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Restoration of adipose function in obese glucose-tolerant men following pioglitazone treatment is associated with CCAAT enhancer-binding protein β up-regulation

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A B S T R A C T

Obese AT (adipose tissue) exhibits increased macrophage number. Pro-inflammatory CD16⁺ peripheral monocyte numbers are also reported to increase with obesity. The present study was undertaken to simultaneously investigate obesity-associated changes in CD16⁺ monocytes and ATMs (AT macrophages). In addition, a pilot randomized placebo controlled trial using the PPAR (peroxisome-proliferator-activated receptor) agonists, pioglitazone and fenofibrate was performed to determine their effects on CD14⁺/CD16⁺ monocytes, ATM and cardiometabolic and adipose dysfunction indices. Obese glucose-tolerant men ($n = 28$) were randomized to placebo, pioglitazone (30 mg/day) and fenofibrate (160 mg/day) for 12 weeks. A blood sample was taken to assess levels of serum inflammatory markers and circulating CD14⁺/CD16⁺ monocyte levels via flow cytometry. A subcutaneous AT biopsy was performed to determine adipocyte cell surface and ATM number, the latter was determined via assessment of CD68 expression by IHC (immunohistochemistry) and real-time PCR. Subcutaneous AT mRNA expression of CEBP β (CCAAT enhancer-binding protein β), SREBP1c (sterol-regulatory-element-binding protein 1c), PPAR γ 2, IRS-1 (insulin receptor substrate-1), GLUT4 (glucose transporter type 4) and TNF α (tumour necrosis factor α) were also assessed. Comparisons were made between obese and lean controls ($n = 16$) at baseline, and pre- and post-PPAR agonist treatment. Obese individuals had significantly increased adipocyte cell surface, percentage CD14⁺/CD16⁺ monocyte numbers and ATM number (all $P = 0.0001$). Additionally, serum TNF- α levels were significantly elevated ($P = 0.017$) and adiponectin levels reduced (total: $P = 0.0001$; high: $P = 0.022$) with obesity. ATM number and percentage of CD14⁺/CD16⁺ monocytes correlated significantly ($P = 0.05$). Pioglitazone improved adiponectin levels significantly ($P = 0.0001$), and resulted in the further significant enlargement of adipocytes ($P = 0.05$), without effect on the percentage CD14⁺/CD16⁺ or ATM number. Pioglitazone treatment also significantly increased subcutaneous AT expression of CEBP β mRNA. The finding that improvements in obesity-associated insulin resistance following pioglitazone were associated with increased adipocyte cell surface and systemic adiponectin levels, supports the centrality of AT to the cardiometabolic derangement underlying the development of T2D (Type 2 diabetes) and CVD (cardiovascular disease).

Key words: adiponectin, CD68, CD14⁺/CD16⁺ monocyte, peroxisome-proliferator-activated receptor (PPAR) agonist, subcutaneous adipose tissue.

Abbreviations: AT, adipose tissue; ATM, AT macrophage; BMI, body mass index; CEBP β , CCAAT enhancer-binding protein β ; C_t , cycle threshold; CV, coefficient of variance; CVD, cardiovascular disease; DBP, diastolic blood pressure; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GLUT4, glucose transporter type 4; HbA_{1c}, glycated haemoglobin; HDL-C, high-density lipoprotein cholesterol; HOMA, homeostatic model assessment; IHC, immunohistochemistry; IRS-1, insulin receptor substrate-1; LDL-C, low-density lipoprotein cholesterol; MCP-1, monocyte chemoattractant protein-1; NEFA, non-esterified 'free' fatty acid; OGTT, oral glucose tolerance test; PBMC, peripheral blood mononuclear cell; PE, phycoerythrin; PPAR, peroxisome-proliferator-activated receptor; RPLP0, ribosomal protein large P0; SBP, systolic blood pressure; SREBP1c, sterol-regulatory-element-binding protein 1c; TAG, triacylglycerol; T2D, Type 2 diabetes; TC, total cholesterol; TNF α , tumour necrosis factor α ; WHR, waist/hip ratio.

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INTRODUCTION

It has been reported that in obesity ATM [AT (adipose tissue) macrophage] numbers increase, in addition to undergoing a phenotypic switch from protective M2 to pro-inflammatory M1 [1–3]. Evidence is mounting to support the contention that paracrine interactions between ATMs and adipocytes play a central role in initiating and maintaining obesity-associated adipose dysfunction [1–4]. It has been speculated that AT dysfunction contributes to the systemic inflammatory status of obesity and, thus, may promote the development of T2D (Type 2 diabetes) and CVD (cardiovascular disease). Therefore, targeting the underlying inflammatory mechanisms may have therapeutic potential in the management of obesity and subsequent CVD risk.

Excess energy intake results in impaired adipogenesis, enlargement of adipocytes and increased secretion of pro-inflammatory adipokines, in addition to a decreased production of the insulin sensitizing adipokine, adiponectin [1]. Circulating levels of adiponectin have been considered a surrogate marker of adipose functionality and, in terms of specific risk biomarkers for CVD and diabetes, a recent publication examining the contribution of different biological pathways to the development of T2D concluded that adiponectin was the most important contributor, explaining one-third of the risk [5]. Pro-inflammatory adipokines, which include TNF α (tumour necrosis factor α), IL-6 (interleukin-6) and MCP-1 (monocyte chemoattractant protein-1), modulate insulin sensitivity, cardiovascular homeostasis and inflammation as well as adipose mass [6]. Large adipocytes release more saturated NEFAs (non-esterified 'free' fatty acids) that can stimulate macrophages to increase TNF α production via NF- κ B (nuclear factor κ B) activation [7,8]. In turn macrophage-derived TNF α activates the adipocytes inducing further lipolysis and secretion of chemokines, such as MCP-1, which promote the diapedesis of peripheral monocytes into the AT and differentiation into macrophages. The pro-inflammatory CD16⁺ peripheral monocytes are thought to drive the inflammatory processes associated with atherosclerosis. A significant association between CD16⁺ monocytes and both obesity and subclinical atherosclerosis has been reported [9]. More recently it has been observed that mass loss can diminish this monocyte subpopulation [10].

PPAR (peroxisome-proliferator-activated receptor) ligands were developed to improve insulin sensitivity; however, they demonstrate additional effects on the arterial wall, which suggest that they also could reduce cardiovascular risk. Previously, we have demonstrated that pioglitazone and fenofibrate treatment of obese, glucose tolerant men reduces inflammation, improves markers of endothelial function and reduces arterial

stiffness [11]. Furthermore, the improved insulin sensitivity observed with pioglitazone treatment was accompanied by increased adiponectin, demonstrating the potential of PPAR agonists to reduce the incidence of premature CVD associated with obesity through effects on the arterial wall and AT. Recent reports indicate that pioglitazone has direct effects on subcutaneous AT promoting adipogenesis in obese, non-diabetic, insulin-resistant subjects [12,13]. Fenofibrate has also been shown to reduce fat mass through increased β -oxidation in various animal models [14,15], but information regarding the effects of fenofibrate in human subcutaneous AT is lacking.

Although previous studies have investigated obesity-associated changes in ATM number or CD16⁺ monocytes, to date these monocyte/macrophage populations have not been examined within a single study. Therefore the present study was undertaken to simultaneously examine obesity-associated changes in peripheral CD14⁺/CD16⁺ monocytes and ATM in order to assess potential relationships between these monocyte/macrophage populations, and between these and cardiometabolic/adipose dysfunction indices in a normoglycaemic, but insulin resistant, obese population. Moreover, in order to investigate the effects of PPAR agonists, pioglitazone and fenofibrate on CD14⁺/CD16⁺ monocytes, ATM number, adipocyte cell surface and subcutaneous AT gene expression, a pilot randomized placebo controlled clinical trial was conducted.

MATERIALS AND METHODS

Study design

The protocol for the randomized placebo controlled trial was approved by Office for Research Ethics Committees Northern Ireland (reference number 06/NIR03/146) and clinical trial details were logged in the EudraCT database (reference number 2006-004296-35). Clinical Trial Authorization was obtained from the Medicines and Healthcare Products Regulatory Agency.

Setting and participants

Obese [BMI (body mass index) ≥ 30 kg/m²] glucose-tolerant males, aged 35–65 years, and lean controls were recruited from the general population (including General Practice patients, hospital and university staff) by clinical trial staff. All lean and obese participants attended the Regional Centre for Endocrinology and Diabetes at the Royal Victoria Hospital for assessment and gave written informed consent. Exclusion criteria were as follows: smoker, clinical cardiac disease, clinical dyslipidaemia, plasma cholesterol >7 mmol/l, fasting TAGs (triacylglycerols) >5 mmol/l, blood pressure $>160/90$ mmHg, diabetes/family history of diabetes, glucose intolerance, or use of hypertensive, cardiac,

non-steroidal anti-inflammatory drugs or lipid-lowering therapies.

Pre-treatment visit

All lean ($n = 16$) and obese ($n = 37$) participants attended hospital after an overnight fast for a medical history and examination, including mass, height and WHR (waist/hip ratio) determination. Blood pressure was measured at the right brachial artery using the OMRON HEM-705CP automated sphygmomanometer. A 75 g OGTT (oral glucose tolerance test) was performed with plasma glucose samples taken at 0, 30, 60, 120 and 180 min to determine glucose tolerance and insulin sensitivity. The HOMA (homoeostatic model assessment) of insulin resistance index was calculated using the following formula: fasting insulin (m-units/l) \times fasting glucose (mmol/l) / 22.5. Blood was drawn and aliquoted for lipid profile, HbA_{1c} (glycated haemoglobin), monocyte isolation, serum adiponectin and TNF α . A subcutaneous fat biopsy was also obtained.

Treatment phase

Obese subjects taking part in the pilot clinical trial ($n = 28$) were randomized to 12 weeks treatment with either fenofibrate (Supralip[®]; Fournier) 160 mg once per day, pioglitazone hydrochloride (ACTOS[®]; Takeda) 30 mg once per day or placebo. For safety purposes, liver function tests were also performed every 4 weeks.

Post-treatment visit

Obese subjects randomized to 12 weeks treatment attended for a post-treatment assessment at which all pre-treatment assessment procedures were repeated.

Biochemical and lipid assessment

HbA_{1c} was assessed by ion-exchange HPLC on an Adams[™] HA-8160 automated analyser (Menarini Diagnostics). Serum insulin was measured by immunoassay on an Abbott IMx analyser (Abbott Diagnostics). Fasting plasma glucose, TC (total cholesterol), HDL-C (high-density lipoprotein cholesterol) and TAGs were measured using slide-based dry chemistry on a VITROS 950 analyser (Ortho-Clinical Diagnostics). LDL-C (low-density lipoprotein cholesterol) was calculated using the Friedewald equation.

Analysis of serum inflammatory markers

Total and high adiponectin were analysed using a human multimeric adiponectin ELISA [ALPCO immunoassays; intra-assay CV (coefficient of variance) total 1.30%, high 2.04%; inter-assay CV total 3.50%, high 2.50%]. TNF α was measured using the Quantikine[®] high sensitivity human TNF α immunoassay kit (R&D Systems; intra-assay CV 3.67%; inter-assay CV 6.40%).

Preparation and analysis of CD14⁺/CD16⁺ PBMCs (peripheral blood mononuclear cells)

PBMCs were isolated by Histopaque (density 1.077 g/l; ratio of blood to histopaque, 1:1) (Sigma–Aldrich) and incubated for 30 min at 4 °C with two fluorescently labelled monoclonal antibodies: FITC-conjugated anti-CD14 (Santa Cruz Biotechnology) and PE (phycoerythrin)-conjugated anti-CD16 (Santa Cruz Biotechnology). Cells were then washed in PBS, centrifuged for 10 min at 250 g and resuspended in PBS/4% (w/v) paraformaldehyde 4:1 (v/v). Fixed CD14⁺/CD16⁺ cells were analysed via flow cytometry (FACSCalibur[™]; Becton Dickinson). Monocytes were identified by forward and side scatter properties. Fluorescence data were collected on 10 000 cells and analysed using CellQuest software (Becton Dickinson).

Adipose analysis

Subcutaneous fat biopsy

Skin was firstly cleaned and anaesthetized with 2% xylocaine. A blunt dissection was then made and a small sample of subcutaneous AT (~1 g) was removed from the periumbilical region using sterile forceps. Collected tissue was washed extensively in PBS and divided into 2 aliquots: (i) an aliquot was formalin fixed and paraffin embedded; (ii) an aliquot was added to RNA later (Ambion), snap frozen and stored at –80 °C until required.

Adipocyte cell surface

Formalin fixed paraffin embedded subcutaneous AT sections (4 μ m) were stained in haematoxylin and eosin, and photographed in triplicate using an Olympus microscope and SPOT Advanced software (SPOT Imaging Solutions). Captured images were examined using Photoshop CS4 Extended software (Adobe Systems). The magnetic lasso tool was used to outline adipocytes and from this the software calculated cell surface in pixels. Pixels were converted manually into μ m² in Excel using a scale conversion of 1 pixel = 2.3543 μ m² [12].

ATM assessment

ATM content was assessed by both IHC (immunohistochemistry) staining for CD68 in formalin fixed paraffin embedded sections and real-time PCR analysis of CD68 mRNA expression, in recognition that this combinatorial approach largely overcomes the limitations of using either method in isolation [16]. Several studies have reported a strong correlation between results obtained via CD68 IHC (Mphi, fraction of CD68-expressing cells) and mRNA expression of CD68 when used to assess AT macrophage number [16–18].

IHC analysis

Sections (4 μm) of formalin fixed paraffin embedded subcutaneous AT were mounted on to APES (3-aminopropyltriethoxysilane)-coated slides, dewaxed in xylene and incubated with a heated citrate buffer (100 °C, 20 min) for antigen retrieval. An avidin/biotin blocking reagent (Avidin/Biotin Blocking Kit, SP-2001; Vector Laboratories) was then applied to the sections, according to the manufacturer's protocol, before being incubated with H₂O₂ for 5 min. Sections were covered with a CD68 PGM1 IgG₃ Kappa primary antibody (N1576; Dako) and incubated for 20 min. Negative control sections were incubated in a universal negative control reagent (N1698; Dako). For staining and development of the sections, a Dako Cytomation LSAB 2 System-HRP Kit (K0673; Dako) was used exactly according to the manufacturer's instructions. The number of CD68-positive cells are expressed as a percentage of the total number of cells counted per slide per subject.

Real-time PCR

Total RNA was extracted from frozen whole subcutaneous AT using the RNeasy[®] Lipid Tissue Midi Kit (Qiagen), exactly according to the manufacturer's protocol. RNA quantity and purification were determined on a ND-1000 NanoDrop[®] spectrophotometer (Thermo Scientific). Total RNA (100 ng) was reversed-transcribed using the Transcriptor High Fidelity cDNA Synthesis Kit (Roche), according to the manufacturer's instructions, and samples were stored at -20 °C until required.

Real-time PCR was performed using FastStart SYBR Green mastermix (Roche) on ABI Prism 7000 sequence detection system (Applied Biosystems) programmed for universal cycling conditions (95 °C for 10 min and 40 cycles of 95 °C for 15 s and 60 °C for 1 min) followed by melting curve analysis. Gene-specific PCR primers were designed using the Primer Express software version 1.5 (Applied Biosystems) and synthesized by Invitrogen Life Technologies. The primers used were as follows: CD68 (GenBank[®] accession no. NM_001251; forward 5'-CCCCACGCAGCACAGTG-3'; reverse 5'-GATCTCGAAGGGATGCATTCTG-3'), CEBP β (CCAAT enhancer-binding protein β ; GenBank[®] accession no. NM_005194; forward 5'-GCCGCC-GCCTGCCTTAAATC-3'; reverse 5'-AGCCAAG-CAGTCCGCCTCGTAG-3'), PPAR γ 2 (GenBank[®] accession no. NM_015869; forward 5'-GGCCAAGGC-TTCATGACAAG-3'; reverse 5'-AAAAGGCTTT-CGCAGGCTCT-3'), SREBP1c (sterol-regulatory-element-binding protein 1c) (GenBank[®] accession no. NM_001005291; forward 5'-TGCAACACAG-CAACCAGAAAC-3'; reverse 5'-TTGCTTTTGTG-GACAGCAGTG-3'), GLUT4 (glucose transporter type 4; GenBank[®] accession no. NM_001042; forward 5'-ATGTTGCGGAGGCTATGGG-3'; reverse 5'-GGAGGACCGCAAATAGAAGGA-3'), IRS-1

(insulin receptor substrate-1) (GenBank[®] accession no. NM_005544; forward 5'-TGAGGATTTAAG-CGCCTATGC-3'; reverse 5'-TTGAGCTACTGACG-GTCCTCTG-3') and TNF α (GenBank[®] accession no. NM_000594; forward 5'-ATCTTCTCGAACC-CCGAGTGA-3'; reverse 5'-GGGTTTGCTACAAC-ATGGGC-3'). PCR was performed in triplicate with C_t (cycle threshold) values calculated automatically using the Sequence detection software version 1.2.3 (Applied Biosystems). The house keeping genes used were GAPDH (glyceraldehyde-3-phosphate dehydrogenase) (GenBank[®] accession no. NM_002046; forward 5'-ATCCATGACAACCTTTGGTATCGTG-3'; reverse 5'-GGCATGGACTGTGGTCATGAG-3'), RPLP0 (ribosomal protein large P0) (GenBank[®] accession no. NM_001002; forward 5'-GGCGTC-CTCGTGGAAGTGACAT-3'; reverse 5'-CAGGGAT-TGCCACGCAGGGT-3') and 18S (GenBank[®] accession no. NR_003286; forward 5'-CGGAGGTT-CGAAGACGATCA-3'; reverse 5'-GGCATCGTTT-ATGGTCGGAA-3'). These housekeeping genes have been used in previous gene expression analyses in AT and, in agreement with previous studies [19–21], in the present study expression of none of the three housekeeping genes were found to be altered by either obesity or treatment. Individual subject gene expression was normalized to the relevant housekeeping gene (ΔC_t). For comparison of lean and obese gene expression, the obese group mean-fold change relative to the lean control group was calculated using the group mean ΔC_t values in the formula $2^{-\Delta\Delta C_t}$. Differences between lean and obese ΔC_t values were analysed using independent Student's *t* tests and a *P* value ≤ 0.05 was considered statistically significant. For pre- and posttreatment comparisons, individual obese subject post-treatment mRNA expression was calculated as a fold change relative to pre-treatment for each participant using the formula $2^{-\Delta\Delta C_t}$. Differences between pre- and post-treatment ΔC_t values were analysed using paired Student's *t* tests. Treatment change (post-pre) was compared with placebo change (post-pre) by independent Student's *t* test. A *P* value ≤ 0.05 was considered statistically significant.

Statistical analysis

Statistical analyses were carried out using SPSS software version 18.0. Lean and obese groups were compared at baseline by independent Student's *t* test; obese treated groups were analysed by calculating the change (post-pre) and comparing with placebo change (post-pre) also using independent Student's *t* tests. Correlations between continuous variables were assessed by Pearson's coefficients for correlations. Logistic regression analysis was used to determine whether existing correlations remained once BMI was added to the model.

Table 1 Anthropometric and biochemical characteristics of study participants at baselineValues are expressed as means \pm S.D. Lean and obese groups were compared at baseline using independent Student's *t* tests. ns, not significant.

Characteristic	Lean controls (<i>n</i> = 16)	Obese (<i>n</i> = 37)	Differences in means (95% CI)	<i>P</i> value
Age (years)	50 \pm 7	47 \pm 7	4 (– 0.09, 7.83)	ns
BMI (kg/m ²)	23.9 \pm 1.4	35.0 \pm 4.0	– 11.1 (– 12.57, – 9.57)	<0.0001
WHR	0.88 \pm 0.10	1.01 \pm 0.05	– 0.12 (– 0.17, – 0.08)	<0.0001
SBP (mmHg)	117 \pm 9	129 \pm 12	– 12 (– 18.09, – 4.98)	0.001
DBP (mmHg)	74 \pm 7	82 \pm 8	– 8 (– 12.53, – 3.62)	0.001
Fasting glucose (mmol/l)	5.1 \pm 0.4	5.3 \pm 0.4	– 0.2 (– 0.45, – 0.002)	0.047
2 h OGTT (mmol/l)	5.8 \pm 1.3	6.4 \pm 1.0	– 0.6 (– 1.25, 0.07)	ns
Fasting insulin (m-units/l)	6.6 \pm 3.0	12.9 \pm 4.9	– 6.3 (– 8.90, – 3.77)	<0.0001
HOMA index	1.4 \pm 0.6	3.2 \pm 1.4	– 1.7 (– 2.36, – 1.10)	<0.0001
HbA _{1c} (%)	5.2 \pm 0.2	5.3 \pm 0.3	– 0.1 (– 0.31, 0.09)	ns
TC (mmol/l)	5.0 \pm 0.8	5.3 \pm 0.6	– 0.4 (– 0.78, 0.07)	ns
LDL-C (mmol/l)	3.1 \pm 0.9	3.4 \pm 0.5	– 0.3 (– 0.79, 0.19)	ns
HDL-C (mmol/l)	1.46 \pm 0.27	1.22 \pm 0.24	0.24 (0.09, 0.39)	0.002
TAG (mmol/l)	1.00 \pm 0.40	1.60 \pm 0.64	– 0.60 (– 0.95, – 0.25)	0.001
TC/HDL-C ratio	3.55 \pm 1.14	4.45 \pm 0.73	– 0.89 (– 1.54, – 0.25)	0.009
LDL-C/HDL-C ratio	2.24 \pm 0.98	2.82 \pm 0.55	– 0.58 (– 1.13, – 0.04)	0.038

Individual subject ΔC_t values were used to assess correlations between mRNA expression and continuous variables and, as higher ΔC_t values reflect lower mRNA expression, negative correlations do not represent inverse relationships between variables. Variables not normally distributed were log transformed to natural logarithms prior to analysis to allow for parametric testing. Serum results were obtained from fasting variables and all results are presented as means \pm S.D. A *P* value \leq 0.05 was considered statistically significant.

RESULTS

Anthropometric and biochemical characteristics of study participants

Baseline anthropometric and biochemical characteristics of study participants are shown in Table 1. As expected, both BMI and WHR were significantly increased in the obese group relative to the lean group. Additionally, the lean group displayed significantly lower SBP (systolic blood pressure) and DBP (diastolic blood pressure) compared with baseline levels in the obese group. The obese group displayed significantly greater glucose levels at baseline. Nonetheless, levels after 120 min of the OGTT were not significantly different between groups, indicating that despite obesity, participants who entered the study had normal glucose tolerance. In support of this, there was no significant difference in HbA_{1c} levels between the groups. There were two surrogate markers of insulin resistance used in the study: fasting insulin levels and HOMA index. Both parameters were significantly lower in the lean participants compared with the obese, signifying insulin resistance within the obese

group. Severe dyslipidaemia was an exclusion criterion in the study; this would indicate why TC and LDL-C were similar between the two groups. In keeping with dyslipidaemic features associated with obesity, HDL-C was significantly higher and TAGs lower in the lean individuals relative to the obese. Additionally, both the TC/HDL-C ratio and LDL-C/HDL-C ratio were significantly increased with obesity.

Cytokine and peripheral monocyte levels and adipocyte cell surface assessment

As expected, baseline levels of TNF α were significantly higher in the obese participants compared with the lean (Table 2). Additionally, levels of total and high adiponectin were significantly reduced with obesity (Table 2). There was no significant difference in the high to total adiponectin ratio between the two groups.

The obese group exhibited a significantly higher percentage of peripheral CD14⁺/CD16⁺ monocytes (13.9 \pm 4.5 and 21.1 \pm 5.6% for lean compared with obese, *P* < 0.0001) (Figure 1b) and greater adipocyte cell surface (1748 \pm 488 and 3334 \pm 538 μ m² for lean compared with obese, *P* < 0.0001) (Figure 1c) compared with their lean counterparts.

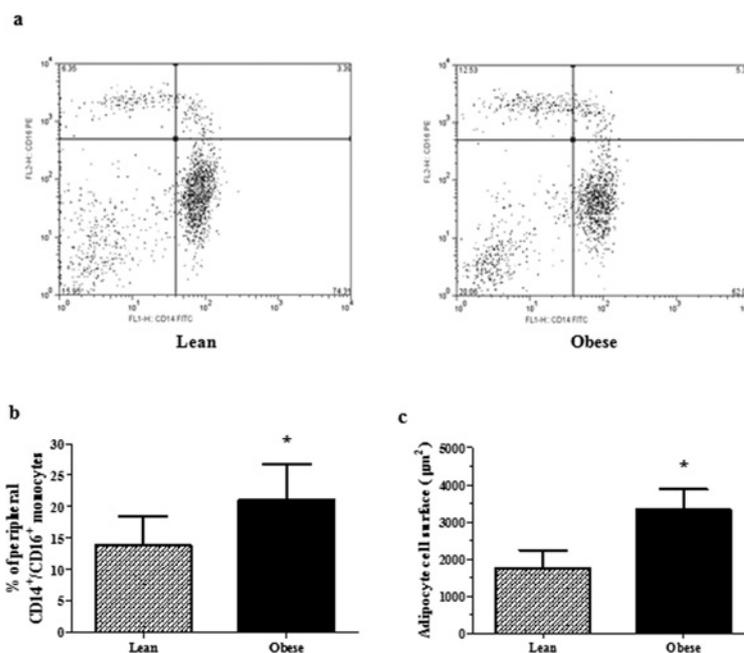
ATM assessment

The percentage of CD68-expressing cells within subcutaneous AT (0.96 \pm 0.69 and 3.95 \pm 3.97% for lean compared with obese, *P* < 0.0001) was significantly elevated with obesity (Figure 2a). In parallel, CD68 mRNA expression followed a similar trend, with a 1.62-fold increase in the obese group relative to the lean group (Figure 2b).

Table 2 Serum levels of inflammatory markers of study participants at baseline

Values are expressed as means \pm S.D. Lean and obese groups were compared at baseline using independent Student's *t* tests. CI, confidence interval.

Inflammatory marker	Lean controls (<i>n</i> = 15)	Obese (<i>n</i> = 37)	Differences in means (95 % CI)	<i>P</i> value
TNF α (pg/ml)	1.62 \pm 0.36	2.14 \pm 0.91	- 0.53 (- 1.01, - 0.04)	0.017
Total adiponectin (μ g/ml)	10.5 \pm 4.5	6.3 \pm 2.1	4.2 (1.59, 6.74)	<0.0001
High adiponectin (μ g/ml)	4.6 \pm 2.6	3.1 \pm 1.4	1.5 (0.01, 3.04)	0.022
High/total adiponectin ratio	0.42 \pm 0.10	0.47 \pm 0.11	- 0.05 (- 0.11, 0.02)	ns

**Figure 1** Baseline analysis of CD14⁺/CD16⁺ peripheral monocyte populations and adipocyte cell surface in lean and obese groups

Representative scatter dot plots showing CD14⁺/CD16⁺ peripheral monocyte populations in lean and obese groups at baseline. PBMCs were isolated by Histopaque and labelled with FITC-conjugated anti-CD14 and PE-conjugated anti-CD16. Fixed monocytes were identified by forward and side scatter properties. Fluorescence data were collected on 10000 cells and analysed using CellQuest Pro software. The percentage of CD14⁺/CD16⁺ cells was calculated by combining the top left and right quadrants of the gated monocyte population (a). Mean percentage of peripheral CD14⁺/CD16⁺ monocytes (b) and mean adipocyte cell surface (μ m²) (c) in lean (*n* = 9–15) and obese (*n* = 23–25) groups at baseline. Error bars indicate S.D. Lean and obese groups were compared at baseline using independent Student's *t* tests: **P* < 0.05.

Adipose tissue gene expression analysis

The observed obesity-associated increases in circulating TNF α levels were reflected in a significant increase in subcutaneous AT expression of this cytokine (Figure 3). Expression of SREBP1c, CEBP β , GLUT4 and IRS-1 were all lower in obese compared with lean AT, however, only the latter was significant (Figure 3). Expression of PPAR γ 2 was similar between lean and obese AT.

Correlations between adipose markers, peripheral monocytes and CVD risk factors

In agreement with the observation of obesity-associated increases in the percentage of CD68 cells within AT

(Figure 2a), BMI and WHR demonstrated positive correlations with the percentage of CD68-expressing cells in subcutaneous AT ($r = 0.595$, $P = 0.001$ and $r = 0.429$, $P = 0.023$ respectively).

As can be seen in Figure 4(a), adipocyte cell surface correlated significantly with BMI, the percentage of CD68-expressing cells in subcutaneous AT and the percentage of peripheral CD14⁺/CD16⁺ monocytes. In addition, adipocyte cell surface correlated significantly with markers of insulin resistance: fasting insulin and HOMA index (Figure 4b). Adipocyte cell surface also correlated significantly with both circulating TNF α ($r = 0.455$, $P = 0.008$) and AT TNF α mRNA levels (ΔC_t : $r = -0.371$, $P = 0.048$), as well as being negatively correlated with total adiponectin ($r = -0.411$, $P = 0.017$).

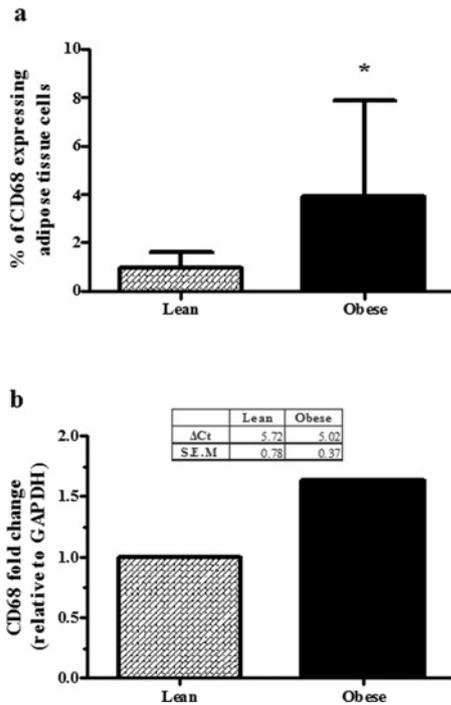
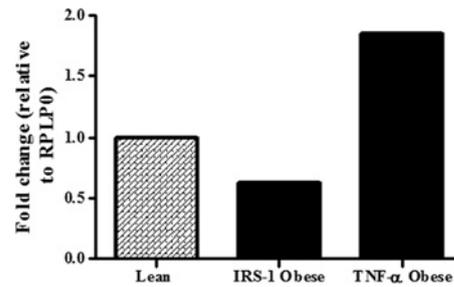


Figure 2 Comparison of mean percentage (\pm S.D.) of CD68-expressing AT cells (a), and mean CD68 mRNA expression (b) in lean ($n=7-13$) and obese ($n=24-28$) groups

Individual subject CD68 mRNA expression was normalized to the housekeeping gene GAPDH using the formula ΔC_t and the mean-fold change relative to the lean control group calculated using the formula $2^{-\Delta\Delta C_t}$ (b). Results are shown as group mean-fold change and statistical analyses were performed on the individual ΔC_t values. Differences between lean and obese groups at baseline were analysed using independent Student's *t* tests: * $P < 0.05$.

Only the correlation between adipocyte cell surface and the percentage CD68-expressing AT cells remained significant ($P=0.014$) after adjusting for BMI.

The percentage of CD68-expressing cells in subcutaneous AT and the percentage of peripheral CD14⁺/CD16⁺ monocytes also demonstrated a significant correlation (Figure 4c); this was lost upon adjusting for BMI. The percentage of CD14⁺/CD16⁺ monocytes also showed a positive correlation with fasting insulin ($r=0.378$, $P=0.048$) and HOMA index ($r=0.422$, $P=0.023$), and a negative correlation with total adiponectin ($r=-0.428$, $P=0.007$), as well as high adiponectin ($r=-0.362$, $P=0.025$). Likewise, the percentage of CD68-expressing AT cells negatively correlated with total (-0.578 , $P=0.001$) and high adiponectin ($r=-0.460$, $P=0.012$). Again, correlations between CD14⁺/CD16⁺ monocytes and indices of insulin resistance and circulating levels of adiponectin isoforms became non-significant when adjusted for BMI, as did correlations between the percentage of CD68-expressing AT cells and adiponectin.



Gene		Lean	Obese
IRS-1	ΔC_t	3.25	3.92*
	S.E.M.	0.24	0.14
TNF- α	ΔC_t	11.67	10.78*
	S.E.M.	0.44	0.18
SREBP1c	ΔC_t	4.88	5.42
	S.E.M.	0.41	0.22
CEBP β	ΔC_t	5.82	6.29
	S.E.M.	0.29	0.18
PPAR γ 2	ΔC_t	1.51	1.62
	S.E.M.	0.17	0.09
GLUT 4	ΔC_t	7.48	8.01
	S.E.M.	0.33	0.15

Figure 3 Comparison of adipose gene expression in lean ($n=12$) and obese ($n=29$) groups

Individual subject IRS-1 and TNF α mRNA expression were normalized to the housekeeping gene RPLP0 using the formula ΔC_t and the mean-fold change relative to the lean control group calculated using the formula $2^{-\Delta\Delta C_t}$. Results are shown as group mean-fold change and statistical analyses were performed on the individual ΔC_t values. Differences between lean and obese groups at baseline were analysed using independent Student's *t* tests: * $P < 0.05$.

Effects of pioglitazone and fenofibrate on anthropometric and biochemical characteristics

The effects of pioglitazone and fenofibrate on anthropometric and biochemical characteristics are shown in Table 3. Fasting insulin levels and HOMA index both improved significantly following pioglitazone treatment, demonstrating its ability to ameliorate obesity associated insulin resistance. As expected, fenofibrate exhibited its lipid-lowering effects by significantly reducing levels of TC, LDL-C and TAG, and improving the TC/HDL-C ratio and the LDL-C/HDL-C ratio. In addition, pioglitazone significantly enhanced HDL-C levels and had similar positive effects to fenofibrate on the TC/HDL-C ratio and the LDL-C/HDL-C ratio.

Effects of pioglitazone and fenofibrate on adiponectin, adipocyte cell surface, ATM and peripheral monocyte numbers

With respect to adiponectin, pioglitazone augmented levels of total (5.5 ± 1.4 and 10.4 ± 5.7 $\mu\text{g/ml}$ for pre- and post- respectively, $P < 0.0001$) and high adiponectin (2.8 ± 1.1 and 6.9 ± 4.6 $\mu\text{g/ml}$ for pre- and

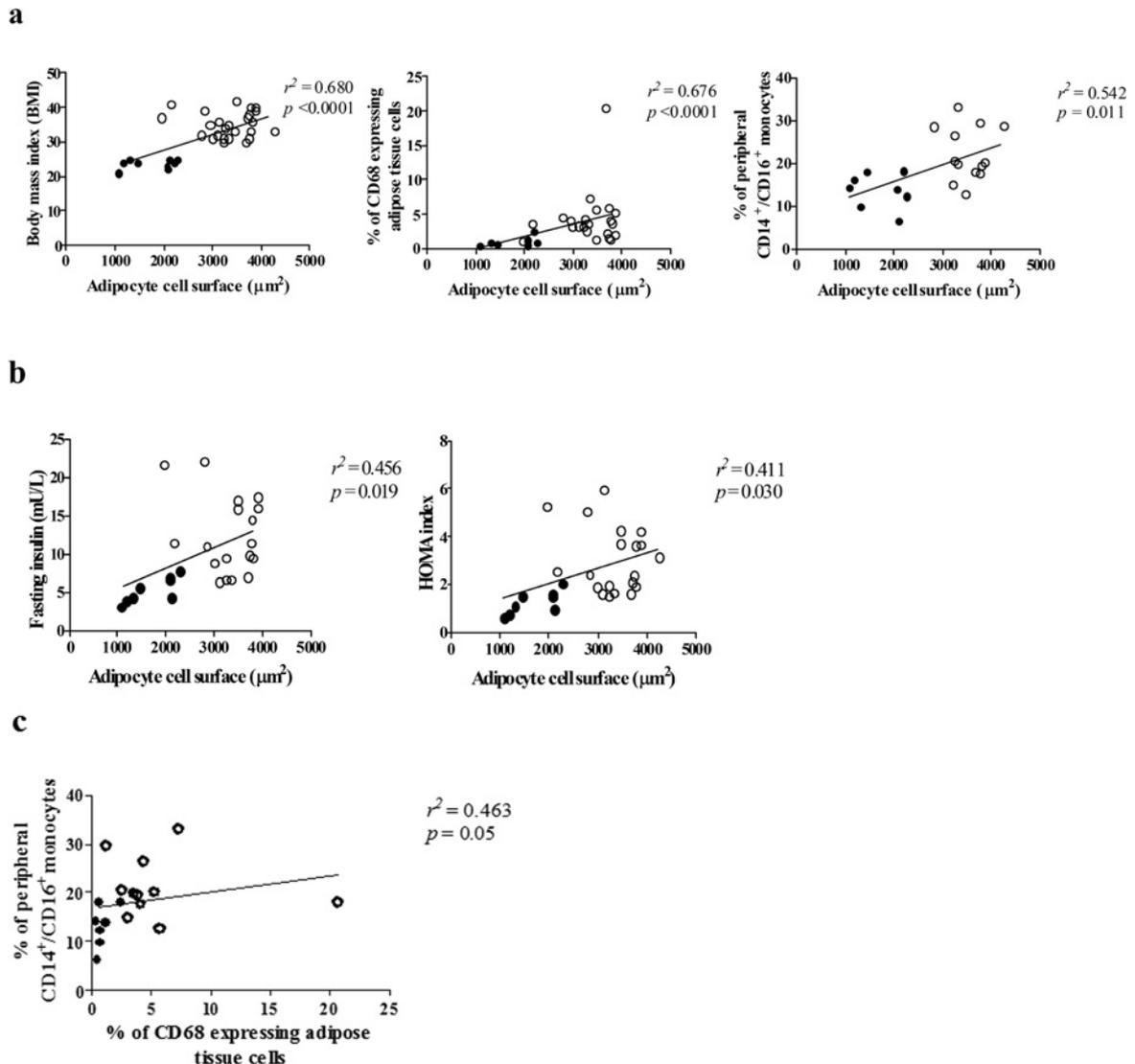


Figure 4 Correlations between (a) adipocyte cell surface (μm^2) and BMI, the percentage of CD68-expressing cells and the percentage of peripheral CD14⁺/CD16⁺ monocytes, (b) adipocyte cell surface (μm^2) and fasting insulin (m-units/l) and the HOMA index, and (c) the percentage of CD68-expressing cells and the percentage of peripheral CD14⁺/CD16⁺ monocytes. Correlations between continuous variables were assessed by Pearson's coefficients for correlations. ○, lean; ●, obese.

post- respectively, $P < 0.0001$) and, additionally, pioglitazone treatment improved the high to total adiponectin ratio (0.49 ± 0.09 and 0.62 ± 0.11 for pre- and post- respectively, $P < 0.0001$).

Neither pioglitazone nor fenofibrate treatment resulted in any significant changes in CD68 mRNA expression or the percentage of CD68-expressing cells within AT, nor did either treatment have any effect on the percentage of peripheral CD14⁺/CD16⁺ monocytes. Following pioglitazone treatment there was, however, a significant increase in adipocyte cell surface (3330 ± 712 and $3655 \pm 712 \mu\text{m}^2$ for pre- and post- respectively, $P = 0.05$).

The effects of pioglitazone and fenofibrate on AT gene expression

Fenofibrate was without effect on the expression levels of any of the genes examined. Pioglitazone significantly increased expression of CEBP β (4.26-fold; Figure 5). Pioglitazone treatment also resulted in increased expression of SREBP1c, PPAR γ 2, GLUT4 and IRS-1, albeit that none of these increases reached significance (Figure 5).

Following pioglitazone treatment, CEBP β expression exhibited significant positive correlations with IRS-1 ($r = 0.979$, $P < 0.0001$) and SREBP1c ($r = 0.976$, $P < 0.0001$) mRNA levels, and a significant negative

Table 3 Anthropometric and biochemical characteristics of obese participants pre- and post-treatment

Values are expressed as means \pm S.D. The obese-treated groups were analysed by calculating change (post–pre) and comparing with placebo change (post–pre) using independent Student's *t* tests: **P* < 0.05 and †*P* < 0.01.

Characteristic	Pioglitazone (<i>n</i> = 6–8)			Fenofibrate (<i>n</i> = 7–11)			Placebo (<i>n</i> = 5–9)		
	Pre	Post	Mean change	Pre	Post	Mean change	Pre	Post	Mean change
BMI (kg/m ²)	36.6 \pm 3.8	36.5 \pm 3.8	0%	34.6 \pm 4.7	35.0 \pm 5.7	1%	34.1 \pm 3.7	34.7 \pm 3.6	2%
WHR	1.02 \pm 0.05	1.01 \pm 0.05	–1%	1.02 \pm 0.08	1.00 \pm 0.06	–2%	0.97 \pm 0.03	0.97 \pm 0.05	0%
SBP (mmHg)	137 \pm 10	136 \pm 15	–1%	126 \pm 8	119 \pm 9	–5%	130 \pm 14	125 \pm 15	–4%
DBP (mmHg)	85 \pm 8	88 \pm 8	4%	79 \pm 10	80 \pm 6	3%	82 \pm 4	81 \pm 6	–2%
Fasting glucose (mmol/l)	5.1 \pm 0.4	5.1 \pm 0.2	0%	5.4 \pm 0.3	5.1 \pm 0.4	–5%	5.3 \pm 0.5	5.3 \pm 0.4	1%
2 h glucose (mmol/l)	6.2 \pm 0.7	5.9 \pm 1.3	–3%	6.4 \pm 1.0	6.3 \pm 1.1	–1%	6.8 \pm 1.3	6.7 \pm 1.4	2%
Fasting insulin (m-units/l)	15.6 \pm 5.1	12.0 \pm 2.9*	–16%	13.0 \pm 5.1	14.4 \pm 8.2	9%	9.9 \pm 3.4	12.5 \pm 5.7	25%
HOMA index	3.6 \pm 1.4	2.7 \pm 0.7*	–15%	3.2 \pm 1.6	3.2 \pm 1.7	2%	2.4 \pm 1.0	3.0 \pm 1.4	27%
HbA _{1c} (%)	5.2 \pm 0.2	5.2 \pm 0.2	0%	5.4 \pm 0.3	5.3 \pm 0.2	–1%	5.3 \pm 0.3	5.3 \pm 0.3	1%
TC (mmol/l)	4.9 \pm 0.4	4.9 \pm 0.8	–1%	5.5 \pm 0.7	4.8 \pm 0.6*	–13%	5.3 \pm 0.8	5.3 \pm 0.5	1%
LDL-C (mmol/l)	3.1 \pm 0.4	3.0 \pm 0.9	–5%	3.7 \pm 0.6	3.1 \pm 0.6*	–14%	3.1 \pm 0.5	3.3 \pm 0.4	9%
HDL-C (mmol/l)	1.15 \pm 0.22	1.19 \pm 0.20*	5%	1.28 \pm 0.23	1.22 \pm 0.23	–4%	1.26 \pm 0.35	1.14 \pm 0.30	–10%
TAG (mmol/l)	1.48 \pm 0.39	1.51 \pm 0.85	7%	1.31 \pm 0.42	1.02 \pm 0.39†	–21%	2.01 \pm 0.83	2.35 \pm 1.37	13%
TC/HDL-C ratio	4.43 \pm 0.91	4.20 \pm 1.00*	–5%	4.40 \pm 0.69	4.04 \pm 0.97†	–8%	4.38 \pm 0.77	4.90 \pm 0.99	12%
LDL-C/HDL-C ratio	2.81 \pm 0.72	2.59 \pm 1.00*	–9%	2.91 \pm 0.49	2.64 \pm 0.79*	–9%	2.50 \pm 0.42	2.94 \pm 0.67	18%

correlation with CD68 ($r = -0.822$, $P = 0.045$) mRNA expression.

DISCUSSION

Using a cohort of lean and obese glucose tolerant subjects, the present study is, to our knowledge, the first to simultaneously investigate obesity-associated changes in both peripheral blood CD14⁺/CD16⁺ monocytes and ATM. The results obtained indicate that obesity is associated with increased peripheral CD14⁺/CD16⁺ monocyte and subcutaneous ATM number, as well as increased subcutaneous adipocyte cell surface, reduced circulating adiponectin levels and lower subcutaneous AT expression of genes involved in macrophage phenotype, adipogenesis and glucose metabolism. Moreover, pioglitazone treatment was found to result in significant improvements in insulin resistance and lipid profile, changes that occurred in parallel with significant increases in subcutaneous AT expression of CEBP β mRNA, adipocyte cell surface and adiponectin levels. Taken together, these results indicate that obesity-associated changes in CD14⁺/CD16⁺ monocyte levels and adipose function (as reflected in reduced systemic levels of adiponectin) are evident prior to the presence of impaired glucose tolerance, and that therapeutic interventions with the ability to target the latter may prove beneficial in reducing CVD risk and the development of T2D.

Pre-diabetic individuals are defined as those with impaired glucose tolerance [2 h glucose, 140–199 mg/dl (7.8–11.0 mmol/l)] or impaired fasting glucose [fasting

glucose concentration, 110–125 mg/dl (5.6–6.9 mmol/l)] or an HbA_{1c} of 5.7–6.4% [22]. A strength of the present study is that the obese subjects recruited did not have impaired glucose tolerance (2 h glucose, 6.4 \pm 1.0 mmol/l; fasting glucose concentration, 5.3 \pm 0.4 mmol/l; HbA_{1c}, 5.3 \pm 0.3%), thereby, enabling obesity-associated changes in primary and secondary endpoints to be investigated and the impact of PPAR agonist treatment on these endpoints to be evaluated. Cardioprotective strategies, including lifestyle modification, have been shown to be most effective in averting or delaying the onset of diabetes when administered at this early stage in the hyperglycaemia/diabetes continuum [23]. The present study has provided evidence that preventative strategies are also effective when administered prior to the development of impaired glucose tolerance.

Subcutaneous and visceral ATM number increase in obesity and evidence is accumulating that ATM are responsible for potentiating the chronic inflammatory processes of obesity [1,2]. The origin of ATM remains to be fully elucidated, it has been reported that these arise from adipokine-dependent extravasated peripheral blood monocytes and evidence has also been presented that multi-potent adipocyte stem cells and pre-adipocytes can differentiate into macrophages [24,25]. Both subcutaneous and visceral ATM number have been reported to correlate with clinical parameters of obesity and its co-morbidities [18]. The results of the current study concur with previous reports: the percentage of CD68-expressing cells within AT was significantly elevated in obesity, while CD68 mRNA

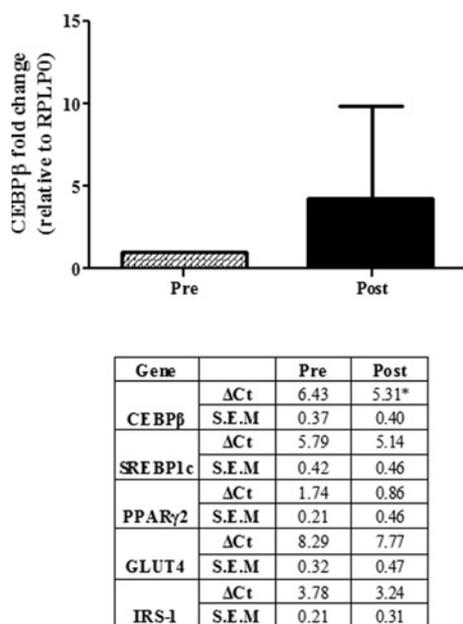


Figure 5 Comparison of adipose gene expression in obese ($n = 7$) subjects pre- and post-pioglitazone treatment

Post-treatment mRNA expression was calculated as a fold change relative to pre-treatment using the formula $2^{-\Delta\Delta C_t}$. Results are shown as mean \pm S.D-fold change and statistical analyses were performed on the individual ΔC_t values. Pioglitazone change (post–pre) was compared with placebo change (post–pre) using independent Student's *t* tests: * $P < 0.05$.

expression followed a similar trend. Moreover, BMI and WHR demonstrated positive correlations with the percentage of CD68-expressing cells in subcutaneous AT. The percentage of CD68-expressing cells also negatively correlated with total and high adiponectin levels, indicating that ATM infiltration is associated with reduced adipocyte function. Adipocyte enlargement is a strong, direct predictor of ATM recruitment and accumulation [26]. Macrophages have been detected in the subcutaneous and visceral AT of obese patients, in which they surround the dead adipocyte in a crown-like arrangement [27]. Given the evidence that adipocyte hypertrophy is a potential stimulus for ATM infiltration, it is of interest that, in the current study, adipocyte cell surface correlated significantly with both the percentage of CD68-expressing cells in subcutaneous AT and the percentage of peripheral CD14⁺/CD16⁺ monocytes. Given the observed obesity-associated increases in the CD14⁺/CD16⁺ peripheral monocyte population, the significant correlation between the percentage of CD68-expressing cells in subcutaneous AT and the percentage of peripheral CD14⁺/CD16⁺ monocytes, and the evidence supporting a role for this population in vascular inflammation, it is tempting to speculate that these represent a source of the increased ATM number

in subcutaneous AT, however, clearly this is an area that requires further analysis.

The observation in the present study that pioglitazone and fenofibrate normalized obesity-associated insulin resistance and/or dyslipidaemia is as would be expected, indeed, in an earlier study similar results were reported by our group [11]. The observation that pioglitazone achieved this without significantly changing the percentage of peripheral CD14⁺/CD16⁺ monocytes or ATM number, but by significantly increasing adipocyte cell surface and improving adipocyte function is a novel one. Taken together, these results suggest a model whereby modulation of adipocyte function, in the absence of effects on CD14⁺/CD16⁺ monocyte expansion or ATM number, results in cardioprotective outcomes. While Di Gregorio et al. [28] have reported a decrease in ATM following pioglitazone treatment, their cohort received a higher dose than used in the current trial (45 mg/day), moreover, their subjects had impaired glucose tolerance and were mixed gender. Hammarstedt et al. [29] have reported that 3-week treatment with a similar dose of pioglitazone in overweight insulin-resistant glucose-tolerant subjects had no effect on adipocyte cell surface, or indeed, in agreement with the results of the current study, adipose macrophage infiltration markers. In contrast with the present study, however, short-term pioglitazone treatment was found to be without effect on lipid levels [29]. PPAR γ agonists are reported to promote NEFAs uptake and storage in adipocytes, thereby preventing lipotoxic trauma to liver and muscle and ameliorating insulin resistance. In support of this, pioglitazone has been demonstrated to increase subcutaneous adipose mass [30]. Moreover, it has been reported that congenital adrenal hyperplasia-associated insulin resistance was improved by pioglitazone treatment, and that this improvement in insulin sensitivity was associated with enlargement of subcutaneous adipocytes [12].

A further novel finding of the present study is that, following pioglitazone treatment, subcutaneous AT CEBP β expression was significantly increased. Expression of CEBP β , SREBP1c, GLUT4 and IRS-1 were all lower in obese versus lean subcutaneous AT, the latter being significantly reduced. These results are in keeping with an obesity-associated impairment in adipogenesis [1]. CEBP β has been recently identified as playing a central role in PPAR γ -mediated gene regulation in both adipocytes and macrophages, two cell types that predominate in obese subcutaneous AT [31,32]. In addition, evidence has been presented that CEBP β plays a non-PPAR γ -dependent role in mitotic clonal expansion during adipogenesis [33]. The observation that pioglitazone up-regulates CEBP β is interesting given the central role of this transcription factor in adipogenesis and macrophage polarization, and provides evidence that pioglitazone, in addition to increasing

the function/size of mature adipocytes, promotes adipogenesis and may facilitate macrophage polarization to the alternative, anti-inflammatory phenotype. It will be of interest in future studies to determine whether pioglitazone-dependent CEBP β up-regulation is reflected in increased protein levels of this transcription factor and whether this is associated with an increase in anti-inflammatory, and a decrease in pro-inflammatory, cytokine expression, as demonstrated in our previous study [11]. Pioglitazone treatment also resulted in increased, albeit non-significant, subcutaneous adipose expression of SREBP1c, PPAR γ 2, GLUT4 and IRS-1. These results are in broad agreement with the findings of Hammarstedt et al. [29], and further support a model whereby pioglitazone treatment facilitates adipocyte terminal differentiation.

In conclusion, the present study has found evidence that increased adipocyte cell surface, expansion of the CD14⁺/CD16⁺ monocyte population and ATM number, and compromised AT function occurs in obese individuals prior to the development of impaired glucose tolerance. Further, significant associations between adipocyte cell surface and increased peripheral monocyte and ATM numbers support the role of adipocyte enlargement as an initiating stimulus in adipose inflammation/dysfunction. The finding that improvements in obesity-associated insulin resistance following pioglitazone were associated with increased adipocyte cell surface and systemic adiponectin levels, supports the centrality of AT to the cardiometabolic derangement underlying the development of T2D and CVD.

AUTHOR CONTRIBUTION

Lesley Powell, Ann McGinty, David McCance, Ian Young and Elisabeth Trimble were involved in the study conception, design and management, data interpretation and drafting of the paper. Paul Crowne, Chenchi Kankara and Jennifer McPeake were involved in the recruitment of the participants, sample collection and analysis, data analysis and paper preparation.

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