Knockdown of a disintegrin A metalloprotease 12 (ADAM12) during adipogenesis reduces cell numbers, delays differentiation, and increases lipid accumulation in 3T3-L1 cells

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Mouse models have shown that a disintegrin A metalloprotease 12 (ADAM12) is implicated during adipogenesis; the molecular pathways are not well understood. Stealth RNA interference was used to knock down ADAM12 in 3T3-L1 cells. Using gene profiling and metabolic enzymatic markers, we have identified signaling pathways ADAM12 impacts upon during proliferation, differentiation, and maturation of adipocytes. ADAM12 reduced cell numbers in proliferating preadipocytes, delayed differentiation of preadipocytes to adipocytes, and increased lipid accumulation in mature adipocytes. The pathway most affected by ADAM12 knockdown was regulation of insulin-like growth factor (IGF) activity by insulin-like growth factor binding proteins (IGFBPs); ADAM12 is known to cleave IGFBP3 and IGFBP5. The IGF/mTOR signaling pathway was down-regulated, supporting a role for ADAM12 in the IGFBP/IGF/mTOR-growth pathway. PPARγ signaling was also down-regulated by ADAM12 knockdown. Gene ontology (GO) analysis revealed that the extracellular matrix was the cellular compartment most impacted. Filtering for matrisome genes, connective tissue growth factor (CTGF) was up-regulated. CTGF and IGFBP3 can interact with PPARγ to hinder its regulation. Increased expression of these molecules could have influenced PPARγ signaling reducing differentiation and an imbalance of lipids. We believe ADAM12 regulates cell proliferation of preadipocytes through IGFBP/IGF/mTOR signaling and delays differentiation through altered PPAR signaling to cause an imbalance of lipids within mature adipocytes.

INTRODUCTION

A disintegrin A metalloprotease 12 (ADAM12) belongs to the metzincin family of proteases characterized by a highly conserved motif of three histidines that bind zinc at the catalytic domain and conserved methionine residue (Sternlicht and Werb, 2001). ADAM12 has the following domains: a signal peptide, propeptide, metalloprotease, disintegrin, cysteine-rich region, epidermal proteins; MNE, mean normalized gene expression; mTOR, mechanistic target of rapamycin; PPARγ, peroxisome proliferator-activated receptor gamma; RNAi, RNA interference.

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growth factor (EGF)-like repeat, transmembrane, and cytoplasmic tail (Duffy et al., 2003). A conserved site of the prodomain, named the cysteine-switch region, coordinates the active zinc site to inhibit catalysis resulting in the protease to remain as azymogen, known as the cysteine-switch mechanism (Loechel et al., 1998; Streuli, 1999; Page-McCaw et al., 2007). Metalloprotease catalysis is dependent on removal of the prodomain by instability of the cysteine switch to expose the active zinc site to enable cleavage of substrates (Loechel et al., 1998). The disintegrin domain and cysteine-rich region are also involved in cell–cell interactions. The disintegrin domain binds integrins and the cysteine-rich region supports syndecan-mediated cell adhesion (Schlondorf and Blobel, 1999; Zollikowska, 1999; Eto et al., 2000; Iba et al., 2000). There are two splice variants of ADAM12, referred to as the long transmembrane form, ADAM12-L, and the short soluble secreted form, ADAM12-S. ADAM12-S has all the extracellular domains of ADAM12-L but lacks the transmembrane domain and cytoplasmic tail; instead, the EGF-like repeat is followed by a unique 33 amino acid sequence. Unlike the transmembrane-bound long form ADAM12-L, ADAM12-S is secreted in the extracellular matrix and detected in serum and urine (Wewer et al., 2006).

ADAM12 is expressed by adipocytes during adipogenesis (Kawaguchi et al., 2002, 2003; Kurisaki et al., 2003; Masaki et al., 2005). Intra- and extracellular roles for ADAM12 during adipogenesis in vitro have been proposed: 1) reorganize the actin cytoskeleton when flat preadipocytes round up, in preparation to lipid-fill into mature adipocytes (Kawaguchi et al., 2003); and 2) to reorganize the fibronectin-rich extracellular matrix, a crucial step in adipogenic differentiation (Kawaguchi et al., 2003). ADAM12 gene knockout mice and transgenic mice overexpressing ADAM12 demonstrate a role for ADAM12 during adipogenesis. Mice overexpressing ADAM12-S and ADAM12-L showed an accumulation of adipocytes within striated skeletal muscle of the abdominal wall, hind limb, and diaphragm indicative of increased adipogenesis (Kawaguchi et al., 2002). Adipocytes in ADAM12-L-overexpressing mice were not as abundant within skeletal muscle when compared with mice overexpressing ADAM12-S (Kawaguchi et al., 2002). ADAM12-S mice lacking the pro- and metalloprotease domain did not display enhanced adipogenesis, suggesting that the catalytic metalloprotease domain is crucial for adipogenesis. PPARy, the master regulator of adipogenesis, was also found to be up-regulated in developing adipocytes found within connective tissue of skeletal muscle in close proximity to blood vessels of mice overexpressing ADAM12 (Kawaguchi et al., 2002). This suggests ADAM12 is involved in the development of adipocytes that originate from mesenchymal progenitor or preadipocytes within the perivascular space of connective tissue (Kawaguchi et al., 2002).

ADAM12 gene knockout mice display a significant reduction in the interscapular brown adipose tissue (BAT) and a mild skeletal muscle defect in the neck and interscapular muscles (Kurisaki et al., 2003). HB-EGF (a substrate of ADAM12) ectodomain shedding was also reduced in ADAM12–deficient mice (Kurisaki et al., 2003). A study by Masaki et al. (2005) found ADAM12 knockout mice were resistant to obesity induced by a high-fat diet, due to a reduced ability of adipocytes to proliferate. HB-EGF was involved in this phenotype but rather inhibited adipogenesis, questioning a role for ADAM12 ectodomain sheddase activity in promoting adipogenesis as suggested by Kurisaki et al. (2003). Another substrate of ADAM12, IGFBP-3 is thought to contribute to IGF-I–dependent proliferation during adipogenesis (Masaki et al., 2005). This is thought to induce proliferation through ADAM12 cleavage of IGFBP-3 to make IGF-I available to activate IGF-I receptor (Shi et al., 2000).

ADAM12 has shown that it is an important regulator of fat development. However, the exact role ADAM12 has during adipocyte proliferation and differentiation is still unclear. This investigation aims to determine the molecular pathways ADAM12 influences during proliferation and differentiation of adipocytes. We have used Stealth RNA interference (RNAi) to knock down ADAM12, and gene profiling in an in vitro murine fat development model to determine the signaling pathways ADAM12 regulates during adipogenesis.

RESULTS

ADAM12 gene knockdown reduced cell numbers and affected differentiation and mature adipocyte development

Phase images demonstrate the morphological change during adipocyte differentiation from flattened preadipocytes (day 6) to mature lipid-filled adipocytes (day 9–day 13; Figure 1). Cell numbers (DNA [µg/ml]) were reduced in ADAM12 RNAi cells for day 3 (control: 5.315 µg/ml; ADAM12 RNAi: 4.731 µg/ml), day 6 (control: 9.426 µg/ml; ADAM12 RNAi: 8.003 µg/ml), and day 9 (control: 6.704 µg/ml; ADAM12 RNAi: 5.207 µg/ml); REML treatment effect, p < 0.05; Figure 1, Day 6, and Figure 2A). Concentration of DNA (µg/ml) peaked on day 6 for control and ADAM12 RNAi (Figure 2A). These results suggest that ADAM12 gene knockdown reduced cell numbers in 3T3-L1 cells. ADAM12 RNAi delayed the rate at which preadipocytes rounded up to form adipocytes (Figure 1). The proportion of preadipocytes to adipocytes differed between ADAM12 RNAi and control cells. On day 9, ADAM12 RNAi–treated cells had a higher proportion of preadipocytes to adipocytes compared with the control (ADAM12 RNAi preadipocytes 55.64%; adipocytes 44.36%; control preadipocytes 20.36%; adipocytes 79.64%; t test, p < 0.01); refer to Figure 2B. Cell size of adipocytes was also found to be different between ADAM12 RNAi and control. On days 9 and 13 the mean diameter of adipocytes was not found to be different between ADAM12 RNAi (29.4 µm)-treated cells and the control (27.6 µm; Figure 2C). The diameter of lipids with one, two, or three droplets was measured in control and ADAM12 RNAi adipocytes. The mean diameter of lipid droplets contained within mature adipocytes was found to be different between the control and ADAM12 RNAi cells. On day 9, adipocytes with two lipid droplets (t test, p < 0.01) were found to be smaller in ADAM12 RNAi cells compared with control cells (control: one droplet, 8.24 µm; two droplets, 7.73 µm; three droplets, 7.14 µm vs. ADAM12 RNAi: one droplet, 6.10 µm; two droplets, 4.84 µm; three droplets, 5.49 µm); see Figure 2D. However, on day 13, lipids containing one (t test, p < 0.01) and three (t test, p < 0.05) droplets were found to be larger in ADAM12 RNAi (control: one droplet, 4.16 µm; two droplets, 4.79 µm; three droplets, 6.84 µm vs. ADAM12 RNAi: one droplet, 11.52 µm; two droplets, 7.61 µm; three droplets, 9.66 µm); refer to Figure 2D. These findings suggest ADAM12 is involved in differentiation of fibroblastic-like preadipocytes into round adipocytes and development of mature lipid-filled adipocytes. To rule out the possibility that increased apoptosis was driving this effect, we evaluated the expression of Bcl2 and Bax, two key regulators of apoptosis. At the early stages of ADAM12 knockdown (day 3), expression of Bcl2 transcript was increased; there was no difference compared with controls at days 6 and 9. At no stage was the expression of Bax affected by inhibition of ADAM12 expression.

ADAM12 gene knockdown affected enzymatic markers of lipogenesis

G3PDH (glycerol-3-phosphate dehydrogenase) enzyme activity was used as an early marker of adipocyte differentiation in response to ADAM12 gene knockdown. Its activity is correlated to the early stages of glucose metabolism (lipogenesis) during adipogenesis.
G3PDH activity was found to be different between ADAM12 RNAi and control cells for day 9, day 12, and day 15 (REML treatment effect, \( p < 0.05 \); refer to Figure 3A). The effect of ADAM12 knockdown on fatty-acid synthesis during latter stages of adipogenesis was assayed by measuring fatty-acid synthase (FAS) activity. This relates to lipid filling (triglyceride anabolism) in maturing adipocytes. FAS activity (nmol of NADH oxidized by FAS per minute per microgram of DNA) was increased in ADAM12 RNAi compared with control on day 9 (t test, \( p < 0.05 \)); see Figure 3B. These results, supported by an increase in the size of lipid droplets at day 13 (Figure 2), suggests there was increased lipogenesis in ADAM12 RNAi cells during stages where adipocytes were lipid-filling.

**Gene profiling**

**Quality control and ADAM12 gene knockdown.** Multidimensional scaling analysis of the filtered and normalized microarray data showed that time was the biggest factor influencing the data, with day 3 (T3), day 6 (T6), and day 9 (T9) samples all showing separation in the first principal component (Figure 4A). A control sample at T3 and ADAM12 RNAi sample at T9 were outliers from their respective groups in the second principal component; however, they did cluster with their corresponding time points in the first principal component (Figure 4A).

With the outlying samples removed, the remaining samples cluster tightly within their time points in the first two principal components (Figure 4B). Clear separation between treatment groups (control and ADAM12 RNAi) can be seen in the fourth principal component, with the outliers (T3 and T9) removed (Figure 4C). Box plots of ADAM12 gene expression show that its expression is reduced in ADAM12 RNAi cells compared with control (Figure 5A), although the knockdown effect did diminish over time, with little difference in expression observed at T9.

**Differentially expressed gene.** T3 showed the highest number of significantly differentially expressed (DE) genes at false discovery rate (FDR) < 0.05 (T3 DE Total: 2508, UP: 1397, DOWN: 1111; Figure 5, B and C). At T6, as the cells differentiated and the magnitude of the gene knockdown diminished, the number of DE genes was reduced (T6 DE total: 1090; UP: 569; DOWN: 521). A further reduction in the number of DE genes was evident at T9 (T9 DE Total: 623; UP: 366; DOWN: 257). Although ADAM12 gene expression returned to control levels in T9, substantial differences are still evident at T9, both at the transcript level and at the protein level, based on the phenotype observed in vitro. We believe that these differences are attributed to changes occurring early in the time course when cells are proliferating and differentiating; in particular, changes in the extracellular matrix which are crucial for adipogenesis. A Venn diagram of the DE genes at each time point shows the greatest overlap between the DE genes at T3 and T6 (308 genes), followed by T6 and T9 (137 genes), then T3 and T9 (92 genes; Figure 5C). We also identified a set of genes that were significantly differentially expressed between control and ADAM12 RNAi cells across all three time points (T3, T6, and T9), irrespective of ADAM12 gene expression at T9. We have named this gene set "ALL." The number of DE genes in the ALL gene list was 1152. Gene lists for DE genes for each time comparison can be found in Supplemental File 1. Heatmaps of the expression levels of the top DE genes for each comparison (FDR < 0.05 and logFC > 2) highlight the differences in gene expression between ADAM12 RNAi and control samples, as well as the changes over time due to the diminishing effect of the knockdown (Figure 6). The samples generally cluster both by time point and treatment, for all comparisons. For the ALL comparison, the difference between the ADAM12 RNAi and control is obvious at all three time points; however, the overall level expression for many of the genes does tend to change substantially over time (Figure 6A). For the comparisons at individual time points, as expected, the difference between treatment and control is most apparent at the time point tested, and tends to be less visible at the other time points (Figure 6, B–D). This is most striking for the genes found to be DE at T3 where the samples fail to cluster based on ADAM12 RNAi treatment by T9 (Figure 6B). This indicates that these are likely to be the genes most directly impacted by the ADAM12 knockdown.
Gene ontology analysis. Gene ontology (GO) analysis on the DE genes for each comparison—T3, T6, T9 and ALL—showed that ADAM12 appears to be impacting the extracellular matrix (ECM). The top 10 GO terms for each comparison can be seen in Figure 7. For the ALL (Figure 7A), T6 (Figure 7C), and T9 (Figure 7D) comparisons, at least 4 of the top 10 GO terms were related to the ECM. At T3 (Figure 7B), the top GO terms were predominantly associated with immune function/response, with only one GO term linked to the ECM. Refer to Supplemental File 2 for a full list of GO terms impacted by ADAM12 knockdown for ALL, T3, T6, and T9.

DE matrisome genes. From the GO analysis we established that the effects of ADAM12 gene knockdown were predominantly impacting the ECM. We then wanted to determine what genes were involved in causing these changes. Using the DE gene lists ALL, T3, T6, and T9, we filtered these genes against a list of known core-matrisome proteins (Naba et al. 2012); this includes a total of 274 genes (43 collagens, 36 proteoglycans, and 195 glycoproteins). Table 1 outlines the top 10 core-matrisome genes differentially expressed (top five up-regulated and five down-regulated) with knockdown of ADAM12; refer to Supplemental File 3 for an extensive list. The total number of core-matrisome genes differentially

FIGURE 2: Effect of ADAM12 knockdown on cell numbers, morphology, and lipid accumulation in mature 3T3-L1 adipocytes. (A) Cell numbers were reduced in ADAM12 RNAi cells (DNA [µg/ml]). (B) Proportion of preadipocytes to adipocytes on day 9 posttransfection was increased in ADAM12 RNAi cells suggesting differentiation was delayed. (C) Cell size (in diameter [µm]) of adipocytes was reduced in ADAM12 RNAi cells. (D) Size of lipid droplets (in diameter [µm]) in mature adipocytes that contain either one droplet, two droplets, or three droplets of lipid on day 9 and day 13 were measured. (E) Size of lipid droplets were increased on day 13 in ADAM12 RNAi cells. Expression of Bcl2 was up-regulated in ADAM12 RNAi cells at day 3 but was not changed at days 6 or 9. (F) The expression of Bax was not affected by inhibition of ADAM12 expression. *, p < 0.05; **, p < 0.01 (n = 3 for control and ADAM12 RNAi at each time point)
Enzymatic markers of differentiation/lipogenesis are increased in ADAM12 RNAi cells. Enzyme activity of glycerol-3-phosphate dehydrogenase (G3PDH; nmol NADH oxidized per min/µg DNA) and enzyme activity of fatty-acid synthase (FAS; nmol NADH oxidized per min/µg DNA) in 3T3-L1 cell lysates from ADAM12 RNAi and control cells. *, p < 0.05 (n = 3 for control and ADAM12 RNAi at each time point).

Ctgf (connective tissue growth factor) was the most highly up-regulated matrisome gene for ALL (1.08-fold), T3 (2.37-fold) and T6 (1.20-fold). Validation by qRT-PCR found Ctgf to be up-regulated at T2 and T3 (p < 0.05). Collagens are important structural ECM proteins fundamental to support the dramatic morphological changes in the adipocytes during differentiation. Proteins associated with collagen binding and synthesis were also found to be the greatest up-regulated core-matrisome genes; these included Dcn (decorin; ALL, 0.87-fold), Lum (lumican; T6, 0.93), Fbn1 (fibrillin 1; ALL, 0.94-fold), and Fbln7 (fibulin 7; ALL, 0.84-fold; T9, 1.39-fold).

In light of these collagen-associated proteins being up-regulated, a number of collagen isoforms were found to be the most down-regulated matrisome genes. These included Col5a3 (ALL), Col5a2, Col4a5, Col11a1 (T3), and Col5a3, Col4a2, Col6a3 (T6). In addition, Lama5 (laminin α5; ALL, T6) and Lamb3 (laminin β3; T9) was also one of the most down-regulated core-matrisome genes. Validation by qRT-PCR found Fbn1 (see Figure 10D later in the paper) to be up-regulated at T2, T3, and T6 (REML treatment effect, p < 0.05), Col6a3 (see Figure 10J later in the paper) down-regulated at T2, T3, T6, and T9 (REML treatment effect, p < 0.05), and Lum (10I) to be up-regulated at T6 (p < 0.05).

In addition to core-matrisome proteins, we were also interested in proteins associated with the matrisome, such as cytokines, chemokines, growth factors, mucins, galectins, plexins, serine proteases, matrix metalloproteases, and other ECM-associated proteins. Using a list of all 619 matrisome genes from the Broad Institute Molecular Signatures Database (MSigDB) curated (C2) set, which includes 177 core-matrisome and 444 matrisome-associated proteins, we found 203 DE genes for T3, 158 for T6, and 142 for T9. Out of these DE genes, 36 were consistently different across all time points (T3, T6, and T9), 41 genes overlap between T3 and T6, 39 between T6 and T9, and 20 between T3 and T9; refer to Figure 8. A summary of the 20 top-ranked genes (FDR < 0.05) is presented in Figure 8 for all comparisons, showing most matrisome genes are up-regulated. MMP3 was in the 20 top-ranked genes for all comparisons. Mfab5 and Fbn1 were in the top ranked for ALL, T6, and T9, and Ctgf was top ranked for T3 and T6. The full list of DE matrisome genes in ADAM12 knockdown cells for each comparison can be found in Supplemental File 4.

Pathway analysis. To determine which pathways were affected in ADAM12 RNAi cells, we performed gene set testing of all the canonical pathways from the MSigDB C2 set. The top 10 canonical pathways for the ALL comparison and the six top-ranked sets for T3, T6, and T9 comparisons are summarized in Table 2; refer to Supplemental File 5 for the full lists. Regulation of IGF activity by IGFBPs was the top-ranked pathway for the ALL comparison; ADAM12 is known to cleave IGFBP3 and IGFBP5 (Loechel et al., 2000; Shi et al., 2000). The same pathway was ranked second at T6 and was also the...
FIGURE 5: Summary of differentially expressed genes in ADAM12 RNAi–treated adipocytes. ADAM12 gene knockdown in ADAM12 RNAi cells compared with control for each time point (T3: day 3 posttransfection; T6: day 6 posttransfection; T9: day 9 posttransfection). (A) Gene knockdown of ADAM12 diminishes with time. (B) Summary of differentially expressed genes up- and down-regulated in ADAM12 RNAi vs. control cells over time (T3, T6, and T9). The biggest impact of ADAM12 gene knockdown on the number of differentially expressed genes was at T3, followed by T6 and T9, respectively. (C) Venn diagram detailing the number of genes differentially expressed in ADAM12 RNAi–treated 3T3-L1 cells vs. control cells, for genes changing at T3, T6, and T9. Values in overlap represent the number of genes found to be different in more than one comparison. T3 and T6 showed the greatest number of genes showing overlap of differentially expressed genes in ADAM12 RNAi cells. n = 3 for control and ADAM12 RNAi at each time point.

top-ranked pathway at T9, suggesting the effects of ADAM12 gene knockdown were maintained even though there was little difference in the gene expression of ADAM12 at T9. Gene expression of Igfbp3 (T3, 0.98-fold; ALL, 0.53-fold) and Igfbp5 (T6, 0.36-fold; ALL, 0.53-fold) was increased in ADAM12 RNAi cells. Validation by qRT-PCR confirmed the gene expression of Igfbp3 (see Figure 10A later in the paper) to be up-regulated at T3 and T6 and Igfbp5 (see Figure 10B later in the paper) up-regulated at T6 (p < 0.05).

The metabolic pathways found to be differentially regulated that may contribute to altered G3PDH and FAS activity were PPAR signaling, mitochondrial fatty-acid beta oxidation, glucose metabolism, and fatty-acid metabolism. These pathways were all

FIGURE 6: Hierarchical clustering of the top differentially regulated genes for each comparison FDR <0.05 and fold change > 2. Genes consistently changing at all time points (A) ALL (T3, T6, and T9), (B) T3, (C) T6, and (D) T9 (T3: day 3 posttransfection; T6: day 6 posttransfection; T9: day 9 posttransfection). n = 3 for control and ADAM12 RNAi at each time point.
down-regulated in ADAM12 RNAi cells suggesting that ADAM12 may have a role to play in these processes. Several pathways related to the ECM were up-regulated in ADAM12 RNAi cells at multiple time points: degradation of the extracellular matrix; keratan sulfate degradation for the ALL comparison; and keratan sulfate degradation, keratan sulfate keratin metabolism, and extracellular matrix organization at T9.

The GO analysis at T3 highlighted GO terms for “immune response.” Three of the top six pathways at T3 were related to an immune response: interferon alpha beta signaling, interferon gamma signaling, and interferon signaling. Other immune-related pathways were chemokine receptors bind chemokines (ALL, T9), graft versus host disease (T6), and allograft rejection (T6).

Based on the results of our analysis, it appears that ADAM12 is either directly or indirectly influencing numerous pathways during adipogenesis. The main pathway impacted by ADAM12 RNAi in adipocytes was regulation of IGF activity by IGFBPs (Figure 9A). This pathway was found to be up-regulated, and qRT-PCR confirmed gene expression of Igfbp3 (T3, T6) and Igfbp5 (T6) were elevated in ADAM12RNAi cells. The mechanism behind this is not apparent from this study, but the absence of cleavage of IGFBP3 and IGFBP5 by ADAM12 knockdown could be driving a positive feedback loop to increase the molecules responsible for activating the regulation of IGFBPs (to release IGF if it is still being bound). This is supported by down-regulation of the IGF/mTOR pathway (p < 0.05; Figure 9F) and the mTOR pathway (p = 0.06; Figure 9I) as IGF/mTOR signaling is a major growth pathway, which could explain the reduced cell numbers found in ADAM12 RNAi cells. Up-regulation of IGF/mTOR has previously been implicated in positive regulation of PPAR. The PPAR signaling pathway (p < 0.001; Figure 9B), Pparg (Figure 10E; REML treatment effect, p < 0.05), and Cebpβ (Figure 10F; T3, p < 0.05) were also found to be down-regulated. In addition, IGFBP3 can regulate the transcription of adiponectin, an adipocytokine important for fatty-acid oxidation through activation of AMPK (adenosine monophosphate-activated protein kinase). The adipocytokine signaling pathway (p < 0.05; Figure 9G), mitochondrial fatty-acid oxidation (p < 0.001; Figure 9D), and AMPK-stimulated fatty-acid oxidation pathways (p = 0.051; Figure 9H) were down-regulated suggesting a role for ADAM12 in their regulation. The mean normalized gene expression of two adipocytokines Adipoq (Figure 10G) and Cd36 (Figure 10H) showed these genes were down-regulated at T6 and T3 and T6 and T9, respectively (p < 0.05). We propose that
| Gene description                        | GenBank accession number | Log fold change |
|----------------------------------------|--------------------------|-----------------|
| ALL                                    |                          |                 |
| Connective tissue growth factor (Ctgf) | NM_010217                | 1.08            |
| Microfibrillar-associated protein 5 (Mfap5) | NM_015776             | 1.03            |
| Fibrillin 1 (Fbn1)                     | NM_007993                | 0.94            |
| Decorin (Dcn)                          | NM_007833                | 0.87            |
| Fibulin 7 (Fbln7)                      | NM_024237                | 0.84            |
| Collagen, type V, α3 (Col5a3)          | NM_016919                | −0.60           |
| Laminin, α5 (Lama5)                    | NM_001081171             | −0.50           |
| SPARC-like 1 (Sparcl1)                 | NM_010097                | −0.50           |
| Nephrocan (Nepn)                       | NM_025684                | −0.43           |
| Cysteine-rich with EGF-like domains 1 (Creld1) | NM_133930            | −0.40           |
|                                         |                          |                 |
| T3                                     |                          |                 |
| Connective tissue growth factor (Ctgf) | NM_010217                | 2.37            |
| Von Willebrand factor homologue (Vwf)  | NM_011708                | 1.80            |
| Bone γ-carboxyglutamate protein 2 (Bglap2) | NM_001032298        | 1.44            |
| Microfibrillar-associated protein 5 (Mfap5) | NM_015776            | 1.23            |
| Dermatopontin (Dpt)                    | NM_019759                | 1.20            |
| Collagen, type V, α2 (Col5a2)          | NM_007737                | −1.28           |
| Transforming growth factor, β induced (Tgfβi) | NM_009369           | −1.24           |
| SPARC-like 1 (Sparcl1)                 | NM_010097                | −0.95           |
| Collagen, type IV, α5 (Col4a5)         | NM_001163155             | −0.91           |
| Collagen, type XI, α1 (Col11a1)        | NM_007729                | −0.90           |
|                                         |                          |                 |
| T6                                     |                          |                 |
| Connective tissue growth factor (Ctgf) | NM_010217                | 1.20            |
| Osteoglycin (Ogn)                      | NM_008760                | 1.03            |
| Microfibrillar-associated protein 5 (Mfap5) | NM_015776            | 1.02            |
| Keratocan (Kera)                       | NM_008438                | 0.94            |
| Lumican (Lum)                          | NM_008524                | 0.93            |
| Collagen, type V, α3 (Col5a3)          | NM_016919                | −0.89           |
| Laminin, α5 (Lama5)                    | NM_001081171             | −0.75           |
| Nephrocan (Nepn)                       | NM_025684                | −0.69           |
| Collagen, type IV, α2 (Col4a2)         | NM_009932                | −0.60           |
| Collagen, type VI, α3 (Col6a3)         | NM_133930                | −0.52           |
|                                         |                          |                 |
| T9                                     |                          |                 |
| Fibulin 7 (Fbln7)                      | NM_024237                | 1.39            |
| Matrix Gla protein (Mgp)               | NM_008597                | 1.00            |
| Keratocan (Kera)                       | NM_008438                | 0.98            |
| Osteoglycin (Ogn)                      | NM_008760                | 0.96            |
| AE binding protein 1 (Aebp1)           | NM_001291857             | 0.94            |
| Laminin, β3 (Lamb3)                    | NM_008484                | −0.77           |
| Nephrocan (Nepn)                       | NM_025684                | −0.43           |

T3: day 3 in culture posttransfection; T6: day 6 in culture posttransfection; T9: day 9 in culture posttransfection; ALL: across all three time points T3, T6, and T9. n = 3 for control and ADAM12 RNAi at each time point. The top five up-regulated and down-regulated genes are presented (FDR < 0.05 and |FC| > 2). Magnitude of regulation is based on fold change.

**TABLE 1:** Core-matrisome genes (Naba et al., 2012) differentially expressed in ADAM12 RNAi cells across all time points (ALL), T3, T6, and T9.
these pathways interact during adipogenesis as a direct result of the absence/reduction of cleavage of IGFBP3 and IGFBP5 by ADAM12.

**DISCUSSION**

Previous studies on ADAM12 have shown it is involved in adipogenesis (Kawaguchi et al., 2002, 2003; Kurisaki et al., 2003; Masaki et al., 2005). We wanted to use an established model of adipogenesis in vitro to investigate this further. Using metabolic markers of adipocyte differentiation and gene profiling we were able to more clearly define pathways involved in regulation of adipogenesis and identify novel pathways for ADAM12 during adipogenesis. 3T3-L1 cells proliferate as a flat-fibroblastic–appearing preadipocyte. Following clonal expansion, the cells arrest and differentiate into a round adipocyte. Following the early stage of differentiation, cells begin lipid-filling to become mature adipocytes. The primary role of this mature adipocyte is to store energy and break down fatty acids to provide ATP when available systemic sources become low. During the course of development the ECM serves as a structure to support the large changes in cell morphology and to harvest and sequester ligands important for signaling proliferation and differentiation.

**TABLE 2:** Top signaling pathways differentially regulated in ADAM12 RNAi cells across all comparisons (ALL), T3, T6, and T9.

| Signaling pathways                                                                 | No. of genes | Direction | p value    |
|-----------------------------------------------------------------------------------|--------------|-----------|------------|
| Regulation of insulin-like growth factor (IGF) activity by insulin-like growth factor binding proteins (IGFBPs) | 26           | UP        | 2.90E-07   |
| PPAR signaling                                                                    | 51           | DOWN     | 1.24E-06   |
| Branched chain amino acid catabolism                                               | 17           | DOWN     | 1.26E-06   |
| Valine leucine and isoleucine degradation                                          | 45           | DOWN     | 1.32E-06   |
| Chemokine receptors bind chemokines                                                | 23           | UP        | 1.94E-06   |
| Degradation of the extracellular matrix                                            | 34           | UP        | 3.17E-06   |
| Keratan sulfate degradation                                                        | 12           | UP        | 8.90E-06   |
| Mitochondrial fatty-acid beta oxidation                                            | 15           | DOWN     | 9.07E-06   |
| Glucose metabolism                                                                | 54           | DOWN     | 6.05E-05   |
| Fatty-acid metabolism                                                             | 37           | DOWN     | 6.54E-05   |
| **T3**                                                                            |              |           |            |
| Interferon alpha beta signaling                                                   | 82           | DOWN     | 2.53E-11   |
| Interferon gamma signaling                                                        | 70           | DOWN     | 4.57E-10   |
| Cholesterol biosynthesis                                                          | 16           | UP        | 5.87E-08   |
| Endosomal vacuolar pathway                                                         | 20           | DOWN     | 1.32E-06   |
| Interferon signaling                                                              | 168          | DOWN     | 6.75E-06   |
| VITCB pathway                                                                     | 18           | DOWN     | 1.44E-05   |
| **T6**                                                                            |              |           |            |
| PPAR signaling pathway                                                            | 51           | DOWN     | 3.17E-08   |
| Valine leucine and isoleucine degradation                                          | 45           | DOWN     | 1.13E-06   |
| Graft vs. host disease                                                             | 28           | UP        | 1.18E-06   |
| Allograft rejection                                                               | 29           | UP        | 1.59E-06   |
| Branched chain amino acid catabolism                                               | 17           | DOWN     | 3.13E-06   |
| CTL pathway                                                                       | 27           | UP        | 4.36E-06   |
| **T9**                                                                            |              |           |            |
| Regulation of insulin-like growth factor (IGF) activity by insulin-like growth factor binding proteins (IGFBPs) | 26           | UP        | 6.76E-08   |
| Keratan sulfate degradation                                                        | 12           | UP        | 4.65E-07   |
| Glycosaminoglycan metabolism                                                      | 82           | UP        | 3.66E-06   |
| Keratan sulfate keratin metabolism                                                | 24           | UP        | 4.22E-06   |
| Extracellular matrix organization                                                  | 74           | UP        | 5.16E-06   |
| Chemokine receptors and chemokines                                                | 23           | UP        | 6.09E-06   |
| T3: day 3 in culture posttransfection; T6: day 6 in culture posttransfection; T9: day 9 in culture posttransfection; ALL: across all three time points T3, T6, and T9. n = 3 for control and ADAM12 RNAi at each time point.

TABLE 2: Top signaling pathways differentially regulated in ADAM12 RNAi cells across all comparisons (ALL), T3, T6, and T9.
ADAM12 is an active protease in the ECM; we have identified pathways ADAM12 influences in the ECM to cause changes in proliferation and differentiation during the course of adipocyte maturation. GO analysis revealed the ECM as being a major compartment of the cell where ADAM12 was impacting. Using genes consistently changing across all time points (ALL gene list), we found the pathway most significantly affected by ADAM12 gene knockdown was regulation of IGF activity by IGFBPs. In vitro studies have shown ADAM12-S binds and cleaves IGFBP3 and IGFBP5 (Loechel et al., 2000; Shi et al., 2000). The main function of IGFBPs is to bind IGF-1 and IGF-2, transport them extracellularly, and protect them from degradation (increasing their half-life; Ruan and Lai, 2010). Once the IGFs are released from IGFBP, they can bind to their IGF receptors (IGFr) and induce IGF-IGFr mediated signaling within the cell, such as induction of cell proliferation (Rajkumar et al., 1999; Firth and Baxter, 2002). Although IGFs are bound to IGFBPs, they can inhibit cell growth by reducing the bioavailability of IGFs to their receptors to regulate cellular activity. Activation of this pathway is consistent with reduced cell numbers in ADAM12 RNAi cells on days 3, 6, and 9. It is plausible knockdown of ADAM12 reduced cleavage of IGFBP3 and IGFBP5 to inhibit release and bioavailability of IGF in the ECM, impeding proliferation to result in reduced cell numbers. In turn, this potentially initiates a feedback loop to increase expression of IGFBPs and other molecules in the pathway responsible for cleavage of IGFBPs to cause it to be up-regulated. In addition, we found downstream signaling pathways of IGF to be affected; these included down-regulation of the IGF/mTOR signaling pathway. IGF/IGFR induces growth through the PI(3)K/Akt/mTOR signaling axis (Bodine et al., 2001; Rommel et al., 2001; Floyd et al., 2007; Laplante and Sabatini, 2012). Suppression of the mTOR signaling pathway suggests that IGF ligand binding to IGFR was affected. This data is in support of previous findings where adipocytes isolated from inguinal white adipose tissue (WAT; a fat depot of high proliferative capacity) of ADAM12−/− mice fed a high-fat diet had reduced cell numbers compared with wild-type mice (Masaki et al., 2005). Collectively these data suggest a role for ADAM12 in proliferation during adipogenesis. Based on these results, a working model of how ADAM12 stimulates proliferation through the IGF/mTOR signaling pathway is provided (Figure 11). In the absence of ADAM12, cleavage of IGFBPs is hindered, in particular its substrates IGFBP3 and IGFBP5, inhibiting release of IGF and reducing its bioavailability to IGFR. This impacts downstream signaling of the mTOR signaling pathway impeding proliferation of preadipocytes.

Three of the top five signaling pathways differentially regulated when preadipocytes were proliferating and knockdown of ADAM12 gene expression was the greatest (day 3) were related to IFN (interferon) signaling, interferon alpha beta signaling, interferon

FIGURE 8: The effect of ADAM12 gene knockdown on gene expression of matrisome genes. (A) Venn diagram detailing the number of matrisome genes (including 177 core-matrisome and 444 matrisome-associated genes) differentially expressed in ADAM12 RNAi-treated 3T3-L1 cells vs. control cells, for genes changing at T3, T6, and T9. Values in the overlap represent the number of genes found to be different in more than one comparison. T3 and T6 showed the greatest number of overlapping differentially expressed genes in ADAM12 RNAi cells. (B–E) Top-ranked matrisome genes (FDR <0.05) for ALL, T3, T6, and T9; bar plots reflect the magnitude of change expression between treated and control cells (log2-fold change). Mmp3 is top ranked for all comparisons. Core-matrisome genes Mfap5, Fbn1, and Ctgf remain as top ranked for ALL, T6, and T9 (Mfap5,Fbn1) and T3 and T6 (Ctgf). Mmp3: matrix metalloprotease 3; Mfab5: microfibrillar-associated protein 5; Fbn1: fibrillin 1; Ctgf: connective tissue growth factor. n = 3 for control and ADAM12 RNAi at each time point.

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gamma signaling, and interferon signaling. IFNs can act as negative regulators of proliferation by blocking the transition from G0/G1 into the S phase of the cell cycle (Clemens and McNurlan, 1985; Hertzog et al., 1994). IFNα (alpha), IFNβ (beta), and IFNγ (gamma) have been found to be potent inhibitors of cell proliferation (Clemens and McNurlan, 1985; Hertzog et al., 1994). All three IFN pathways were down-regulated in proliferating ADAM12 RNAi preadipocytes. It is not clear from this study whether suppression of IFN signaling is in response to impeded cell growth as a mechanism to maintain proliferation or if ADAM12 directly impacts IFN signaling by remodeling of the ECM or via direct interaction. This is of further interest as both ADAM12 and IFNs are modulated in tumor growth (Clemens and McNurlan, 1985; Hertzog et al., 1994; Kveiborg et al., 2008).

Following proliferation and growth arrest of preadipocytes, we investigated the effect of ADAM12 knockdown on enzymatic markers of differentiation. The activity of G3PDH was increased from day 6 to day 15 and FAS was elevated at day 9 in ADAM12 RNAi cells. We also measured when preadipocytes differentiated to round adipocytes, the size of mature lipid-filled adipocytes, and the size of large lipid droplets in mature adipocytes. We found on day 9 that the

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**FIGURE 9:** Barcode plots for a selection of growth signaling pathways differentially regulated in ADAM12 RNAi cells (ALL comparison across all time points T3, T6, and T9). (A) Regulation of insulin-like growth factor (IGF) activity by insulin-like growth binding proteins IGFBPs and (C) degradation of the extracellular matrix were up-regulated with ADAM12 gene knockdown. Pathways down-regulated which are potentially acting antagonistically or down-regulated in response to up-regulation of A were (B) PPAR signaling pathway, (D) mitochondrial fatty-acid beta oxidation, (E) glucose metabolism, (F) IGF/mTOR pathway, (G) adipocytokine signaling pathway, (H) activated AMPK (adenosine monophosphate-activated protein kinase) stimulated fatty-acid oxidation, and (I) mTOR pathway. n = 3 for control and ADAM12 RNAi at each time point.
FIGURE 10: Validation of microarray gene expression by quantitative real-time PCR (qRT-PCR). Mean normalized gene expression (MNE) of (A) Igfbp3, (B) Igfbp5, (C) Ctgf, (D) Fbn1, (E) Pparg, (F) Cebpβ, (G) Adipoq, (H) Cdf, (I) Lum, and (J) Col6a3 using Ppia as the housekeeping gene. Igfbp3: insulin-like growth factor binding protein 3; Igfbp5: insulin-like growth factor binding protein 5; Ctgf: connective tissue growth factor; Fbn1: fibrillin 1; Pparg: peroxisome proliferator-activated receptor gamma; Cebpβ: CCAAT/enhancer binding protein beta; Adipoq: adiponectin; Cdf: complement factor D (adipsin); Lum: lumican; Col6a3: collagen type VI alpha 3 chain; Ppia: peptidylprolyl isomerase A (cyclophilin A). Note: These data are from a trial independent to the microarray. *, p < 0.05; **, p < 0.01 (n = 3 for control and ADAM12 RNAi at each time point).
IGFBP3 cleavage in ADAM12 RNAi cells and increased expression, we observe from day 3 to day 9 during the fundamental stages of differentiation, that it is possible IGFBP3 could be impairing differentiation by hampering the RXRα/PPARγ interaction to reduce induction of PPARγ-regulated genes and therefore the PPARγ signaling pathway. Mice overexpressing ADAM12 found PPARγ was up-regulated in developing adipocytes found within connective tissue of skeletal muscle further supporting a role for ADAM12 in PPARγ signaling (Kawaguchi et al., 2003).

Similarly, connective tissue growth factor (CTGF) shows many parallels with IGFBP3, also reported to inhibit differentiation in 3T3-L1 cells (Tan et al., 2008). Ctgf was up-regulated in ADAM12 RNAi cells (ALL, T3, and T6); validation by qRT-PCR confirmed this at T2 and T3. CTGF inhibits adipocyte differentiation by targeting CCAAT/enhancer binding protein-β (C/EBPβ) to block PPARγ. Gene expression of Cebpβ and Pparg were down-regulated in ADAM12 RNAi cells suggesting PPARγ signaling was impacted. CTGF up-regulates tissue inhibitor of matrix metalloproteases 1 (TIMP-1; McLennan et al., 2004); TIMP-1 blocks cleavage of IGFBP3 by matrix metalloproteases (MMP1, MMP2, and MMP3; Fowlkes et al., 1994) inhibiting proteolysis of IGFBP3 by other MMPs. Mmp3 was up-regulated (ALL, T3, T6, and T9); however, Timp1 (ALL, T6, and T9), Timp2 (ALL, T6, and T9), and Timp3 (T6) also had increased gene expression, potentially induced by increased Ctgf which could hinder any compensatory cleavage of IGFBP3. The inverse relationship that Igfbp3 and Ctgf have with ADAM12 gene expression and their potential impact on PPARγ signaling is unknown but is of further interest.

Increased lipogenesis found in ADAM12 RNAi cells as observed by elevated G3PDH, FAS, and larger lipids in mature adipocytes suggests that lipogenesis is dominating over fatty-acid oxidation. We found the mitochondrial fatty-acid beta oxidation pathway (ALL gene list) to be down-regulated. Linked to this, adipocytokine signaling pathway and activated AMPK stimulates fatty-acid oxidation were also down-regulated (ALL gene list). As mentioned above, IGFBP3 can interfere with regulation of PPARγ-regulated genes; the adipocytokine adiponectin (Adipoq) is one of them (Zappala and Rechler, 2009). IGFBP3 can inhibit expression of Adipoq via interaction with PPARγ (Zappala and Rechler, 2009). Adiponectin is an energy sensing cytokine which stimulates AMPK to increase fatty-acid oxidation, reducing the triglyceride content of adipocytes in adipose tissue and skeletal muscle when energy is low. Reduced expression of adiponectin and another adipocytokine, Cfd (adipsin), is associated with hypertrophy of adipocytes in obesity and insulin resistance in obesity and type II diabetes (Rosen et al., 1989; Kadowaki and Yamauchi, 2005; Zappala and Rechler, 2009). The gene expression of Adipoq and Cfd was decreased in ADAM12 RNAi adipocytes (qRT-PCR). Other adipocytokines that regulate AMPK-stimulated fatty-acid oxidation that may have caused these pathways to be down-regulated are leptin and IL-6; however, these were not differentially regulated in ADAM12 RNAi cells. Further studies are required to determine what is driving increased lipogenesis and reduced signaling of fatty-acid oxidation pathways as a result of ADAM12 gene knockdown. We believe reduced PPARγ signaling due to increased expression of Igfbp3 and Ctgf and potentially reduced cleavage of IGFBP3 may be altering adipocytokine and downstream fatty-acid oxidation pathways. As a result, lipids accumulate in ADAM12 RNAi cells; a working model is provided in Figure 12.

Previous findings in ADAM12 knockout mice and mice overexpressing ADAM12 suggest ADAM12 promotes adipogenesis in vivo. However, in our study, we show that ADAM12 knockdown in vitro increases lipid accumulation. This result may not be representative in vivo due to other tissues able to secrete molecules such as adipocytokines which can then be made available to adipocytes. For example, adiponectin is also expressed by muscle (Krause et al., 2008), potentially making it available to bind to adiponectin receptors on adipocytes. This could counteract the impaired adipocytokine signaling we see in ADAM12 RNAi cells. We also believe that the effects of ADAM12 on adipogenesis in vivo are predominantly driven by the impact on proliferation through IGF/mTOR signaling as this was the top pathway affected in vitro as described above.

Final remarks
Mice overexpressing ADAM12 have increased adipocytes within skeletal muscle (Kawaguchi et al., 2002) and in the absence of ADAM12, mice are resistant to a high-fat diet (Masaki et al., 2005).
ADAM12 is important for signaling proliferation of preadipocytes, differentiation of flat-fibroblastic preadipocytes into round adipocytes, and for maintaining the balance of lipids within mature adipocytes. We postulate increased expression of \( \text{Igfbp3} \) and \( \text{Ctgf} \), both of which are known to inhibit expression of PPAR\( \gamma \), the master regulator of adipogenic differentiation genes. Knockdown of ADAM12 in vitro causes increased expression of \( \text{Igfbp3} \) and \( \text{Ctgf} \). The expression of WAT genes was unaltered (PPAR\( \gamma \), C/EBP\( \alpha \), AKT-1) suggesting ADAM12-S influences cellular plasticity of BAT but not WAT cells. The cellular pathways ADAM12S influences to cause reprogramming of embryonic fibroblasts into BAT cells are of interest and may be responsible for reduced interscapular BAT in ADAM12 knockout mice (Zhou et al., 2013).

In addition, ADAM12 is implicated in many cancers, including mammary, bladder, liver, lung, oral, stomach, colon, brain, and bone (Kveiborg et al., 2008). IGFBP/IGF/mTOR signaling by ADAM12 may also be driving tumor growth in these cancers. Pharmacological inhibitors of ADAM12 may prove beneficial in controlling adipocyte expansion in disorders such as obesity and metabolic disease.

**MATERIALS AND METHODS**

The cell line used for this study was a well-established murine preadipocyte cell line, 3T3-L1. Each well of a six-well plate was seeded with...
1.98 \times 10^4 cells and incubated overnight in DMEM plus 10% fetal bovine serum (FBS) in a humidified CO\textsubscript{2} incubator. Preadipocytes at 80% confluence were transfected using Lipofectamine 2000 (Invitrogen, Australia) with either 20 pmol (in Opti-MEM I Reduced Serum Media without serum or antibiotics) of ADAM12 Stealth RNAi (CCA ACU CCU GUG ACC UCC CAG AUU) or Stealth RNAi Negative Control Medium GC Duplex #2 (Invitrogen, Australia) as the control per manufacturers guidelines. Transfection efficiency (>95%) was determined using the BLOCK-TT Fluorescent Oligo (Invitrogen, Australia). After 6 h transfection, media was aspirated and replaced with Opti-MEM I Reduced Serum Media plus 10% (vol/vol) FBS. Fresh growth media was added to 3T3-L1 cells every second day. On day 3 cells were placed in differentiation media (DMEM and 10% [vol/vol] FBS, 0.5 mM IBMX, 1 mM dexamethasone, 10 µg/ml insulin, and 10 µg/ml biotin) until cells differentiated. 3T3-L1 adipocytes were then placed in postdifferentiation media on day 9 (DMEM and 10% [vol/vol] FBS plus 10 µg/ml insulin) to accelerate lipid-filling of adipocytes. 3T3-L1 cells were incubated in postdifferentiation media until development of mature adipocytes.

**Morphometrics on preadipocytes and adipocytes**

Morphometrics were conducted on phase contrast images (n = 3 for each treatment/time point) of 3T3-L1 preadipocytes and adipocytes using Leica Microsystems QWin image analysis software (Cambridge, UK), adapted from a previously described method (McDonough et al., 2009). Differentiation was measured by counting the number of preadipocytes (flattened fibroblastic-appearing cell) and adipocytes (rounded cell) in independent images. The proportion of preadipocytes to adipocytes was then calculated (pre-dipocytes/adipocytes). Mature adipocyte development (lipid filling) was determined by first measuring the diameter of adipocytes for each cell present in an independent image (n = 2 images). The diameter of lipid droplets contained within adipocytes was also measured for cells containing one, two, and three lipid droplets present in the image. Only adipocytes containing one, two, or three lipid droplets were measured due to the complexity of counting adipocytes containing more than three lipid droplets. Measurements were grouped according to the number of lipid droplets contained within the cell (one, two, and three lipid droplets).

**DNA quantitation to assay cell numbers**

Cell numbers were measured by the amount of DNA (µg/ml). Cells were lysed with 0.1 M PBS, 50 mM MES, 50 mM trizma base, 1 mM MgCl\textsubscript{2}, 10% [vol/vol] glycerol, and 0.2 mM dithiothreitol). Cells were collected using an 18-cm cell scraper and incubated on ice for 45 min. Lysates were then centrifuged at 10,000 \times g for 3 min at 4°C. Supernatants (15 µl for G3PDH activity and 45 µl for FAS activity) were added to reaction buffer (125 mM triethanolamine-HCl, pH 7.5, 2.5 mM EDTA, 0.125 mM β-mercaptoethanol, 0.5 mM NADH, and 1.1 mM dihydroxyacetone phosphate) for G3PDH activity. For FAS activity, supernatants were added to FAS reaction buffer (50 nM KH\textsubscript{2}PO\textsubscript{4}, 2.5 nM β-mercaptoethanol, 0.25 mM β-NADPH), and 0.1 mM malonyl coenzyme A and acetyl coenzyme A were added to each sample. Absorbance was measured kinetically at 340 nM (20 s) using Skanit Software 2.4.2 RE for Multiskan Spectrum (Thermo Scientific, Scoresby, Australia). The change in absorbance per minute was used in the formula sourced from Alhauud (2001) to determine enzyme activity (nmol/min/mg) for each sample.

**RNA purification and hybridization to microarrays**

Microarray analysis was conducted on total cellular RNA collected from cells transfected with Stealth ADAM12 RNAi (ADAM12 RNAi) and Stealth RNAi Negative Control (control) on day 3 (n = 3), day 6 (n = 3), and day 9 (n = 3) posttransfection using the Qiagen RNeasy Mini Kit. Doubled-stranded cDNA was amplified from total cellular RNA (200 ng) using the T7 Primer Promoter from Low Input Quick Amp Labeling Kit (Agilent Technologies). cDNA was then synthesized using T7 RNA polymerase and labeled with cyanine 3-CTP (Low Input Quick Amp Labeling Kit). Amplified cRNA were purified using Qiagen RNeasy Mini Kit. The amount of cRNA was quantitated using NanoDrop ND-1000 UV-VIS Spectrophotometer (V3.2.1) to determine the specific activity (pmol Cy3 per µg cRNA) for each reaction. Activity greater than six was deemed viable. The quality of cRNA was also assessed using a BioAnalyzer 2100 (Agilent Technologies). Cy3-labeled cRNA (600 ng) was fragmented and incubated at 60°C for exactly 30 min. GEEx Hybridization Buffer Hi-RPM was added and centrifuged for 1 min at 13,000 rpm. Four samples were loaded into an Agilent Microarray SureHyb Hybridization Chamber (Santa Clara, CA). SureHyb hybridization chambers were placed into a hybridization oven (Santa Clara, CA) overnight (17 h) at 65°C. Hybridization chambers were removed from hybridization ovens and slides were disassembled and placed in a slide rack immersed in GE wash buffer 1. Slides were then transferred to GE wash buffer 2 at 37°C. Slides were then removed and placed into the scanning cassette of a high-resolution Agilent microarray scanner (Santa Clara, CA).

**Microarray analysis**

All data analysis was performed using the R (3.3.1) statistical programming language, primarily using the limma (3.30.13) Bioconductor (3.4) package (Ritchie et al., 2015). The raw fluorescence signal was background-corrected (Ritchie et al., 2007) and quantile normalized (Bolstad et al., 2003). The 95th percentile of the negative control probes on each array was calculated; only probes ≥10% brighter than the negative controls on at least three arrays were retained for further analysis. The signal from all probes measuring the same gene was averaged, resulting in a single expression value for each gene in each sample. Genes without Entrez IDs were also removed, leaving 14,162 genes for differential expression analysis.

Gene-wise linear models were fitted using limma to determine differences in gene expression between treated and control samples, across all three time points and at each individual time point. Empirically estimated array weights, which indicate the relative reliability of each array, were used to down-weight outlying samples (Ritchie et al., 2006). Statistically significant DE genes were identified using empirical Bayes moderated t tests (Smyth, 2005), allowing for a mean-variance trend and performing robust empirical Bayes shrinkage of the gene-wise variances to protect against hypervariate genes (Phipson et al., 2016). p values were adjusted for false discovery rate using the Benjamini-Hochberg method (Benjamini and Hochberg, 1995).
Overrepresentation of GO terms among significantly DE genes was tested using one-sided hypergeometric tests as implemented in limma (Ritchie et al., 2007). The sets of matrisome genes (Naba et al., 2012) extracted from the C2 curated gene sets in the Broad Institute MSigDB were tested for differential expression using the “roast” self-contained gene set testing method (Mu et al., 2010).

All canonical pathways from the C2 curated gene sets in the Broad Institute MSigDB were tested using the “camera” competitive gene set testing method (Wu and Smyth, 2012). “Camera” accounts for intergene correlation while testing whether a set of genes is highly ranked relative to other genes in terms of differential expression.

Quantitative real-time PCR

Reverse transcription and qRT-PCR were done as described (Hunt et al., 2013) on an independent trial to the microarray. Mean normalized expression value (MNE) was calculated using PpaI (peptidylprolyl isomerase A, also known as cyclophilin A) as the housekeeping gene. Oligonucleotide primer sequences can be found in Supplemental Table 1.

Statistical analysis

Statistical analyses used GenStat 16.0 (VSN International Ltd., UK). Student’s t-test (unpaired-two-sample) was used to compare differences between single measures for control and ADAM12 RNAi. Where three or more time points were measured, REML linear mixed models were used to assess differences between ADAM12 RNAi and control and the effect of time. p < 0.05 was considered to be statistically significant. Results are presented as mean ± SEM.

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