *Agricultural Biotechnology Journal*, *14*(3), 243-256. https://doi.org/10.22103/jab.2022.20199.1428

Mohammadabadi, M., Shaban Jorjandy, D., Arabpoor Raghabadi, Z., Abareghi, F., Sasan, H. A., & Bordbar, F. (2022b). The role of fennel on DLK1 gene expression in sheep heart tissue.

Agricultural Biotechnology Journal, *14*(2), 155-170. https://doi.org/10.22103/jab.2022.19402.1399

Noori, A. N., Behzadi, M. R. B., & Mohammadabadi, M. R. (2017). Expression pattern of Rheb gene in Jabal Barez Red goat. *The Indian Journal of Animal Sciences*, *87*(11), 1375–1378. https://doi.org/10.56093/ijans.v87i11.75890

Quek, J., Chan, K. E., Wong, Z. Y., Tan, C., Tan, B., Lim, W. H., Tan, D. J. H., Tang, A. S. P., Tay, P., Xiao, J., Yong, J. N., Zeng, R. W., Chew, N. W. S., Nah, B., Kulkarni, A., Siddiqui, M. S., Dan, Y. Y., Wong, V. W., Sanyal, A. J., … Ng, C. H. (2023). Global prevalence of non-alcoholic fatty liver disease and non-alcoholic steatohepatitis in the overweight and obese population: A systematic review and meta-analysis. *The Lancet Gastroenterology & Hepatology, 8*(1), 20–30. https://doi.org/10.1016/S2468-1253(22)00317-X

Rajapaksha, I. G., Gunarathne, L. S., Asadi, K., Laybutt, R., Andrikopoulous, S., Alexander, I. E., Watt, M. J., Angus, P. W., & Herath, C. B. (2022). Angiotensin converting enzyme-2 therapy improves liver fibrosis and glycemic control in diabetic mice with fatty liver. *Hepatology Communications, 6*(5), 1056–1072. https://doi.org/10.1002/hep4.1884

Rezamand, G., Mahmoudi, T., Tabaeian, S. P., Farahani, H., Shahinmehr, F., Nobakht, H., Dabiri, R., Asadi, A., Mansour-Ghanaei, F., & Zali, M. R. (2021). The "GG" genotype of rs26802 variant in the ghrelin gene is a potential protective factor against nonalcoholic fatty liver disease. *Physiological International, 108*(3), 342–352. https://doi.org/10.1556/2060.2021.00183

Rinella, M. E., Lazarus, J. V., Ratziu, V., Francque, S. M., Sanyal, A. J., Kanwal, F., Romero, D., Abdelmalek, M. F., Anstee, Q. M., Arab, J. P., Arrese, M., Bataller, R., Beuers, U., Boursier, J., Bugianesi, E., Byrne, C. D., Castro Narro, G. E., Chowdhury, A., Cortez-Pinto, H., … Newsome, P. N. (2023). A multisociety Delphi consensus statement on new fatty liver disease nomenclature. *Hepatology, 78*(6), 1966–1986. https://doi.org/10.1097/HEP.0000000000000520

Roudbar, M.A., Mohammadabadi, M., & Salmani, V. (2015). Epigenetics: A new challenge in animal breeding. *Genetics in the Third Millennium*, 12(4), 3900–3914.

Safaei, S. M. H., Dadpasand, M., Mohammadabadi, M., Atashi, H., Stavetska, R., Klopenko, N., & Kalashnyk, O. (2022). An *Origanum majorana* leaf diet influences *Myogenin* gene expression, performance, and carcass characteristics in lambs. *Animals, 13*(1), 14. https://doi.org/10.3390/ani13010014

Safaei, S. M. H., Mohammadabadi, M., Moradi, B., Kalashnyk, O., Klopenko, N., Babenko, O., Borshch, O. O., & Afanasenko, V. (2024). Role of fennel (*Foeniculum vulgare*) seed powder in increasing testosterone and *IGF1* gene expression in the testis of lamb. *Gene Expression, 23*(2), 98-105. https://doi.org/10.14218/GE.2023.00020

Shahsavari, M., Mohammadabadi, M., Khezri, A., Borshch, O., Babenko, O., Kalashnyk, O., Afanasenko, V., & Kondratiuk, V. (2022). Effect of fennel (*Foeniculum vulgare*) seed powder consumption on *insulin-like growth factor 1* gene expression in the liver tissue of growing lambs. *Gene Expression, 21*(2), 21-26. https://doi.org/10.14218/GE.2022.00017

Shiha, G., Korenjak, M., Eskridge, W., Casanovas, T., Velez-Moller, P., Högström, S., Richardson, B., Munoz, C., Sigurðardóttir, S., Coulibaly, A., Milan, M., Bautista, F., Leung, N. W. Y., Mooney, V., Obekpa, S., Bech, E., Polavarapu, N., Hamed, A. E., Radiani, T., … Eslam, M. (2021). Redefining fatty liver disease: An international patient perspective. *The Lancet Gastroenterology & Hepatology, 6*(1), 73–79. https://doi.org/10.1016/S2468-1253(20)30294-6

Shokri, S., Khezri, A., Mohammadabadi, M., & Kheyrodin, H. (2023). The expression of MYH7 gene in femur, humeral muscle and back muscle tissues of fattening lambs of the Kermani breed. *Agricultural Biotechnology Journal*, *15*(2), 217-236. https://doi.org/10.22103/jab.2023.21524.1486

Smith, G. I., Shankaran, M., Yoshino, M., Schweitzer, G. G., Chondronikola, M., Beals, J. W., Okunade, A. L., Patterson, B. W., Nyangau, E., Field, T., Sirlin, C. B., Talukdar, S., Hellerstein, M. K., & Klein, S. (2020). Insulin resistance drives hepatic de novo lipogenesis in nonalcoholic fatty liver disease. *Journal of Clinical Investigation, 130*(3), 1453–1460. https://doi.org/10.1172/JCI134165

Sveinbjornsson, G., Ulfarsson, M. O., Thorolfsdottir, R. B., Jonsson, B. A., Einarsson, E., Gunnlaugsson, G., Rognvaldsson, S., Arnar, D. O., Baldvinsson, M., Bjarnason, R. G., DBDS Genomic Consortium, Eiriksdottir, T., Erikstrup, C., Ferkingstad, E., Halldorsson, G. H., Helgason, H., Helgadottir, A., Hindhede, L., Hjorleifsson, G., … Stefansson, K. (2022). Multiomics study of nonalcoholic fatty liver disease. *Nature Genetics, 54*(11), 1652–1663. https://doi.org/10.1038/s41588-022-01199-5

Tabaeian, S. P., Mahmoudi, T., Sabzikarian, M., Rezamand, G., Dabiri, R., Nobakht, H., Asadi, A., Farahani, H., Mansour-Ghanaei, F., & Zali, M. R. (2021). The Leu72Met (rs696217 G>T) polymorphism of the ghrelin gene might be a protective factor for nonalcoholic fatty liver disease. *Journal of Gastrointestinal and Liver Diseases, 30*(2), 233–239. https://doi.org/10.15403/jgld-2703

Teng, M. L., Ng, C. H., Huang, D. Q., Chan, K. E., Tan, D. J., Lim, W. H., Yang, J. D., Tan, E., & Muthiah, M. D. (2023). Global incidence and prevalence of nonalcoholic fatty liver disease. *Clinical and Molecular Hepatology, 29*(Suppl), S32–S42. https://doi.org/10.3350/cmh.2022.0365

Tuero, C., Becerril, S., Ezquerro, S., Neira, G., Frühbeck, G., & Rodríguez, A. (2023). Molecular and cellular mechanisms underlying the hepatoprotective role of ghrelin against NAFLD progression. *Journal of Physiology and Biochemistry, 79*(4), 833–849. https://doi.org/10.1007/s13105-022-00933-1

Wang, Z., Du, H., Zhao, Y., Ren, Y., Ma, C., Chen, H., Li, M., Tian, J., Xue, C., Long, G., Xu, M., & Jiang, Y. (2023). Response to pioglitazone in non-alcoholic fatty liver disease patients with vs. without type 2 diabetes: A meta-analysis of randomized controlled trials. *Frontiers in Endocrinology, 14,* 1111430. https://doi.org/10.3389/fendo.2023.1111430

Yang, M., Ma, X., Xuan, X., Deng, H., Chen, Q., & Yuan, L. (2020). Liraglutide attenuates non-alcoholic fatty liver disease in mice by regulating the local renin-angiotensin system. *Frontiers in Pharmacology, 11,* 432. https://doi.org/10.3389/fphar.2020.00432

Yang, Y., Cai, J., Yang, X., Wang, K., Sun, K., Yang, Z., Zhang, L., Yang, L., Gu, C., Huang, X., Wang, Z., & Zhu, X. (2022). Dysregulated m6A modification promotes lipogenesis and development of non-alcoholic fatty liver disease and hepatocellular carcinoma. *Molecular Therapy, 30*(6), 2342–2353. https://doi.org/10.1016/j.ymthe.2022.02.021

Zhang, C., Xu, Q., Xu, C., Yang, K., Xia, T., Hasi, W., Hao, M., & Kuang, H. (2024). Sex differences in the association between AST/ALT and incidence of type 2 diabetes in Japanese patients with nonalcoholic fatty liver disease: A retrospective cohort study. *Endocrine Research, 49*(1), 1–11. https://doi.org/10.1080/07435800.2023.2262034

مجله بیوتکنولوژی کشاورزی
شاپا چاپی: ۶۷۰۵-۲۲۲۸ شاپا الکترونیکی: ۶۵۰۰-۲۲۲۸

ارتباط بیان ژنی ACE و GHRL با بیماری مزمن کبد چرب: بینش‌های بالینی و متابولیک

طارق حسین مغیر

گروه شیمی و بیوشیمی، دانشکده پزشکی، دانشگاه بابل، عراق. ایمیل: tariq-almgheer@yahoo.com

تاریخ دریافت: ۱۴۰۴/۰۴/۲۸ تاریخ دریافت فایل اصلاح شده نهایی: ۱۴۰۴/۰۷/۰۳ تاریخ پذیرش: ۱۴۰۴/۰۷/۰۴

چکیده

هدف: بیماری کبد چرب (FLD) یا استئاتوز کبدی، یک وضعیت پاتولوژیک است که با تجمع بیش از حد چربی در کبد بیش از ۵ تا ۱۰ درصد وزن آن تعریف می‌شود. با توجه به علل چندعاملی این بیماری که شامل اختلالات متابولیک و زمینه‌های ژنتیکی است، این پژوهش با هدف بررسی ارتباط میان شاخص‌های بیوشیمیایی، بیان ژنی ACE و GHRL و متغیرهای جمعیت‌شناختی مانند سن و شاخص توده بدنی (BMI) در بیماران مبتلا به FLD در مقایسه با افراد سالم انجام شد.

مواد و روش‌ها: در این مطالعه ۲۰۰ نفر شرکت کردند که شامل ۱۰۰ بیمار مبتلا به FLD تأیید شده با سونوگرافی (G2) و ۱۰۰ فرد سالم همسان از نظر سن و قومیت (عراقی) به عنوان گروه کنترل (G1) بودند. تمامی افراد بزرگسال غیرسیگاری با محدوده سنی ۲۰ تا ۶۰ سال بودند که از بیمارستان آموزشی دیوانیه، عراق انتخاب شدند. آزمایش‌های بیوشیمیایی استاندارد برای اندازه‌گیری کراتینین، اوره خون، انسولین، قند خون ناشتا (FBS)، هموگلوبین گلیکوزیله (HbA1c)، کلسترول تام (TC)، تری‌گلیسرید (TG)، لیپوپروتئین با چگالی بالا (HDL)، لیپوپروتئین با چگالی بسیار پایین (VLDL)، آلانین آمینوترانسفراز (ALT)، آسپارتات آمینوترانسفراز (AST)، نسبت AST/ALT و آلکالین فسفاتاز (ALP) انجام شد. همزمان، تحلیل کمی بیان ژن ACE و GHRLصورت گرفت و سطوح بیان برای ارتباط بالینی با اختلالات متابولیک در FLD بررسی شد.

نتایج: بیماران مبتلا به FLD در مقایسه با گروه کنترل دارای مقادیر بالاتر معنی‌دار در شاخص توده بدنی، کراتینین، اوره خون، انسولین، FBS، HbA1c، TC، TG، VLDL، ALT، ASTو ALP بودند، در حالی که سطح HDL به‌طور معناداری پایین‌تر بود ($P < 0.05$). به‌طور مهم، سطح بیان ژن‌های ACE و GHRL در گروه FLD افزایش قابل توجهی داشت که با ناهنجاری‌های بیوشیمیایی مشاهده‌شده همبستگی نشان داد. این نتایج تعامل میان تغییرات بیان ژن و اختلالات متابولیک در پاتوفیزیولوژی FLD را تقویت می‌کند.

نتیجه‌گیری: مقادیر P به‌طور مداوم کمتر از ۰/۰۵، استحکام ارتباطات مشاهده‌شده را تأیید می‌کند. تغییر در بیان ژن‌های ACE و GHRL می‌تواند به عنوان نشانگرهای مولکولی قابل اعتماد برای شناسایی افراد در معرض خطر بالاتر پیشرفت FLD به‌کار رود. افزون بر این، ارزیابی گسترده شاخص توده بدنی، شاخص‌های عملکرد کلیوی، شاخص‌های گلیسمی، پروفایل‌های چربی و فعالیت آنزیم‌های کبدی، بینش ارزشمند بالینی فراهم کرده و از رویکرد یکپارچه برای تشخیص زودهنگام و مدیریت FLD پشتیبانی می‌کند.

واژگان کلیدی: بیماری کبد چرب، استئاتوز کبدی، ژن ACE، ژنGHRL، نشانگرهای زیستی

نوع مقاله: پژوهشی

استناد: طارق حسین مغیر (۱۴۰۴). ارتباط بیان ژنی ACE و GHRL با بیماری مزمن کبد چرب: بینش‌های بالینی و متابولیک. *مجله بیوتکنولوژی کشاورزی*، ۱۷(۴)، ۲۸۵-۳۰۴.

Publisher: Shahid Bahonar University of Kerman & Iranian Biotechnology Society.