Research Article
Green Tea Prevents NAFLD by Modulation of miR-34a and miR-194 Expression in a High-Fat Diet Mouse Model

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Received 19 December 2018; Revised 11 October 2019; Accepted 5 November 2019; Published 4 December 2019

Background/Aims. Nonalcoholic fatty liver disease (NAFLD) is considered the hepatic manifestation of metabolic syndrome. It is currently the most common chronic liver disease with complex pathogenesis and challenging treatment. Here, we investigated the hepatoprotective role of green tea (GT) and determined the involvement of miRNAs and its mechanism of action.

Methods. Male C57Bl/6 mice were fed with a high-fat diet for 4 weeks. After this period, the animals received gavage with GT (500 mg/kg body weight) over 12 weeks (5 days/week). HepG2 cell lines were transfected with miR-34a or miR-194 mimetics and inhibitors to validate the in vivo results or were treated with TNF-α to evaluate miRNA regulation.

Results. GT supplementation protects against NAFLD development by altering lipid metabolism, increasing gene expression involved in triglycerides and fatty acid catabolism, and decreasing uptake and lipid accumulation. This phenotype was accompanied by miR-34a downregulation and an increase in their mRNA targets Sirt1, Pparα, and Insig2. GT upregulated hepatic miR-194 by inhibiting TNF-α action leading to a decrease in miR-194 target genes Hmgcs/Apoa5.

Conclusion. Our study identified for the first time that the beneficial effects of GT in the liver can be due to the modulation of miRNAs, opening new perspectives for the treatment of NAFLD focusing on epigenetic regulation of miR-34a and miR-194 as green tea targets.

1. Introduction

Nonalcoholic fatty liver disease (NAFLD) is currently the most common chronic liver disease in Western countries, affecting about 30% of the worldwide population [1–3]. The NAFLD is considered the hepatic manifestation of metabolic syndrome and it is highly related to obese patients [4]. The mechanisms underlying the development and progression of NAFLD are displayed in a multiple hit model that involves insulin resistance (IR), nutritional factors overload, gut microbiota dysfunction, endoplasmic reticulum (ER) stress, inflammatory liver environment (cytokine release), and genetic and epigenetic factors [5–7].

Green tea (GT) is one of the most consumed beverages in the world and its high content of polyphenols guarantees health beneficial effects. Among the main biological effects attributed to GT polyphenols, we can highlight the antioxidant, anti-inflammatory, antitumor, antiobesity, and hepatoprotective activities [8, 9]. Several studies have related the GT consumption to the improvement and prevention of NAFLD [10–13]. The administration of EGCG, the main polyphenol in GT, improves liver function and morphology, as well as reducing body weight and ameliorates insulin sensitivity [14].

The activity of EGCG on pathways such as TLR4/NFkb and PI3K/AKT/FoxO1 is essential for attenuating inflammation, endoplasmic reticulum stress, oxidative stress, and fibrosis in NAFLD [10]. In addition, green tea extract increases the expression of genes related to lipid oxidation, preventing the accumulation of liver fat through the activation of AMPK [11, 13]. Despite the evidence of the beneficial effects of the green tea and its compounds against NAFLD,
the mechanism by which polyphenols exert their effects on the different pathways highlighted here has not been fully elucidated.

In the last decade, the discovery of epigenetic mechanisms of small noncoding RNAs known as microRNAs (miRNAs) has emerged as potential therapeutic targets for several diseases [15]. Increasing evidence suggests that NAFLD is related to alterations in miRNA expression [16–20]. Jin et al. reported for the first time the difference in the pattern of miRNA expression between NAFLD and normal liver, evidencing the possible contribution of miRNAs for NAFLD pathogenesis and its potential as therapeutic targets and diagnosis [21]. miR-122 is the major miRNA known to be differentially expressed during NAFLD, and it is currently suggested as a predictive marker of fibrosis [22]. The link between miRNA and NAFLD is in the ability of these small molecules to modulate cellular metabolism, especially lipid metabolism in hepatocytes. Recently, it has been observed that the increase of miR-34a is responsible for the decrease in the expression of miR-103, miR-107, and their retention time with those of standard solutions. As a result, the activation of hepatic miR-24 leads to an increase in the expression of miR-24 and consequent steatosis development [23]. In addition, inhibition of hepatic miR-24 leads to an increase in the expression of miR-103, miR-107, and miR-122 [24]. Some studies suggest that the prevention of NAFLD in polyphenol-treated animals is associated with miRNA modulation [25, 26]. Also, it has been demonstrated that the administration of plant-derived polyphenols prevents hepatic steatosis in association with changes in the expression of miR-103, miR-107, and miR-122 [27]. In this context, this study is aimed at evaluating the hepatoprotective role of GT in a high-fat diet (HFD) mouse model of NAFLD and at determining the involvement of miRNAs in vivo and in vitro.

2. Material and Methods

2.1. Animals and Green Tea Supplementation. Twelve-week-old male C57Bl/6 mice were obtained from the University of São Paulo (USP, Brazil) and were housed in the animal facility of the Cruzeiro do Sul University for a one-week period of acclimation. Mice were kept in a room with controlled temperature (24 ± 2°C), light/dark cycle 12:12, and were given water and balanced diet (NUVILAB-CR1, Nuvital Nutrientes LTDA, Brazil) ad libitum. This study has been approved by the Ethics Committee on Animal Experimentation of the Cruzeiro do Sul University (CEUA Cruzeiro do Sul, 135/2014) and all animals received humane care according to the criteria outlined in the Guide for the Care and Use of Laboratory Animals. A total of thirty mice were randomly divided into 3 groups: (i) control (Cont) fed with chow diet, (ii) high-fat diet (HFD) fed with hyperlipidemic diet, and (iii) high-fat diet supplemented with green tea (HFD+GT). The protocol was performed twice with fifteen animals each. The chow diet consisted of 32% protein, 55% carbohydrates, and 13% lipids (2.88 kcal/g). On the other hand, HFD (Prag-Soluções, São Paulo, Brazil) was composed of 20% protein, 36% carbohydrates, and 34% lipids (5.31 kcal/g). Animals were fed an HFD ad libitum, for 16 weeks. After the 4th week, the animals were submitted to a daily (Monday through Friday) oral gavage with 500 mg/kg body weight (BW) of green tea aqueous extract (HFD+GT group) or vehicle (Cont and HFD) for over 12 weeks. The powdered green tea extract was commercially acquired from Tovani Benzaquen, São Paulo, SP, Brazil. The dose of GT was based on previous in vivo studies from our group [29, 30]. The human equivalent dose (HED) was determined following equation: HED (mg/kg = animal NOAEL mg/kg) × (weight animal (kg)/weight human (kg)) (1−0.67). The dose by the factor method applies an exponent for body surface area, which accounts for the difference in metabolic rate, to convert doses between animals and humans [31]. HED = 500 mg/kg × 0.022 kg/70 kg0.33 = 34.9 mg/kg or 2.44 g/70 kg. Therefore, we believe that until a total of 2.44 g/day/70 kg could be used in humans to promote health beneficial effects. That dose of GT can easily be ingested as capsules as a nutraceutical supplement and is therefore of physiological relevance. GT extract was weighed daily and then solubilized in distilled water at 70°C. After GT was at room temperature, it was administered by gavage to mice prior to the feeding period (between 6:00–7:00 pm) in a final volume of 100 μL. The GT extract and standards (EC, EGCG, EGC, ECG, catechin, quercetin, and caffeine) were analyzed in an analytical LC (Varian 210) system with a ternary solvent delivery system equipped with an autosampler, a photodiode array detector (PDA) monitored at λ = 200–800 nm. The catechins, quercetin, and caffeine were identified in GT extract by comparing their retention time with those of standard solutions. As obtained by the HPLC analysis, polyphenol, catechin, and caffeine contents in the extract were 39%, 30%, and 0.4%, respectively [29].

After 16 weeks into the experimental protocol, animals were euthanized by decapitation (between 9:00 and 12:00 h). Blood samples were drawn into heparinized tubes and centrifuged for 10 min at 1200×g, and plasma was stored at −80°C, to the subsequent determination of triglycerides (TG), aspartate aminotransferase (AST), and alanine transaminase (ALT) as well as the determination of cytokines and adipokines. The Aspartate Aminotransferase Activity Assay Kit provides a simple and direct procedure for measuring AST activity. In this kit, the transfer of an amino group from α-ketoglutarate results in the generation of glutamate, resulting in the production of a colorimetric (450 nm) product proportional to the AST enzymatic activity present. One unit of AST is the amount of enzyme that will generate 1.0 μmol of glutamate per minute at pH 8.0 at 37°C. The ALT Activity Assay Kit provides a simple and direct procedure for measuring ALT activity. ALT activity is determined by a coupled enzyme assay, which results in a colorimetric (570 nm)/fluorometric (λex = 535/Aem = 587 nm) product, proportional to the pyruvate generated. One unit
Liver tissue was fixed in 4% phosphate-buffered paraformaldehyde for 24 h. Fixed samples were dehydrated by sequentially increased ethanol concentrations, cleared in xylene, and then embedded in paraffin wax. The embedded samples were cut into 5μm sections and stained with hematoxylin and eosin (H&E). Histological assessment and scoring of steatosis, hepatocellular ballooning, and lobular inflammation were performed by a pathologist blinded to the study. NAFLD stage were established using the histological criteria outlined by Kleiner et al. [32]. The degree of macrovesicular steatosis was graded using the following 4-point scale, namely, grade 0, steatosis involving <5% of hepatocytes; grade 1, steatosis involving up to 33% of hepatocytes; grade 2, steatosis involving 33–66% of hepatocytes; and grade 3, steatosis involving >66% of hepatocytes. Lobular inflammation was also graded on a 4-point scale, namely, grade 0, no foci; grade 1, fewer than 2 foci per ×20 field; grade 2, 2 to 4 foci per ×20 field; and grade 3, more than 4 foci per ×20 field. Hepatocyte ballooning was graded on a 3-point scale: 0, none; 1, a few balloon cells; and 2, any/prominent balloon cells. For NAS, features of steatosis, lobular inflammation, and hepatocyte ballooning were combined with values from 0 to 8. The OCT-embedded (optimal cutting temperature) frozen livers were sectioned at 10 μm with a cryostat to detect neutral lipids by Oil Red-O staining. Briefly, slides were fixed in 10% (v/v) formalin for 10 min, stained with Oil Red-O working solution (Sigma-Aldrich, St. Louis, MO, USA), and counterstained with Hematoxylin.

2.4. Glycogen Analysis. Liver glycogen content was measured after extraction with KOH and precipitation with ethanol followed by determination of glucose through phenol-sulfuric hydrolysis [33]. Liver samples (60 mg) were placed in plastic tubes containing 1.0 mL of 6N KOH and were incubated in a boiling water bath for 10 minutes until complete dissolution. 250 μL of the homogenate was mixed to 3 mL of 95% ethanol and 100 μL of 10% K₂SO₄. A cloudy white precipitate was formed and the supernatant was discharged after centrifuging (150g for three minutes). Afterward, 300 μL of each sample was analyzed at a wavelength of 490 nm on a Tecan spectrophotometric reader (Salzburg, Austria). A standard curve of oyster glycogen (Sigma) was prepared for the final quantification, expressed in μmol/60 mg of hepatic tissue.

2.5. Plasma Insulin and Cytokines/Chemokines and Adipokines. Plasma insulin, cytokines/chemokines (IL-1β, IL-6, TNF-α), and adiponectin levels were measured using Multiplex MAP magnetic bead-based multianalyte panels (Mouse Cytokine/Chemokine Panel I (Cat. No. MCTMAG-70K), Mouse Adipokine (Cat. No. MADKMAG-71K), and Mouse Adiponectin Single Plex (Cat. No. MADPNMAG-70K-01)) (Millipore, Billerica, MA, USA) according to the manufacturer’s guidelines.

2.6. MicroRNA Expression Analysis. Total RNA was extracted using miRNA isolation kit (Ambion, Foster City, USA), according to the manufacturer’s instructions. Total RNA (200 ng/μL) was reverse-transcribed using miScriptII RT kit (Qiagen®, USA) according to the manufacturer’s instructions. After reverse transcription, the expression of miR-34a and miR-194 was evaluated by qRT-PCR (Table 1). The results were normalized to U6. The ΔΔCt method (2-ΔΔCt) was used to calculate relative changes in miRNA expression.

2.7. HepG2 Cell Treatment. Human hepatoma cells were a gift from Dr. Bruno Cogliati (HepG2; University of São Paulo). Cells were maintained at 37 °C in 5% carbon dioxide in high-glucose (11.1 mmol/L) Dulbecco’s modified Eagle’s medium (DMEM) with 10% FBS and 10,000 U/mL penicillin-streptomycin. The HepG2 cell line at 70% confluence was used to validate the expression of target genes of miR-34a and miR-194. Cells were transfected with miRNA mimics or inhibitors using Lipofectamine 3000 (Invitrogen) according to the manufacturer’s instructions. For inhibition of miR-34a and miR-194, anti-hsa-miR-34a and anti-hsa-miR-194 were used at final concentration of 40 nM. For the overexpression of pre-hsa-miR-34a and pre-hsa-miR-194 (Ambion), they were also used at 40 nM. Cells were also treated with GT extract (0.19%) in the presence of miR-34a and anti-miR-194. After 24 h of transfection, the cells were collected and stored at -80 °C for further RNA extraction and qRT-PCR analysis of target genes (Table 1).

In another set of experiments, the HepG2 cells at 90% confluence were treated for 24 h with TNF-α (10ng/mL) to evaluate if this cytokine can modulate the expression of miR-34a and miR-194. Moreover, cells were treated with 2 μM of a mix of catechins (epigallocatechin-3-gallate 1 μM; epicatechin gallate 300 nM; epigallocatechin 500 nM and epicatechin 200 nM) or with GT extract (0.19%) to prevent the TNF-α effect. After 24 h, cells were collected and stored at -80 °C for further miRNA expression analysis (Table 1). The dose of catechins in vitro and GT extract used was previously obtained in our laboratory as an effective dose to reduce the triglyceride content in HepG2 cells (data not shown).

2.8. qRT-PCR Analysis. Total RNA from the liver and HepG2-treated cells was extracted as previously described.
Total RNA was quantified and its integrity confirmed using agarose gel electrophoresis. Total RNA (2 μg) was used to synthesize cDNA using random primers and 200 U SuperScript II RNase H reverse transcriptase at 42°C for 50 min, following the manufacturer’s instructions.

The qRT-PCR was carried out using 30 ng of cDNA and 5× HOT FIREPol EvaGreen® qPCR Mix Plus (Solis Bio-dyne), and gene expression was assessed in an Agilent AriaMx Real-Time PCR under the following conditions: 50°C for 2 min, 95°C for 10 min, and 40 cycles of 95°C for 15 sec, 60°C for 1 min.

| Gene          | Primer sense (5’ to 3’) | Primer anti-sense (5’ to 3’) |
|---------------|-------------------------|-----------------------------|
| miR-34a-5p    | TGGCCACTGGTCTTATGCTGTTG | CGAGGTTGACCTTTCCAGATATTCTT |
| miR-194-5p    | TGTAACAGCAACTTCATTTAGC   | TTACAGGGGCTCTGAAAGAGTTT  |
| Universal_MS2_R | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| hsa-18s       | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| hsa-Apoa5     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| hsa-Hmgcs2    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| hsa-Insig2    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| hsa-Ppara     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| hsa-Sirt1     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-18s       | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Acs13     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Adipor1   | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Adipor2   | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Apoa5     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Cd36      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Cd86      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Fasn      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Fg21r     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Foxo1     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Hmger     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Hmgcs2    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ikkb      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Insig2    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ir        | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Irs2      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Mcr1      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Nkb       | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Nrlh3     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-P3k3      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Pnpla2    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-PPrara    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-PPrard    | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ppargc1a  | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ppargc1b  | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ppargc1c  | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ppargc1s  | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Sirt1     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Tlr       | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Tnf       | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Traf6     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Ucp2      | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |
| mmu-Xbp1s     | TGGCCACTGGTCTTTAGCTGTTG   | TGTTGATGATCTCAGAGGAAG |

[29].
15 s, 60°C for 20 s, and 72°C for 30 s. Dissociation protocols were used to test the effectiveness of the primers in amplifying the genes specifically. In our experiments, the results were normalized by constitutive gene control (18S), determined in accordance with the pattern of tissue expression in each tissue analyzed. To identify predicted or validated targets mRNAs for the selected miRNAs (miR-34a and miR-194), the miRWalk and DIANA-miRPath databases were used. The ΔCt method (2−ΔΔCt) was used to calculate relative changes in mRNA/miRNA expression.

2.9. Statistical Analysis. Our results are given as mean ± SEM. The variance of the data was verified by the Levene test. The interaction (diet, D × green tea, GT) was evaluated through a factorial two-way ANOVA using Tukey as post-test (P < 0.05). The main effect (diet, D, and/or green tea treatment, GT) was assessed by a factorial two-way ANOVA (P < 0.05) when the interaction was not statistically significant. Student’s t-test (P < 0.05) was used for in vitro cell analysis. We used SPSS/Windows version 22 statistical package (SPSS Inc., Chicago, IL, USA) and GraphPad Prism statistics software package version 5.0 for Windows (GraphPad Software, San Diego, CA, USA).

3. Results

3.1. Green Tea Prevents Obesity Attenuating Inflammation in HFD-Induced NAFLD. During the 16 experimental weeks, the body weight of the mice was evaluated. GT-supplemented mice showed attenuated body weight gain, decreased fat pad depots, resulting in a decreased adiposity index when compared to the HFD group (Figures 1(a)–1(f)). GT exhibited significant anti-inflammatory activity through the reduction of plasmatic inflammatory cytokine levels (IL-1β, IL-6, and TNF-α), also increasing plasmatic adiponectin level (Figure 1(g)) compared with the HFD group. Mice supplemented with GT exhibited lower fasting glycemia, plasma insulin level, and higher kITT, promoting lower HOMA index. Besides that, the liver of HFD+GT mice presented higher expression of insulin signaling genes such as Ins2 and Pikh, and higher hepatic glycogen depot (Figures 1(h)–1(m)). Altogether, these data indicate that GT supplementation protects against systemic insulin resistance (IR) improving hepatic insulin sensitivity.

3.2. Green Tea Has Hepatoprotective Effects in HFD-Induced NAFLD. To characterize our NAFLD model, we analyzed the hepatic lipid droplet accumulation through histological images using Oil Red-O staining and biochemical analysis of liver tissue. GT supplementation was effective in reducing lipid accumulation in the liver of HFD-fed mice (Figure 2(a)). GT-supplemented mice had lower activity score of NAFLD when compared to mice only fed with HFD (Figure 2(b)). Supplementation with GT reversed the changes in lipid profile induced by HFD in the liver reducing the macrovesicular steatosis, TG, and cholesterol content (Figures 2(c)–2(e)). We also evaluated the biochemical changes that contribute to the NAFLD characterization and we observed that the supplementation with GT minimizes liver damage induced by HFD (Figures 2(f) and 2(g)). To determine the inflammatory, liver profile evaluated the gene expression of some classical markers of inflammation. GT-supplemented mice showed higher expression of Mrcl, an anti-inflammatory macrophage (M2) marker, and lower expression of inflammatory genes TLR (TLR4), Tnafs, Nkjb (NF-kB), and Tnf (TNF-α) when compared to the HFD group (Figure 2(h)).

3.3. Prevention of Steatosis by Green Tea Extract Is Mediated by Modulating of Lipid and Cholesterol Metabolic Genes. To understand the metabolic changes that accompanied the phenotype of NAFLD, we evaluated the expression of key genes involved in the lipid and cholesterol hepatic metabolism. In general, the supplementation with GT increased lipid catabolism genes increasing the expression of Adipor1/Adipor2 (adiponectin receptors) and Fgf21r—an important receptor that mediates lipid oxidation in the liver (Figure 3(a)). GT supplementation induces genes related to lipolysis and β-oxidation pathway, such as Ffox1, ATGL (Pnpla2), β subunit of PKA (Prkacb), Sirt1, Rxrβ and Acsl3, AMPK alpha subunit (Prkaa2), PGCC1α (Pparγ1a), PPAR-α, LXRs (Nr1h3), and Ucp2 when compared to the HFD group (Figures 3(a)–3(c)). Consistent with the histological analysis, we observed an increase in the expression of genes involved in TG accumulation, fatty acid (FA) uptake, and synthases such as Apoa5, CD36, and Fasn in HFD-fed mice, while GT supplementation reverted Apoa5 and Cd36 expression, decreasing the transcription factor PPAR-γ (Ppar) (Figure 3(d)).

Regarding the cholesterol metabolism, we observed that GT supplementation reduces Hmgcs2 (HMG-CoA synthase) and Hmgcr (HMG-CoA reductase) expression, key genes of cholesterol biosynthesis, while there is an increase in Inisig2 expression, responsible for HMG-CoA reductase cleavage and inactivation when compared to HFD group (Figure 3(e)). These data suggest that GT inhibits cholesterol biosynthesis, thereby decreasing the hepatic lipid content (Figure 2(e)).

3.4. Green Tea Modulates the Expression of miR-34a and miR-194 in Murine HFD-Induced NAFLD. To evaluate the involvement of miRNAs in the mechanism of action of GT, we evaluate the expression of miRNA 34a that is classically known to be involved in the regulation of lipid metabolism and is highly expressed in liver diseases. Also, miR-194 is poorly studied but it is highly expressed in the liver and has been implicated as a modulator of the inflammatory pathway [34].

GT supplementation was effective in reversing miR-34a expression induced by HFD. Inversely, miR-194 was shown to be decreased in the NAFLD, whereas supplementation with green tea increased its expression (Figures 4(a) and 4(b)). After GT treatment, a positive correlation (P < 0.05) between miR-34a expression with miRNAs levels of adipor2 (r² = 0.66), Prkacb (r² = 0.62), and Hmgcs2 (r² = 0.73) was found.

To identify predicted or validated targets mRNAs for the selected miRNAs (miR-34a and miR-194), the miRWalk and
Figure 1: Continued.
Figure 1: Continued.
DIANA-miRPath databases were used. Initially, target genes involved in processes related to NAFLD pathogenesis such as glucose and IR, metabolism, inflammation, and lipid metabolism were selected. From this search, there were identified some targets that had their expression modulated by NAFLD and/or GT in an inverse manner to their respective miRNA, the selected genes were Sirt1, Ppara, and Insig2 for miR-34a; Apoa5 and Hmgcs2 for miR-194 (Figure 4(c)). These targets were then selected for validation in HepG2 cells transfected with miR-34a or miR-194 mimetics and inhibitors, in order to outline the possible mechanism by which the modulation of these miRNAs is related with the development and prevention of NAFLD by HFD and GT, respectively.

3.5. Validation of Target mRNAs Regulated by miR-34a and miR-194 in HepG2 Cells. We initially confirmed that transfection of anti-miR-34a and miR-34a mimic was effective in our cell system (Figure 5(a)). Consistent with our outcomes found in vivo in the HFD-fed mice, cells transfected with miR-34a mimic showed decreased Sirt1, Insig2, and Ppara expression. In addition, anti-miR-34a transfection leads to increased Sirt1, Ppara, and Insig2 expression, similar to the results of mice in the HFD+GT group (Figures 5(b)–5(d)). Cells transfected with miR-34a and treated with GT have presented increased mRNA levels of Sirt1, Ppara, and Insig2. Taken together, these results suggest that the gene regulation of Sirt1, Ppara, and Insig2 occurs through the modulation of miR-34a promoted by GT.

Transfection of HepG2 cells with miR-194 mimic and inhibitor was also effective (Figure 5(e)). We observed that anti-miR-194 transfection increased Hmgcs2 expression when compared to the group transfected with miR-194
Figure 2: Continued.
mimic, corroborating with the result found in vivo (HFD group). Similar to the GT-supplemented group in vivo, miR-194 mimic transfection decreased Hmgcs2 expression. Apoa5 expression was lower in cells transfected with miR-194 mimic as compared to the anti-miR-194 treated cells as observed in GT-supplemented mice compared to HFD mice (Figures 5(f) and 5(g)). GT treatment of cells transfected with anti-miR-194 has decreased both Hmgcs2 and Apoa5 mRNA expression. These results evidenced that Hmgcs2 and Apoa5 gene regulation occurs through miR-194 modulation. We found a positive correlation ($P < 0.05$) between miR-194 expression ($r^2 = 0.77$) and mRNA levels of insig2 in HFD-fed mice and for insR in the HFD+GT group.

To understand the mechanism by which miR-34a and miR-194 are modulated in NAFLD condition, we evaluated their expression in HepG2 cells exposed to TNF-α, which was used to mimic the in vivo inflammation observed during NAFLD. The expression of miR-34a was independent of TNF-α exposure (Figure 5(h)), whereas the expression of miR-194 was directly affected by adding TNF-α in the cell culture. Interestingly, cells incubated with TNF-α and treated with a mix of catechins or the GT extract restored the expression of miR-194 (Figure 5(i)). These results support the idea that TNF-α regulates miR-194 expression and the modulation of GT occurs through its anti-inflammatory activity.

4. Discussion

In the present study, we demonstrate that the GT supplementation protects against obesity and NAFLD development in HFD-fed mice by altering lipid metabolism, increasing genes involved in TG catabolism and fatty acid oxidation, and also decreasing lipid uptake and accumulation as well as cholesterol synthesis. We have some evidence that the underlying mechanism by which the GT alters hepatic metabolism could involve epigenetic regulation of miR-34a and miR-194 that control the expression of target genes such as Sirt1/Ppara/Insig2 and Hmgcs2/Apoa5, respectively. The mechanism by which miR-34a modulation occurs during NAFLD remains unknown, although we have demonstrated that miR-194 expression is downregulated by TNF-α and it was restored by GT.

Our experimental model of HFD was able to induce NAFLD in mice. In contrast, the livers from mice supplemented with green tea extract were protected against the lipid accumulation and inflammation. The GT extract dose used in this study was based in a systematic review of the literature published up to 2013 [35] that concluded, based on an analysis of the reports from 34 randomized clinical trials, that liver-related adverse events were rare after GT supplementation (seven cases in 1405 human subjects that had received dried GT extracts versus one case in 1200 controls) and that liver-related adverse effects were generally mild. Mice fed
**Figure 3: Continued.**

(a) mRNA expression fold change for Adipor1, Adipor2, Fg21r, Prkacb, and Prkaa2 across Cont, HFD, and HFD+GT.

(b) mRNA expression fold change for Sirt1, Fox o1, Pnpla2, Pparg c1a, and Ppara across Cont, HFD, and HFD+GT.

(c) mRNA expression fold change for Nr1h3, Rxr, Ppard, Acox3, and Ucp2 across Cont, HFD, and HFD+GT.
with HFD showed higher expression of hepatic genes involved in lipid accumulation pathways (Apoa5, Cd36, and Fas). Green tea supplementation decreased genes involved in lipid accumulation via such as Cd36 and Apoa5 and increased the expression of key genes involved in FA catabolism such as Pnpla2, Fgf21r, Adipor1, Adipor2, Prkacb, Prkaa2, Sirt1, Foxo1, Ppargc1a, Ppara, Nr1h3, Rxrβ, Ppard, and Acsl3. (d) Genes associated with lipid accumulation (Apoa5, Cd36, Pparg, Fasn). (e) Genes associated with cholesterol biosynthesis (Hmgcs2, Hmgcr, Insig2). Results are presented as mean ± SEM of at least 06 animals per group. ANOVA one- and two-way and Student’s t-test were used for all the statistical analysis. When the difference was statistically significant, the following overwritten letters were used: aCompared to the Cont group. bCompared to the HFD group.

Figure 3: Prevention of steatosis by green tea extract is mediated by modulating of lipid and cholesterol metabolic genes. (a–c) Analysis of expression of genes involved in catabolism Adipor1, Adipor2, Fgf21r, Prkacb, Prkaa2, Sirt1, Foxo1, Pnpla2, Ppargc1a, Ppara, Nr1h3, Rxrβ, Ppard, and Acsl3. (d) Genes associated with lipid accumulation (Apoa5, Cd36, Pparg, Fasn). (e) Genes associated with cholesterol biosynthesis (Hmgcs2, Hmgcr, Insig2). Results are presented as mean ± SEM of at least 06 animals per group. ANOVA one- and two-way and Student’s t-test were used for all the statistical analysis. When the difference was statistically significant, the following overwritten letters were used: aCompared to the Cont group. bCompared to the HFD group.

A wide range of dietary factors, including micronutrients and bioactive compounds such as polyphenols, can modify the expression of miRNAs; additionally, these small regulators have significant contribution in pathways related to the development of NAFLD [24, 36]. Recently, miR-34a has been reported as a miRNA specifically modulated in liver diseases. Circulating levels of miR-34a are high in NAFLD patients as
well as its hepatic expression in animal models of steatosis [23, 37]. Similarly, our NAFLD model showed increased hepatic expression of miR-34a, whereas the GT supplementation mitigates that induction. miR-34a expression in HFD-fed mice was positively correlated with liver cholesterol level ($r^2 = 0.98$), TNF-α ($r^2 = 0.69$), and steatosis ($r^2 = 0.66$). Important lipid-related genes that were modulated in our in vivo study are a target of miR-34a. The genes Sirt1, Ppara, and Insig2 had their expression inversely proportional to miR-34a expression in vivo and in vitro and GT treatment in vitro abolished miR-34a inhibitory effects on Sirt1, Ppara, and Insig2 suggesting a direct effect of GT on miR-34a. Yamakuchi et al. have demonstrated that the Sirt1 is a direct target of miR-34a [38]. In agreement with that data, our mice with NAFLD showed a decrease in the expression of Sirt1 while supplementation with green tea has reverted Sirt1 expression. Furthermore, Ding et al. [23] reported that inhibition of miRNA-34a improves hepatic steatosis of mice by increasing the expression of Ppara and Sirt1, enhancing phosphorylation of AMPKα and, consequently, increasing lipid oxidation. Our results suggest that green tea protects against NAFLD by enhancing the SIRT1/AMPK/PPAR-α signaling axis leading to increased lipid oxidation, with miR-34a mediating those effects corroborating with phenotype of liver tissue observed in histological images.
miR-34a expression
fold change
Scramble miR-34a anti-miR-34a

(a)

Scramble miR-34a anti-miR-34a miR-34a+GT

(b)

Scramble miR-34a anti-miR-34a miR-34a+GT

(c)

Scramble miR-34a anti-miR-34a miR-34a+GT

(d)

miR-194 expression
fold change
Scramble miR-194 anti-miR-194

(e)

Scramble miR-194 anti-miR-194 anti-miR-194+GT

(f)

Figure 5: Continued.
MiR-194 is known by downregulating the TLR4 signaling pathway through suppression of TRAF6 [39]. Although poorly studied, miR-194 presented an interesting modulation being negatively regulated during NAFLD and restored after green tea supplementation. Target genes involved in lipid and cholesterol metabolism, such as Apoa5 and Hmgcs2, had their expression inversely proportional to miR-194 expression.

Camporez et al. [40] reported that ApoA5 knockout mice fed with HFD showed improvement in systemic insulin sensitivity and reduced liver steatosis. Corroborating with that, the expression of miR-94 was decreased in the liver of HFD-fed mice beside an increase of Apoa5 that could, along with other factors, be responsible for the impairment of insulin sensitivity and liver steatosis observed in our study. Positive modulation of miR-194 expression promoted by green tea could be responsible for the decrease of Apoa5 gene expression and improved insulin sensitivity observed, as well as prevention of hepatic fatty accumulation. Our in vitro outcomes validate the modulation of all selected target genes with their respective miRNAs, evidencing that the protective effects of GT on the liver are mediated by direct regulation of miR-34a and miR-194.

It is well established that NAFLD development and evolution are influenced by cytokines and adipokines from adipose tissue, establishing a communication between adipose and hepatic tissues [41]. This crosstalk mediates several events and metabolic alterations [42]. TNF-α has been extensively investigated in this context, and several studies have revealed the regulation of different miRNAs (e.g., miR-142, miR-155, miR-335) by this cytokine [43, 44]. Recently, our group demonstrated that GT prevents obesity and improves adipose tissue metabolism through the miR-335 regulation mediated by TNF-α repression [45].
In view of the notoriety of TNF-α in regulating miRNA expression accompanied of increased plasma level and hepatic expression of TNF-α found in our study, we decided to evaluate the in vitro regulation of miR-34a and miR-194 in cells exposed to TNF-α and treated with catechins or GT extract. TNF-α was able to downregulate the miR-194 expression similar to observed in our HFD-induced NAFLD mouse model. HepG2 cells treated with catechins or GT extract were able to restore miR-194 expression to basal levels, similar to the profile found in vivo following GT supplementation. These data suggest that TNF-α regulates miR-194 expression and the restoration of miR-194 by GT occurs through its anti-inflammatory activity. The modulation of miR-194 via TNF-α has evidenced a crosstalk between adipose tissue and liver mediated by adipocytokines. Since GT also increases adiponectin plasma levels as well as their hepatic receptors AdipoR1/R2 that are responsible for promoting beneficial metabolic actions, we are also suggesting the involvement of adiponectin as a mediator of the GT mechanism of action as proposed and presented in Figure 6.

In summary, this study has provided new evidence that the protective effects of GT in the liver presenting NAFLD are at least in part, mediated by miR-34a and miR-194 modulation. This study showed for the first time important findings such as the modulation of Insig2 by miR-34a, the involvement of miR-194 in lipid and hepatic cholesterol metabolism, and their regulation by TNF-α. However, further studies are needed to determine whether the modulation of miR-194 by GT and its catechins is mediated by an anti-inflammatory effect on TNF-α or by a direct effect on the expression of miRNA-194. Understanding the pathways shown herein reveals new targets for the prevention and therapeutic intervention for NAFLD and evidence of the involvement of miR-34a and miR-194 in the mechanism of action of green tea polyphenols.
Data Availability
Data availability will be provided when requested.

Conflicts of Interest
The authors declare that there are no conflicts of interest.

Acknowledgments
The authors thank Prof. Dr. Rodrigues AC for the contribution in the definition of the experimental design used in this study. This research was supported by the São Paulo Research Foundation (FAPESP, 2015/21785-1, 2013/22293-0) and the Cruzeiro do Sul University.

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