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Aquaporin-9 is involved in the lipid-lowering activity of the nutraceutical silybin on hepatocytes through modulation of autophagy and lipid droplets composition

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ABSTRACT

Hepatic steatosis is the hallmark of non-alcoholic fatty liver disease (NAFLD), the hepatic manifestation of the metabolic syndrome and insulin resistance with potential evolution towards non-alcoholic steatohepatitis (NASH), cirrhosis and hepatocellular carcinoma. Key roles of autophagy and oxidative stress in hepatic lipid accumulation and NAFLD progression are recognized. Here, we employed a rat hepatoma cell model of NAFLD progression made of FaO cells exposed to oleate/palmitate followed or not by TNFα treatment to investigate the molecular mechanisms through which silybin, a lipid-lowering nutraceutical, may improve hepatic lipid dyshomeostasis. The beneficial effect of silybin was found to involve amelioration of the fatty acids profile of lipid droplets, stimulation of the mitochondrial oxidation and upregulation of a microRNA of pivotal relevance in hepatic fat metabolism, miR-122. Silybin was also found to restore the levels of Aquaporin-9 (AQP9) and glycerol permeability while reducing the activation of the oxidative stress-dependent transcription factor NF-κB, and autophagy turnover. In conclusion, silybin was shown to have molecular effects on signaling pathways that were previously unknown and potentially protect the hepatocyte. These actions intersect TG metabolism, fat-induced autophagy and AQP9-mediated glycerol transport in hepatocytes.

1. Introduction

Non-alcoholic fatty liver disease (NAFLD) is accompanying the growing epidemics of obesity, type 2 diabetes, and metabolic syndrome worldwide [1]. In this context, hepatic steatosis is the response to high levels of fatty acids (FA) from diet and adipose tissue, as well as from intrahepatic *de novo* lipogenesis and defective export as very low density lipoproteins (VLDL) [2]. FA entering the hepatocytes are mainly esterified with glycerol to originate triglycerides (TG). The saturated palmitic acid (PA, 16:0) and the monounsaturated oleic acid (OA, 9-cis 18:1) are the most abundant FA in both diet and serum, and they show different lipotoxicity. In rodent hepatocytes cultured *in vitro*, excess PA induces apoptosis, whereas OA prevents cell death and promotes TG secretion [3]. The formation of monounsaturated fatty acids (MUFAs) from saturated fatty acids (SFAs) is catalyzed mainly by the stearoyl-CoA desaturase (SCD-1) [4]. In hepatocytes, TG are either packed as lipid droplets (LD) for storing, or as VLDL for secretion [5].

The proprotein convertase subtilisin/kexin type 9 (PCSK9) is a hepatic protease that degrades the low-density lipoprotein receptor (LDLR) thereby elevating plasma LDL cholesterol levels [6]. Moreover,

Abbreviations: AQP, aquaporin; Atg, autophagy-related proteins; COX, cytochrome *c* oxidase; FA, fatty acids; FAME, fatty acid methyl ester; G3P, glycerol-3-phosphate; LC3: Atg8/MAP1LC3, microtubule associated protein 1 light-chain 3; LD, lipid droplets; miRNA, microRNAs; MUFA, monounsaturated fatty acid; NAFLD, non-alcoholic fatty liver disease; NASH, non-alcoholic steatohepatitis; NEFA, non-esterified fatty acid; OA, oleic acid; PA, palmitic acid; PCKS9, proprotein convertase subtilisin/kexin type 9; SCD-1, Stearoyl-CoA desaturase; SFA, saturated fatty acid; TG, triglycerides; UCP2, uncoupling protein 2; VLCAD, very long-chain acyl-CoA dehydrogenase; VLDL, very low density lipoproteins

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PCSK9 is involved in TG metabolism by acting on degradation of CD36, a major receptor involved in transport of long-chain FA and TG storage [7].

Although storing of lipids inside LD is beneficial, excess hepatocyte enlargement may result in cell dysfunction [8,9], and benign hepatic steatosis can progress to non-alcoholic steatohepatitis (NASH), cirrhosis and hepatocellular carcinoma [10]. Adipokines, interleukins and Tumor Necrosis Factor α (TNFα) are known mediators of NAFLD progression [11]. As a defense mechanism, excess TG accumulation promotes autophagy of LD (lipophagy) [12]. Conventional autophagy is driven by a concerted action of a suite of "autophagy-related" molecules (Atg). The Atg8/MAP1LC3 (microtubule associated protein 1 light-chain 3, hereafter referred to as LC3) acts in elongation and maturation of the autophagosome, while Atg7 mediates the conversion of LC3-I to the active form LC3-II [13]. Autophagy dysfunction has been linked to development of NAFLD [14].

The mobilization of lipids from LD results in excess FA entering oxidation pathways [2]. The long chain FA are oxidized mainly in mitochondria, where the very long-chain acyl-CoA dehydrogenase (VLCAD) catalyzes the first step of oxidation [15], the cytochrome *c* oxidase (COX) in the respiratory chain converts molecular oxygen to water [16], and the uncoupling protein 2 (UCP2) in the inner membrane dissipates excess energy by separating oxidative phosphorylation from ATP synthesis [17].

Stimulation of fat oxidation induces oxidative stress that promotes increased production of TNFα in adipose tissue and in the liver, which, in turn, may induce mitochondrial dysfunction. On the other hand, oxidative stress and stimulated autophagy activate the transcription factor NF-κB which regulates the expression of a broad range of antioxidants genes [18], plays anti-apoptotic and pro-inflammatory functions and inhibits autophagy [19].

MicroRNAs (miRNAs) are non-protein-coding, small single-stranded RNA, that bind to the 3′-UTR of the nucleotide sequence leading to inhibition of translation or mRNA degradation [20]. Dysregulation of miRNA expression has been observed in rodent models of NAFLD, often aligning with the changes observed in patients with steatosis and NASH [21,22]. In the liver, miR-122 represents about 70% of total miRNA and its down- or up-regulation can modify FA and cholesterol metabolism [23].

Aquaporin-9 (AQP9) belongs to *Aquaglyceroporins*, a branch of the *Aquaporin* family of membrane channels allowing permeation of glycerol and, to a lesser extent, water, hydrogen peroxide, urea and ammonia [24,25]. In liver, AQP9 represents the major route through which hepatocytes import glycerol [26–29]. Reduction in hepatic AQP9 levels resulting in reduced glycerol permeability decreases substrate availability for the TG synthesis in the cell [28,30]. Hepatic AQP9 is regulated by insulin and leptin [31], and its pathophysiological relevance was shown in both cell and animal models of NAFLD, and in liver biopsies of obese patients with NAFLD [32–35]. Male rats fed a high-fat diet (HFD) show reduction in liver steatosis after knock-down of liver *Aqp9* at disease onset [36]. Leptin-deficient mice, an animal model of NAFLD, have decreased levels of hepatic AQP9 [32]. Therefore, AQP9 might become an additional therapeutic target for treatment of NAFLD/NASH [37,38]. The possible correlation between AQP9 and autophagy in hepatic lipid metabolism needs to be investigated [14], as changes in AQP9 may prevent or reduce TG accumulation through autophagy [38].

So far, therapeutic options in NAFLD and NASH are lacking, and currently the best approach is limited to changes of lifestyles (*i.e.* balanced diet, regular physical exercise, and reduction of overweight) [39]. As oxidative stress seems to have a central role in hepatic cell injury in the context of NASH, the influence of several antioxidants such as the phytochemical silybin and other compounds are being actively investigated. Silybin is the most relevant flavonolignan of silymarin, the extract of milk thistle seed (*Silybum marianum*). Silybin has antioxidant, anti-inflammatory and cytoprotective actions and it has been used in patients with NAFLD with some beneficial effects [40,41]. Here, in addition to a significant amelioration of the lipid profile of LD, we report involvement of AQP9 in the lipid-lowering activity of silybin on a hepatocyte model of NAFLD through modulation of autophagy.

2. Materials and methods

2.1. Chemicals

All chemicals, unless otherwise indicated, were supplied by Sigma-Aldrich Corp. (Milan, Italy).

2.2. Cell treatments

Rat hepatoma FaO cells [The European Collection of Authenticated Cell Cultures (ECACC)], [42] were grown in Coon's modified Ham's F12 with 10% foetal bovine serum (FBS). Cells grown until 80% confluence were incubated in high-glucose medium with 0.25% bovine serum albumin (BSA) to increase stability and solubility of FA [43]. A condition mimicking human steatosis (SS) was induced by incubating FaO cells for 3 h with an oleate/palmitate mixture (2:1 M ratio, final concentration 0.75 mM). A steatohepatitis (SH) condition was mimicked by incubating SS cells for 24 h with 10 ng/mL TNFα [44]. After replacing the medium, both SS and SH cells were treated for 24 h with 50 μM silybin (Sil) (Istituto Biochimico Italiano, Lorenzini SpA, Italy) [45,46]. Silybin stock (10 mM) was prepared in dimethyl sulfoxide (DMSO).

2.3. Lipid droplet imaging

Cells grown on coverslips were rinsed with PBS and neutral lipids were visualized by optical microscopy using the selective Oil-Red-O (ORO) dye [47]. Briefly, after fixing in 4% paraformaldehyde for 20 min at room temperature, cells were washed with PBS, stained for 30 min with 0.3% ORO solution in isopropanol 60%. After fixation and washing, cells were mounted with 4′,6-diamidino-2-phenylindole (DAPI). Images were obtained using a Leica DMRB light microscope equipped with a Leica CCD camera DFC420C (Leica, Wetzlar, Germany). A first image was obtained by acquiring the ORO-stained LD with bright field set-up, then a second image of the DAPI stained nuclei was acquired with fluorescence set-up. Images were captured with 40× objective and merged [48]. Both the average size and the number of LD/cell were evaluated on acquired images using the open source image processing program ImageJ free software (http://imagej.nih.gov/ij/). At least five images from random fields in each sample were acquired for each experiment set, and at least forty cells for each image were analyzed. Values were expressed as mean ± S.D. from at least three independent experiments.

2.4. Lipid droplet isolation and composition

Lipid droplets were isolated from cells following a standard protocol with minor modifications [49]. FaO cells were scraped from the dishes. Cell suspension (about 40×10^6 cells/sample) was homogenized with a glass dounce homogenizer on ice, and centrifuged at 800 ×*g* for 10 min at 4 °C. The supernatant was centrifuged at 5000 ×*g* for 20 min. Then the supernatant was further centrifuged at 43,000 rpm in SW55 rotor (230,000 ×*g*) for 2 h at 4 °C. The LD fraction forming a distinct white band on the surface of the preparation was collected. Lipids were then extracted from isolated LD using the method of Folch et al. [50] as previously described [51]. Briefly, the lipid phase was saponified with methanolic KOH (3 M) and the non-saponifiable lipids were extracted by diethylether, and the aqueous phase was acidified and extracted with n-hexane. The hexane phases containing NEFAs were collected, the solvent evaporated, and the residue derivatized by acid-catalyzed esterification [52]. Then, samples resuspended in hexane were injected in a HP5890 series II gas chromatograph coupled to a HP5970 mass

spectrometer equipped with an electron impact ionization source (Agilent). Separation was performed on a DB5MS capillary column (Phenomenex, 0.25 mm × 30 m); the helium gas flow was 1 mL/min. The oven temperature gradient was as follows: initial temperature of 100 °C, isothermal at 100 °C for 3 min, 100 to 300 °C (rate, 15 °C/min) and isothermal at 300 °C for 5 min. The MS analysis was performed in full-scan mode. FAME (fatty acid methyl ester) quantification was performed using a calibration curve obtained injecting different FAME standards referring to selected ions. The most abundant and specific ions were used for the quantification of FAMEs: *m/z* 74 was used for saturated FAMEs and *m/z* 55 for monosaturated FAMEs. The regression curves were linear in the range of the FAME concentrations used for the analysis.

2.5. RNA extraction and real-time qPCR

RNA was isolated using Trizol reagent, cDNA was synthesized and quantitative real-time PCR (qPCR) performed in quadruplicate using 1× IQ™SybrGreen SuperMix and Chromo4™ System apparatus (Biorad, Milan, Italy) as previously described [53]. The relative quantity of target mRNA was calculated by the comparative Cq method using glyceraldehyde 3-phosphate dehydrogenase (GAPDH) as housekeeping gene, and expressed as fold induction with respect to controls [45,46]. Primer pairs designed *ad hoc* starting from the coding sequences of *Rattus norvegicus* (http://www.ncbi.nlm.nih.gov/Genbank/GenbankSearch.html) and synthesized by TibMolBiol (Genova, Italy) are listed in Table 1.

Expression of miRNA 122 (miR-122) was measured as described elsewhere [54]. Briefly, reverse transcription was performed using the High capacity cDNA kit (ThermoFisher Scientific, Milan, Italy), following manufacturer's instructions, and the miRNA-specific reverse-transcription primers provided with the TaqMan MicroRNA Assay (ThermoFisher Scientific, Milan, Italy). Amplification was performed using the Stepone plus Real-Time PCR system (ThermoFisher Scientific) at 50 °C for 2 min and at 95 °C for 10 min followed by 40 cycles at 95 °C for 15 s and 60 °C for 1 min. Probe and primers for both miRNA-122-5p (4427975-002245) and miRNA U6 (4427975-001973) were purchased from ThermoFisher Scientific. The relative quantity of miRNA-122-5p was calculated by the comparative Cq method using miRNA U6 as housekeeping gene and expressed as fold induction with respect to controls.

2.6. Immunofluorescence of LC3 and AQP9

Cells grown on poly-L-lysine coated coverslips were rinsed with phosphate-buffered saline (PBS) at pH 7.4, fixed with 4% paraformaldehyde for 20 min and then permeabilized with 0.1% Triton X-100 for 15 min at room temperature (RT). After several washings (3 times for 5 min), slides were blocked with 0.1% gelatin in PBS for 15 min and incubated for 2 h at RT with rabbit polyclonal anti-LC3 (14600-1-AP; Proteintech, Manchester, UK) and/or anti-AQP9 affinity-purified antibodies (AQP9-1A; Alpha Diagnostics International, San Antonio, TX) at a concentration of 3 μg/mL and 4 μg/mL, respectively, in blocking solution (PBS added with 0.1% gelatin). Successively, slides were washed and incubated with fluorescein-isothiocyanate (FITC)-conjugated secondary antibody (Alexa Fluor 488; Thermo Fisher Scientific, Milano, Italy) diluted 1:1000 in blocking solution for 1 h at RT. After staining, slides were washed thoroughly with PBS and mounted with an anti-fade medium containing DAPI (Vectashield, DBA, Segrate, Italy). Finally, slides were sealed and viewed with a Nikon Eclipse 600 photomicroscope equipped with a Nikon DMX 1200 camera (Nikon Instruments SpA, Calenzano, Italy).

2.7. Cytochrome C oxidase activity

Cytochrome C oxidase (COX) is the terminal enzyme complex in the respiratory chain. COX activity was assayed according to Moyes and coworkers [55] following the decrease in absorbance at 550 nm. Briefly, 50 μM reduced cytochrome *c* was dissolved in 0.5% Tween-20 in 20 mM Tris-HCl (pH 8.0). Cytochrome c was reduced with ascorbate and dialyzed overnight to remove unreacted ascorbate. Then, the concentration of reduced cytochrome *c* was determined using an $\varepsilon_{550} = 28.5\ mM^{-1}$. Immediately before the assay, cell extracts (about $3–10 \times 10^4$ cells) were added to the assay medium and incubated for 5 min. The reaction was started by adding 10 μM reduced cytochrome *c* and the change in absorbance was recorded at 550 nm for 3 min.

2.8. Western blotting

Immunoblotting analyses to assess the protein level of LC3α/β and of NF-kB were performed as previously described [16]. For LC3α/β immunoblotting cells were lysed on ice in lysis buffer (NaCl 150 mM, Tris HCl pH 7.4, 50 mM, SDS 0.33%). For of NF-kB, nuclei were isolated by suspending the cellular pellet in 400 μL ice-cold Buffer A (20 mM Tris-HCl pH 7.8, 50 mM KCl, 10 μg/mL Leupeptin, 0.1 mM Dithiothreitol-DTT, 1 mM phenylmethanesulfonyl fluoride-PMSF); and 400 μL Buffer B (Buffer A plus 1.2% Nonindet P40). The suspension was vortex-mixed for 10 s, centrifuged, and washed. The nuclear pellet was re-suspended in 100 μL Buffer B, mixed thoroughly in ice for 15 min and finally centrifuged. The supernatant containing the nuclear extracts was collected. About 30–50 μg proteins were electrophoresed on 10% sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) [56]. Membrane was blocked in 5% fat-free milk/PBST (pH 7.4) and probed overnight at 4 °C using rabbit NF-kB p65 antibody (SC-109; Santa Cruz Biotechnology, DBA, Milan, Italy), or mouse anti-MAP LC3α/β p (SC-398822 Santa Cruz Biotechnology) in PBST buffer (PBS

Table 1
Characteristics of the primer pairs used for the RT-qPCR analysis.

Primer name	Primer sequence (5′- > 3′)	Annealing temperature (°C)	Accession ID
GAPDH-Fw	GACCCCTTCATTGACCTCAAC	60	DQ403053
GAPDH-Rv	CGCTCCTGGAAGATGGTGATGGG		
ATG7-Fw	CCTCAGCGGATGTATGGACC	60	NM_001012097.1
ATG7-Rv	AGCCACATTACACCCCAAGG		
AQP9- Fw	CGTAGGAGAAAATGCAACAGC	60	NM_022960
AQP9-Rv	TGGCAAAGACGATCAGAAGG		
SCD-1 Fw	CACACGCCGACCCTCACAACT	60	AF509569
SCD-1 Rv	TCCGCCCTTCTCTTTGACAGCC		
PCSK9 Fw	GCTTCAGCGGCTTGTTCCT	60	NC_005104.4
PCSK9 Rv	TGCTCCTCCACTCTCCACATAA		
VLCAD Fw	TGAATGACCCTGCCAAG	60	NM 012891
VLCAD Rv	CCACAATCTCTGCCAAGC		
UCP2 Fw	CGTCGGACCTAGCCGTCTGCA	56	BC062230
UCP2 Rv	CGGAGTCGGGAGGGTGCTTTG		

with 0.1% Tween 20) at 4 °C [57]. Membranes were washed and incubated with horseradish peroxidase (HRP)-conjugated secondary antibody in PBST for 1 h at room temperature. Immune complexes were visualized using an enhanced chemiluminescence Western blotting analysis system (Bio-Rad ChemiDoc XRS System). Films were digitized and band optical densities were quantified against the actin band using a computerized imaging system and expressed as Relative Optical Density (ROD, arbitrary units). ROD of each band was expressed as percentage respect to control and about 30–50 μg proteins of cellular homogenates were electrophoresed on SDS polyacrylamide gel electrophoresis (SDS-PAGE).

2.9. Measurement of extracellular glycerol

Glycerol content was measured in cellular medium after a brief centrifugation (14,000 ×*g* for 3 min at 4 °C) after separation in chloroform:methanol (2:1). The water-soluble glycerol was determined by using the 'Triglycerides liquid' kit (Sentinel, Milan, Italy) [45,46]. Varian Cary 50 spectrophotometer (Agilent, Milan, Italy) was used for spectrophotometric analysis. Data were expressed as percent glycerol content relative to controls.

2.10. Statistical analysis

Data were expressed as means ± standard deviation (S.D.) of at least three independent experiments in triplicate. Statistical analysis was performed using ANOVA with Tukey's post-hoc test (GraphPad Software, Inc., San Diego, CA, USA).

3. Results

3.1. Effect of silybin on the fatty acid composition of LD

The cytosolic accumulation of TG in the different steatotic conditions, as visualized by ORO staining, was associated with a marked increase in LD number and size compared to control cells (Fig. 1A–C). Control FaO cells showed only few (about 72 LD/cell) and small (about 0.9 μm average diameter) LD, while both number and size of LD resulted significantly increased in SS and SH cells. While the number of LD was comparable between SS and SH cells (about 295 LD/cell), the average size of LD in SH was smaller than in SS cells (1.3 μm *vs* 1.5 μm, respectively). In SS cells silybin reduced the LD diameter to a value similar to that of control cells (1.1 μm), without effects on the number of LD. No change in LD diameter was seen in the SH cells exposed to silybin.

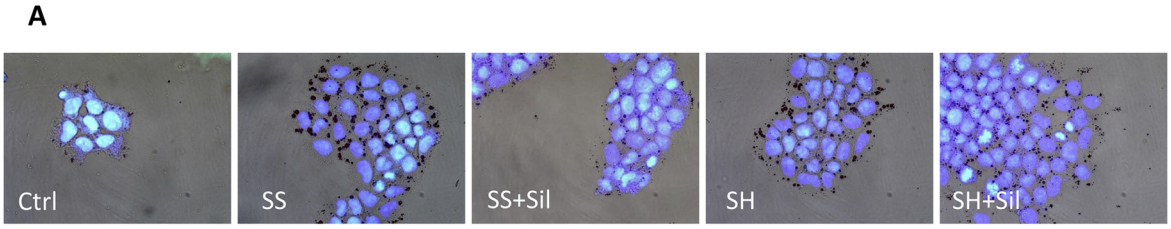
Gas chromatography analysis of LD purified from steatotic cells (Fig. 2A) revealed an acyl composition of the TG in LD consistent with that typically found in mammalian cells in terms of both saturated (SFA) and unsaturated (UFA) fatty acids. The most abundant fatty acids stored in LD included SFA such as myristic acid (MA, 14:0), palmitic acid (PA, 16:0), stearic acid (SA, 18:0), and UFA such as oleic acid (OA, 18:1) and linoleic acid (LA, 18:2). Analytically, the acyl profile in LD from SS cells showed a prevalence of PA (50.1%), followed by SA (27.4%), OA (10.8%), MA (7.4%) and LA (4.2%). SH cells exhibited an increase in PA content (65.6%) and a decrease in OA (6.4%), MA (1.1%) and LA (0.6%) contents, while SA did not change (26.2%). Silybin did not markedly modify the FA pattern in SS cells whereas in SH cells led to a reduction in PA (to 46.5%) and SA (to 20.2%) content and to an increase in OA (to 11.5%) and MA (to 13.8%) levels.

Of note, SH cells showed a marked increase in SFA/UFA ratio compared to SS cells (13.7 *vs* 5.7 in SH and SS cells, respectively), and a reduction in the content of short-medium chain FA (< C16) (4.3% *vs* 11.6% in SS and SH cells, respectively) (Fig. 2A, panel). Treatment with silybin rescued the altered FA profile since the SFA/UFA ratio decreased when SH cells were treated with silybin (from 13.6 to 7.0% in SH and SH + Sil cells). On the other hand, treatment with silybin increased the amount of FA < C16 that reached mean values of 15.9% and 18.6% in SS + Sil and SH + Sil conditions, respectively.

As shown in Fig. 2B, both SS and SH cells showed a decrease in SCD-1 mRNA expression compared to control (0.39- and 0.62-fold induction, respectively; $p \leq 0.01$ and $p \leq 0.05$, respectively), while treatment with silybin increased SCD-1 mRNA level of +249% ($p \leq 0.05$) and + 292% ($p \leq 0.001$) with respect to their counterpart SS and SH, respectively.

3.2. Effect of silybin on hepatocyte AQP9, glycerol uptake and autophagy of LD

Since liver steatosis *in vivo* has been reported to lead to AQP9 dysregulation [32,33,36] and dysfunctional autophagy [14] we assessed



B

LDs number / cell

	Ctrl	SS	SS+Sil	SH	SH+Sil
Mean	72	294 *	248 *	296 *	328 *
Std. Deviation	1.41	161	24	58.7	9.19

* p≤0.001 vs Ctrl

C

LD diameter (μm)

	Ctrl	SS	SS+Sil	SH	SH+Sil
Mean	0.93	1.49	1.11 #	1.33 #	1.22 #
Std. Deviation	0.60	1.38	1.12	1.47	1.22

p≤0.001 vs SS

Fig. 1. Effect of silybin on fatty acid accumulation.
FaO cells were incubated in the presence of oleate/palmitate (SS), or oleate/palmitate and TNFα (SH), then treated for 24 h with 50 μM silybin (Sil). Untreated FaO cells were used as control (Ctrl). A. Representative micrographs of FaO cells stained with DAPI and Oil-Red-O (ORO) (magnification 40×). B–C. Average size of LDs and number of LDs/cells. Values are mean ± S.D. from at least three independent experiments. Statistical significance between groups was assessed by ANOVA followed by Tukey's test. Symbols: Ctrl *vs*. all treatments *$p \leq 0.001$; SS *vs*. all treatments & $p \leq 0.001$.

A

	SS	SS+Sil	SH	SH+Sil
SFA/UFA	5.66	7.56	13.63	6.98
<C16 (%)	11.59	15.88	4.29	18.56

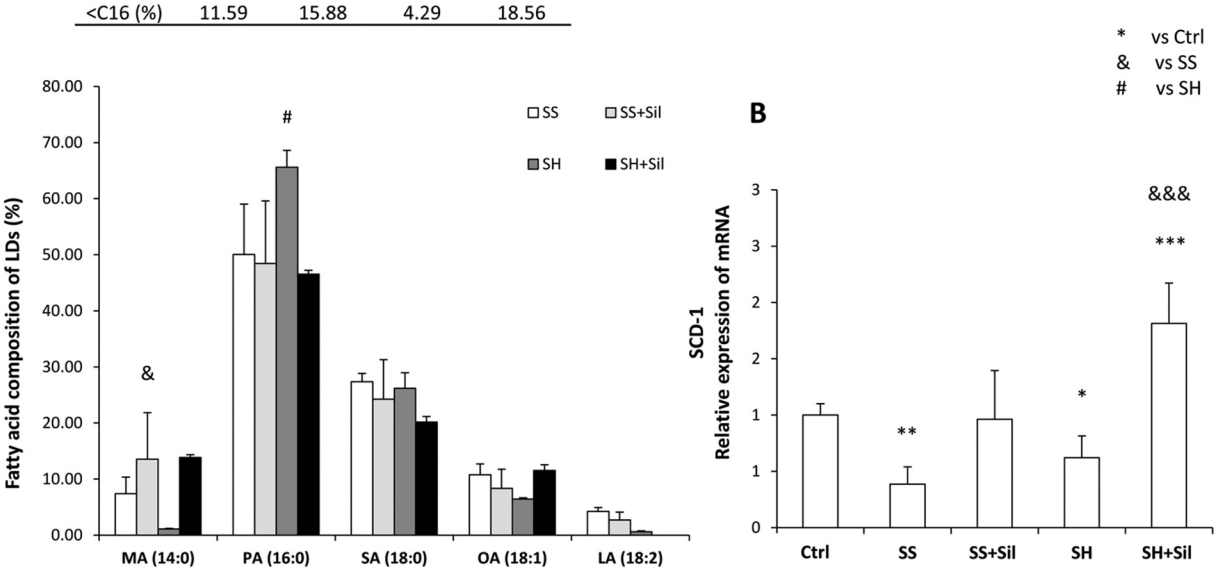


Fig. 2. Effect of silybin on fatty acids composition of LDs.
FaO cells were incubated in presence of oleate/palmitate (SS), or oleate/palmitate and TNFα (SH), then treated for 24 h with 50 μM silybin (Sil). Untreated FaO cells were used as control (Ctrl). A. Acyl composition of LDs purified and analyzed by gas chromatography. B. Real-time qPCR analysis of SCD-1 transcriptional expression. Values are mean ± S.D. from at least three independent experiments. Statistical significance between groups was assessed by ANOVA followed by Tukey's test. Symbols: Ctrl *vs*. all treatments *$p \leq 0.05$, **$p \leq 0.01$, ***p ≤ 0.001; SS *vs*. all treatments &$p \leq 0.05$, &&&p ≤ 0.001; SH *vs*. all treatments # $p \leq 0.05$.

the possible changes in AQP9 expression, glycerol import and autophagic process in FaO cells in the different experimental conditions.

By real-time qPCR, no differences in *AQP9* transcript levels occurred in both steatotic SS and SH cells compared to control (Fig. 3A), whereas marked upregulation of AQP9 was observed in SS and SH cells exposed to silybin (1.55- and 1.72-fold induction *vs* control cells, in SS and SH cells, respectively; $p \leq 0.001$) (Fig. 3A). In terms of protein, SS and SH cells showed a significant reduction of plasma membrane AQP9 immunoreactivity compared to control cells (Fig. 3B, C, E), and silybin restored the levels of AQP9 protein in SS and SH cells (Fig. 3D, F) to extents comparable to those of the control FaO cells. No changes in the transcript and protein levels of AQP9 were seen in control cells receiving silybin (data not shown).

Given the role of AQP9 in glycerol transport within hepatocytes, we measured the glycerol concentration in the culture medium in the attempt of correlating the levels of AQP9 with those of the glycerol influx. The extracellular level of glycerol for both SS and SH cells was similar to that of control cells, while it was significantly reduced by the treatment with silybin (−41% for SS + Sil *vs* SS; −46% for SH + Sil *vs*. SH; $p \leq 0.001$) (Fig. 3G).

The possible effects of silybin on cell autophagy were investigated by assessing the intracellular expression and distribution of LC3-II, and by quantifying the LC3-II/LC3-I ratio [58]. In control conditions, only few punctuate structures, seen as green dots, were observed indicating LC3 recruitment on autophagosomes (Fig. 4A). Both SS and SH hepatocytes showed an increase in these cytosolic puncta (Fig. 4B, D), a profile indicating increased autophagy turnover accompanying NAFLD progression. The immunofluorescence was of wider diffusion when SS and SH were treated with silybin (Fig. 4C, E), resulting in a pattern more similar to that of the control cells (Fig. 4A). In line with these results, Western blot analysis (Fig. 4F) showed a significant increase in LC3-II/LC3-I ratio in both SS and SH cells (+24% and +17%, respectively, *vs* control; $p \leq 0.001$ and $p \leq 0.05$), while silybin counteracted this increase in both steatotic conditions (−29% and − 31%, respectively, *vs* their counterparts; $p \leq 0.001$). No changes in LC3-II/LC3-I ratio were seen in control FaO cells receiving silybin (data not shown).

In both steatotic conditions the Atg7 mRNA was overexpressed, but the increase was larger in SH cells compared to SS cells (2.84 *vs* 1.53-fold induction *vs* control, respectively; $p \leq 0.01$ and $p \leq 0.001$) (Fig. 4G). On the other hand, silybin was able to restore Atg7 expression near to control in SH hepatocytes (−60% *vs* SH; $p \leq 0.001$).

Since autophagy is known to activate NF-κB we assessed by immunoblotting the NF-κB activation as a downstream effect of autophagy stimulation (Fig. 4H). A significant decrease in NF-κB activation was seen when both SS and SH hepatocytes were treated with silybin (about −30% for both SS and SH; $p \leq 0.05$).

3.3. Effects of silybin on genes of hepatic lipid metabolism

Uptake of circulating FA by hepatocytes is also regulated by PCSK9. Analysis by qPCR showed that *PCSK9* mRNA expression was downregulated in both SS and SH cells, with respect to control (0.59- and 0.45-fold induction, respectively; $p \leq 0.001$), and silybin partially reversed this downregulation as *PCSK9* mRNA expression increased significantly in SH cells (+102% *vs* SH; $p \leq 0.01$) (Fig. 5A).

Mitochondria are the final destination of long chain FA for β-oxidation. In mitochondria, expression of VLCAD (Fig. 5B), the shuttle for FA, was up-regulated in SS and SH cells with respect to control (1.61- and 1.86-fold induction, respectively; $p \leq 0.05$), and it was further stimulated when cells were treated with silybin (2.21- and 4.47-fold induction *vs* control, respectively; $p \leq 0.01$). COX acting in the mitochondrial electron transport chain (Fig. 5D) increased significantly its activity only in SH cells (+97% *vs* control; $p \leq 0.001$), but not in SS cells, and silybin was able to stimulate COX activity in SS cells (+27% *vs* control), but not in SH cells (Fig. 5C). Expression of the uncoupling protein UCP2 (Fig. 5D) was also up-regulated in SS and SH cells with respect to control (1.72- and 2.97-fold induction *vs* control; $p \leq 0.01$

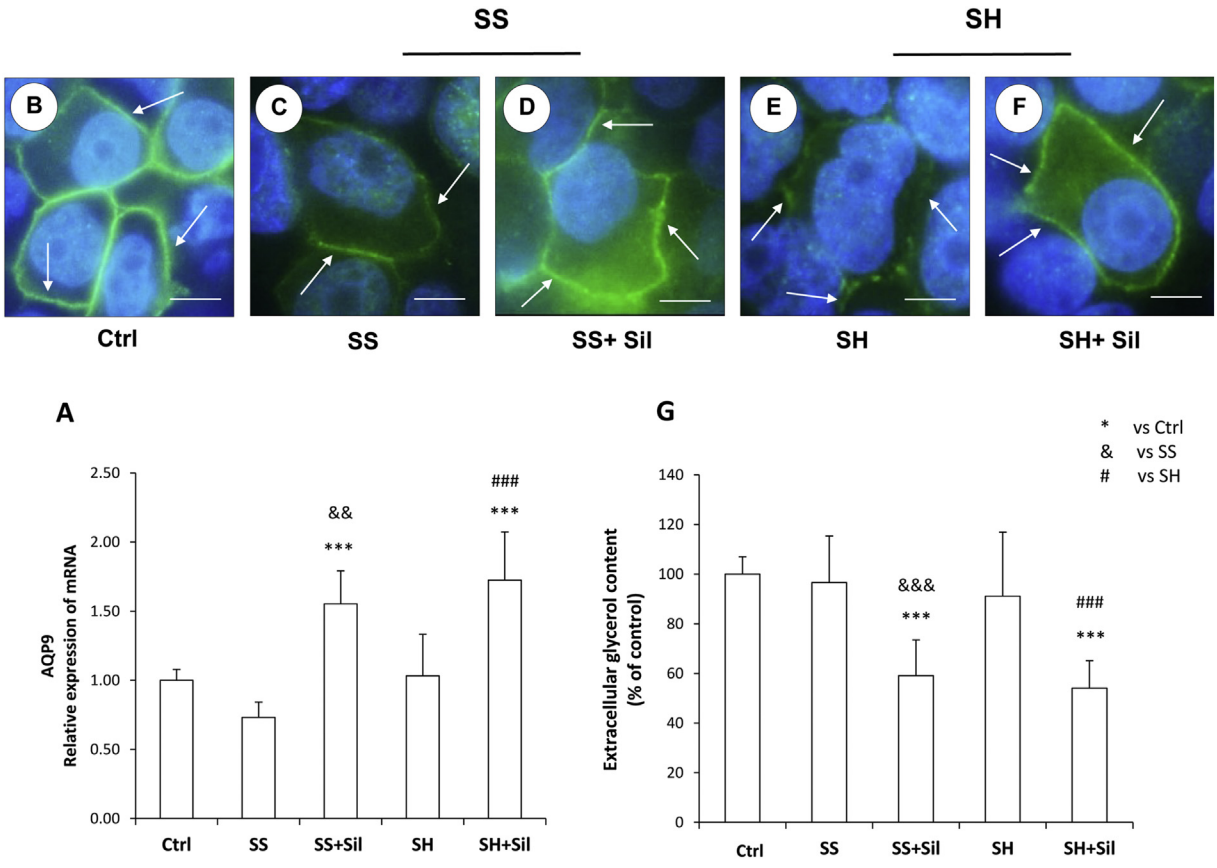


Fig. 3. Effect of silybin on AQP9 expression and glycerol import.
FaO cells were incubated with oleate/palmitate (SS), or oleate/palmitate and TNFα (SH), then treated for 24 h with 50 μM silybin (Sil). Untreated FaO cells were used as control (Ctrl). A. Real-time qPCR analysis of *AQP9* transcriptional expression. B–F. Immunofluorescence analysis. AQP9 immunoreactivity (*green fluorescence*) is seen over the plasma membrane. Nuclei are stained by DAPI (*blue fluorescence*). G. Glycerol content of culture medium. Values are mean ± S.D. from at least three independent experiments. Statistical significance between groups was assessed by ANOVA followed by Tukey's test. Symbols: Ctrl *vs*. all treatments ***p ≤ 0.001; SS *vs*. all treatments &&*p* ≤ 0.01, &&&p ≤ 0.001; SH *vs*. all treatments ### p ≤ 0.001.

and $p \leq 0.0011$, respectively), and silybin counteracted this upregulation (−31% with respect to SH cells; $p \leq 0.01$). Silybin did not play any significant effect on the expression/activity of these proteins in control FaO cells (data not shown).

In hepatocytes miR-122 is recognized to be a major regulator of lipid metabolism [59]. A significant increase in miR-122 level was observed in SS cells upon treatment with silybin (2.01-fold induction *vs* control; $p \leq 0.001$) (Fig. 5E).

4. Discussion

NAFLD is a worrisome health problem worldwide commonly encountered with the metabolic syndrome. No established therapy exists for NAFLD, and changes in lifestyles remain the most common approaches to treat overweight, obesity, insulin resistance, and liver steatosis. The nutraceutical silybin has shown beneficial effects in patients with NAFLD [41], and potential hepatoprotective effects in both animal and cellular models of NAFLD [16,45,46,60,61].

In the present study, employing a cellular model of NAFLD progression widely employed in previous studies [9], we found that the beneficial effect of silybin on hepatic steatosis involves amelioration of the FA profile of LD, stimulation of the mitochondrial oxidation and upregulation of miR-122 expression. Interestingly, silybin is also found to restore the levels of AQP9 and glycerol permeability while reducing the autophagy triggered by the ectopic accumulation of lipids. These results suggest a rather complex and pleiotropic role for silybin in the hepatic cells, involving several key molecular intracellular pathways active during liver steatosis.

The accuracy of the cellular model of NAFLD progression was verified by a series of morphometric and biochemical parameters. First of all, steatotic FaO cells showed an increase in number/size of LD compared to controls. However, the LD diameter was smaller in SH cells than in SS cells, suggesting that these conditions mimic microvesicular and macrovesicular steatosis, respectively. Of note, differences in type of histological steatosis might correlate with distinct phenotypic and prognostic manifestations of liver steatosis. For example, in drug-induced liver injury, acute steatosis is severe, and usually microvesicular because of disrupted mitochondrial beta-oxidation of lipids and oxidative energy production [62]. Also, acute liver failure of pregnancy occurs as microvesicular steatosis [63]. More chronic forms of liver damage, by contrast, occur with macrovesicular steatosis as [64]. However, treatment with silybin was able to reduce the number of LD in both SS and SH cells and the diameter of LD in SS cells, while did not play detectable effects on the size of LD in SH cells. Another sign that silybin improves hepatic steatosis is the increase in miR-122 level in SS cells upon treatment with silybin according to previous studies showing the involvement of miR-122 in NAFLD [59]. Indeed, *in vitro* studies showed downregulation of miR-122 in fatty hepatocytes, and reduced expression of major lipogenic genes upon upregulation of miR-122 in HepG2 cells [21].

In terms of acyl composition, the LD of SS cells are rich in the saturated fatty acids PA and SA, and of the unsaturated OA. The PA content increases in SH cells (+15% *vs* SS cells) being partially balanced by a reduction in OA content (−4% *vs* SS cells). SH cells showed also a lower content of short-medium chain FA (< C16) compared to SS cells. The changes in SFA/UFA ratio might be a sign of more severe

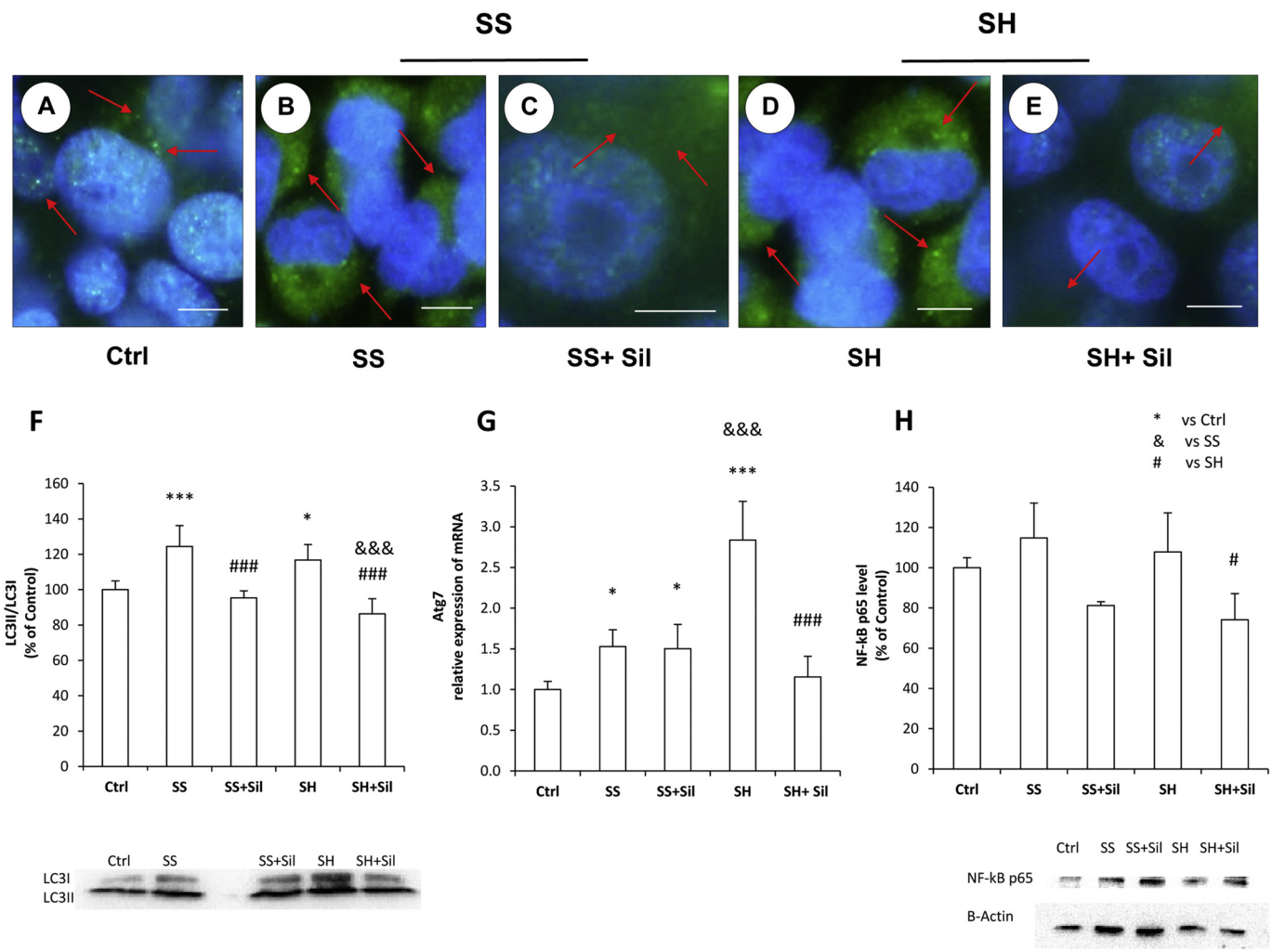


Fig. 4. Effect of silybin on hepatocyte autophagy.

A–E. Immunofluorescence analysis. LC3-II immunoreactivity (*green fluorescence*) is seen over the plasma membrane. Nuclei are stained by DAPI (*blue fluorescence*). Control cells (A) show few punctuate structures (*green dots*) indicating LC3 recruitment on autophagosomes. Both SS (B) and SH (D) hepatocytes show an increase in these cytosolic puncta reflecting an increase in autophagy turnover. The immunofluorescence becomes more diffuse in SS and SH cells were treated with silybin (C, E), resulting in a pattern more similar to that of control cells. F. Western blot analysis of LC3-II/LC3-I ratio. Both SS and SH cells show a significant increase in LC3-II/LC3-I ratio, while silybin counteracts this increase in both steatotic conditions. G. Real-time qPCR analysis of *Atg7* transcriptional expression. In both steatotic conditions, Atg7 mRNA results overexpressed, largely in SH cells compared to SS cells. The treatment with silybin restores the Atg7 expression near to control in SH hepatocytes. H. Western blot analysis of NF-κB. A significant decrease in NF-κB activation is observed when both SS and SH hepatocytes are treated with silybin. Values are mean ± S.D. from at least three independent experiments. Statistical significance between groups was assessed by ANOVA followed by Tukey's test. Symbols: Ctrl *vs*. all treatments *p ≤ 0.05, ***p ≤ 0.001; SS *vs*. all treatments &&&p ≤ 0.001, SH *vs*. all treatments ###p ≤ 0.001.

steatosis in SH cells compared to SS cells. Of note, the beneficial effect of silybin in SH cells was accompanied to a reduction in content of the saturated fatty acids PA and SA, and to an increase in content of the unsaturated OA, as well as to an increase in the amount of short-medium chain FA. In both SS and SH cells, the changes in the FA profile of LDs could be sustained by downregulation of the *SCD-1* mRNA expression. Interestingly, silybin was able to counteract the SCD-1 mRNA downregulation.

Uptake of FA by hepatocytes is regulated by PCSK9, and this effect is independent of its action on LDLR [7]. Indeed, PCSK9 binds LDLR resulting in its internalization and degradation [65], but PCSK9 promotes also degradation of CD36, which is involved in FA uptake and TG storage/secretion. Indeed, *Pcsk9*$^{-/-}$ mice develop hepatic steatosis with liver sections showing accumulation of LD and marked increase in TG content [7]. In the present experimental steatogenic setting, *PCSK9* mRNA was downregulated in both SS and SH cells. This condition would likely promote FA entry in hepatocytes, a mechanism potentially counteracting the excess of external FA. Notably, silybin significantly reversed *PCSK9* downregulation in SH cells, and apparently restored cellular function while reducing FA influx in the hepatocyte. The potential "double sword" effect of PCSK9 inhibition/activation in the hepatocyte, and the action of silybin, needs to be shortly commented, due to potential effects on systemic lipid metabolism. *In vivo* dysfunctional PCSK9 leads to persistently elevated serum LDL-cholesterol and increased risk of coronary heart disease [6], nevertheless loss-of-function mutations are frequently associated with decreased LDL-cholesterol and low risk of heart disease [66,67]. Of note, statins, acting as hypolipemic drugs, lead to increased levels of PCSK9 resulting in a LDL-C-lowering effect *in vitro* [68], but clinical studies do not confirm this effect [69]. In this study, it appears that liver steatosis leads to dysregulation of PCSK9 (and possibly LDLR), while silybin restores at least in part the hepatocyte function. Furthermore, silymarin (and its main constituent silybin) are deemed as adjuvants in hyperlipoproteinemia [70] and reduce LDL lipid peroxidation. Silybin exerts an inhibitory effect on HMG-CoA reductase *in vitro* while, *in vivo*, reducing cholesterol synthesis [71].

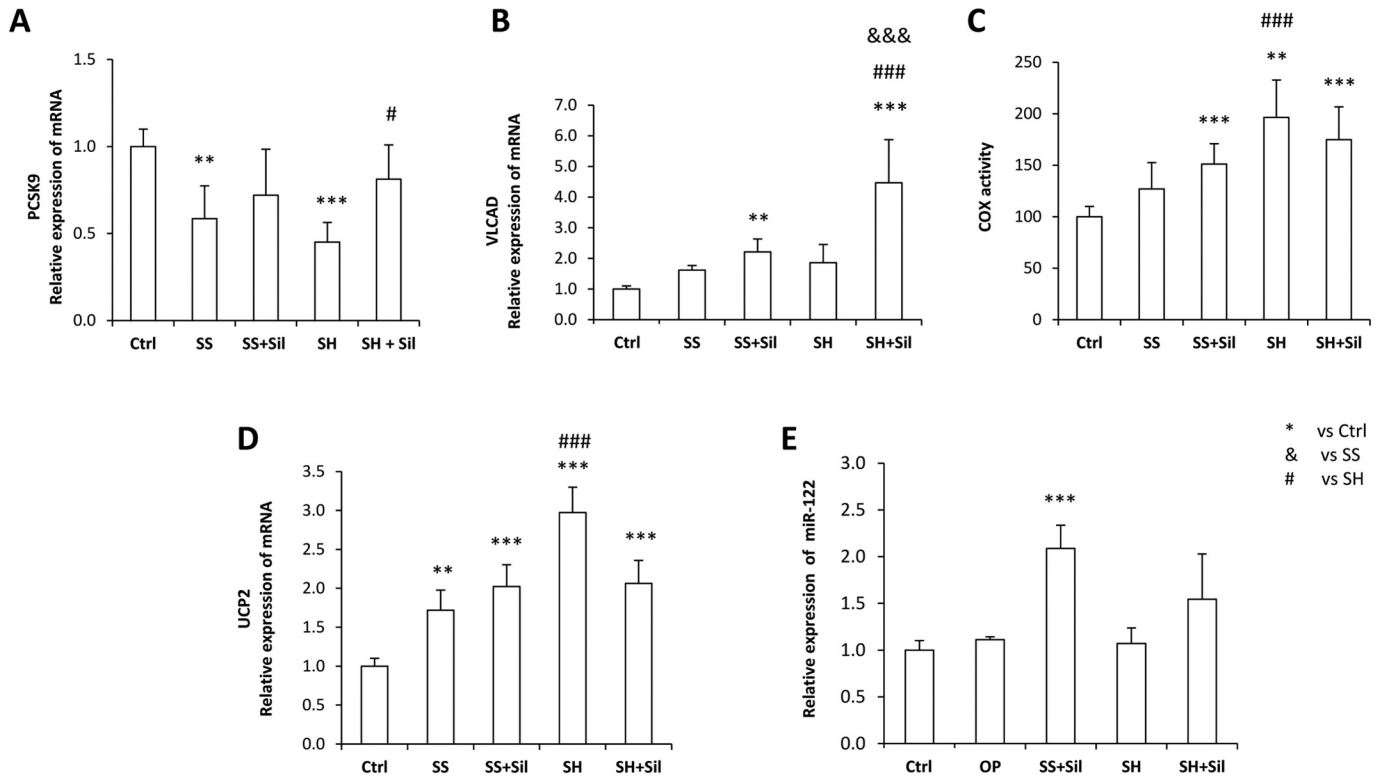


Fig. 5. Effects of silybin on genes of hepatic lipid metabolism.
FaO cells were incubated in the presence of oleate/palmitate (SS), or oleate/palmitate and TNFα (SH), then treated for 24 h with 50 μM silybin (Sil). Untreated FaO cells were used as control (Ctrl). A. Real-time qPCR analysis of *PCSK9* transcriptional expression. B. Real-time qPCR analysis of VLCAD transcriptional expression. C. Cytochrome C oxidase activity measured by enzymatic assay. D. Real-time qPCR analysis of UCP2 transcriptional expression. E. Real-time qPCR analysis of miR-122 transcriptional expression. The level of miR-122 is increased in SS cells upon treatment with silybin. Values are mean ± S.D. from at least three independent experiments. Statistical significance between groups was assessed by ANOVA followed by Tukey's test. Symbols: Ctrl *vs*. all treatments ** $p \leq 0.01$, ***$p \leq 0.001$; SS *vs*. all treatments &&&$p \leq 0.001$; SH *vs*. all treatments ###$p \leq 0.001$.

Together with the effect on other biomarkers of cardiovascular risk, the net effect of silymarin appears to be rather protective on the liver and on serum lipids [72], although further studies need to investigate *in vivo* the effect of silybin on PCSK9-mediated effects during ongoing liver steatosis.

Mitochondria are the final destination of long chain FA for β-oxidation. In both SS and SH cells, UCP2 expression was upregulated in the attempt to avoid the excess synthesis of ATP. Moreover, as a response of toxic TG accumulation, SH cells stimulated the COX activity in the respiratory chain. The lipid lowering activity of silybin in both SS and SH cells was associated to increased long chain FA entering mitochondria through up-regulation of VLCAD expression.

Our results suggest that the anti-steatotic action of silybin implies upregulation of AQP9 and increase of glycerol permeability in hepatocytes. This result is an important insight into the full understanding of the role played by this aquaglyceroporin in NAFLD/NASH. In humans, AQP9 is highly expressed in liver [73], where in post-prandial conditions it sustains the hepatic import of extracellular glycerol for the *ex-novo* synthesis of TG. Likely, silybin might increase the AQP9 levels through an epigenetic mechanism as most bioactive plant polyphenols do [74].

Moreover, silybin is found to diminish the fat-stimulated autophagy as demonstrated by the downregulation of the LC3-II and Atg7 expression in both SS and SH hepatocytes. Indeed, the autophagosome formation is regulated by Atg7 [75]. The parallel reduction in NF-κB activation upon treatment with this phytocompound well fits with the role of NF-κB activation in promoting autophagic process [76].

The inverse correlation found between AQP9 levels and autophagy is compelling. Low levels of hepatocyte AQP9 were associated with the increased autophagy accompanying the TG overaccumulation, whereas the opposite was observed after restoring the levels of AQP9. This finding is consistent with hepatocyte AQP9 expression being positively regulated by the mammalian target of rapamycin (mTOR) [31], a paramount signaling pathway in the regulation of autophagy as the initiation of autophagosome formation by phosphorylating UNC51-like kinase 1 (ULK1) is inhibited by mTOR [77,78]. Of note, AQP9 might have good potentials as drug target in preventing or treating NAFLD/NASH [38], and small compounds selectively and potently gating the AQP9 channel are already available [27,79,80]. The present results lead to the attractive idea that pharmacological modulation of AQP9 may prevent or reduce TG over accumulation and consequent liver dysfunction through autophagy.

In summary, the beneficial effect of silybin on the *in vitro* model of NAFLD and NASH implies (*i*) amelioration of the profile of FA stored in LD with an increase the short/medium chain FA ratio and a decrease of the saturated/monounsaturated FA ratio, (*ii*) stimulation of mitochondrial FA oxidation through upregulation of VLCAD and UCP2 and stimulation of COX activity, (*iii*) increase of the master regulator of hepatic lipid metabolism miR-122, (*iv*) increase of AQP9 expression and glycerol permeability, and (*iv*) diminution of fat-stimulated autophagy.

Altogether, these results show that silybin has molecular effects on signaling pathways that were previously unknown and potentially protect the hepatocyte. These effects intersect TG metabolism, fat-induced autophagy and AQP9-mediated glycerol transport in hepatocytes.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to

influence the work reported in this paper.

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