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ARTICLE

Fatty acid desaturases in human adipose tissue: relationships between gene expression, desaturation indexes and insulin resistance

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Abstract
Aims/hypothesis Fatty acid desaturases introduce double bonds into growing fatty acid chains. The key desaturases in humans are Δ^5-desaturase (D5D), Δ^6-desaturase (D6D) and stearoyl-CoA desaturase (SCD). Animal and human data implicate hepatic desaturase activities in insulin resistance, obesity and dyslipidaemia. However, the role of desaturase activity in adipose tissue is uncertain. We therefore evaluated relationships between adipose mRNA expression, estimated desaturase activities (fatty acid ratios) in adipose tissue and insulin resistance.
Methods Subcutaneous adipose tissue mRNA expression of *D5D* (also known as *FADS1*), *D6D* (also known as *FADS2*) and *SCD* was determined in 75 individuals representative of the study population of 294 healthy 63-year-old men. Desaturation indexes (product/substrate fatty acid ratios) were generated from adipose tissue fatty acid composition in all individuals. Insulin resistance was defined as the upper quartile of the updated homeostasis model assessment (HOMA-2) index.
Results The relevant desaturation indexes (16:1/16:0, 18:1/18:0, 20:4/20:3 and 18:3/18:2) reflected expression of *SCD*, but not of *D5D* or *D6D* in adipose tissue. Insulin-resistant individuals had a higher adipose tissue 18:1/18:0, but not 16:1/16:0 ratio than insulin-sensitive individuals. Individuals with a high adipose tissue 18:1/18:0 ratio were 4.4-fold (95% CI 1.8–11.8) more likely to be insulin resistant [threefold (95% CI 1.1–8.6) after adjustment for waist circumference and plasma triacylglycerol]. In a multiple regression model predicting HOMA-2, the independent effect of the 18:1/18:0 ratio was borderline (p=0.086).
Conclusions/interpretation Adipose tissue desaturation indexes of SCD reflect the expression of the gene encoding the enzyme in this tissue. Elevated SCD activity within adipose tissue is closely coupled to the development of insulin resistance.

Keywords Adipose tissue · Desaturase · Fatty acid composition · Human · Insulin resistance · Stearoyl-CoA desaturase

Abbreviations

CRP	C-reactive protein
D5D	Δ^5-desaturase
D6D	Δ^6-desaturase
HOMA-2	updated homeostasis model assessment (for insulin sensitivity)
SCD	stearoyl-CoA desaturase

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Introduction

Insulin resistance and metabolic disturbances are increasing continuously throughout the world, with a correspondingly discouraging future prognosis for type 2 diabetes and cardiovascular disease [1]. To counter this development, it is necessary to understand the complex aetiology underlying these traits.

One component implicated in the insulin-resistant state is a disturbed fatty acid metabolism. Desaturases are key enzymes in the remodelling of fatty acids, introducing a double-bond at the Δ^5, Δ^6 or Δ^9 carbon of the growing fatty acid chain (Fig. 1). These desaturases are consequently termed Δ^5-desaturase (D5D), Δ^6-desaturase (D6D) and Δ^9-desaturase. Stearoyl-CoA desaturase (SCD) is the key Δ^9-desaturase in man. The activities of these enzymes produce fatty acids with a greater degree of desaturation, which are required for the efficient synthesis of more complex lipids, such as triacylglycerols [2]. Both animal and human studies suggest that fatty acid desaturases play a role in various metabolic disturbances, such as insulin resistance and dyslipidaemia [3–5].

Special attention has been paid to SCD, which is the main enzyme responsible for converting saturated fatty acids into monounsaturated fatty acids (16:0 to 16:1 and 18:0 to 18:1). The potential importance of SCD activity has been extensively studied in mouse models, indicating a considerable impact of SCD on dyslipidaemia and obesity [4]. SCD knockout mice display markedly reduced triacylglycerol synthesis with subsequent reductions in plasma triacylglycerol concentrations, effects that have been attributed to the lack of SCD in the liver of these mice. In addition, SCD knockout mice are resistant to diet-induced obesity [6], possibly due to the absence of SCD activity in adipose tissue. However, the literature contains only very limited data on the importance of desaturase activities in adipose tissue.

Studies on desaturases in humans are few and predominantly based on estimates of desaturation activities derived from the circulating fatty acid composition of fasting blood samples. In the fasting state, most lipids in the circulation are derived from the liver. Therefore, calculating the product/substrate ratio of fatty acids in circulating lipids generates desaturation indexes that are believed to predominantly reflect hepatic desaturase activity. In line with the findings in SCD knockout mice, a couple of studies have suggested a major lipidaemic effect of SCD also in man [7, 8]. Furthermore, the characteristic fatty acid composition of circulating lipids in insulin-resistant individuals indicates that they have increased SCD and D6D activities and decreased D5D activity [5]. The concept that desaturase activities might affect insulin resistance is supported by a recent study in which estimates of hepatic desaturase activity predicted development of the metabolic syndrome [9]. Importantly, however, these studies have not addressed the role of adipose desaturase activities, an issue that is currently unresolved. Finally, the question of whether adipose tissue desaturation activity can be accurately estimated by desaturation indexes (generated from fatty acid product/substrate ratios) is presently unclear.

Against this background, we determined the expression of *D5D* (also known as *FADS1*), *D6D* (also known as *FADS2*) and *SCD* mRNAs in adipose tissue of healthy 63-year-old Swedish men with a range of insulin sensitivities and from

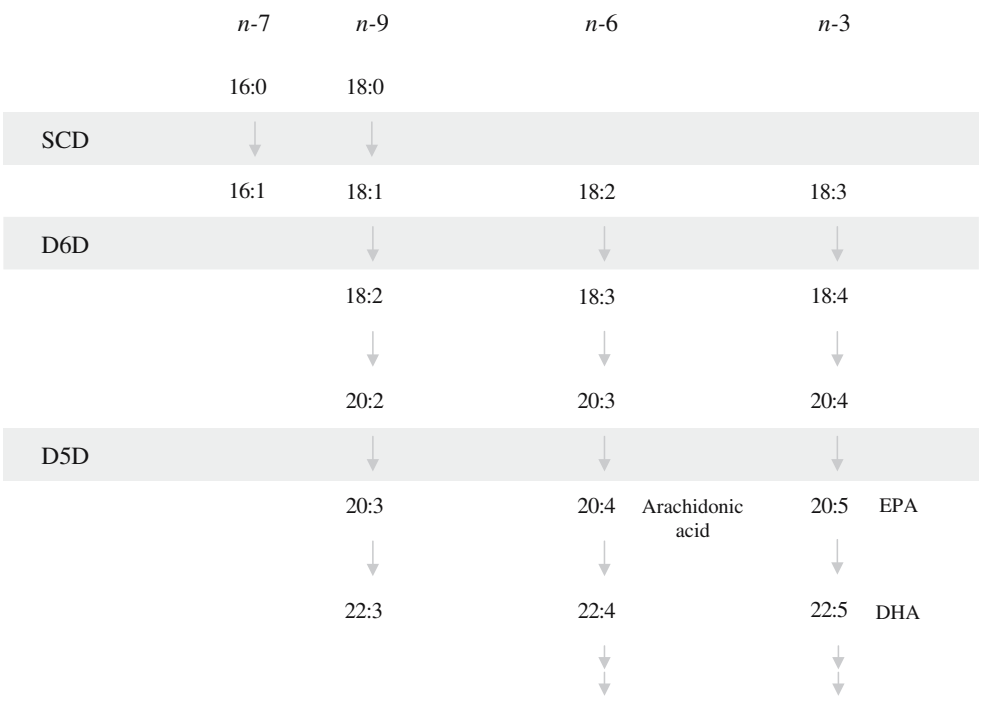

Fig. 1 Schematic representation of the major steps in fatty acid remodelling and the roles of desaturases. Vertical pathways represent the different fatty acid families *n*-7, *n*-9, *n*-6 and *n*-3. EPA, eicosapentaenoic acid; DHA, docosahexaenoic acid

whom adipose tissue fatty acid composition and detailed metabolic profiles were available. Estimates of adipose tissue desaturase activity (fatty acid ratios) and their relationships to desaturase gene expression and insulin resistance were investigated.

Methods

Participants A biobank and data set comprising a total of 294 healthy, 62- to 64-year-old men (mean 63±0.6 years), randomly recruited from a larger population-based cohort of 2039 men living in Stockholm county, was used for this study [10]. The men were selected to represent a wide range of fasting plasma insulin concentrations. Recruitment details, exclusion criteria, clinical procedures and dietary assessment (7 day dietary records) have been described previously [11]. Subcutaneous adipose tissue biopsies were taken from the left upper buttock for subsequent analysis; smaller biopsies were taken from all individuals for fatty acid composition analysis and larger biopsies were taken from a subset of 87 individuals (equally distributed throughout the tertiles of fasting insulin concentrations). Adequate amounts of RNA for expression analysis were obtained from 75 individuals. The Ethics Committee of Karolinska Institutet approved the study and all participants gave informed consent.

Laboratory procedures Methods for determination of plasma glucose, insulin, proinsulin, uric acid, triacylglycerol, LDL peak particle size distribution and cholesterol in VLDL, LDL and HDL have been described previously [11]. Circulating levels of oxidised LDL, C-reactive protein (CRP), TNFα and IL-6 were derived as described previously [12]. RNA was extracted from the subset of larger adipose tissue biopsies and cDNA synthesised as described previously [13]. The expression of *SCD*, *D5D* and *D6D* mRNAs was quantified in the 75 samples by real-time PCR using an ABI 7000 SDS (Applied Biosystems, Foster City, CA, USA) and normalised for expression of the housekeeping gene *RPLP0*. Assay numbers for the respective genes were: *SCD*, Hs00748952_s1; *D5D*, Hs00203685_m1; *D6D*, Hs00188654_m1; and for the housekeeping gene *RPLP0*, Hs99999902_m1 (Assays-on-demand; Applied Biosystems). Expression levels were quantified in arbitrary units using a five-point serially diluted cDNA standard curve. The fatty acid composition of subcutaneous adipose tissue was analysed by gas liquid chromatography as described previously [14]. The relative amount of each fatty acid quantified was expressed as the percentage of the total amount of fatty acids.

Estimation of desaturase activity The product/substrate ratios of individual fatty acids in adipose tissue were calculated to estimate the activities of different desaturases as follows: SCD, 16:1/16:0 and 18:1/18:0; D5D, 20:4/20:3; and D6D, 18:3/18:2 (for D5D and D6D, all fatty acids were *n*-6).

Statistical procedures JMP 6.0 software (SAS Institute, Cary, NC, USA) was used for statistical analysis, with significance level set to $p<0.05$. Skewed data were logarithmically transformed, but arithmetic means (±SD) are presented for ease of understanding. Spearman rank correlation analysis was used to test for relationships between desaturase mRNA expression levels and desaturation indexes and unpaired *t* test was used to analyse differences in continuous variables between insulin-sensitive and insulin-resistant individuals. Pearson correlation analysis was used in univariate analysis, with the log of the calculated updated homeostasis model assessment (HOMA-2) value as the dependent variable. HOMA-2 of insulin sensitivity was derived as described previously [15]. Five individuals were excluded with this approach, due to glucose or insulin values outside the ranges of 3.5–25 mmol/l and 20–400 pmol/l, respectively [16]. Accordingly, 289 individuals remained for group comparisons. Insulin-resistant individuals were defined as those in the upper quartile of HOMA-2 index ($n=61$). Furthermore, logistic regression analysis, unadjusted and adjusted for (1) high waist circumference and (2) high waist circumference and high plasma triacylglycerol (according to the cutoffs defined by the National Cholesterol Education Program Adult Treatment Panel III (NCEP/ATPIII) for metabolic syndrome components [17]), was used to determine the association between high adipose tissue 18:1/18:0 fatty acid ratio (i.e. upper vs lower quartile of the ratio) and insulin resistance. To evaluate the additional prediction of the 18:1/18:0 ratio, a single parsimonious model was constructed using forward stepwise selection to identify any significant parameters that made additional contributions to the prediction of log [HOMA-2]. Selection of predictor variables was done in forward stepwise fashion with strict variable entry and elimination criteria. Consequently, the final parsimonious model included only those measures that made independent contributions to the prediction of log[HOMA-2] (waist circumference and plasma triacylglycerol) plus the adipose tissue 18:1/18:0 ratio.

Results

Quantification of adipose tissue mRNA levels in the subset of 75 individuals revealed expression levels of *D5D*, *D6D* and *SCD* to be correlated (Table 1). In particular, a strong relationship between the mRNA levels of *D5D* and *D6D* was found. To investigate whether the fatty acid composition of lipids in adipose tissue reflected the mRNA levels of the different desaturases, desaturation indexes were created from the fatty acids considered to be the typical products

Table 1 Relationships between the mRNA expression levels of different desaturases and indexes of desaturase activity in human subcutaneous adipose tissue

	Adipose tissue mRNA expression		
	SCD	*D5D*	*D6D*
SCD		0.39*	0.47**
D5D			0.70**
Adipose tissue FA ratios			
16:1/16:0 Δ9	0.36*		
18:1/18:0 Δ9	0.35*		
20:4/20:3 Δ5		0.19	
18:3/18:2 Δ6			0.12

n=75
Associations are presented as Spearman rank correlation coefficients
Levels of mRNA expression were normalised to *RPLP0*
*p<0.01; **p<0.0001
FA, fatty acid

and substrates of the respective enzymes. The adipose tissue fatty acid ratios 16:1/16:0 and 18:1/18:0 were both significantly correlated with the expression of *SCD*, but there were no significant relationships between the fatty acid ratios 20:4/20:3 and 18:3/18:2 and the expression of *D5D* and *D6D*, respectively (Table 1). The two estimates of SCD activity, 16:1/16:0 and 18:1/18:0, were strongly correlated (r=0.78, p<0.0001).

In the study population as a whole (composed of individuals with a range of fasting plasma insulin concentrations), the HOMA-2 index was calculated to estimate the degree of insulin sensitivity. Participants in the upper quartile of HOMA-2 index were classified as insulin resistant and compared with the remaining individuals, who were considered to be insulin sensitive (Table 2). Marked differences were found between the groups, with insulin-resistant individuals having significantly higher plasma concentrations of insulin, proinsulin, glucose, triacylglycerol, uric acid and CRP as well as higher anthropometric measurements and blood pressure. LDL particle size and HDL-cholesterol were significantly lower in the insulin-resistant group, while no significant differences were found for total cholesterol, LDL-cholesterol, oxidised LDL, IL-6 or TNFα. Investigation of estimates of SCD activity in adipose tissue (i.e. fatty acid ratios 16:1/16:0 and 18:1/18:0) revealed 18:1/18:0 to be significantly higher in insulin-resistant individuals, but no difference for 16:1/16:0 was found. Differences in dietary fatty acid intake did not seem be able to explain this discrepancy, since the reported intake of 16:0, 16:1, 18:0, 18:1 and the respective ratios did not differ between the insulin-resistant and insulin-sensitive groups (data not shown).

Table 2 Characteristics of participants grouped as insulin-sensitive or insulin-resistant

	Insulin-sensitive (n=228)	Insulin-resistant (n=61)	p value
Clinical characteristics			
HOMA-2 index	0.6±0.2	1.4±0.4	<0.0001
Insulin (pmol/l)	31±10	76±23	<0.0001
Proinsulin (pmol/l)	3.1±1.7	5.9±4.4	<0.0001
Glucose (mmol/l)	4.9±0.5	5.2±0.6	<0.0001
BMI (kg/m^2)	25±3	28±3	<0.0001
Waist (cm)	94±8	103±7	<0.0001
Uric acid (μmol/l)	331±56	365±66	0.0001
Systolic BP (mmHg)	133±14	142±19	0.0001
Diastolic BP(mmHg)	80±8	85±9	<0.0001
Lipids			
Triacylglycerol (mmol/l)	1.1±0.5	1.6±0.7	<0.0001
Cholesterol (mmol/l)	5.9±1.1	5.8±1.0	0.65
HDL-C (mmol/l)	1.7±0.4	1.5±0.3	<0.0001
LDL-C (mmol/l)	3.7±1.0	3.7±0.9	0.95
LDL peak (Å)	239±4	237±5	0.0004
oxLDL (U/l)	62±19	61±18	0.75
oxLDL/LDL-C	17±4	17±5	0.78
Markers of inflammation			
TNFα (ng/l)	2.2±1.2	2.1±0.9	0.51
CRP (mg/l)	1.8±2.2	2.6±3.2	0.0068
IL-6 (ng/l)	1.4±1.2	1.7±2.1	0.088
Adipose tissue FA ratios			
20:4/20/3 (Δ5)	2.6±0.7	2.5±0.6	0.69
18:3/18:2 (Δ6)	0.004±0.002	0.005±0.002	0.43
16:1/16:0 (SCD)	0.36±0.09	0.37±0.12	0.56
18:1/18:0 (SCD)	14.3±3.3	16.2±4.0	0.0004

Values are means±SD
Insulin-resistant individuals were identified according to upper quartile of HOMA-2 index
The p values were calculated from log-transformed data with unpaired t tests
C, cholesterol; FA, fatty acid; oxLDL, oxidised LDL

Although the desaturation indexes for D5D and D6D did not correlate with the mRNA expression level of the respective enzyme (see above), D5D and D6D desaturation indexes in insulin-sensitive and insulin-resistant individuals are presented in Table 2, but there were no significant differences between the groups.

To investigate predictors of insulin sensitivity, univariate analysis was performed with HOMA-2 as the dependent variable (Table 3). HOMA-2 was positively related to BMI, waist circumference, uric acid, blood pressure, triacylglycerol, CRP and the adipose tissue 18:1/18:0 ratio; it was negatively related to HDL-cholesterol and LDL peak. Since adipose tissue 18:1/18:0, but not 16:1/16:0, was related to insulin resistance, the former desaturation index was used in logistic regression analysis to further investigate the impact of the adipose tissue 18:1/18:0 ratio on insulin resistance (Fig. 2). Individuals with a high adipose tissue 18:1/18:0 ratio were 4.4 times (95% CI 1.8–11.8) more likely to be insulin resistant. This relationship remained significant after adjusting for the two strongest predictors of HOMA-2, waist circumference and plasma triacylglycerol (odds ratio 3.0, 95% CI 1.1–8.6). The adipose tissue 18:1/18:0 ratio correlated with both BMI and waist circumference (r=0.34, p<0.0001 for both), but replacing waist circumference with BMI in the model did not alter the relationships between 18:1/18:0 and insulin resistance (data not shown). In a final multiple regression model predicting the quantitative level of HOMA-2, which included the strongest predictors of HOMA-2 (waist circumference and plasma triacylglycerol), the independent effect of the 18:1/18:0 ratio was borderline (p=0.086; Table 3).

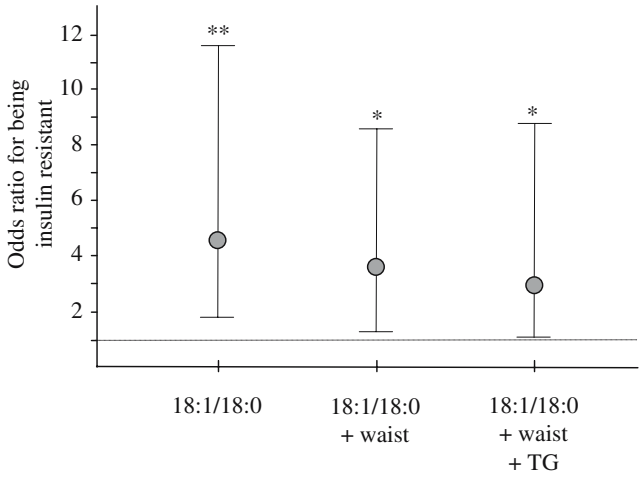

Fig. 2 Odds ratios (95% CI) for the effect of the adipose tissue 18:1/18:0 ratio on insulin resistance according to logistic regression analysis (n=289). *p<0.05, **p<0.01. Waist, waist circumference; TG, plasma triacylglycerol

Discussion

Data from this cohort of 62- to 64-year-old men have been reported previously [11–13, 18, 19]. Here, novel information on the expression of desaturase genes in human adipose tissue, relationships to desaturation indexes and association with insulin resistance are presented.

We show that mRNA expression levels of different fatty acid desaturases in adipose tissue are related to each other and that, to some extent, the fatty acid composition of adipose tissue can be used as a biomarker of desaturase gene

Table 3 Univariate and multivariate linear regression analyses for HOMA-2 index

	Univariate analysis		Multivariate analysis[a]	
	r value	p value	β±SE	p value
BMI	0.55	<0.0001		
Waist circumference	0.55	<0.0001	0.025±0.003	<0.0001
Uric acid	0.29	<0.0001		
Systolic blood pressure	0.19	0.0012		
Diastolic blood pressure	0.24	<0.0001		
Triacylglycerol	0.46	<0.0001	0.78±0.14	<0.0001
HDL-cholesterol	−0.34	<0.0001		
LDL peak	−0.34	<0.0001		
C-reactive protein	0.25	<0.0001		
Adipose tissue 16:1/16:0	0.01	0.93		
Adipose tissue 18:1/18:0	0.27	<0.0001	0.46±0.27	0.086

n=289

Prior to analysis, HOMA-2 index, BMI, uric acid, triacylglycerol, CRP and the adipose tissue ratios 16:1/16:0 and 18:1/18:0 were log-transformed

[a] Parsimonious multivariate model (adjusted R^2 =0.36). From the variables investigated in univariate analysis, independent predictors of HOMA-2 were identified using a forward stepwise approach (BMI and LDL peak were not included in the model due to strong co-linearity with waist and triacylglycerol, respectively). The final model includes these independent predictors (waist circumference and plasma triacylglycerol) plus the 18:1/18:0 ratio

expression. The relevant desaturation indexes (i.e. the 16:1/16:0, 18:1/18:0, 20:4/20:3 and 18:3/18:2 ratios) reflected the expression of *SCD*, but not *D5D* or *D6D*. Individuals with insulin resistance had a higher 18:1/18:0, but not 16:1/16:0 ratio than insulin-sensitive individuals. Indeed, a high 18:1/18:0 ratio was associated with a significantly higher risk of insulin resistance in logistic regression analysis, with the 18:1/18:0 ratio tending to predict insulin resistance in a multiple linear regression model. These results suggest that adipose tissue desaturation indexes of SCD reflect expression of the enzyme in this tissue and that elevated SCD activity within adipose tissue accompanies the development of insulin resistance.

To our knowledge, only one study has previously presented relationships between levels of adipose tissue *SCD* mRNA and insulin resistance in man. An improvement in insulin sensitivity (by thiazolidinedione treatment) in 24 overweight individuals with type 2 diabetes was concomitant with increased adipose tissue *SCD* expression, but no direct relationship between changes in *SCD* expression and enhanced insulin sensitivity was found [20]. That study, however, was small and no data were available to relate *SCD* expression levels to estimates of SCD activity in adipose tissue. The inherent difficulty of measuring desaturase activities directly has led to the use of fatty acid product/substrate ratios as surrogate estimates of desaturase activities. This approach is supported to some degree by results from animal studies [21–24], but compelling evidence is lacking. Importantly, the absence of human data on the validity of these relationships is of concern, since mice, in contrast to humans, express various isoforms of SCD with different affinities for the precursor fatty acids [4]. In the current study, SCD desaturation indexes (derived from adipose tissue fatty acid composition) were significantly related to the level of adipose tissue *SCD* mRNA expression. In contrast, no relationships were found between desaturation indexes and the expression of *D5D* or *D6D*. This could be explained by the high bioactivity of the products of D5D and D6D, resulting in fatty acid ratios that reflect a range of pathways, rather than just the enzyme activities as such. Thus our expression data indicate that fatty acid ratios can be used to estimate SCD but not D5D or D6D activities in human adipose tissue.

The important role of SCD as a metabolic regulator has been described in various mouse models [4]. SCD-deficient mice are resistant to diet-induced obesity and have increased energy expenditure, reduced lipogenesis and increased insulin sensitivity. The underlying explanation is not clear, but includes enhanced phosphorylation of insulin-receptor substrates and activation of AMP-kinase [25]. Human studies report relationships between estimates of hepatic SCD activity and both plasma triacylglycerol concentrations and obesity [7, 8, 26]. However, these studies have not addressed desaturation activity in adipose tissue, since fatty acid ratios derived from circulating lipids primarily reflect hepatic desaturation activity.

Our results suggest that elevated SCD activity in adipose tissue could contribute to the development of insulin resistance. Indeed, a high adipose tissue 18:1/18:0 ratio was associated with a threefold risk of being insulin resistant, even after adjusting for waist circumference and plasma triacylglycerol. A recent publication identified obesity as being mainly responsible for explaining the association between higher hepatic SCD activity (as estimated from plasma desaturation indexes) and elevated risk of developing the metabolic syndrome [9]. However, the present findings indicate that the relationship between adipose tissue SCD activity and insulin resistance is at least partly independent of obesity (as shown in both logistic and linear regression models). This effect might be mediated through abrogation of insulin signalling pathways and/or AMP-kinase activity, as indicated in animal studies [25]. On the other hand, it is also possible that increases in adipose tissue SCD activity are merely a consequence of the development of insulin resistance. However, thiazolidinedione (insulin-sensitiser) treatment of patients with type 2 diabetes leads to increases in adipose tissue *SCD* expression, suggesting a beneficial effect of increased adipose tissue SCD activity in these individuals [20, 27]. One interpretation of these seemingly conflicting data is that the consequences of increased adipose tissue SCD activity depend on the current metabolic status. In insulin-sensitive adipose tissue, there may be a flexible and appropriately regulated balance between up- and downregulation of SCD activity, a balance that shifts according to metabolic demand. However, in insulin-resistant adipose tissue an inappropriately prolonged and maintained increase in SCD activity may have detrimental consequences. Indeed, the complexity of the consequences of altering SCD activity was highlighted recently, when SCD deficiency was shown to improve insulin sensitivity in lean mice, but to worsen diabetes in obese littermates [28].

The fact that the 16:1/16:0 ratio, another estimate of SCD activity, did not relate to insulin resistance in this study (as did the 18:1/18:0 ratio) calls for some attention. It is not presently clear which ratio most accurately mirrors SCD activity. The corresponding mouse SCD (namely SCD-1, the enzyme knocked out in SCD-deficient mice) preferentially converts 18:0 to 18:1 rather than 16:0 to 16:1 [4]. Whether this is the case for human SCD is not clear and both fatty acid ratios have been used in the literature, but not usually concurrently. In contrast to our results, Warensjö et al. [9] identified the circulating 16:1/16:0 ratio, but not 18:1/18:0 ratio, as a predictor of the metabolic syndrome. The authors

suggested that dietary factors could explain the absent relationship for 18:1/18:0, since the diet is normally high in 18:1, which might attenuate the impact of SCD on this specific ratio. Although dietary habits have been shown to influence SCD activity [4], the differing relationships between SCD indexes 16:1/16:0 and 18:1/18:0 and insulin resistance observed in the present study did not appear to be explained by differences in fatty acid intake. Therefore differences in the metabolism of individual fatty acids within adipose tissue may underlie the inconsistent relationships for the two desaturation indexes, but the specific nature of these differences remains unknown.

There are certain limitations to the current study. First, the study is cross-sectional, restricting possibilities of drawing causal conclusions. Second, actual activities of the desaturases were not determined. Instead, mRNA expression levels of desaturases in adipose tissue and the corresponding fatty acid ratios were used as estimates of enzyme activity. Since SCD protein undergoes rapid degradation [29], this could suggest that SCD activity is determined primarily by transcription of the gene and hence by *SCD* mRNA levels. Finally, the present findings are restricted to SCD in subcutaneous adipose tissue. It is, however, possible that SCD activity in other tissues (such as liver and skeletal muscle) or in other adipose tissue depots has different metabolic consequences. Indeed, a central role has been ascribed to intra-abdominal fat in the development of insulin resistance and differences in SCD activity between subcutaneous and visceral adipose tissue may be important in this context.

In summary, we have shown that the adipose tissue desaturation indexes (fatty acid ratios) of 16:1/16:0 and 18:1/18:0 reflected *SCD* expression in adipose tissue. In contrast, desaturation indexes for D5D and D6D were not related to their respective gene expression levels. A high SCD desaturation index (18:1/18:0) in adipose tissue increased the risk of being insulin resistant, even after adjusting for waist and plasma triacylglycerol; this index also contributed to a predictive model for insulin resistance. Collectively, these results suggest that derangements in adipose tissue SCD activity might reflect disturbed adipose tissue metabolism, which is closely coupled to the development of insulin resistance.

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Duality of interest The authors declare that there is no duality of interest associated with this manuscript.

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