



Cite this: *Food Funct.*, 2015, **6**, 3282

# Suppressive effects of saponin-enriched extracts from quinoa on 3T3-L1 adipocyte differentiation

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This study was performed to investigate the effect of quinoa saponins (QS) on the differentiation of 3T3-L1 preadipocytes. QS inhibited triglyceride (TG) accumulation in the mature adipocytes, evidenced by oil-red O staining and intracellular quantification. Real time-PCR analysis and western blot analysis showed that QS significantly down-regulated the mRNA and protein expression of key adipogenic transcription factors, peroxisome proliferator-activated receptor  $\gamma$  (PPAR $\gamma$ ), and CCAAT/enhancer-binding protein alpha (C/EBP $\alpha$ ), however, they had no significant effect on CCAAT/enhancer-binding protein beta (C/EBP $\beta$ ) and CCAAT/enhancer-binding protein delta (C/EBP $\delta$ ) which are the upstream regulators for adipogenesis compared with mature adipocytes. QS also reduced mRNA and protein expression of sterol regulatory element-binding protein-1c (SREBP-1c) related to the late stage of adipogenesis. Furthermore, lipoprotein lipase (LPL), adipocyte protein 2 (aP2) and glucose transporter 4 (Glut4), as adipocyte specific genes, were decreased in mature adipocytes by QS treatment. These findings indicate that QS are capable of suppressing adipogenesis and therefore they seem to be natural bioactive factors effective in adipose tissue mass modulation.

Received 15th June 2015,  
Accepted 18th July 2015

DOI: 10.1039/c5fo00716j

www.rsc.org/foodfunction

## 1. Introduction

Obesity has reached epidemic proportions worldwide, leading to the development of many common medical conditions, such as type 2 diabetes and metabolic syndrome with a high increasing rate, accelerated cardiovascular diseases and increased cancer risk.<sup>1</sup> Intraabdominal visceral fat accumulation, which depends on adipocyte proliferation and differentiation of pre-adipocytes, would directly contribute to the occurrence of obesity.<sup>2</sup> During adipocyte differentiation, adipogenic transcription factors, such as peroxisome proliferator-activated receptor  $\gamma$  (PPAR $\gamma$ ), CCAAT/enhancer-binding protein alpha (C/EBP $\alpha$ ), and sterol regulatory element-binding protein-1c (SREBP-1c), are considered to be key regulators of adipogenesis, which govern the expression of genes involved in the induction of adipocyte phenotypes.<sup>3–5</sup> Several studies suggest that suppression of transcription factors such as PPAR $\gamma$ ,

C/EBP $\alpha$ , and SREBP-1c, which are necessary for adipogenesis to occur, can inhibit preadipocyte differentiation.<sup>6–8</sup>

Quinoa (*Chenopodium quinoa* Willd.) saponins have been found in all parts of the quinoa plant such as leaves, flowers, fruits, seeds, and seed coats.<sup>9</sup> The saponins of quinoa are bitter and represent the major antinutritional factor in the grain. In Ecuador, the seeds of quinoa are commonly soaked in water to remove the bitter saponins before cooking.<sup>10</sup> There is now much interest in the saponins in quinoa for their physiological functionalities, such as anti-inflammatory activity,<sup>11</sup> antifungal activity,<sup>12</sup> antitumor activity,<sup>13</sup> and antioxidant activity.<sup>14</sup> However, little is known about quinoa saponins on preadipocyte differentiation and the formation of mature adipose cells. In this study, we investigated the effects of QS on 3T3-L1 cell preadipocyte differentiation. Furthermore, we investigated the regulatory effects of QS on the mRNA expression of transcriptional factors, PPAR $\gamma$ , C/EBP $\alpha$  and SREBP1c, lipoprotein lipase (LPL), adipocyte protein 2 (aP2) and glucose transporter 4 (Glut4).

## 2. Materials and methods

### 2.1. Materials

3T3-L1 cells were obtained from the Institutes for Biological Sciences, Chinese Academy of Sciences (Shanghai, China). Fetal bovine serum (FBS), Dulbecco's modified Eagle's

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medium (DMEM), insulin, dexamethasone (DEX) and 1-methyl-3-isobutylxanthine (IBMX) were purchased from Sigma Chemical Co. (St Louis, MO).

## 2.2. Extraction of QS

QS was prepared as we previously described.<sup>11</sup> Quinoa seeds were finely powdered and defatted at room temperature with petroleum ether and extracted with MeOH by exhaustive maceration. The residue was successively dissolved in water and partitioned with EtOAc and *n*-BuOH, respectively. After filtration, the extracts were loaded onto a macroreticular resin column (type: AB-8) and eluted with 30, 50, 70, and 90% of methanol-ethanol solution. The 50% resultant QS was concentrated and spray-dried. Individual components in QS were determined using high-performance liquid chromatography (HPLC). The QS sample was analyzed by an Agilent 1200 series liquid chromatograph containing an autosampler coupled with a 6300 series ion-trap mass spectrometer (Agilent, Santa Clara, CA). On the basis of peak areas, QS contained 14.52 g kg<sup>-1</sup> 3-*O*-hexose-pentose-pentose phytolaccagenic acid

28-*O*-hexose, 98.25 g kg<sup>-1</sup> 3-*O*- $\alpha$ -L-arabinopyranosyl phytolaccagenic acid 28-*O*- $\beta$ -D-glucopyranosyl ester, 84.28 g kg<sup>-1</sup> 3-*O*- $\beta$ -D-glucopyranosyl-(1 $\rightarrow$ 3)- $\alpha$ -L-arabinopyranosyl phytolaccagenic acid 28-*O*- $\beta$ -D-glucopyranosyl ester, 142.68 g kg<sup>-1</sup> 3-*O*- $\alpha$ -L-arabinopyranosyl-(1 $\rightarrow$ 3)- $\beta$ -D-glucuronopyranosyl serjanic acid 28-*O*- $\beta$ -D-glucopyranosyl ester, 35.54 g kg<sup>-1</sup> 3-*O*- $\beta$ -D-xylopyranosyl-(1 $\rightarrow$ 3)- $\beta$ -D-glucuronopyranosyl hederagenin 28-*O*- $\beta$ -D-glucopyranosyl ester, 149.25 g kg<sup>-1</sup> 3-*O*- $\beta$ -D-glucopyranosyl-(1 $\rightarrow$ 3)- $\alpha$ -L-arabinopyranosyl hederagenin 28-*O*- $\beta$ -D-glucopyranosyl ester, 135.48 g kg<sup>-1</sup> 3-*O*- $\beta$ -D-glucopyranosyl-(1 $\rightarrow$ 3)- $\alpha$ -L-arabinopyranosyl serjanic acid 28-*O*- $\beta$ -D-glucopyranosyl ester, and 32.44 g kg<sup>-1</sup> 3-*O*- $\beta$ -D-glucuronopyranosyl oleanolic acid 28-*O*- $\beta$ -D-glucopyranosyl ester.

## 2.3. Cell culture

3T3-L1 cells were cultured according to the provider's established protocol. 3T3-L1 cells were grown in DMEM containing 4.5 g L<sup>-1</sup> D-glucose with 10% heat-inactivated FBS, 1% penicillin and 1% HEPES buffer at 37 °C under a humidified atmosphere of 5% CO<sub>2</sub>.

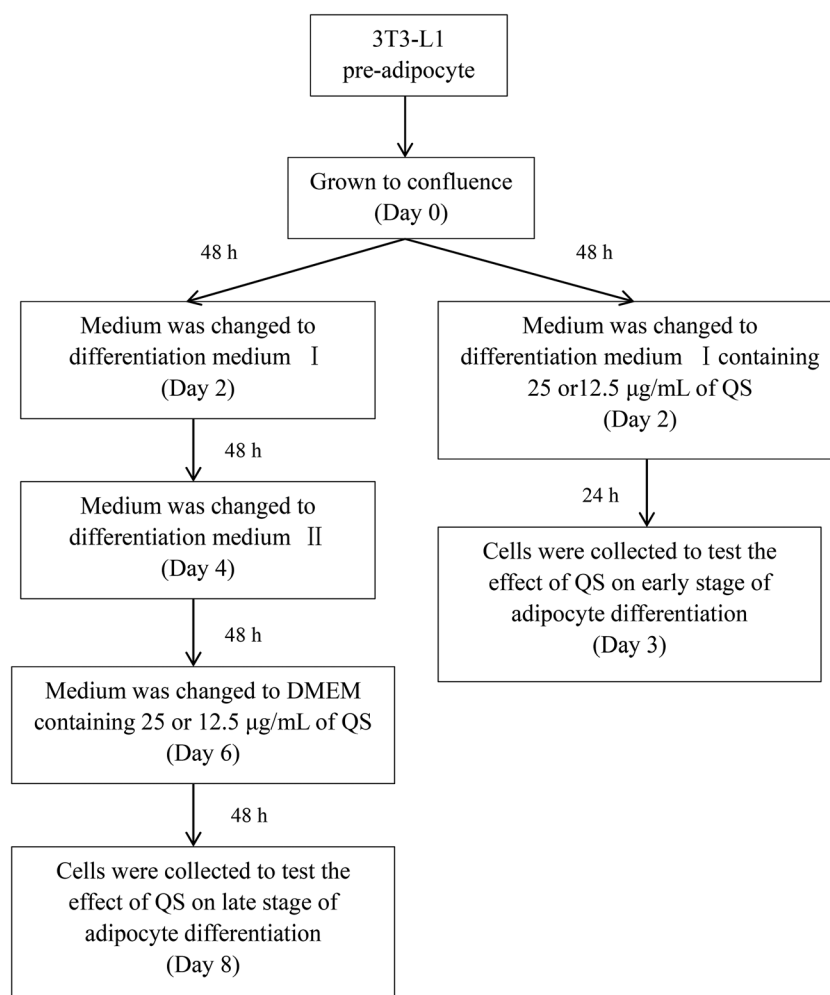


Fig. 1 Procedure for QS treatment during 3T3-L1 differentiation.

**Table 1** The primer sequence used for real-time PCR

Gene name	Forward primer	Reverse primer	Accession no.
PPAR $\gamma$	TTTCAAGGGTGCCAGTTTC	AATCCTTGGCCCTCTGAGAT	NM_011146
C/EBP $\alpha$	TTACAACAGGCCAGGTTTCC	GGCTGGCGACATACAGTACA	NM_007678
C/EBP $\beta$	CCTTTAAATCCATGGAAGTGG	GGGCTGAAGTCGATGGC	NM_005194.2
C/EBP $\delta$	ACGACGAGAGCGCCATC	TCGCCGTCGCCCCAGTC	TRCN0000013697
SREBP1c	TGTTGGCATCCTGCTATCTG	AGGGAA AGCTTTGGGGTCTA	NM_011480
LPL	CATCGAGAGGATCCGAGTGAA	TGCTGAGTCCTTTCCCTTCTG	NM_008509
ap2	GGCCAAGCCCAACATGATC	CACGCCAGTTTGAAGGAAA	NM_024406
Glut4	ACGACGGACACTCCATCTGTTG	GGAGACATAGCTCATGGCTGGAA	NM_009204
$\beta$ -actin	CCACAGCTGAGAGGGAATC	AAGGAAGGCTGGAAGAGAGC	X03672

#### 2.4. MTT viability assay

Cell viability was assessed by the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay.<sup>15</sup> 3T3-L1 cells were grown in 96-well plates (10 000 cells per well) and allowed to adhere overnight. After 24 h, culture media containing QS was added to each well. The control culture was treated in DMEM medium. The cells were incubated for 48 h at 37 °C under a humidified atmosphere of 5% CO<sub>2</sub>. After 48 h, the culture medium and test samples were replaced with 20  $\mu$ L of MTT (1 mg mL<sup>-1</sup>) in a culture incubator in the dark for 4 h. Then the MTT reagent was removed, and formazan crystals were solubilized in 200  $\mu$ L of DMSO. The absorbance of each well was read at 570 nm using a microplate reader (Bio-Rad, MA, USA).

#### 2.5. 3T3-L1 cell pre-adipocyte differentiation

A pre-adipocyte differentiation assay was assessed according to the modified method of Yim, Hosokawa, Yoshida, Saito, & Miyashita.<sup>16</sup> 3T3-L1 pre-adipocytes were cultured in DMEM with 10% FBS, 100 U mL<sup>-1</sup> penicillin, and 100  $\mu$ g mL<sup>-1</sup> streptomycin at 37 °C under an atmosphere of 5% CO<sub>2</sub> and grown to confluence. 48 h after confluence, the medium was changed to differentiation medium I containing 10  $\mu$ g mL<sup>-1</sup> insulin, 0.5 mM IBMX, and 0.1  $\mu$ M DEX in DMEM and was incubated for an additional 48 h. Cells were then incubated in differentiation medium II containing 5  $\mu$ g mL<sup>-1</sup> insulin in DMEM for 48 h and further cultured in DMEM without insulin, which was replaced with fresh medium for 48 h. QS were added to DMEM after a 48 h incubation period with differentiation medium II. The final QS concentration in the medium was adjusted to 25 and 12.5  $\mu$ g mL<sup>-1</sup>, respectively. QS was firstly dissolved in DMSO and diluted to 1000  $\mu$ g mL<sup>-1</sup> with DMEM medium. To test the effect of QS on the early stage of adipocyte differentiation, the QS stock solution was added to differentiation medium I after a 48 h confluence. Cells were collected after 24 h of DM induction. On the other hand, to test the effect of QS on the late stage of adipocyte differentiation, the QS stock solution was added to the DMEM medium after a 48 h incubation period with differentiation medium II. Cells were collected at day 8. The final QS concentration in the medium was adjusted to 25 and 12.5  $\mu$ g mL<sup>-1</sup> without cytotoxicity, respectively (Fig. 1).

#### 2.6. Oil-red O staining and OD measurement

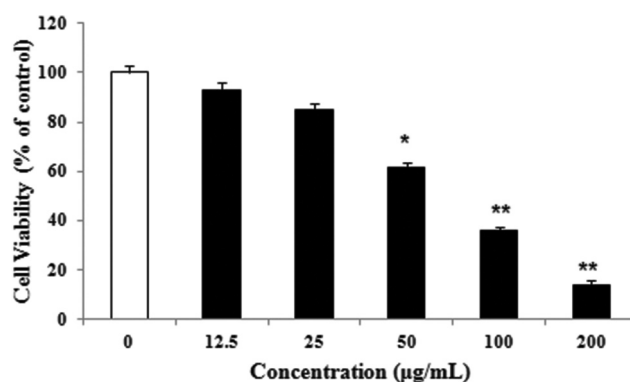
After induced for 8 days, the cells were washed with PBS twice, fixed with 10% formalin at room temperature for 10 min, and stained with oil red O (Sigma, St. Louis, MO, USA) at 60 °C for 10 min.<sup>7</sup> The pictures were taken using an Olympus (Tokyo, Japan) microscope, then they were extracted with isopropanol and O.D. absorbance measured at 492 nm using a microplate reader (Bio-Rad, MA, USA).

#### 2.7. Quantification of intracellular triglyceride (TG)

TG was measured according to the method previously described with slight modifications.<sup>17</sup> The mature adipocytes (day 8) were washed twice and collected in 1 ml of ice-cold PBS (0.1 mol L<sup>-1</sup>, pH 7.4) using a cell scraper, and then sonicated (300 W, 15 min, repeated 3 times). The cell was re-suspended by vortex (60 s) before sonicating each time. The suspension was used to measure the intracellular TG content, which was then analysed with the enzymatic kit (Nanjing Jiancheng Bioengineering Institute, China) at 510 nm. The TG content was normalized to the cell protein content.

#### 2.8. RNA extraction and real-time reverse transcription polymerase chain reaction (RT-PCR)

Total mRNA was extracted and isolated from 3T3-L1 cells collected at 24 h or day 8 using the Trizol Reagent (Invitrogen,



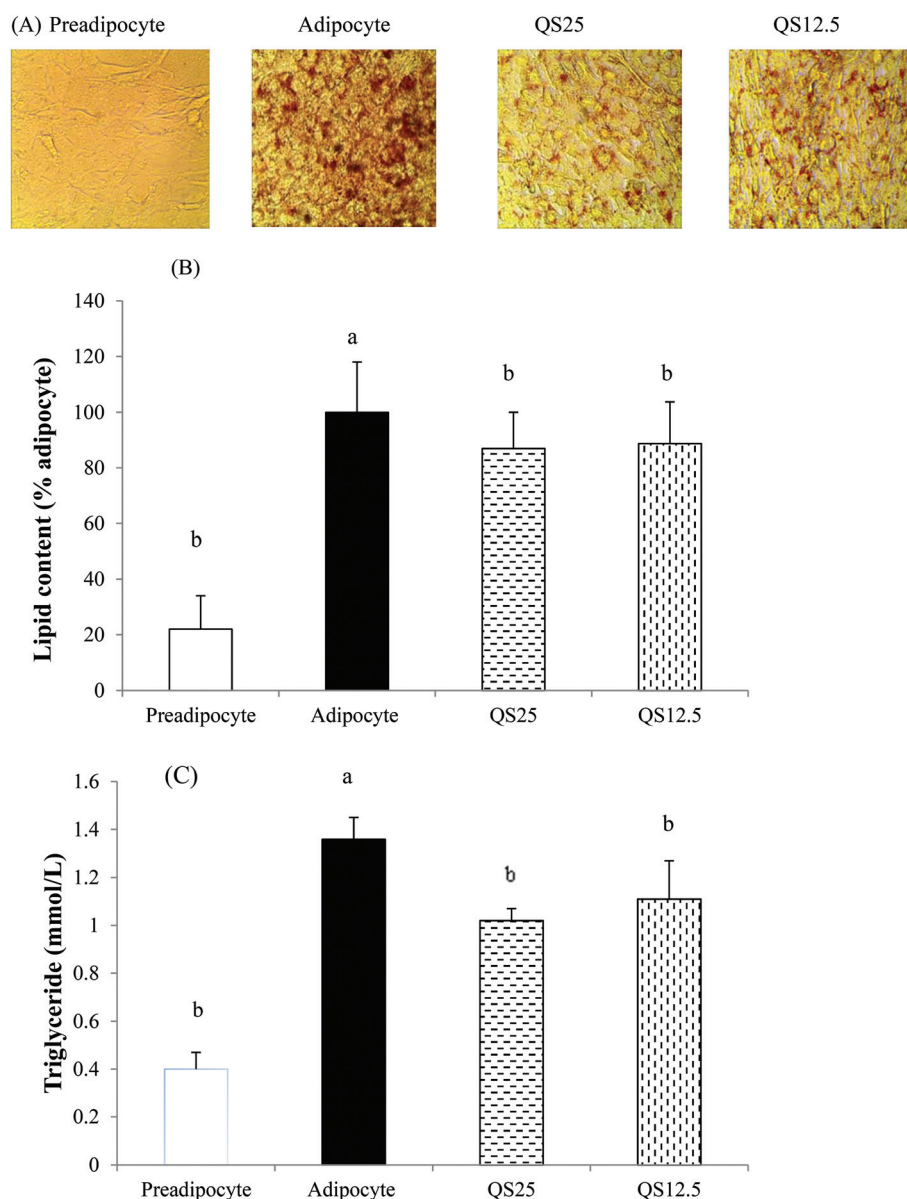
**Fig. 2** MTT cell viability of QS. Cultures in basal medium served as control. Three independent experiments were performed and the data are shown as mean  $\pm$  SD. \* $p$  < 0.05 vs. control; \*\* $p$  < 0.005 vs. control.

Carlsbad, CA, USA) according to the manufacturer's instruction. Total RNA was converted to complementary DNA (cDNA) using the High Capacity cDNA Reverse Transcription kit (Applied Biosystems, Foster City, CA, USA). Quantification of gene expression in 3T3-L1 cells treated with QS was measured using a 7300 Real Time PCR System (Applied Biosystem). All primers used for real-time PCR for these genes are listed in Table 1. Real-time PCR was performed using a TaqMan Fast Universal PCR Master Mix (Applied Biosystems). The relative amount of each gene was calculated using the  $2^{-\Delta\Delta CT}$  method. The level of transcripts was normalised using  $\beta$ -actin as an internal standard. Levels of each different mRNA in the control cells were designated as 1, and the relative levels of the

gene transcripts of the samples were expressed as the fold change. Analysis was carried out in triplicates.

## 2.9. Western blot analysis

Western blot analysis was performed according to the method previously described by Yim *et al.*<sup>16</sup> Ice-cold lysis RIPA buffer (20 mM Tris-HCl, pH 7.4), 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, 0.1% sodium dodecyl sulfate (SDS), 0.1 mg mL<sup>-1</sup> phenylmethanesulfonyl fluoride (PMSF), 50  $\mu$ g mL<sup>-1</sup> aprotinin, and 1 mM sodium orthovanadate were used to lyse cells. Cell lysates were centrifuged at 12 000g for 20 min at 4 °C. The supernatant was collected and estimated for protein measurement. Ten micrograms of protein was separated



**Fig. 3** Effect of QS on intracellular lipid accumulation in 3T3-L1 cells. 3T3-L1 cells were treated with QS (50 or 25  $\mu$ g mL<sup>-1</sup>) for day 8. (A) The mature adipocytes were stained with oil-red O, and the (B) OD value (% adipocyte) and (C) TG content (mmol L<sup>-1</sup>) were measured to quantify intracellular lipid content. Three independent experiments were performed and the data are shown as mean  $\pm$  SD. Values which do not share the same letter are significantly different ( $p < 0.05$ ).

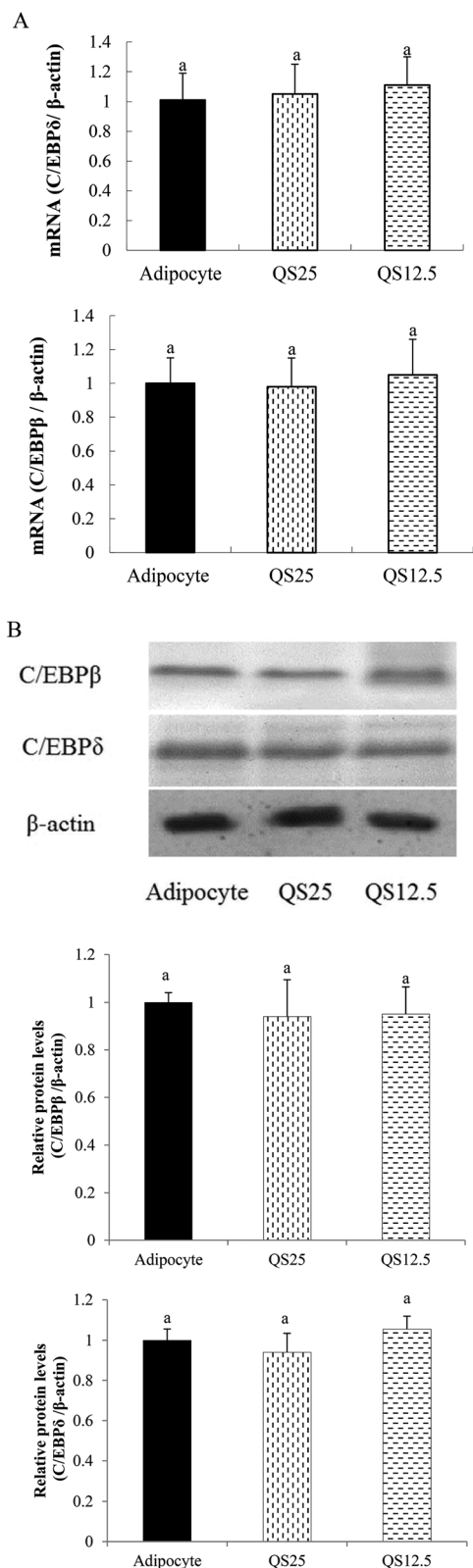


Fig. 4 Effect of QS on the mRNA expression (A) and protein levels (B) of C/EBPδ and C/EBPβ in 3T3-L1 cells. Three independent experiments were performed and the data are shown as mean  $\pm$  SD. Values which do not share the same letter are significantly different ( $p < 0.05$ ).

by 10% SDS-polyacrylamide gel electrophoresis (PAGE) and transferred to the polyvinylidene difluoride (PVDF) membrane. After being blocked for 1 h at room temperature in 5% skim milk in tris-buffer salt containing 0.1% Tween-20 (TBST), anti-PPAR $\gamma$ , C/EBP $\alpha$ , C/EBP $\beta$ , C/EBP $\delta$ , SREB1c, LPL, aP2, Glut4 and  $\beta$ -actin antibody (Santa Cruz, CA) were respectively added and incubated for 2 h at room temperature. The membrane was then washed with TBST three times for 5 min each time, incubated with a HRP-conjugated secondary antibody for 1 h at room temperature, and washed with TBST three times for 10 min each time. The signal was detected using a SuperSignal ELISA Pico Chemiluminescent Substrate (Thermo Fisher Scientific, USA).

## 2.10. Statistics

Data, which were expressed as the mean  $\pm$  SD, included at least three replicates per sample. ANOVA and Tukey's test were performed using SPSS (Statistics for Social Science) version 17.0. All graphical representations were performed using Sigma plot version 11.0 (SPSS, USA). Statistical significance was set at  $p < 0.05$ .

## 3. Results and discussion

### 3.1. Cell viability analysis

Toxic concentrations of QS were assessed *via* the MTT viability assay. There were no significant ( $p > 0.05$ ) differences in the viability of 3T3-L1 cells at a concentration of up to 25  $\mu\text{g mL}^{-1}$  for QS compared with the control (Fig. 2). The results showed that the viability of 3T3-L1 cells significantly ( $p < 0.05$ ) decreased at a concentration of 50  $\mu\text{g mL}^{-1}$  and higher for QS compared with the control (Fig. 2). A 27% decrease in viability was observed at a concentration of 50  $\mu\text{g mL}^{-1}$  of QS, suggesting that QS exerts a toxic effect on 3T3-L1 cells at a concentration higher than 50  $\mu\text{g mL}^{-1}$ . It was therefore decided that the non-cytotoxic concentrations of 25 and 12.5  $\mu\text{g mL}^{-1}$  of QS will be used in the following experiments.

### 3.2. Effect of QS on intracellular lipid accumulation in 3T3-L1 cells

To determine the effects of QS on pre-adipocyte differentiation, we treated confluent 3T3-L1 cells with or without QS for 8 days. Following various treatments, differentiated 3T3-L1 cells in plates were subjected to oil-red O staining. Representative images of oil-red O staining demonstrate that QS suppressed lipid accumulation. This result was consistent with a previous study, which reported that the ginsenoside Rh2, an active component of *Panax ginseng*, effectively blocked adipocyte differentiation.<sup>18</sup> This result was supported by quantitative data obtained by spectrophotometric analysis of oil-red O-stained cells eluted with isopropanol (Fig. 3A), which revealed that QS significantly inhibited adipogenic differentiation compared with control 3T3-L1 cells ( $p < 0.05$ , Fig. 3B). These observations were confirmed by the TG content assay (Fig. 3C). The TG contents of QS-treated 3T3-L1 cells were lowered by 25.01% and 18.38% respectively, compared with control ( $p < 0.05$ ). Thus,

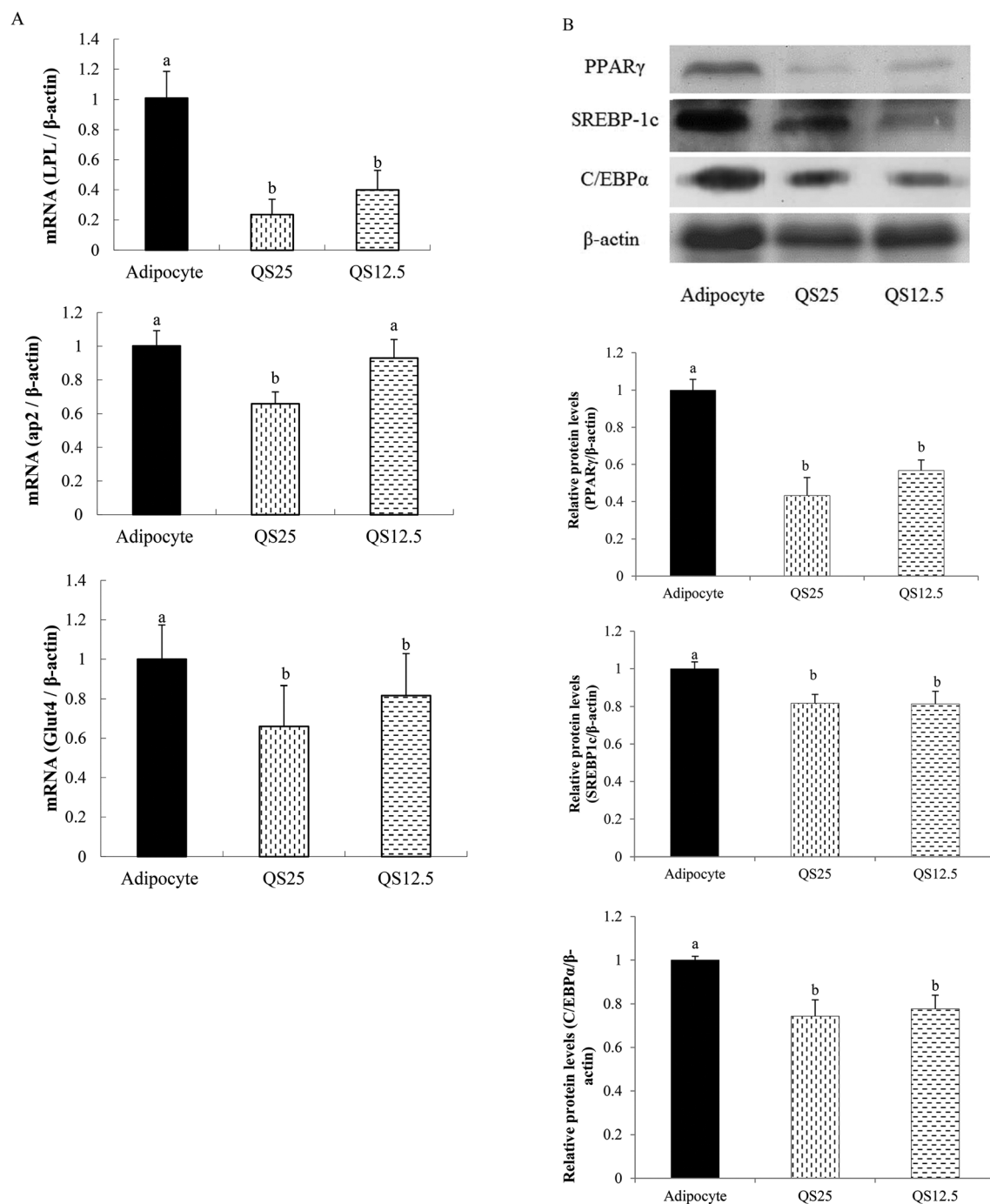


treatment of 3T3-L1 cells with QS during induction resulted in inhibition of adipocyte differentiation.

### 3.3. Effect of QS on mRNA expression and protein levels of PPAR $\gamma$ , C/EBP $\alpha$ , C/EBP $\beta$ , C/EBP $\delta$ and SREBP1c

The mRNA levels of PPAR $\gamma$ , C/EBP $\alpha$ , C/EBP $\beta$ , C/EBP $\delta$  and SREBP1c were measured after the induction of the differentiation process (day 8) in the 3T3-L1 cells, in the presence of

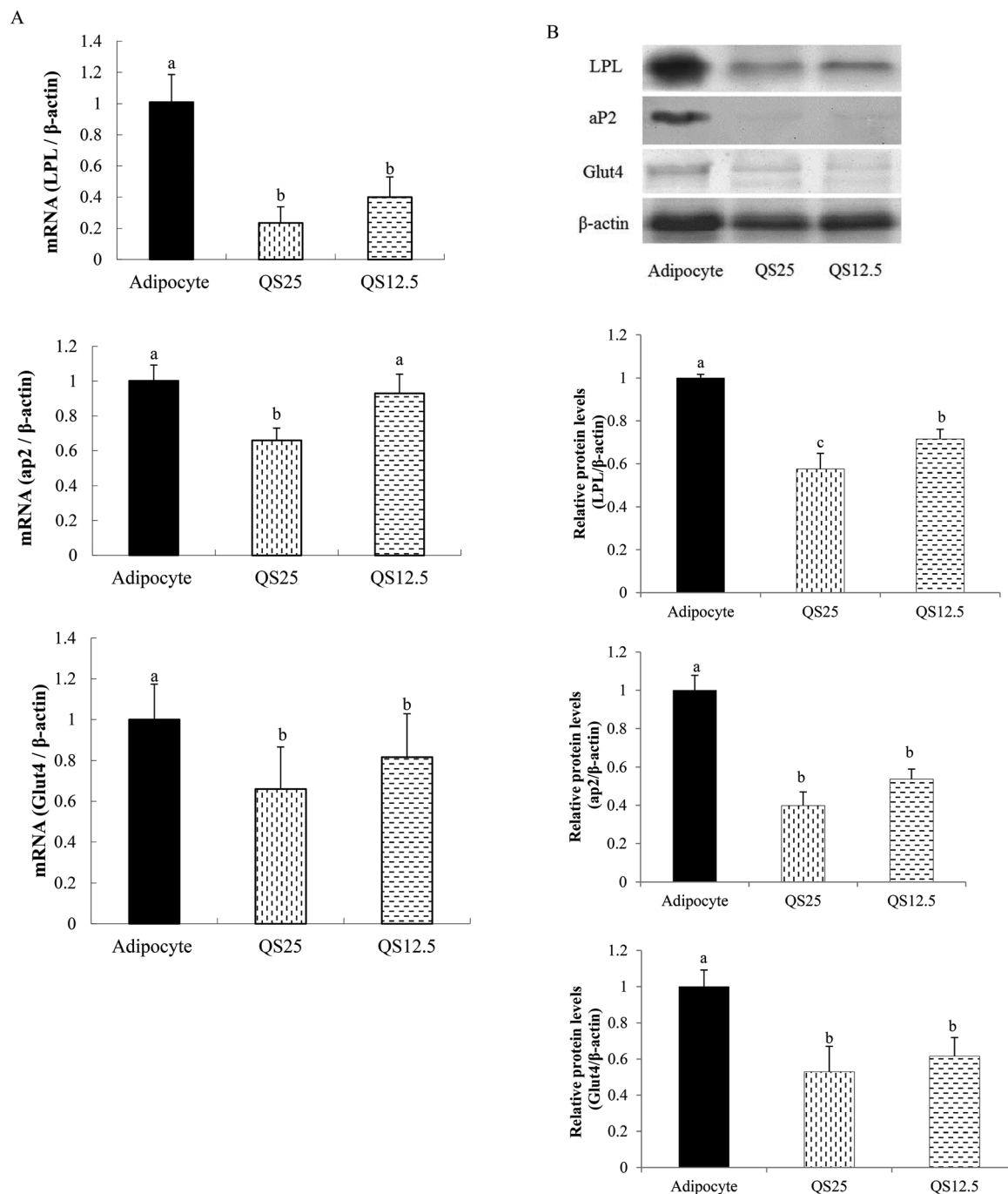
QS, at concentrations of 12.5 and 25 mg mL<sup>-1</sup>. Consistent with previous studies on saponins from *Panax notoginseng*,<sup>19</sup> ginseng<sup>18</sup> and platycodin,<sup>20</sup> our results indicated that QS suppressed the expression of PPAR $\gamma$ , C/EBP $\alpha$  and SREBP1c compared with control adipocytes ( $p < 0.05$ ) (Fig. 4A and 5A). These results were consistent with a study of Foucault *et al.*,<sup>21</sup> who observed that quinoa extract reduced adipose tissue development of diet-induced obesity in mice by regulating the



**Fig. 5** Effect of QS on the mRNA (A) and protein (B) expression of PPAR $\gamma$ , C/EBP $\alpha$  and SREBP1c in 3T3-L1 cells. Three independent experiments were performed and the data are shown as mean  $\pm$  SD. Values which do not share the same letter are significantly different ( $p < 0.05$ ).

expression of adipocyte-specific genes in PPAR $\gamma$ , C/EBP $\alpha$  and SREBP1c. However, QS didn't significantly affect the expression of C/EBP $\beta$  and C/EBP $\delta$ , which are the upstream regulators for adipogenesis, compared to the control ( $p > 0.05$ ) (Fig. 4A). QS significantly down regulated mRNA expression of PPAR $\gamma$  and C/EBP $\alpha$ , which are the central determinants of the transcriptional factor during adipocyte differentiation. These two major transcription factors work sequentially and cooperatively in stimulating fat cell differ-

entiation. PPAR $\gamma$  is necessary to promote adipogenesis and C/EBP $\alpha$  is influential in maintaining the expression of PPAR $\gamma$ .<sup>22</sup> Hwang *et al.*<sup>18,23</sup> have reported that ginsenoside Rg3 and Rh2 from ginseng reduced preadipocyte viability and the differentiation from preadipocyte to adipocyte through a down-regulation of the PPAR $\gamma$ . Kim *et al.*<sup>24</sup> have also observed that saponins isolated from *Cheonggukjang* inhibited adipocyte differentiation and triglyceride accumulation in 3T3-L1 preadipocyte cells.



**Fig. 6** Effect of QS on the mRNA (A) and protein (B) expression of LPL, ap2 and Glut4 in 3T3-L1 cells. Three independent experiments were performed and the data are shown as mean  $\pm$  SD. Values which do not share the same letter are significantly different ( $p < 0.05$ ).

PPAR $\gamma$  and C/EBP $\alpha$  transcription factors activate the expression of genes involved in adipogenesis, such as aP2, LPL, fatty acid transporter and others, which participate in creating the adipocyte phenotype.<sup>25</sup> SREBP1c increases the expression of many lipogenic genes, including fatty acid synthase (FAS).<sup>25</sup> Inhibited SREBP1c and normal C/EBP $\beta$  and C/EBP $\delta$  compared to the control indicate that QS regulates the intermediate stage of adipocyte differentiation by inhibiting the expression of genes critical for adipogenesis without affecting the expression of upstream regulators such as C/EBP $\beta$  and  $\delta$ .<sup>17</sup>

Besides, we further examined PPAR $\gamma$ , C/EBP $\alpha$  and SREBP1c expression levels by western blotting. Consistent with mRNA expression, the PPAR $\gamma$ , C/EBP $\alpha$ , C/EBP $\beta$ , C/EBP $\delta$  and SREBP1c protein expression levels showed a similar pattern (Fig. 4B and 5B). These results suggested that QS suppresses PPAR $\gamma$ , C/EBP $\alpha$ , C/EBP $\beta$ , C/EBP $\delta$  and SREBP1c protein expression by down-regulating their mRNA transcription.

### 3.4. Effect of QS on mRNA expression and protein levels of LPL, aP2 and Glut4

The mRNA expression levels of LPL, aP2 and Glut4 were down-regulated by QS ( $p < 0.05$ , Fig. 6A). Western blot analysis confirmed the reduction, and QS markedly inhibited the protein expression levels of LPL, aP2 and Glut4 at concentrations of 25 and 12.5  $\mu\text{g mL}^{-1}$  (Fig. 6B). LPL and aP2 mRNA are adipocyte specific genes involved in fatty acid metabolism regulated by PPAR $\gamma$  and C/EBP $\alpha$ .<sup>26–28</sup> From these results, the suppressive effects on adipocyte specific mRNA expression are suggested to be mediated by the down regulation of PPAR $\gamma$  and C/EBP $\alpha$  mRNA expression. Glut4 creates and maintains the adipocyte phenotype and is a key regulator of whole-body glucose homeostasis.<sup>29</sup> Sim, Xu, Wong, Sim, & Lee<sup>30</sup> reported that increased Glut4 translocation improved hyperglycaemia and insulin resistance.

## 4. Conclusion

Our data demonstrate that QS suppressed 3T3-L1 adipocyte differentiation and decreased cell viability in mature adipocyte cultures. QS reduced the lipid accumulation during the differentiation process and down-regulated the adipogenesis-related transcriptional factors, PPAR $\gamma$ , C/EBP $\alpha$ , C/EBP $\beta$ , C/EBP $\delta$  and SREBP1c, and adipocyte-specific molecules, LPL, aP2 and Glut4. These findings are helpful in understanding the anti-adipogenic properties of QS, however further *in vivo* studies should also be conducted in order to confirm the anti-obesity effect of QS.

## Acknowledgements

This project was supported by the Hong Kong, Macao and Taiwan Science & Technology Cooperation Program of China (2013DFT3050), the Special Fund for Agro-scientific Research

in the Public Interest (201303063) and the Agricultural Science and Technology Program for Innovation Team on Identification and Excavation of Elite Crop Germplasm, CAAS.

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