



**„THE ROLE AND FUNCTION OF ADIPOSE TISSUE-DERIVED DPP4 IN
INTRA- AND INTERORGAN CROSSTALK“**

Inaugural-Dissertation

zur Erlangung des Doktorgrades
der Mathematisch-Naturwissenschaftlichen Fakultät
der Heinrich-Heine-Universität Düsseldorf

vorgelegt von

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Düsseldorf, Dezember 2016

Dieser Arbeit wurde angefertigt am

Deutschen Diabetes-Zentrum

Paul-Langerhans-Gruppe für Integrative Physiologie

Leibniz-Zentrum für Diabetes-Forschung

an der Heinrich-Heine-Universität Düsseldorf

Gedruckt mit der Genehmigung der
Mathematisch-Naturwissenschaftlichen Fakultät der

Heinrich-Heine-Universität Düsseldorf

Referent: Prof Jürgen Eckel

Korreferent: Prof. Ulrich Rüther

Tag der mündlichen Prüfung: 09.02.17

„Der Zweifel ist der Beginn der Wissenschaft. Wer nichts anzweifelt, prüft nichts. Wer nichts prüft, entdeckt nichts. Wer nichts entdeckt, ist blind und bleibt blind.“

- Teilhard de Chardin (1881-1955), frz. Theologe, Paläontologe u. Philosoph -

ZUSAMMENFASSUNG

Weißes Fettgewebe galt lange Zeit als reines Energiespeicher-Depot. Heutzutage ist weithin anerkannt, dass weißes Fettgewebe ein endokrines Organ darstellt, das eine Vielzahl an Proteinen freisetzt, die sogenannten Adipokine. Das Fettgewebe ist ein heterogenes Organ, das sich aus verschiedenen Zelltypen zusammensetzt, zu denen sowohl Präadipozyten, Fibroblasten, Immunzellen als auch reife Adipozyten zählen. Bei positiver Energiebilanz kommt es zu einer dysfunktionellen Ausdehnung des Fettgewebes, welches durch chronische niedriggradige Inflammation, Insulinresistenz und Veränderung des sekretorischen Profils charakterisiert ist. Durch die Kommunikation mit anderen insulin-sensitiven Geweben, wie Leber und Skelettmuskel sind übergewichtige Individuen besonders prädestiniert, chronische metabolische Erkrankungen zu entwickeln. Zu diesen gehören Typ 2 Diabetes mellitus (T2DM), Herz-Kreislauf Erkrankungen und nicht-alkoholische Fettleber. In unserer westlichen Gesellschaft hat sich Fettleibigkeit zu einer der größten Gesundheitsbelastungen entwickelt, die mittlerweile epidemische Ausmaße annimmt. Um dieses komplexe Krankheitsbild zu bekämpfen, ist es nötig, die zugrunde liegenden molekularen Mechanismen, die Fettleibigkeit mit metabolischen Erkrankungen verbinden, zu verstehen. In diesem Zusammenhang entwickelten sich Adipokine, die vom Fettgewebe freigesetzt werden, zu einem Forschungsschwerpunkt in den letzten Jahrzehnten.

Durch Proteomanalyse des humanen Adipozytensekretoms wurde Dipeptidylpeptidase 4 (DPP4) als neues Adipokine identifiziert. DPP4 ist eine ubiquitär exprimierte Zelloberflächen-Protease. Aufgrund ihrer katabolen Eigenschaft gegenüber den Inkretin-Hormonen, welche maßgeblich für die postprandiale Insulinfreisetzung verantwortlich sind, wurde DPP4 zu einem wichtigen therapeutischen Ziel für die Behandlung von T2DM. DPP4 wird nicht nur auf der Zelloberfläche exprimiert, sondern auch in die Zirkulation freigesetzt, wo es sowohl para- als auch endokrine Funktionen in Zielorganen erfüllt. Frühere Studien weisen außerdem darauf hin, dass DPP4 ein neuer Faktor sein könnte, der Fettleibigkeit mit Parametern von metabolischen Erkrankungen, wie BMI, Taillenumfang und Insulinsensitivität verbindet. Dennoch sind der Mechanismus und die Regulation der Freisetzung von DPP4 weitestgehend unbekannt. Aus diesem Grund war der Ausgangspunkt dieser Arbeit, den Freisetzungsmechanismus und dessen Regulation *in vitro* aufzuklären. Die Ergebnisse legen nahe, dass konstitutive

Freisetzung von löslichem DPP4 (sDPP4) über hydrolytische Spaltung von der Zelloberfläche erfolgt, welche auch „shedding“ genannt wird. Ich konnte zeigen, dass dieser Prozess verschiedene Proteasen involviert, wie beispielsweise Matrixmetalloproteasen oder Cathepsine, und Zelltyp-spezifisch ist. Außerdem deuten meine Ergebnisse darauf hin, dass die beteiligten Enzyme über eine katalytische Kette aktiviert werden. Ein identifizierter regulatorischer Faktor der DPP4 Freisetzung in vaskulären Zellen ist Hypoxie. Diese führt zu einer gesteigerten Expression von Metalloproteasen, was zu einer erhöhten DPP4 Freisetzung beiträgt.

Obwohl frühere Studien bereits belegen konnten, dass das Fettgewebe eines der wichtigen Quellen für sDPP4 darstellt, blieb die Rolle von DPP4 innerhalb des Fettgewebes weitestgehend unbekannt. Ein weiteres Untersuchungsziel dieser Thesis war die Charakterisierung der Rolle von DPP4 im Fett *in vitro* durch siRNA-vermittelte Reduktion von DPP4 in Präadipozyten. Um klarzustellen, ob die beobachteten Effekte durch die enzymatische Aktivität von DPP4 vermittelt werden, wurden Schlüsselexperimente unter Verwendung von etablierten DPP4 Inhibitoren wiederholt. Die erhobenen Daten zeigen, dass DPP4 keine zentrale Rolle in der Adipozyten-Differenzierung zu spielen scheint. Weiterhin konnten keine Effekte einer DPP4 Reduktion auf Ebene der TNF α -induzierten Inflammation hinsichtlich NF κ B Aktivierung oder Expression von NF κ B Zielgenen beobachtet werden. Effekte einer siRNA-induzierter Reduktion von DPP4 hinsichtlich der Änderung des Adipozyten Sekretoms können auf Grundlage meiner Ergebnisse derzeit nicht ausgeschlossen werden. Interessanterweise führt die Verminderung von DPP4 zu einer verbesserten Insulin Signalweiterleitung, welche zumindest teilweise über die enzymatische Aktivität vermittelt wird. Zusammen mit unseren bereits publizierten Ergebnissen zu direkten Effekten von sDPP4 auf den Insulinsignalweg postuliere ich, dass die vorhandene Menge an DPP4 speziell in fettleibigen insulin-resistenten Patienten einen Mediator der Insulinresistenz darstellt.

Mäuse mit einem kompletten DPP4 Knockout (KO) sind vor diät-induzierter Fettleibigkeit geschützt, indem metabolische Parameter wie Glukosetoleranz und hepatische Fettakkumulation verbessert werden. Die Interpretation der Ergebnisse mit diesem Mausmodell gestaltet sich allerdings schwierig, da auch Nahrungsaufnahme, Körpergröße und Immunzellen vom KO beeinflusst werden. Zusätzlich kann keine Aussage zu organspezifischen Effekten eines DPP4 KO getroffen werden. Aufgrunddessen war ein weiteres Ziel die lokale und systemische Rolle von fettgewebs-

spezifischem DPP4 unter Generierung eines gewebe-spezifischen KO zu untersuchen. Um weiterhin die Rolle von fettgewebs-spezifischem DPP4 in der Fettleibigkeit zu untersuchen, wurden die Mäuse für 24 Wochen einer Hoch-Fett-Diät (HFD) ausgesetzt. In diesem Zusammenhang konnte trotz erhöhtem Körpergewicht eine verbesserte orale Glukosetoleranz in den KO Tieren unter HFD beobachtet werden. Interessanterweise scheint das gewebs-spezifisches Modell speziell die hepatische Insulinsensitivität in Hinsicht auf endogene Glukoseproduktion zu verbessern. Ich postuliere, dass dies über eine verminderte Freisetzung von Insulin-like Growth Factor Binding Protein 3 (IGFBP-3) aus dem Fettgewebe mediiert wird, welche zu erhöhtem Level von freiem Insulin-like Growth Factor 1 (IGF1) führt. Daraus resultiert eine Verbesserung der Glucose Toleranz und der hepatischen Insulinresistenz. Die Beobachtungen deuten außerdem darauf hin, dass es zu einer vorteilhaften Fettgewebsmodellierung unter HFD kommt. Diese zeichnet sich durch ein optimiertes Verhältnis von M1 zu M2 Makrophagen, verminderter Fibrose und einer reduzierten Adipozytengröße aus. Besonders hervor zu heben ist diesbezüglich, dass die beobachteten Effekte unabhängig von der Inkretin-Achse zu sein scheinen und eher direkt über die Wirkung von DPP4 oder über alternative Substrate erfolgen.

Zusammengefasst verdeutlichen die erzielten Erkenntnisse die negative Rolle von DPP4 in der Entwicklung der Fettleibigkeit. Diese Arbeit zeigt, dass DPP4 vor allem in der Fettleibigkeit lokal den Metabolismus und die Struktur des Fettgewebes beeinflusst. Außerdem konnten meine Ergebnisse maßgeblich zu einem besseren Verständnis der DPP4 Freisetzung beitragen, was besonders im Hinblick auf die Kommunikation mit anderen Geweben von großem Interesse ist. Beispielhaft wurde dies in dieser Arbeit hinsichtlich der Wirkung von DPP4 auf die hepatische Insulinsensitivität im fettgewebs-spezifischen KO Mausmodell gezeigt. Diese Thesis bekräftigt weiterhin die Rolle von DPP4 als therapeutisches Mittel für die Behandlung von metabolischen Erkrankungen wie T2DM, welche auch über die Inkretin-vermittelte Wirkung hinausgeht.

SUMMARY

White adipose tissue (AT) has long been considered as a mere energy storage organ. Nowadays, it is widely accepted that AT is a real endocrine organ releasing various metabolically active proteins, the so-called adipokines. AT is a heterogeneous organ comprising different cell types such as preadipocytes, fibroblasts, immune cells and mature adipocytes. Due to positive energy balance AT mass is expanding during obesity, leading to a dysfunctional tissue, which is characterized by a chronic low-grade inflammation, insulin resistance and an altered secretory profile. Via crosstalk to other insulin sensitive tissues like liver and skeletal muscle, obese individuals are predisposed to the development of chronic metabolic diseases like type 2 diabetes mellitus (T2DM), cardiovascular disease (CVD) or non-alcoholic fatty liver disease (NAFLD). In our western society obesity became one of the greatest health burdens reaching epidemic dimensions now. To combat this complex disease scenario it is necessary to understand the underlying molecular mechanisms linking obesity to metabolic diseases. In this context, adipokines released by AT became a major research topic in the last decades.

By proteomic profiling of the human adipocyte secretome, dipeptidylpeptidase 4 (DPP4) has been identified as a novel adipokine. DPP4 is a ubiquitously expressed cell-surface protease. Due to its catabolism of the incretin hormones, which are important for post-prandial insulin secretion, it became a therapeutic target for the treatment of T2DM. DPP4 is not only expressed as a cell-surface molecule, but is also released into the circulation, thus exerting para- and endocrine functions on target tissues. Previous studies also revealed that DPP4 might be a novel factor linking obesity to parameters of metabolic diseases like BMI, waist circumference and insulin sensitivity. However, the mechanism and regulation of DPP4 release were largely unknown. Therefore the starting point of this thesis was to elucidate the mechanism and regulation of DPP4 release *in vitro*. Our findings suggest that constitutive sDPP4 release occurs via hydrolytic cleavage from the cell surface, in a process which is termed shedding. I postulate that this process involves different types of proteases like matrix metalloproteases and cathepsins in a cell-type specific manner. Furthermore, I propose a catalytic cascade being involved in the activation of the responsible sheddases. One regulating factor of sDPP4 release in vascular cells seems to be hypoxia, which leads to an upregulation of MMP gene expression, thereby increasing DPP4 shedding.

Although previous studies support the notion that AT is an important source of circulating DPP4, its functional role within AT remained elusive. A second topic of this thesis was to study the effects of DPP4 ablation on AT *in vitro* by siRNA-mediated silencing of DPP4 in preadipocytes. To verify if the observed effects are mediated through DPP4 enzymatic activity selected experiments were repeated with established DPP4 inhibitors. The present thesis reveals that DPP4 seems to play no role in adipocyte differentiation *in vitro*. There have also been observed no effects of DPP4 silencing on TNF α -induced inflammation in respect to NF κ B activation or gene expression of NF κ B target genes. Effects of DPP4 on the adipocyte secretome can not be excluded with the obtained data. Interestingly, DPP4 knock-down improves insulin signaling in mature adipocytes which seems to be at least partly mediated through its enzymatic activity. Together with previously published results on direct effects of sDPP4 on insulin signaling, I postulate that the amount of DPP4 is potentially a regulating factor in insulin sensitivity especially in obese insulin-resistant patients.

Whole body knock-out (KO) animals revealed that DPP4 ablation protects from diet-induced obesity and improves metabolic parameters like glucose tolerance and hepatic lipid accumulation. However, the interpretation of these findings is difficult because of an effect of the KO on food intake, body size and immune cells. Furthermore, these studies fail to ascribe the observed effects to a particular DPP4 releasing tissue. Therefore, another aim of the thesis was to elucidate local and systemic effects of AT-derived DPP4 with a tissue-specific KO approach. To further reveal the importance of AT-derived DPP4 in the development of obesity, adipose-specific DPP4 KO mice were challenged with 24 weeks of high-fat diet (HFD) feeding. In this context improved oral glucose tolerance was observed despite increased body weight in the KO animals under HFD. Most interestingly, the AT-specific KO model seems to selectively improve hepatic insulin sensitivity via improving endogenous glucose production. I propose that this might be mediated by a downregulated insulin-like growth factor binding protein 3 (IGFBP-3) release from AT into the circulation. In this respect the findings further indicate that AT-specific DPP4 KO leads to a beneficial AT remodeling under HFD with improved M1 vs M2 macrophage ratio, less fibrosis and a significant reduction of adipocyte diameter. Of note is, that the observed effects seem to be independent of incretin hormones and might rather be mediated via direct effects of DPP4 or via alternative DPP4 substrates.

Taken together, the findings highlight the importance of DPP4 as a negative modulator during the development of obesity. This thesis indicates that DPP4 acts locally on the metabolism and structure of AT especially in obesity. Furthermore, my results contributed significantly to a better understanding of DPP4 release which is important in understanding the underlying effects of DPP4 in the cross-talk to other tissues. As an example of this cross-talk DPP4 was identified as a mediator of hepatic insulin resistance via cross-talk mechanisms in the AT specific KO mouse model. This thesis further strengthens the role of DPP4 as a therapeutic target for the treatment of metabolic disease like T2DM also beyond its incretin-mediating action.

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LIST OF ABBREVIATIONS

ADA	adenosine deaminase
AS160	Akt substrate of 160kDa
AT	adipose tissue
ATGL	adipocyte triglyceride lipase
cAMP	cyclic adenosine-mono-phosphat
CM	conditioned medium
CVD	cardiovascular disease
ECM	extracellular matrix
ER	endoplasmatic reticulum
GIP	glucose-dependent insulintropic peptide
GLP-1	glucagon-like peptide 1
Glut	glucose transporter
HFD	high-fat diet
Hif1 α	hypoxia inducible factor 1 α
HOMA-IR	homeostatic model assessment-insulin resistance
HSL	hormone sensitive lipase
IL	interleukin
InsR	insulin receptor
IRS	insulin receptor substrate
JNK	c-Jun N-terminal kinase
Loxl1	lysyl oxidase homolog 1
MHO	metabolically healthy obese
mTOR	mammalian target of rapamycin
MUNW	metabolically unhealthy normal weight
NEFA	non-esterified fatty acids
NF κ B	nuclear factor kappa-light-chain-enhancer of activated B cells
oGTT	oral glucose tolerance test
PDE3b	phosphodiesterase 3B
PI3K	phosphoinositide 3-kinase
PKA	proteinkinase A
PKC	proteinkinase C
PLIN1	perilipin

Rab	ras-related in brain
SMC	smooth muscle cell
T2DM	type 2 diabetes mellitus
TNF α	tumor necrosis factor α

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1. GENERAL INTRODUCTION

1.1. ADIPOSE TISSUE AND ITS DYSFUNCTION IN OBESITY

Adipose tissue (AT) is a heterogeneous cell population consisting of energy storing, lipid-loaden mature adipocytes, its precursors the preadipocytes, collagenous and reticular fibre, neurons, blood vessels, lymph nodes, immune cells and fibroblasts (1;2). There are two distinct types of classical AT in mammals, classical brown, which is mainly responsible for thermoregulation (3) and classical white. The latter will be the focus of this thesis and has the main energy regulating function via storage and mobilization of triglycerides (TG). Another important feature of white AT is only known since several years and shifted the relevance of AT from a mere energy storing depot to an active endocrine organ. This feature is the secretion of various factors, the so called adipokines (2).

During obesity optimal body composition shifts to increasing adipose tissue (AT) mass. The classification of patients is defined according to their percentage of body fat, which is defined by certain cut-offs depending on gender and age (4). Obesity in males is defined by the cut-off of 20.6-24.2% fat per bodyweight depending on age whereas in females it ranges from 36-37%. Obesity is one of the greatest health burdens in our western society since it is linked to the development of chronic diseases like type 2 diabetes mellitus (T2DM)(5), cardiovascular disease (CVD)(6), non-alcoholic fatty liver disease (NAFLD) (7;8) and certain types of cancer (9). The following sections deal with the complex alterations of AT occurring during the progression of obesity and leading to insulin resistance within AT. Insulin resistance is influenced by various mechanisms. On the one hand insulin action itself on adipocytes in respect of lipolysis and glucose uptake is impaired, but also adipocyte hypertrophy, hypoxia, fibrosis as well as macrophage infiltration and the development of a chronic low-grade inflammation are contributing to insulin resistance. All of these aspects will shortly be discussed in the following sections.

1.1.1. INSULIN ACTION ON GLUCOSE UPTAKE AND LIPOLYSIS

Insulin is produced by the beta cells of the pancreas and reaches its target tissues via the blood stream. Post-prandially insulin levels are rising which leads to a subsequent

activation of Akt within the target cells (10). Interestingly, insulin is increasing the blood-flow after meal ingestion or physical activity and thereby enhances its own delivery and that of other signaling substrates to the target tissues (11;12). The increase in post-prandial AT blood-flow is also associated with insulin sensitivity independent of body-weight as shown by Karpe and colleagues (13). Furthermore, it is well known that ectopic fat accumulation leads to impaired insulin sensitivity in tissues like liver and muscle (14;15). There is a tight cross-talk between anabolic processes mediated by insulin and catabolic processes mediated by catecholamines. On the one hand insulin is able to counteract lipolysis, and on the other hand mediators of lipolysis are able to interfere with glucose uptake. This complex association was already described by Randle in 1963 and is known as the “Randle cycle” and was redefined throughout the years by more in depth knowledge (16). The first part of this section will deal with lipolysis and how insulin affects this process.

AT lipolysis is the catabolic pathway which leads to a sequential breakdown of triglycerides into glycerol and fatty acids (17). It is the key regulator of energy mobilization and storage and therefore lipolysis is under tight control according to nutritional status of an individual. In T2DM patients there is an insufficient suppression of lipolysis which results in an increased fatty acid spillover to the circulation (18;19). Akt despite being a key component in the phosphoinositide 3-kinase (PI3K) pathway which leads to glucose uptake also phosphorylates phosphodiesterase 3b (PDE3b). PDE3b catalyzes cAMP hydrolysis, which is usually built during fasting upon activation of adenylyl cyclase via β -adrenergic receptor activation (20). Thereby insulin acts antilipolytic in AT. However there are also Akt-independent pathways described by which insulin acts on lipolysis. Especially at low submaximal levels of catecholamines insulin might rather act through protein kinase C-dependent pathways or through the regulation of lipid droplet trafficking by Rab proteins (21). Another inhibitory pathway of lipolysis might be mediated through lactate (22). Preferentially under conditions where glucose uptake is enhanced lactate production is upregulated. Lactate is able to activate the G-protein-coupled receptor GPR81 and thereby counteracts the effect of catecholamines on β -adrenoceptors (22). Not only the suppression of lipolysis by insulin is disturbed in T2DM patients, but also basal fat cell lipolysis is elevated in obesity and is closely associated with insulin resistance (14;23). Since it is well-known that fat cell size positively correlates with basal lipolysis rate this could be one possible reason for elevated basal lipolysis in obese subjects (24). However this is not applicable for the

sensitivity to insulin. It was shown on the contrary that larger adipocytes are more sensitive to the inhibitory action of insulin on lipolysis (25;26). Disturbances in antilipolytic action of insulin as seen in obese individuals seem to be rather mediated through impaired insulin binding (27). Furthermore, it is reported that in metabolically healthy humans insulin acts very quickly as an antilipolytic agent after glucose ingestion via alterations at the post-receptor level, which is not the case in obesity (28).

Although AT accounts for only approximately 10% of whole body glucose disposal capacity, glucose uptake is still crucial for normal AT function (29). Impaired glucose uptake is altering esterification of fatty acids, lipid biosynthesis (30) and endocrine function of AT (31). The following section will deal with glucose uptake and how lipid products generated during lipolysis may counteract this process in AT.

Insulin-stimulated glucose uptake in AT is dependent on the presence of the glucose transporter isoform 4 (Glut4). This protein is absent from fibroblastic, pre-adipocyte states and is progressively upregulated upon adipocyte differentiation (32). Another glucose transporter isoform is also expressed in AT and accounts for basal glucose uptake. Glut1 is already detectable in adipocyte precursor cells and is gradually decreased during adipocyte differentiation. At least human adipocyte precursor cells are not sensitive to insulin and basal glucose uptake is decreased throughout differentiation. During obesity Glut4 protein levels are reduced and thereby glucose disposal rate is diminished in AT. This was shown in diabetic rats where Glut4 levels in the membrane fraction of adipose cells are markedly reduced even in the insulin-stimulated state (33). In contrast, it was reported that Glut1 levels are unaffected. It seems that the intracellular Glut4 pool in diabetic rats is decreased and therefore less Glut4 is available for translocation (33). In humans it was shown that already in patients with impaired glucose tolerance Glut4 mRNA levels are diminished, thus the regulation of glucose transport is already affected at pretranslational level (34). Mullins and colleagues found out that lipid products generated during lipolysis lead to a dissociation of mammalian target of rapamycin (mTOR) complexes. Especially via decrease of mTORC2 a subsequent decrease of glucose uptake occurs (35). mTORC2, which consists of mTOR and rictor together with other proteins, is responsible for phosphorylation of Akt at Ser473 upon insulin stimulation (36). This in turn is required for activation of Akt substrate of 160kDa (AS160) and translocation of Glut4 to the plasma membrane which results in glucose uptake.

1.1.2. ADIPOSE TISSUE HYPERTROPHY VERSUS HYPERPLASIA

Obesity is a heterogeneous condition which is influenced by genetics, lifestyle habits and behavior and is characterized as an excessive accumulation of body fat (37). Although AT is a heterogeneous tissue, adverse effects which are observed due to obesity are mainly linked to adipocytes (38). Interestingly not all obese individuals develop T2DM and there is also a subgroup of individuals who are lean, but not cardiometabolically healthy. These two subgroups are classified as metabolically healthy obese (MHO) or metabolically unhealthy normal weight (MUNW) individuals (37). MHO individuals are characterized by a BMI above 30 but normal insulin sensitivity, fasting glucose and blood lipids (39) whereas MUNW individuals have a BMI below 25, which is still accompanied by elevated plasma triglycerides, and LDL-Cholesterol with lowered HDL-Cholesterol (40).

There are two possible ways how AT can react on positive energy balance. First, mature adipocytes could increase in diameter by storing more triacylglycerol in lipid droplets, which would make them hypertrophic (41). Indeed, large lipid-laden adipocytes can be predominant in white AT and may exceed a volume of 800pL (42). And second, new mature adipocytes can be generated from pre-adipocytes by differentiation which forms a hyperplastic AT (41). More smaller adipocytes are protective against metabolic abnormalities in respect of lipid profile, glucose and insulin levels as normally seen in hypertrophic obesity (43). Functional adipogenesis is therefore crucial to prevent development of insulin resistance. It has been demonstrated that polymorphisms in PPAR γ , which renders it unfunctional, are associated with higher risk to develop T2DM (44). In contrast to that, polymorphisms without loss-of-function have no effect on insulin sensitivity. Additionally, the level of circulating adiponectin, which is a key mediator of adipogenesis, is a strong predictor of insulin sensitivity (45). Larger adipocytes are characterized by an increased basal and catecholamine-stimulated lipolysis (46). Especially in the postprandial period lipid storage capacity in obese individuals is reduced. This might be due to the fact that adipocytes have a maximum size threshold which could already be exceeded during obesity (47). On top of that, the lipolysis rate is increased during fasting in obese AT so that there is a higher efflux of non-esterified fatty acids (NEFA) into other tissues and this could impair whole body

insulin sensitivity (48). There is evidence, that hypertrophy is more likely to lead to insulin resistance and T2DM than hyperplasia (49;50). Interestingly MHO individuals tend to have lower ectopic fat accumulation in liver and skeletal muscle than their metabolically unhealthy obese counterparts (39;51). Studies suggest that MHO individuals preserve their white AT function via increasing hyperplasia instead of hypertrophy (49;52). This is achieved e.g. via increasing the expression of genes related to adipocyte differentiation (50). The mean and maximum volume of adipocytes is associated with whole body insulin sensitivity, increased parameters of inflammation and oxidative stress in the circulation, and increased macrophage number within AT (42). One possible explanation might be the activation of stress kinases like JNK or p38MARK during hypertrophy and adipocyte differentiation which leads to an alteration of the secretome, to insulin resistance and stimulates macrophage infiltration (53-55).

Another important explanation for the existence of MHO and MUNW individuals might be the location of AT. It has been demonstrated that MUNW have increased VAT (56;57). It was also shown that in MHO and MUO individuals matched for percentage of body fat MHO have reduced amounts of VAT (58). Although it is hypothesized that MHO preferentially store excess fat in SAT, the literature is controversial and some studies did not find differences in SAT between MHO and MUO (51;59-61).

A novel study by Lackey and colleagues suggests that another difference between MHO and MUO might be ECM characteristics like tensile strength, collagen and proteolytic enzymes (62).

Blood vessels within white AT might also function as an adipocyte progenitor niche providing expanding AT with new pre-adipocytes (38;63). Another important function of blood vessels is the supply with oxygen and there might be a difference between MHO and MUO in angiogenic potential as proposed by Sun and colleagues (64).

1.1.3. FIBROSIS AND HYPOXIA

Hypoxia and fibrosis are tightly linked to each other in the progression of obesity. Fibrosis is defined as the excessive deposition of fibrous connective tissue within a certain organ or tissue. In AT, fibrosis results from a higher synthesis of fibrillary components like collagen I, II and VI (65). To accommodate hypertrophic adipocytes properly during nutrient overload, the extracellular matrix (ECM) is underlying constant remodeling. During obesity adipocyte size increases to 140-180µm in diameter and at

some point the size of these adipocytes exceeds the possibility to efficiently vascularize and innervate these cells (66). Efficient oxygen diffusion is possible until approximately 100µm apart from blood vessels (67). Therefore at some point during obesity AT becomes hypoxic (64). This leads to an increase in hypoxia-inducible factor 1 α (Hif1 α) expression (68). Hypoxia also leads to inflammation via upregulation of IL-6 and macrophage inflammation factor 1 (MIF1) by Hif1 α (69). Inflammation further triggers expression and secretion of collagens by macrophages and preadipocytes, thus highlighting the correlation of AT fibrosis and inflammation (70). Furthermore hypoxia stimulates fibrosis of AT since lysyl oxidase homolog 1 (Loxl1), which crosslinks collagens and elastin (68), is a Hif1 α target gene. Obesity in humans is associated with increased fibrosis via excessive collagen deposition (71). Fibrosis limits AT expandability and makes it more “stiff”, which leads to adipocyte cell death and triggers inflammation (65). On the other hand hypoxia induces angiogenesis to counteract AT growth and oxygen demand (72). Therefore obese subjects are characterized by increased vessel size in AT in comparison to lean individuals (73). However, this counteraction is not enough to sufficiently react on the oxygen need of the expanding tissue. VAT seems to be more prone to fibrotic strokes than SAT and limited hypertrophy also increases the risk for ectopic lipid accumulation (74). However the exact molecular link between obesity and fibrosis is mainly unknown.

1.1.4. CHRONIC LOW-GRADE INFLAMMATION

During the progression of obesity, AT undergoes massive metabolic and morphologic changes due to hypertrophy, apoptosis and stresses such as inflammation and hypoxia. These changes are summarized in Fig 1. Taken together, these changes in AT lead to an alteration of the secretory profile towards a more pro-inflammatory status (75). Pro-inflammatory cytokines like interleukin 6 (IL-6) and tumor necrosis factor α (TNF α) are known to inhibit adipocyte differentiation and to induce apoptosis in pre- and mature adipocytes (76-78). These modifications lead to a decrease in hyperplastic potential of AT and thereby reduces its storage capacity resulting in higher NEFA production (79). NEFA on the one hand can then systemically impair insulin sensitivity and further elevate the risk to develop T2DM, but on the other hand NEFA also have local effects like elevating MCP-1 and IL-6 levels in pre-adipocytes and further support development of a pro-inflammatory secretome (80).

Furthermore, the population of immune cells in white AT tissue changes during the progression of obesity and metabolic dysfunction. Whereas in healthy white AT, resident macrophages are mainly of the anti-inflammatory M2 phenotype, during obesity a switch of these macrophages towards a more pro-inflammatory M1 subset occurs (81). In addition to a phenotypic switch also the number of macrophages is elevated during low-grade chronic inflammation. This occurs both due to local proliferation as well as recruitment of circulating macrophages (82). Pro-inflammatory cytokines like MCP-1 attract more macrophages to the inflamed AT and macrophages themselves also produce MCP-1, and thereby close the vicious cycle (83;84). Macrophages are typically infiltrating AT especially around necrotic adipocytes which are called crown-like structures (85).

In addition to macrophages, another important cell type associated with insulin resistance and T2DM are CD4⁺ T-cells (86;87). Also other cells of the innate and adaptive immune system are involved in the pathology of T2DM and obesity. These cells are e.g. B-cells, neutrophils and dendritic cells, as recently reviewed by Apostopoulos (88). The amount of these cells positively correlates with the severity of the metabolic disorder (37).

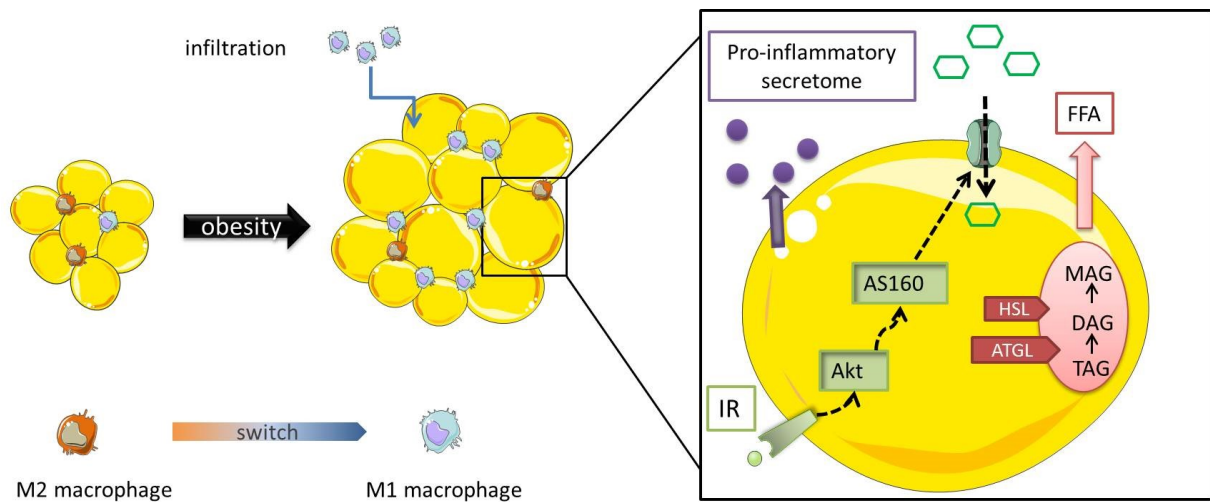


FIGURE 1: ADIPOSE TISSUE AND ITS DYSFUNCTION IN OBESITY

During obesity adipocytes are increasing in size and number. Furthermore, a phenotypic switch of macrophages from anti-inflammatory M2 to more pro-inflammatory M1 occurs, plus new macrophages are recruited into AT. Within adipocytes more pro-inflammatory adipokines are released. Due to impaired insulin sensitivity more free fatty acids are released and glucose uptake is diminished. FFA free fatty acids; MAG monoacylglycerol; DAG diacylglycerol; TAG triacylglycerol; HSL hormone sensitive lipase; ATGL adipose triglyceride lipase; PLIN perilipin; IR insulin resistance; Akt protein kinase B; AS160 Akt-substrate of 160kDa

1.2. ADIPOSE TISSUE IN THE CROSS-TALK TO CELLS AND ORGANS

Through the release of circulating factors, AT is not only able to regulate its own function but also to interact with surrounding or distant organs and tissues. Although the list of newly identified secreted factors is expanding rapidly most of them are incompletely characterized. It is well-accepted that many of these factors released by AT have an impact on the function of other organs. However, it is often unknown how these factors emerge AT or how and if these factors are involved in adipogenesis, AT growth or function. The next section deals with the role of AT as an endocrine organ, the general export mechanisms for the secreted factors, and gives examples of some factors and their role in intra- and inter-organ crosstalk. This complex interplay is summarized in Fig 2.

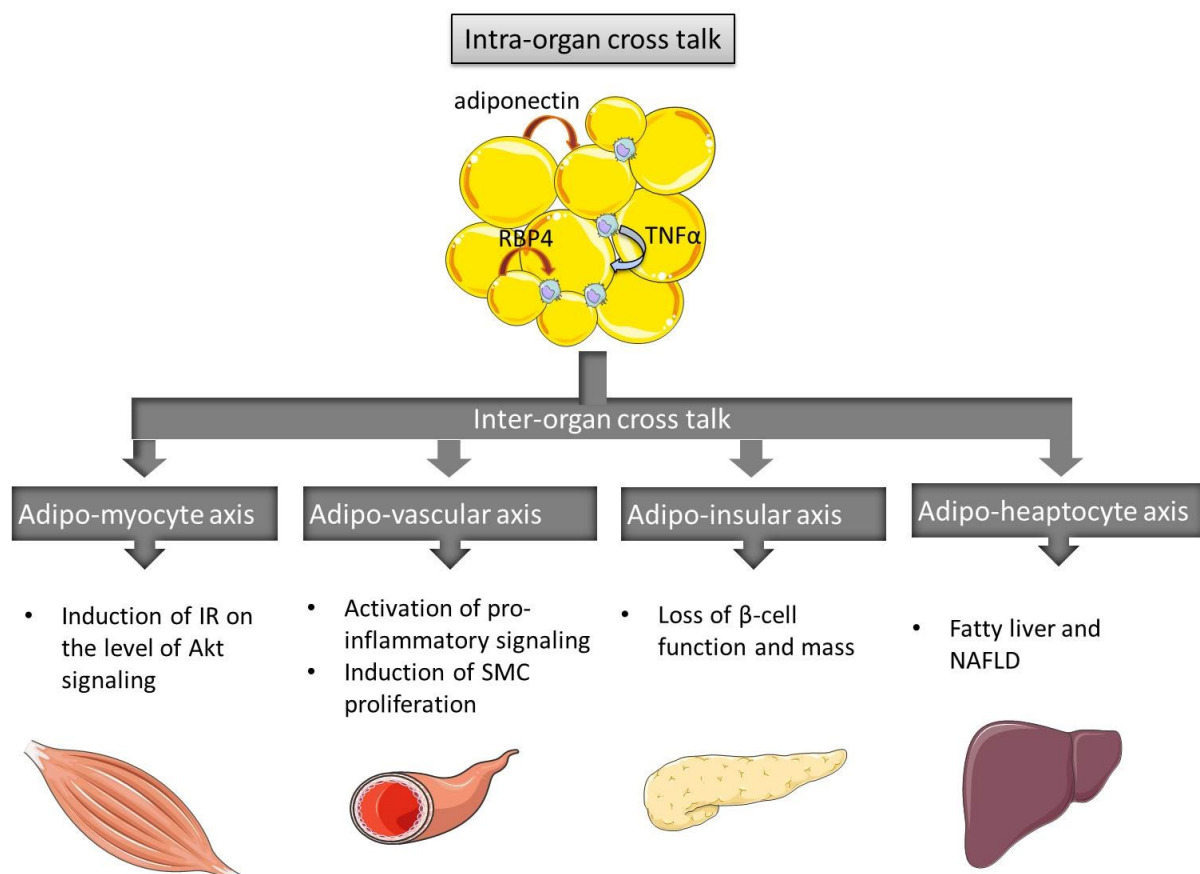


FIGURE 2: ADIPOSE TISSUE IN THE CROSS-TALK TO OTHER CELLS

AT is an active endocrine organ releasing a variety of factors. Thereby it is able to communicate locally with adipocytes or immune cells within AT or systemically with target tissues like skeletal muscle, vascular cells, pancreas or liver. RBP4 retinol binding protein 4; TNFα tumor necrosis factor α; NAFLD non-alcoholic fatty liver disease

1.2.1. ADIPOSE TISSUE AS AN ENDOCRINE ORGAN

For a long time it was believed that AT is an inactive tissue mainly responsible for the storage and mobilization of lipids according to need. Already in 1987, when AT was identified as the major site of sex steroid metabolism and as producer of adipsin, this view changed (89). The discovery and characterization of leptin in 1994 opened up the road to a new era of research on AT (90). Nowadays, it is widely accepted that AT is an endocrine organ and the number of identified secreted factors, the so called adipokines, is increasing at a tremendous rate over the last decades (91-93). The released adipokines are able to act locally within AT or systemically on other peripheral target tissues thus influencing developmental, metabolic or inflammatory processes. Furthermore, adipocytes are equipped with receptors necessary to receive signals from other cells and distant organs thus enabling it to not only actively interfere in processes, but also to react on signals (94). Although many of the secreted factors are derived from the non-adipocyte fraction of AT, still all components are one functional unit and thus AT is a true endocrine organ. Attempts to identify novel adipokines and to characterize the whole secretome revealed hundreds of secreted factors (91). It could be shown that the majority of the identified factors have an altered expression in obesity. Most significantly, upregulated gene sets at mRNA level are associated with ECM organization, cell-cell adhesion, and acute inflammatory response (95). If one keeps in mind that the body is composed of >25% AT in obese individuals and obesity is associated with numerous diseases, it is necessary to understand the role and function of these adipokines.

1.2.2. DIFFERENT SECRETORY PATHWAYS FOR ADIPOKINES

As already mentioned above, research on the human adipokinome revealed numerous novel adipokines. However, the precise mechanism of secretion of many adipokines is still unknown. There are several mechanisms by which adipokines can exit the cell into the extracellular space. These mechanisms can be separated into the classical, or endoplasmatic reticulum (ER)-Golgi-mediated pathway, and non-classical secretory pathways.

To exit adipocytes via the classical pathway, adipokines need to be equipped with an N-terminal signal sequence (96). Thereby these factors are translocated to the ER, correctly folded and assembled and then exit the compartment via COPII-coated vesicles to enter the Golgi complex (97). Inside this compartment adipokines are sorted

according to their destination and packed into vesicles. These vesicles fuse with the plasma membrane afterwards to release their content into the extracellular space (98). One representative adipokine of this export mechanism is adiponectin (99).

For the non-classical secretion mechanism, there are several possibilities with at least three distinct ways described until now, namely transporter-mediated export, microvesicle/exosome release and selective post-translational hydrolysis from the cell surface (100). All of these mechanisms have in common, that the exported factors lack the typical signal sequence which targets them to the ER and are therefore also called “leaderless”. Furthermore, this makes them also insensitive to brefeldin A or monensin treatment (101). One example for transporter-mediated export is fibroblast growth factor 2 (FGF2), which is exported via the plasma membrane Na^+/K^+ -ATPase which was shown by treatment with the inhibitor ouabain (102;103). IL-1 β is a classical representative of vesicle mediated transport. It is able to exit the cell via at least three possible vesicle routes like lysosomes, shed plasma membrane vesicles, or exosomes from multi-vesicular bodies (104). One non-classical secretory pathway is especially interesting in the context of the presented PhD thesis. The selective post-translational hydrolysis from the cell surface, called shedding, is a proposed export route for dipeptidylpeptidase 4 (DPP4) (105). As a member of the type II transmembrane protease family of proteins, DPP4 contains a predicted signal sequence which is located at the transmembrane domain and serves as the anchor sequence for DPP4 inside the plasma membrane (106). It was already speculated that DPP4 is released via shedding, but the exact underlying mechanism is unknown (107). Furthermore, it was already shown that it is insensitive to brefeldin A treatment in skeletal muscle cells (108). Another member of this secretory pathway is TNF α which is released into the extracellular space by proteolytic cleavage at Ala76-Val77 by TNF α converting enzyme (TACE) (109).

The release of adipokines can be constitutively active or it can be triggered by a certain stimulus. These stimuli can originate from the cross-talk with other cells within adipose tissue and this will be discussed in the following section.

1.2.3. INTRA-ORGAN CROSS-TALK

AT it is a heterogeneous tissue which does not only consist of adipocytes and precursor cells, but is also highly infiltrated by immune cells. Via the secretion of cytokines and adipokines these different cell-types are in close communication. This cross-talk is not unidirectional but a rather complex interplay between the different partners (110).

The cross-talk can influence AT on different levels like mediation of adipogenesis (111) or inflammation (112). Furthermore, some mediators are also known to have an impact on adipocyte function like lipolysis and glucose uptake (113;114).

Although also adipocytes are able to release TNF α and IL-6, the main sources of these cytokines within AT are macrophages (115;116). TNF α is known to inhibit adipogenesis by preventing peroxisome proliferator activated receptor (PPAR) γ and CCAAT/enhancer binding protein (C/EBP) α expression (117). Both TNF α and IL-6 are associated with insulin resistance in AT (118;119). The release and expression of cytokines and adipokines is tightly regulated and can be influenced bidirectional via cytokines or adipokines. Especially TNF α is able to increase the release of some adipokines like chemerin (120), or decrease the release of adipokines like retinol binding protein 4 (RBP4) (121). Adipokines can also impair macrophage secretory function. As such RBP4 is able to induce MCP-1, TNF α and IL-6 release in macrophages (122). IL-6 is able to regulate its own expression and release, as it was shown by several groups (118;123). The impact of cytokines on adipocyte function can be versatile. In this respect TNF α is able to impair lipolysis by interfering with the expression and activity of LPL and fatty acid binding transport proteins (113). But it is also involved in regulation of glucose uptake. Several mechanisms are known by which TNF α can interfere with glucose uptake. First, TNF α is able to lower PPAR γ expression and activity, and thereby reduces Glut4, insulin receptor (InsR) and IRS1 levels (124). Second, it actively inhibits tyrosine phosphorylation of the InsR and IRS-1, and thereby impairs insulin signaling (125;126). Furthermore, TNF α elevates intracellular ceramides and diacylglycerol levels which are impairing insulin signaling (127;128). In obesity, lipolysis is dysregulated and basal as well as isoprenaline-stimulated lipolysis are upregulated, which might be mediated by IL-6 (129).

Well-characterized adipokines which are positively mediating adipogenesis are adiponectin and chemerin. A known negative mediator of adipogenesis is RBP4. Low levels of circulating adiponectin are correlated with obesity, insulin resistance, T2DM and CVD (130;131). Since mature adipocytes are the main source of this adipokine, the

role and function of adiponectin within AT have been studied intensively. Fu and coworkers found out that adiponectin promotes adipocyte proliferation and differentiation and is able to prolong gene expression of C/EBP2, PPAR γ and sterol regulatory element-binding protein (SREBP1c) (132). Furthermore, adiponectin is able to suppress PPAR γ coactivator (PGC-1 α) expression, all of which is leading to an augmented programmed gene expression of adipogenesis markers (132). Additionally, mature adipocytes are characterized by a higher number and increased size of lipid droplets. Adiponectin also mediates insulin-stimulated glucose uptake by elevating Glut4 expression and recruitment to the plasma membrane (132).

Chemerin is mainly derived from mature adipocytes (120). It is influencing adipogenesis by impairing the mitotic expansion phase during the initial days of differentiation, thus potentially providing new adipocytes during phases of hypertrophy (133).

RBP4 is a negative regulator of adipogenesis, which is upregulated during differentiation of adipocytes (134). High levels of RBP4 are associated with obesity, T2DM and metabolic syndrome (135;136). RBP4 affects adipogenesis by downregulating the expression of differentiation markers like aP2 and PPAR γ and by reducing the lipid content of adipocytes (137). Furthermore it impairs insulin signaling locally within AT by blocking phosphorylation of IRS-1.

1.2.4. INTER-ORGAN CROSS-TALK TO OTHER TISSUES

Since the discovery of the first adipokines and the acceptance of AT as a real endocrine organ, researchers all over the world are interested in the cross-talk of AT with other tissues and organs. Especially visceral AT is known to play a central role in the progression and pathogenesis of metabolic diseases (138;139). However, the cross-talk scenario is an extremely complex multidirectional network of factors and the field of interacting factors is mere endless. Every day the list of factors secreted by other tissues and influencing each other is broadening. Despite the classical cytokines and the well-known adipokines and myokines (140), nowadays there are also hepatokines (141), cardiokines (142), or batokines (143) described. To add more complexity to this whole scenario one has to keep in mind that most of the factors are not exclusively produced by one tissue but by several, and especially adipokines and myokines are overlapping, contributing both to the circulating level (108). By proteomic profiling of the secretome of different tissues novel factors are easily identified, but the role within the cross-talk remain often poorly understood. To study inter-organ cross-talk some basic tools have

been established and most of them are either *in vitro* or *ex vivo*. The co-culture of adipocytes with cells of the tissue of interest is the first important tool for investigation of cross-talk mechanisms. The advantage of this method is the bidirectional way of action of the released factors. Another option is to use conditioned medium (CM) either generated *in vitro* during the culture of adipocytes or *ex vivo* from AT explants. Whereupon, the latter has the advantage of getting all factors released from all cells within AT. However, both of these CM techniques lack the bidirectionality. Though, the complexity of the inter-organ cross-talk makes it very difficult to study isolated factors *in vivo*. The following section deals with different axis of interaction between AT and other tissues.

1.2.4.1. ADIPO-MYOCYTE AXIS

Skeletal muscle besides liver is the main target organ for glucose disposal and thus important for the regulation of insulin sensitivity in the body (144). Co-culture experiments of myocytes and adipocytes have revealed an interaction on the insulin signaling axis, as adipokines seem to induce insulin resistance by affecting Akt phosphorylation and Glut4 translocation thus lowering glucose uptake (145). This notion was further supported by experiments with CM generated from adipocytes that is also able to induce insulin resistance on the level of Akt phosphorylation and downstream (146). Furthermore, CM generated from adipocytes increases oxidative stress and ceramide level paralleled with reduced mitochondrial capacity and elevated lipotoxic potential of palmitate (147). A well-known adipokine which promotes insulin sensitivity in skeletal muscle cells is adiponectin (148).

Resistin is at least in rodents an AT-derived factor which is clearly linked to insulin resistance (149). It impairs insulin-stimulated glucose transport in muscle of rodents via regulating IRS-1 and Akt activity and via impairing Glut4 trafficking (150).

1.2.4.2. ADIPO-VASCULAR AXIS

During obesity, a switch towards a more pro-inflammatory secretion profile of AT occurs which is associated with endothelial dysfunction and inflammation (112). Some adipokines such as fatty acid binding protein 4 (FABP4) and lipocalin-2 are well-known for their activation of pro-inflammatory signaling pathways in vascular cells and are predictors of cardio-vascular disease (151-154). Through the release of classical vasoactive factors or adipokines, or the release of fibrinolysis regulating factors,

adipocytes affect vascular homeostasis thus actively promote the progression of atherothrombotic disease (155;156). One example for the action of adipokines on vascular cells is their impact on smooth muscle cells (SMC). Our group was able to show that CM generated from adipocytes affects SMC in various ways. CM is able to induce insulin resistance on the level of Akt and PRAS40 phosphorylation via the dysregulation of certain miRNAs (157). Furthermore, CM-induced proliferation and elevated migration seems to be mediated by dipeptidylpeptidase 4, vascular endothelial growth factor and CD36 (158). Lamers and co-workers could show that CM not only increases VEGF release but also the expression level of VEGF receptor, thus potentiating the proliferative effect of VEGF on SMC. Furthermore, activation of NF κ B and p38MAPK signaling was elevated by CM.

1.2.4.3. ADIPO-INSULAR AXIS

During the progression of T2DM, loss of β -cell function and mass occurs due to glucotoxicity, lipotoxicity and islet cell amyloid (159). Adiponectin is one example of a positive cross-talk from adipocytes to the pancreas. On the one hand adiponectin is able to protect β -cells by inhibiting apoptotic effects of cytokines, palmitate or high glucose (160;161). On the other hand adiponectin actively promotes insulin secretion via elevated insulin gene expression and exocytosis of insulin granules (162). This might also lead to the rescued impairment of insulin secretion by FFA and cytokines (160). In a study by Schinner and colleagues the cross-talk of Ins-1 cells and adipocytes was investigated via the generation of CM. They revealed that adipocytes release Wnt-signaling molecules which induce β -cell proliferation and insulin secretion which might link obesity to hyperinsulinemia (163).

1.2.4.4. ADIPO-HEPATOCYTE AXIS

Cross-talk of AT and liver is essential for the regulation of glucose and lipid metabolism. Thus, elevated pro-inflammatory markers in the circulation are associated with fatty liver and non-alcoholic fatty liver disease (NAFLD) (164). In a study by Zhou and colleagues it could be shown that HepG2 cells have impaired insulin sensitivity upon treatment with adipocyte-derived CM (165). Another group could induce steatosis in hepatocytes with CM which was generated from white AT explants (166). They postulate that the observed effect is mediated by MCP-1, which lowered Apolipoprotein

B secretion and increases phosphoenolpyruvate carboxykinase mRNA expression thus leading to triglyceride accumulation in hepatocytes.

It is well-known that adiponectin sensitizes hepatocytes for insulin signaling and acts as an anti-inflammatory agent via lowering the levels of TNF α and IL-6 (110;167). Adiponectin is involved in the regulation of genes involved in glucose and lipid metabolism, which was demonstrated by RNA sequencing analysis in adiponectin KO mice (168). Recently Nishijima-Matsunobu and coworkers established a three-dimensional culture model to investigate the cross-talk of white AT and hepatocytes (169). Thereby they confirmed an induction of lipotoxicity especially by VAT and a downregulation of FA production in VAT by hepatocytes to counteract the lipotoxic effects. These model could be very helpful for future research on cross-talk scenarios of AT with other tissues.

1.3. DIPEPTIDYLPEPTIDASE 4

Dipeptidylpeptidase 4 (DPP4) is a well-known target for the treatment of T2DM since several years. It is well known for its deactivation of the incretin hormones glucagon like peptide 1 (GLP-1) and glucose-dependent insulintropic polypeptide (GIP), which are to a large extent responsible for the postprandial insulin release (170). Thereby DPP4 inhibitors like sitagliptin, which was the first approved gliptin, prolong the half-life of incretins and are used as monotherapy (171) or in combination with e.g. metformin to treat T2DM (172). Interestingly, DPP4 was one of the highest scored adipokines identified by comprehensive proteomic profiling of the adipocyte secretome (91). The following section deals with a short characterization of DPP4 in respect of structure and function. Furthermore, the multi-faceted role of DPP4 in the context of T2DM will be highlighted.

1.3.1. GENERAL ASPECTS OF DPP4

Dipeptidylpeptidase 4 (DPP4) was first described by Hopsu-Havu and Glenner in 1966 (173). This type II transmembrane protease belongs to the serine peptidase subfamily S9B, where it groups together with fibroblast activation protein α (FAP), DPP8, DPP9, DPP6 and DPP10. All of them share a typical α/β hydrolase fold.

The 110kDa protein consists of four domains, namely the short cytoplasmic domain [aa 1-6], the transmembrane domain [aa 7-28], a flexible stalk region [aa 29-39] and the

extracellular domain [aa 40-766] (107). The latter can be further subdivided into a highly glycosylated region, a cysteine-rich region, and the catalytic region. The domain architecture of DPP4 is displayed in Fig 3.

Although DPP4 contains a signal peptide which targets the protein to the ER and is responsible for the translocation across the cell membrane, this signal is not cleaved off like in classically secreted proteins, but serves as an anchor inside the cell membrane (107). The hydrolytic cleavage of DPP4 occurs within the flexible stalk region and releases a soluble, fully functional form of DPP4 (sDPP4) into the circulation (107).

DPP4 is ubiquitously expressed on numerous cell types. It is believed that substitution with different carbohydrates, which account for approximately 20% of the total molecular mass, are responsible for the heterogeneity depending on the location of DPP4 on different cell types (174). The DPP4 gene is located on chromosome 2 with a size of 70kb, which consists of 26 exons (107). Consensus sites for different transcription factors are located within the promoter region of DPP4. Amongst them e.g. NF κ B and epidermal growth factor receptor (EGFR) are known consensus sites (175).

Dimers are the predominant form of DPP4 and dimerization is necessary for enzymatic activity of the protease (176). Dimerization occurs through the cysteine-rich region of DPP4 either with another DPP4 molecule, or as a heterodimer with other partners like FAP or adenosine deaminase (ADA) (177;178).

DPP4 is a multifunctional molecule which, on one hand, cleaves as an exopeptidase dipeptides from the N-terminal penultimate position of its substrates. Thereby it can generate novel bioactive compounds or inactivate its substrates (105). On the other hand, DPP4 exerts enzyme-independent functions either through binding of partner molecules as membrane-bound form or through binding of receptors as soluble form. This complex function of DPP4 is also displayed in Fig.3. By binding to ADA, DPP4 is involved in tissue remodeling through MMP activation (179) or mediates inflammatory processes like T-cell proliferation (180). Furthermore, DPP4 plays a role in glucose homeostasis via adenosine through ADA binding (181;182). Via the binding to receptors on its target cells, soluble DPP4 is involved in different intracellular signaling processes, and thereby exerts paracrine or endocrine effects. However, the knowledge on potential receptors for DPP4 is scarce and so far only mannose-6 phosphat/insulin-like growth factor 2 receptor and protease activated receptor 2 are described as potential acceptors for DPP4 (183;184).

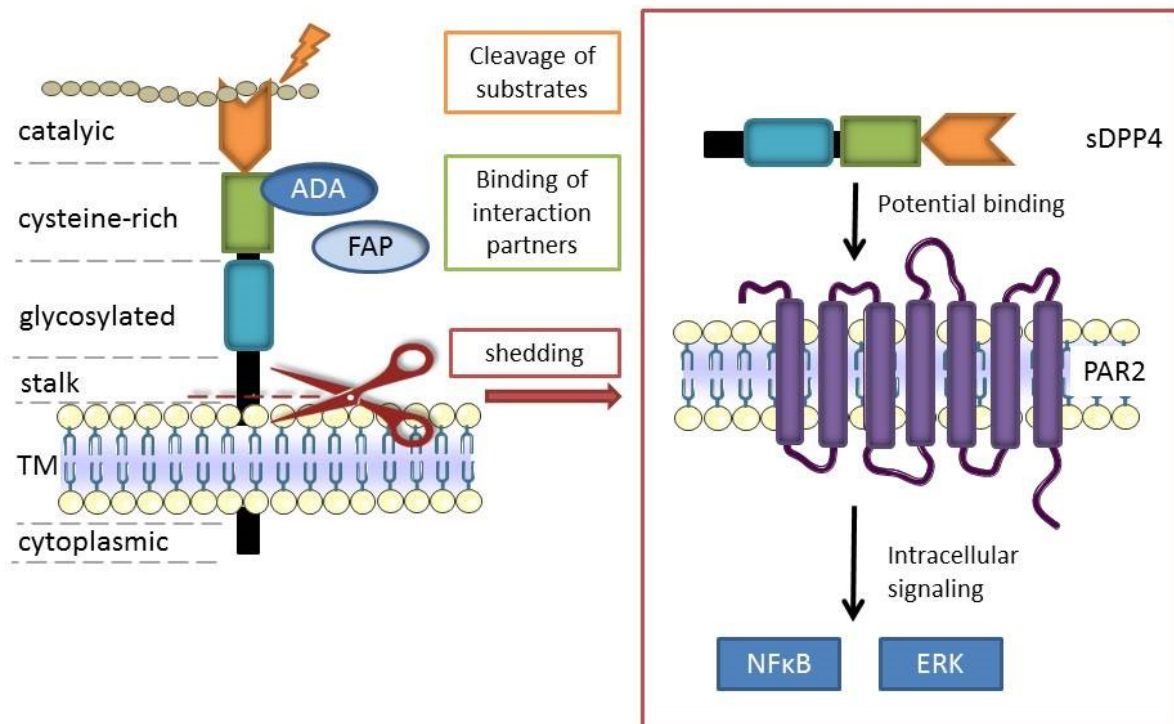


FIGURE 3: DPP4 AS A MULTIFUNCTIONAL ENZYME.

DPP4 domain architecture displays its multifunctional properties as binding partner for various proteins like FAP and ADA and its proteolytic action on numerous substrates. Upon shedding sDPP4 is released, which then is able to bind to potential receptors like PAR2. Thereby DPP4 is able to initiate intracellular signaling processes. TM transmembrane domain; ADA Adenosine Deaminase; FAP fibroblast activation protein; sDPP4 soluble DPP4; PAR2 protease activated receptor 2; NFκB nuclear factor of activated B-cells; ERK Extracellular-signal Regulated Kinase

1.3.2. DPP4 AS A NOVEL ADIPOKINE

As already mentioned above, DPP4 is ubiquitously expressed on numerous cell types. In 2011 our group was the first to describe DPP4 as a novel adipokine potentially linking obesity to the metabolic syndrome (185). In this study it was shown, that DPP4 expression and release is upregulated in a differentiation-dependent manner. Although macrophages also release DPP4, it was postulated that the major contribution of sDPP4 from adipose tissue arises from mature adipocytes, since they account for 2/3 of the cellular content within AT (185). Furthermore, it was shown that DPP4 release can be triggered by inflammatory stimuli like TNFα but also by metabolic stimuli like insulin. Both of these stimuli are especially interesting in the context of AT dysregulation during

the progression of obesity. Recombinant sDPP4 exerted direct effects on adipocytes themselves, on skeletal muscle cells (SkMc) and SMC, where it induced insulin resistance in a dose-dependent manner. This could be blocked by a specific DPP4 inhibitor. Additionally sDPP4 induced proliferation in SMC (185). Taken together, these observations illustrate the potential of sDPP4 to be involved in obesity-associated diseases like T2DM and atherosclerosis, which will be discussed in the following section in more detail.

Interestingly, serum levels of DPP4 are elevated in obese patients and positively correlate with clinical and biochemical markers like BMI, adipocyte surface area and insulin levels (185). DPP4 expression in AT biopsies of obese patients is significantly higher in visceral than in subcutaneous fat, and the release of DPP4 from these biopsies correlates with parameters of the metabolic syndrome (MetS) (185;186). Together with the fact that insulin-sensitive obese patients release significantly less DPP4 than obesity-matched insulin-resistant patients, DPP4 may be a marker for visceral obesity, insulin resistance and MetS (186).

1.3.3. DPP4 AND ITS ROLE IN DIABETES

1.3.3.1. DPP4 AS A DRUG-TARGET FOR THE TREATMENT OF T2DM

DPP4 is a serine-type protease which cleaves dozens of substrates equipped with appropriate residues at the penultimate position. Although there is a clear preference for proline at this position also other residues, which possess a similar stereochemistry are accepted (187). The scientific interest in DPP4 dramatically rose with the discovery that it cleaves the incretin hormones, GLP-1 and glucose-dependent insulintropic peptide (GIP) in 1993 by Mentlein and coworkers (188). Incretin hormones are responsible for approximately 50% of the postprandial insulin secretion and are very rapidly inactivated upon DPP4 cleavage. This discovery promoted the development of DPP4 inhibitors as a treatment option for T2DM. After sitagliptin was approved in 2006, more and more of these inhibitors with improved pharmacologic functions came to the market (189;190). They can be classified into two subgroups, peptidomimetics (sitagliptin, teneligliptin, vildagliptin, saxagliptin and anagliptin) and non-peptidomimetics (alogliptin and linagliptin) (reviewed by (191)). The disadvantage of the first developed inhibitors was their unstability and unselectivity for DPP4. Because they possessed an electrophilic trap such as a nitrile group, they build a covalent bond

with Ser630 of the catalytic triad, which is very conserved and also present in family members like DPP8 and DPP9 (192). This was improved during the further development of the inhibitors. Gliptins are orally administered drugs that prevent the rapid degradation of incretins, thereby raising the postprandial levels of active GLP-1 and GIP which leads to an improved glycemic control. Upon cleavage by DPP4 both GLP-1 and GIP lose their receptor activating properties (193;194). It is even reported that cleaved GIP is a weak antagonist of its receptor *in vivo* (195). The majority of effects seen upon DPP4 inhibitor treatment are addressed to the rise in GLP-1 levels. DPP4i are able to lower DPP4 activity by 70-90% and a clear benefit of a gliptin therapy is the indifference on bodyweight and a low risk of hypoglycemia in patients (196). As already mentioned before, DPP4 serum levels are elevated in obese patients and circulating levels and DPP4 release from AT is linked to parameters of the MetS (185). So it can be speculated that enlarged visceral adipocytes might substantially contribute to augmented sDPP4 levels during obesity (197). Interestingly, there are more and more beneficial effects of DPP4i reported that go beyond the incretin axis. *Ex vivo* and *in vitro* studies on effects of acute DPP4 inhibition by vildagliptin revealed Src-Akt-eNOS mediated nitric oxide release, which leads to vasodilation (198). Another example is a study by Shirakawa and colleagues, who could show that AT hypertrophy and linoleic-acid induced inflammation is prevented upon des-fluoro sitagliptin treatment in a specific mouse model (199). Because of a lack of GLP-1 receptors in AT, these effects have to be mediated incretin-independently, most likely through alternative DPP4 substrates.

In addition to the incretin hormones, there are other substrates of DPP4 that might be linked to its important role in diabetes. One of these substrates is stromal cell derived factor 1 α (SDF-1 α), which is reported to protect stem-cell derived insulin-producing cells from glucotoxicity (200). Furthermore, SDF-1 α enhances β -cell survival via Akt activation (201). Also the polypeptide family with its members peptide YY (PYY) and neuropeptide Y (NPY) are involved in β -cell survival and improved glucose homeostasis and are known physiological targets of DPP4. Upon DPP4 truncation, the affinity of these peptides towards their receptors is shifted thereby altering their biological function (202;203). Substance P is another physiological substrate of DPP4, which is reported to promote insulin resistance in preadipocytes *in vitro* (204).

All of these data indicate that obesity-associated processes like inflammation, AT hypertrophy and insulin resistance are closely linked to DPP4 expression and release by AT.

1.3.3.2. DPP4 DEFICIENCY IN ANIMAL MODELS

DPP4 deficiency is preferentially studied in rodents. In rats with a loss of function mutation in the DPP4 gene, which leads to a global KO phenotype, insulin resistance was induced by high fat diet (HFD)-challenge (205). These DPP4-deficient rats showed an improved homeostatic model assessment-insulin resistance (HOMA-IR) value and improved oral glucose tolerance test (oGTT) which was attributed to higher levels of active GLP-1. This in turn also leads to improved insulin levels. Furthermore, it could be shown that these rats are characterized by an improved lipid profile and improved insulin sensitivity. Additionally, improved adipocyte maturation could be observed in parallel to less AT inflammation in DPP4-deficient rats (206). The same group also observed an improved liver function under HFD (207). Basically the same improvements were also shown in global DPP4 KO mice. In addition to displaying an improved glucose tolerance (208), also improved insulin sensitivity with sustained islet morphology was described in global DPP4 KO mice (209). KO mice also showed an improved liver biology in respect of lipid accumulation and gene expression levels, like already described for DPP4-deficient rats (209). A drawback of these animal models is, however, that central regulation of food intake is impaired by DPP4 KO. This impedes to dissect the role of DPP4 in metabolic complications under diet-induced obesity, as animals consume less food and gain less weight. Another disadvantage of these models is the fact that the global KO also affects immune cells. Infiltration of these cells plays a central role in obesity-related AT inflammation and might be modulated by DPP4 deficiency. Furthermore, the role of selected organs in the contribution to circulating levels of DPP4 remains unclear.

1.4. OBJECTIVES

Obesity is a hallmark of the metabolic syndrome and increasing at an alarming rate worldwide. The fact that it increases the risk for cardiometabolic diseases or the development of T2DM highlights how important it is to understand the progression and causes of this disease. During obesity, AT needs to store excess lipids in lipid droplets and this leads on one hand to AT hypertrophy, but also to a recruitment and differentiation of novel adipocytes. However, at some point AT is no longer able to sustain its normal function, and not only more free fatty acids (FFA) and triglycerides are released, but also a shift towards a more proinflammatory secretion of adipokines occurs. Both facts are associated with increasing insulin resistance in peripheral organs such as skeletal muscle or liver. Currently we believe that adipokines display the missing link between obesity, insulin resistance and β -cell dysfunction during AT expansion (210). To combat the metabolic complications it is necessary to understand the role and function of adipokines. One of these adipokines which was identified by comprehensive proteomic profiling of the adipocyte secretome was DPP4 (91). Because of its incretin inactivating property, DPP4 is already a key therapeutic target for the treatment of T2DM. Furthermore, it was already known that it is dysregulated in obese subjects especially in visceral AT and that mature adipocytes might be the most important source of sDPP4 within AT (185;186).

- As a member of the type II transmembrane protease family DPP4 is not classically secreted, but cleaved off the cell surface in a process called shedding. However, which enzymes are contributing to the shedding of DPP4, and how this process is regulated remains elusive. The first objective of this thesis was to identify the enzymes involved in DPP4 shedding from human adipocytes and human SMC, and to elucidate the regulation of this process *in vitro*. Therefore, human adipocytes and SMC were treated with different protease inhibitors and the impact on DPP4 release was assessed. Furthermore, the influence of low oxygen levels on the release of DPP4 and the expression of involved proteases was analyzed.
- Although DPP4 is a well characterized adipokine, which potentially links obesity to the metabolic syndrome, and might be a marker for visceral obesity and insulin resistance, the role of DPP4 within adipose tissue is unknown so far. The second objective of this thesis was to elucidate the role of DPP4 within human adipocytes *in vitro*. This was addressed by siRNA-mediated silencing of DPP4 throughout adipocyte differentiation and the impact on differentiation,

inflammation and secretory output of adipocytes was analyzed. Furthermore, the influence of DPP4 silencing on adipocyte function in respect of insulin signaling was assessed. Additionally, to investigate whether the seen effects can be allocated to the enzymatic function of the protein, selected experiments were repeated after administration of the well-known DPP4 inhibitors sitagliptin and saxagliptin.

Although generation of global DPP4 knock-out (KO) mice has already shown an improvement in glucose tolerance, and a resistance to diet-induced obesity and insulin resistance (209), it remains difficult to dissect the role of DPP4 on peripheral metabolism since the food intake is affected by the KO. Furthermore, a global KO also leads to an ablation of DPP4 in immune cells, which are critical components in the development of AT inflammation during the progression of obesity. It is also unclear how much AT contributes to the level of circulating DPP4, and how this affects general insulin sensitivity in peripheral organs like liver or skeletal muscle.

- Based on our previously published data it might be speculated that AT is a key source for circulating DPP4 during obesity. To address which role AT-derived DPP4 plays in the development of obesity-associated disorders like T2DM, we developed a unique AT-specific DPP4 KO mouse model. These mice were challenged with a high fat diet (HFD) to characterize the impact of AT-derived DPP4 on the metabolic phenotype. Furthermore, the role of DPP4 within AT was assessed *in vivo* and *ex vivo* by analyzing the AT phenotype and metabolic parameters like marker gene expression.

2. PUBLISHED STUDIES

2.1. STUDY 1: DPP4 IN DIABETES

DPP4 IN DIABETES

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Published in: Front Immunol. 2015 Jul 27;6:386. doi: 10.3389/fimmu.2015.00386. eCollection 2015. Review.

Keywords: CD26/DPP4, soluble DPP4, type 2 diabetes mellitus, incretins, DPP4 inhibitors/Gliptins, multifunctional enzyme

Dipeptidyl peptidase 4 (DPP4) is a glycoprotein of 110 kDa, which is ubiquitously expressed on the surface of a variety of cells. This exopeptidase selectively cleaves N-terminal dipeptides from a variety of substrates, including cytokines, growth factors, neuropeptides, and the incretin hormones. Expression of DPP4 is substantially dysregulated in a variety of disease states including inflammation, cancer, obesity, and diabetes. Since the incretin hormones GLP-1 and GIP are major regulators of post-prandial insulin secretion, inhibition of DPP4 by the gliptin family of drugs has gained considerable interest for the therapy of type 2 diabetic patients. In this review, we summarise the current knowledge on the DPP4 - incretin axis, and evaluate most recent findings on DPP4 inhibitors.

Furthermore, DPP4 as a type II transmembrane protein is also known to be cleaved from the cell membrane involving different metalloproteases in a cell-type specific manner. Circulating, soluble DPP4 has been identified as a new adipokine which exerts both para- and endocrine effects. Recently, a novel receptor for soluble DPP4 has been identified and data are accumulating that the adipokine-related effects of DPP4 may play an important role in the pathogenesis of cardiovascular disease. Importantly, circulating DPP4 is augmented in obese and type 2 diabetic subjects and it may represent a molecular link between obesity and vascular dysfunction. A critical evaluation of the impact of circulating DPP4 is presented and the potential role of DPP4 inhibition at this level is also discussed.

INTRODUCTION

Dipeptidylpeptidase (DPP) 4, which is also known as CD26, is a ubiquitously expressed glycoprotein of 110 kDa, which was first characterized by Hopsu-Havu and Glenner 1966 (1). DPP4 is a type II transmembrane protein, which is also cleaved off the membrane and released into the circulation by a process called shedding (2;3). The importance of DPP4 for the scientific and medical community raised substantially since the approval of DPP4 inhibitors for the treatment of type 2 diabetes mellitus (T2DM). These so called gliptins increase the incretin levels and therefore prolong the postprandial insulin action. Since soluble DPP4 is characterized as an adipokine (4) and also correlates with parameters of the metabolic syndrome (5), it might also be an important molecular biomarker. DPP4 is a multifunctional enzyme which serves as a binding partner for numerous peptides amongst which are adenosine deaminase (ADA) and extracellular matrix proteins (2;6;7). Moreover, as a serine protease DPP4 cleaves numerous substrates, which further amplifies its complexity of action. Thus, DPP4 is involved in signaling processes, immune cell activation, and its dysregulated expression and release is associated with numerous diseases.

In the present review we wanted to emphasize the complex function of DPP4 with special focus on its association to T2DM. Furthermore, we wanted to offer a different perspective of the current view of DPP4 beyond the inhibition of its protease activity (8-10). The first part of the present review is dealing with general informations about DPP4 and its

numerous biological functions in regard to T2DM and its treatment. The last section collects the current knowledge about how DPP4 with its pleiotropic functions, as described before, affects several organs, thereby playing a pivotal role in the development of T2DM and its comorbidities.

GENERAL INFORMATION ON DPP4

BIOLOGY OF DPP4

The following part will deal with the domain architecture and respective relevance of these domains for the functionality of DPP4.

DPP4 (EC3.4.14.5) is a type II transmembrane protein which groups together with fibroblast activation protein α (FAP), the resident cytoplasmic proteins DPP8 and DPP9 and the non-enzymatic members DPP6 and DPP10 to the serine peptidase subfamily S9B. All of these proteins share a typical α/β hydrolase fold (2;6). The DPP4 protein consists mainly of 4 domains: a short cytoplasmic domain [1-6], a transmembrane domain [7-28], a flexible stalk segment [29-39], and the extracellular domain [40-766], which can be further separated by a highly glycosylated region, the cysteine-rich region and the catalytic region (Fig. 1).

As a member of the type II transmembrane proteins DPP4 contains a typical signal peptide which is necessary for the targeting to the endoplasmatic reticulum and the initiation of the translocation across the cell membrane. In contrast to the classically secreted proteins the signal peptide is not cleaved off, but serves as a membrane anchor. We were able to show that the circulating

form of DPP4 (sDPP4), which lacks the cytoplasmic domain and the transmembrane region, is cleaved off the membrane of human adipocytes and smooth muscle cells in a process called shedding by involvement of matrix metalloproteases (3).

Within the transmembrane domain (TMD) it could be shown that proline residues play an important role for the translocation of membrane-anchored proteins such as DPP4. Chung and colleagues (11) studied single proline substitution throughout the TMD of DPP4. They were able to show that translocation and integration into the membrane are determined by the hydrophobicity, conformation and also the location of proline within the TMD. Furthermore, the position of proline relative to other prolines and the location of highly hydrophobic residues within the TMD are

important for correct translocation and membrane-integration of DPP4.

In addition to the TMD also the glycosylation of DPP4 is also important for the correct trafficking of DPP4. Carbohydrates account for approximately 20% of the total molecular mass of DPP4 and cause heterogeneity of this protein depending on the location on different cell types. Two highly conserved glutamate residues (205 and 206) within the glycosylated region are essential for the activity of DPP4 (12). Interestingly, six of the nine N-glycosylation sites are located within the glycosylated region. These glycosylation sites are mostly conserved among species. They are necessary for folding, stability and intracellular trafficking (13). Other modifications like sialylation and/or O-glycosylation have an impact on targeting DPP4 to the cell membrane. Sialylation of DPP4 increases

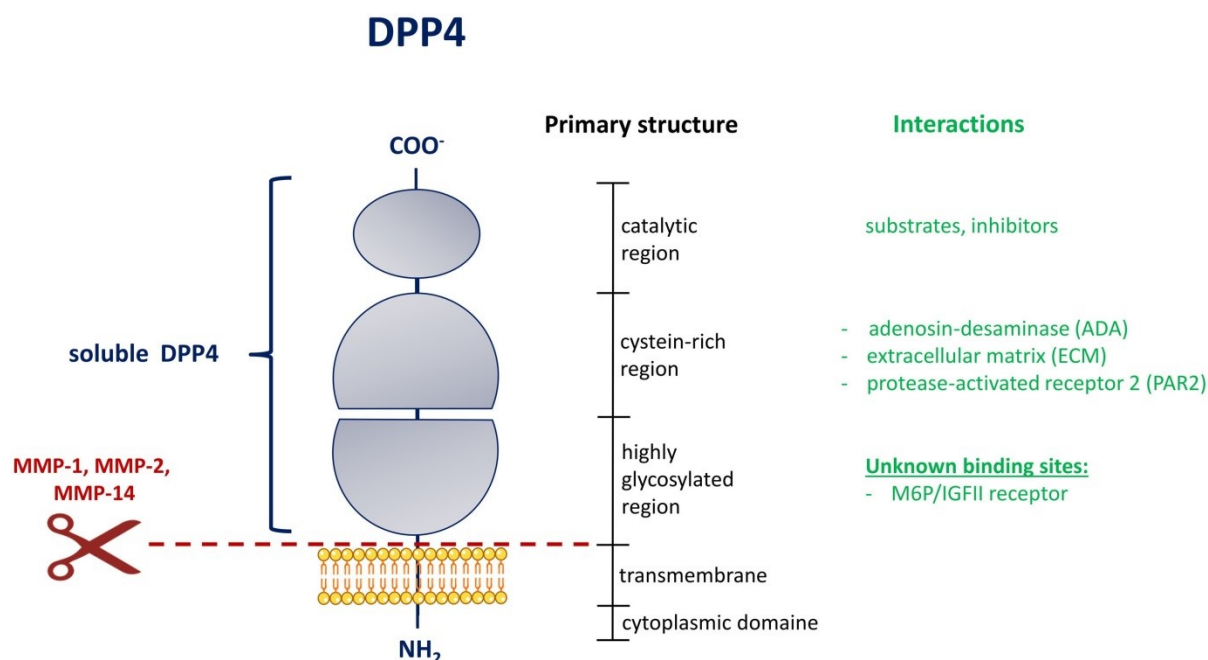


FIGURE 1 | Domain structure of DPP4 [adapted from Ref. (2)]. Schematic representation of the membrane-bound DPP4 monomer. The extent of the circulating and soluble form of DPP4 is illustrated on the left in blue. The shedding of DPP4 from the membrane by indicated matrix metalloproteinases is shown by a scissors symbol in red. The vertical black bar on the right represents the primary structure with the delineation of the different regions. In green are interactions collected, which occur in the indicated region of the DPP4 structure. MMP, matrix metalloproteinase; M6P/IGFII, mannose-6 phosphate/insulin-like growth factor 2.

significantly with age and hypersialylation occurs in patients with HIV-infection (14). Not only glycosylation and residues within the TMD are important for the cellular function of DPP4 but also dimerization. DPP4 can be found as monomer, as homodimer or even as homotetramer on the cell surface of cells. DPP4 needs dimerization for enzymatic activity and this form is the predominant form of DPP4 (15). Dimerization occurs upon interaction with DPP4 itself or with other binding partners e.g. FAP (16;17), and occurs via interaction with the cysteine rich region. Through its interaction with several proteins DPP4 can act also in an enzymatic activity-independent way. Through this interaction DPP4 is linked to various mechanisms like immune response and tumor invasion. The heterodimerization and interaction with different binding partners will be discussed in a later section.

The serine in the active site of DPP4 is located in the sequence Gly-Trp-Ser-Tyr-Gly and is part of the catalytic triad (Ser 630, Asp 708, His 740) within the catalytic region of DPP4. DPP4 is an exopeptidase which cleaves dipeptides from the penultimate N-terminal position of its substrates and thereby either inactivates these peptides and/or generates new bioactive compounds (7). There are numerous different DPP4 substrates known to date and they will be addressed in a separate section within this review.

DPP4 EXPRESSION AND ITS REGULATION

DPP4 is ubiquitously expressed on numerous different cell types among which are epithelial cells, fibroblasts and leukocyte subsets. Mechanisms that regulate DPP4 gene transcription and enzymatic activity are not fully

understood so far and may be dependent on the studied cell type.

The human DPP4 gene is located on chromosome 2, spans 70 kb and consists of 26 exons (2). The DPP4 promoter region contains consensus sites for different transcription factors like NF κ B, SP-1, EGFR and AP-1 factor NF-1(18). At least in chronic b lymphocytic leukemia cells it could be shown that there is a consensus interferon γ -activated sequence (GAS) which is a binding motif for STAT1. The interferons α , β and γ stimulate STAT1 α binding to this region and thus lead to an increased DPP4 expression and activity (19). Interleukin (IL) 12, which is a key factor in differentiation of naïve T-cells into the Th1 subtype, is also able to upregulate DPP4 expression. Therefore DPP4 is important in immune cell activation (20;21). Our group was able to show that release of soluble DPP4 is increased upon TNF α stimulation and insulin *in vitro* (4). However IL-12 and TNF α also seem to play a regulatory role in translation and translocation of DPP4. In activated lymphocytes IL-12 upregulates DPP4 translation whereas TNF α decreases cell surface expression, which might be due to elevated sDPP4 release (22). Also transcription factors, such as HIF-1 α and HNFs target DPP4 expression (23), which fits to the observation of our group that hypoxia induces DPP4 release in human smooth muscle cells, which might be mediated by MMPs (3).

NON-ENZYMATIC INTERACTIONS OF DPP4

Through its cysteine-rich region which is separated from the catalytic region, DPP4 is able to interact with different proteins, and further broadens its spectrum of

activity and highlights its multifunctional role in different processes.

BINDING PARTNERS OF MEMBRANE-BOUND DPP4

The best studied interaction in this regard is certainly the binding of DPP4 and adenosine deaminase (ADA). It was already identified in 1993 by Morrison and colleagues (24). Importantly, the interaction of DPP4 and ADA preserves the enzymatic function of both binding partners. It has been shown that residues 340-343 of DPP4 are essential for the interaction with ADA. Regulation of the DPP4/ADA interaction occurs e.g. via tetramerisation of DPP4 or glycosylation at Asn281 which interferes with ADA binding (25). Also the HIV envelope glycoprotein gp120, which interacts with DPP4 on lymphocytes via its C3 region, is able to inhibit the association with ADA (2). Upon ADA binding, activation of plasminogen-2 occurs, which raises plasmin levels. This leads to a degradation of matrix proteins and an activation of matrix metalloproteases (MMP), thereby indicating that the interaction of DPP4 and ADA might be involved in tissue remodeling (26).

Furthermore, ADA catalyzes the irreversible deamination of adenosine and 2'-deoxyadenosine and is therefore a crucial player in the cellular and humoral immunity. Via interaction with CD45 the complex of ADA and DPP4 enhances T-cell activation. Interestingly, DPP4 is also able to promote T-cell proliferation independent from ADA binding or even its enzymatic activity (27). Zhong *et al.* were able to show that the interaction of DPP4 and ADA on dendritic cells might potentiate inflammation in obesity upon activation and proliferation of T-cells,

which could be competitively inhibited by exogenous sDPP4, but not by inhibiting DPP4 enzymatic function (28). Furthermore, ADA activity is elevated in T2DM patients and may serve as a marker of inflammation and obesity (29).

Beside its role in inflammation adenosine is also an important player in glucose homeostasis. Already in 1988 it was shown that by lowering endogenous adenosine levels, ADA contributes to a reduced insulin sensitivity of glucose transport stimulation (30). Additionally, adenosine seems to facilitate insulin action in adipocytes (31). Another study could show a correlation of increased ADA activity in T2DM with fasting plasma glucose, HbA1c, aspartate and alanine aminotransferase. DPP4-inhibitors exert no additional effects on ADA activity despite glycemic control or HbA1c-dependent effects (32). All these studies emphasize that the effects of ADA/DPP4-interaction are independent of DPP4 enzymatic activity.

Another known interaction partner of DPP4 is Caveolin-1 which is present on antigen presenting cells (APCs) and binds to residues 630 and 201-211 of DPP4 expressed on T-cells. Thereby an upregulation of CD68 occurs and initiates a signaling cascade which might be implicated in the pathogenesis of arthritis, and may be relevant for other inflammatory diseases as well (33). Intracellular signaling is also initiated by DPP4 via interaction with Caspase recruitment domain containing protein 11 (CARMA-1) (6).

Another well-known interaction of DPP4 is with extracellular matrix proteins like collagen and fibronectin (34;35). The interaction of DPP4 with fibronectin was

revealed via nitrocellulose binding assays in rat hepatocytes and seems to play a role in the interaction of these cells with the ECM and with matrix assembly (36). Interaction of DPP4 with FAP α leads to a local degradation of ECM and thus migration and invasion of endothelial cells (37).

POTENTIAL RECEPTORS FOR sDPP4

Since DPP4 is shedded from the membrane of cells with intact enzymatic and cysteine-rich region, it can also exert biological functions in a paracrine or endocrine manner. These functions might also involve intracellular signaling events in the targeted cells. Therefore it would be of great importance to know receptors of sDPP4 to better understand the multiple role of sDPP4 on different cells and in different disease conditions where serum levels are elevated. However, there is not much known about DPP4 receptors so far. Ikushima *et al.* were able to show that DPP4 needs to associate with mannose-6-phosphat/IGFIIR to exhibit its function as T-cell activator. This is due to the fact that for this activation, internalization of DPP4 is necessary, but DPP4 lacks a signal for exocytosis. The binding with M6P/IGFIIR occurs via M6P residues in the carbohydrate moiety of DPP4 and the complex is then internalized and able to exert its biological function (38).

Our group showed that at least in human vascular smooth muscle cells protease activated receptor 2 (PAR2) might be activated by sDPP4. We were able to show that sDPP4-mediated ERK activation and proliferation, as well as upregulation of inflammatory cytokines could be prevented by silencing of PAR2. The same was shown by use of a specific PAR2 antagonist. We propose that sDPP4 acts as

an activator of PAR2, since a sequence within the cysteine-rich region of DPP4 is highly homologous to the auto-activating tethered ligand of PAR2 (39).

GENETIC ALTERATIONS OF DPP4 AND PREDISPOSITION TO T2DM ASSOCIATED DISEASES

There are only few studies aiming to identify modifications in the DPP4 gene and their association with T2DM. Some of these are reviewed in the following section.

In 2009 Bouchard *et al.* analyzed single nucleotide polymorphisms (SNPs) in the DPP4 gene and searched for association with blood pressure, lipids and diabetes-related phenotypes in obese individuals, to verify whether DPP4 gene polymorphisms could explain the individual risks of obese patients to develop metabolic complications. Three of the analyzed SNPs showed significant association with plasma total-cholesterol levels or plasma triglyceride level or total cholesterol level. But none of the polymorphisms or cardiovascular disease risk factors showed a significant correlation with DPP4 mRNA levels in omental adipose tissue. Therefore, the authors concluded that at least in their studied group DPP4 gene polymorphisms seem to be unrelated to the inter-individual risk of developing obesity-related metabolic complications (40).

In another study visceral adipose tissue DNA of 92 severely obese, non-diabetic female patients was analyzed for methylation rate in the DPP4 promoter CpG island, and compared between different DPP4 polymorphisms. These cysteine and guanine rich regions are prone to epigenetic modification like methylation, and thus inactivate or

activate transcription of certain genes. Different methylation levels of the DPP4 gene were identified in three DPP4 SNPs. Interestingly, the methylation level was negatively associated with DPP4 mRNA abundance and positively with plasma total/HDL-cholesterol ratio. These observations suggest that plasma lipid profile is improved by a higher methylation status of the investigated CpGs (41). Two years later the same group analyzed DPP4 gene methylation levels between obese subjects with and without the metabolic syndrome in visceral adipose tissue. They observed no significant difference in the percentage of methylation levels of the CpGs within or near the second exon of the DPP4 gene between non-diabetic severely obese subjects with or without metabolic syndrome. However, they were able to show a correlation between plasma cholesterol levels and the percentage of methylation when the subjects were classified into quartiles (42). This further underpins a link between epigenetic modification of the DPP4 gene and plasma lipid metabolism.

Aghili N. *et al.* analyzed 875 patients with angiographically documented coronary artery disease (CAD), and divided them in two subgroups dependent of their myocardial infarction (MI) status. By a genome-wide association study, loci which predispose to MI were assessed and associated with SNPs in the DPP4 gene. They found that polymorphisms in the DPP4 gene increase the risk of MI and progression of atherosclerosis in terms of plaque stability in patients with already existing CAD. Especially one SNP was identified in both dominant and additive inheritance modes, which associates with

low plasma DPP4 levels and which may increase the risk of MI in CAD patients (43).

Dyslipidemia which is characterized by excessive lipids in the blood is a common feature of T2DM. The status of this risk factor is quantifiable by the measurement of apolipoprotein B (ApoB) in the blood. In a very recent study by Baileys and colleagues they aimed to identify novel SNPs associated with ApoB level. Especially in South Asians which tend to develop risk factors for T2DM and MI at younger ages and lower BMI they found an association of a DPP4 SNP with ApoB level (44).

THE DPP4 DEFICIENCY IN ANIMAL MODELS

To date there are several studies dealing with the question which role DPP4 plays *in vivo*. Animal models are useful tools to study the involvement of DPP4 in different organs. Upon triggering different diseases like insulin resistance (IR) or myocardial infarction (MI) it is possible to understand the role of DPP4 in these comorbidities of T2DM.

DPP4 DEFICIENCY IN RATS

A major part of the literature is dealing rather with DPP4-KO in rats than in mice. Most research groups work with the F344/DuCrj (DPP4 deficient)-strain. Rats developing insulin resistance due to high-fat diet (HFD) feeding showed improved HOMA-IR values and blood glucose levels in oral glucose tolerance test (oGTT) and more active GLP-1 and insulin in plasma (45). The same improved glucose tolerance with increased GLP-1 and leptin levels was found in DPP4 depleted Dark Agouti rats with diet-induced obesity (46).

Another research group also found improvement in serum lipid profile despite increased visceral fat. They also performed insulin tolerance tests (ITT) in addition to GTT and saw an increased phosphorylation of Akt and reduced expression of gluconeogenic genes, concluding that DPP4-KO improved insulin sensitivity. Furthermore, the KO rats showed increased adipocyte maturation by increased expression of genes involved in triglyceride uptake and in PPAR γ expression and increased adiponectin and leptin levels. In addition, adipose tissue is less inflamed illustrated by lower TNF α , IL-6, PAI1 and CCL7 levels (47). The observed effects were attributed to elevated GIP levels in the KO rats. Furthermore, the same group could also show attenuated liver damage under HFD challenge in the KO rats due to improved bile secretory function. They postulate that the enhanced export of bile acids out of hepatocytes and a reduction of bile acid synthesis via inhibition of CYP7A1, which converts cholesterol to bile acids, were mediated by increased GLP-1 in DPP4 KO rats (48). Interestingly, at least Yasuda and colleagues also saw a significant reduced food intake in the KO rats irrespective of the diet (45) which might be due to changed receptor-specificity of NPY, which was shown to be more potent in KO rats to influence food intake and feeding motivation (49). Although several independent working groups saw increased NPY levels in KO rats (49-51), the effect on food intake is controversial (45;50). When diabetes is induced via streptozotocin (STZ) treatment in F344/DuCrj-DPP4-deficient rats, onset of hyperglycaemia was delayed, but KO rats showed impaired creatinine clearance and more severe dyslipidemia, which might be

caused by a dysregulated expression of factors involved in steroid and lipid metabolism (52;53). The authors concluded that DPP4 might be responsible for preservation of renal function. Another effect of the whole-body KO of DPP4 in rats is induction of behavioural changes like a blunted stress phenotype (46;51) and also effects on the immune-regulatory system like blunted NK cell and T-cell function and differential leukocyte subset composition or altered cytokine levels (46;47).

DPP4 DEFICIENCY IN MICE

Most of the observations already described in deficient(54;55) rats are also true in whole-body DPP4 KO mice. Marguet *et al.* showed enhanced glucose tolerance, lower plasma glucose and higher plasma insulin and GLP-1 after a 15 min oral glucose load without further characterizing the diet, age or sex of the used C57BL/6 DPP4 KO mice (56). Conarello and colleagues found less weight-gain independent of the diet, and marked hypertrophy in the HFD-fed KO mice in epididymal white (eWAT) and brown adipose tissue (BAT). Importantly, they admitted that the reduction in caloric intake accounted for ~70% of the observed changes in bodyweight. Although they still observed differences in the bodyweight between KO and WT when they used pair-feeding, they carried out their further analysis in ad libitum fed mice and it is therefore difficult to judge the influence of DPP4 irrespective of bodyweight. However, they found improved insulin sensitivity and islet morphology, and improved liver biology in respect to lipid content and marker gene expression (57). The observation that DPP4 might be involved in the immune-

regulatory system was also investigated in DPP4-KO mice, which were treated with pokeweed mitogen which stimulates growth and proliferation of B-cells. DPP4 seems to be involved in maturation and migration of immune cells, cytokine secretion and percentages of spleen lymphocytes (58).

All these studies have in common that they use whole-body KO animals. The disadvantage here is that one cannot distinguish between direct effects of the KO and side effects caused for example by different immune cell status or decreased caloric intake. To really decipher the role of DPP4 in different tissues and their crosstalk with other target tissues it is of great importance to study tissue-specific KO models.

Because of this and because we were the first to describe DPP4 as a novel adipokine linked to parameters of the metabolic syndrome (4), we decided to develop an adipose tissue-specific KO mouse model. The AT-specific DPP4 KO mouse was generated using a Cre-lox strategy under control of the aP2 promoter on the C57BL/6J background. Interestingly, we found out that KO mice gained significantly more weight, fat and lean mass under HFD with no effect on energy expenditure or food intake. However, KO mice showed improved HOMA-IR and lower fasting insulin. The observations that within AT KO mice display a shift towards significantly more smaller adipocytes, and an increased expression of M2 macrophage marker genes, points towards a beneficial role of DPP4 deletion in adipose tissue remodeling during HFD (54;55).

ENZYMATIC FUNCTION OF DPP4

DPP4 exerts its enzymatic action by clipping dipeptides from the penultimate position of its substrates. The active center, which is housed in an internal cavity, is surrounded by the β -propeller domain and the catalytic domain. Inhibitors and substrates enter/leave the active center by a so-called “side opening” (59;60). The following section deals with known substrates of DPP4 in respect of T2DM, and with DPP4 as a drug target for T2DM treatment, which will include current knowledge on DPP4-inhibitors and the impact of DPP4 on organs involved in complications of T2DM.

DPP4 SUBSTRATES

In theory, numerous peptides are potential DPP4 substrates since they contain the cleavable amino acid sequence at their penultimate position, but not for all of them it could be shown that DPP4 is able to cleave them *in vivo*. There seems to be a size limitation at least for cytokines, where DPP4 is more prone to cleave substrates of around 24 amino acids (aa) length. Furthermore the substrate recognition is also dependent on the aa sequence around the penultimate position (61;62). It turned out to be difficult to find physiological targets of DPP4 in the literature, reasons of that are excellently summarized in a recent review by Mulvihill and Drucker (6). We decided to focus here on the (potential) substrates of DPP4, which might play a role in T2DM or its complications. The list of DPP4 substrates mentioned here is not fully complete and aims to highlight the importance of DPP4 in T2DM also beyond its well-known incretin effect.

INCRETIN HORMONES

The incretin hormones account for approximately 50 % of the insulin secretion after meal intake and are secreted from the gut within minutes after the meal intake. Through binding to distinct receptors on beta-cells in the pancreas they stimulate insulin secretion and suppress glucagon release depending on the blood glucose level. Most potent in their glucose-lowering action are glucagon-like peptide 1 (GLP-1) and glucose-dependent insulintropic polypeptide (GIP). Both peptides belong to the same glucagon peptide superfamily and share significant aa character.

GLP-1 is secreted from L-cells of the gut into the bloodstream. Upon binding to G-protein coupled receptors on the beta cells, intracellular cAMP level is elevated and the protein kinases Epac1 and 2 are activated, which leads to an increase of insulin secretion. Furthermore, GLP-1 enhances beta-cell mass by mediating proliferation and differentiation and inhibiting apoptosis (8). By inhibiting gastric emptying GLP-1 also improves blood sugar excursion, delays food absorption, and is therefore a regulator of satiety and appetite also through the hypothalamus (63).

GIP is a 42 aa peptide which mainly originates from enteroendocrine K-cells (64). Subjects with diabetes or impaired glucose tolerance show significantly reduced levels of meal-stimulated circulating GIP and the levels are negatively correlated with the severity of insulin resistance in the patients (65;66). GIP has in contrast to GLP-1 no effect on glucagon secretion, but also regulates fat metabolism in adipocytes (67).

Since inhibition of DPP4 due to genetic deletion or use of DPP4-inhibitors was shown to elevate GLP-1 / GIP levels in

numerous studies, this effect is the main focus of developing therapeutic targets for treatment of T2DM. There are numerous reviews which focus on DPP4 and GLP-1 mediated effects and this will topic not be further discussed here.

STROMAL CELL-DERIVED FACTOR 1A (SDF-1A)/ CXCL12

This factor is important in the homing of stem cells and is thus discussed in the literature as one of the mediators of cardioprotective effects addressed to the use of DPP4-inhibitors. It is a well-known physiological target of DPP4 (68;69). SDF-1 α also plays a role in diabetes itself by protecting stem-cell derived insulin-producing cells from glucotoxicity under high glucose conditions (70) or promoting pancreatic beta cell survival in mice via Akt activation (71). Furthermore, it was shown that some genetic variants of SDF-1 α are associated with late stage complications in T2DM patients (72;73).

NPY AND PYY

Neuropeptide Y and Peptide YY are members of the polypeptide family. They are highly expressed in the hypothalamus but are also present in peripheral tissues like islets. NPY regulates energy balance, memory and learning, while PYY reduces appetite, inhibits gastric motility, and increases water and electrolyte absorption in the colon (74). Both NPY together with PYY play a role in beta cell survival and in glucose homeostasis (74). NPY is able to suppress insulin secretion acutely (75). Both polypeptides have in common that DPP4 truncation shifts their receptor specificity and thus alters their biological role in different cellular processes. *In vitro* experiments in adipocytes could show that DPP4 inhibition has an impact on lipid metabolism mediated by NPY (76;77).

SUBSTANCE P

Substance P is a physiological target of DPP4 which is sequentially converted to SP [3-11] and SP[5-11] *in vivo* in F344-DPP4 positive rats (78). SP is a neurotransmitter and -modulator which is involved in neurogenic inflammation. Serum levels in diabetes are controversially discussed with one study showing a decrease in diabetic patients (79), and another one showing an increase in fasting blood samples with correlation to diabetic risk factors like BMI and blood pressure (80). This discrepancy in serum levels could be addressed to the fact that it is not always stated which form of SP (full length vs. truncated) is measured. However, SP was shown to promote insulin resistance *in vitro* in human preadipocytes by interacting with proteins that are involved in the inhibitory phosphorylation of IRS-1. Furthermore, SP can directly inhibit insulin-dependent glucose metabolism in rat adipocytes (81). SP also promotes diabetic corneal wound healing, as shown by Yang and colleagues (82).

BRAIN NATRIURETIC PEPTIDE (BNP)

BNP is responsible for vasodilation, natriuresis and suppresses renin secretion. It is so far only a predicted DPP4 substrate, which was cleaved *in vitro* by DPP4 to BNP[3-32]. This truncation was inhibited by a DPP4-inhibitor in a dose-dependent manner (83). Truncated forms of BNP with lower enzymatic activity are discussed as an indicator of heart failure severity. In 2013, dos Santos *et al.* could show an improved cardiac performance in sitagliptin-treated rats, which they attributed to increased levels of active BNP (84).

PITUITARY ADENYLATE CYCLASE-ACTIVATING POLYPEPTIDE (PACAP)

PACAP is very rapidly degraded by DPP4 to the fragments [3-27], [5-27] and [6-27]. These fragments lack PACAPs insulinotropic ability, but are no feasible treatment options for T2DM because of their actions on glucose homeostasis and glucagon secretion (85). Several studies have shown that PACAP is a powerful stimulator of insulin secretion, which enhances glucose uptake in adipocytes and augments antilipolytic action of insulin (86;87). After DPP4-inhibitor treatment in mice, PACAP-induced insulin secretion was enhanced (88). However, a proof that PACAP also plays a role in humans is lacking so far.

REGULATED ON ACTIVATION, NORMAL T-CELL EXPRESSED AND SECRETED (RANTES)/CCL5

RANTES recruits leukocytes into inflammatory sites and is cleaved by DPP4 to RANTES[3-68]. Due to this truncation, RANTES [3-68] is not able anymore to increase cytosolic calcium concentrations and to induce chemotaxis of human monocytes *in vitro*. This is explained by a shift in receptor subtype-specificity towards enhanced activation of CC-Motiv-Chemokin-Receptor 5 (CCR5) (89). Elevated serum levels of RANTES in T2DM are associated with postprandial hyperglycaemia (90). Interestingly, RANTES and its receptor CCR5 are important mediators of obesity-induced inflammation which was shown in CCR5 KO mice (91). Levels of RANTES and CCR5 were reduced in adipose tissue of obese patients upon exercise (92). RANTES reduces glucose-stimulated GLP-1 secretion *in vitro* and *in vivo* in mice, by acting most probably through the intestinal glucose transporter SGLT1 (93).

EOTAXIN/CCL11

Eotaxin mediates mobilization of eosinophils into the bloodstream, which was shown to be increased in DPP4-deficient F344 rats (94). DPP4 cleaves eotaxin to eotaxin[3-74]. However there was no significant correlation of eotaxin seen in patients with T2DM or impaired glucose tolerance in the KORA cohort (95).

DPP4 AS A DRUG TARGET FOR THE TREATMENT OF T2DM

DEACTIVATION OF DPP4 ENZYMATIC ACTIVITY

DPP4-inhibitors

Major DPP4 substrates are the so called incretin hormones which are key regulators of postprandial insulin release. DPP4 inhibition leads to greater bioavailability of these proteins and therefore prolongs the half-life of insulin action. The majority of effects seen upon DPP4-inhibitor treatment are ascribed to an increase in GLP-1 levels. Because of this, DPP4 became a major target for the treatment of T2DM. This section deals with the most recent knowledge around DPP4-inhibitors, their mode of action - if known - and the newest developments in the inhibition of DPP4 enzymatic activity. There are numerous modifications and potential optimizations of the five so far approved gliptins reported. However, most of them are not in clinical trials yet and not much is known about their advantage in a head to head comparison to established gliptins. Therefore we decided to focus on the most recent data on approved gliptins in this review. The data are also summarized in Tab. 1.

DPP4-inhibitors lower DPP4 activity by 70-90%. They do not pass the blood-brain

barrier and have no direct effect on satiety or on altering gastric emptying (8). The benefit for diabetes therapy clearly is their indifference on bodyweight gain and the low risk of hypoglycemia. There are five gliptins approved so far for clinical use, namely sitagliptin, vildagliptin, saxagliptin, linagliptin and alogliptin. Another gliptin, teneligliptin is only approved in the Japanese and Korean market. Despite the same mode of action, the different gliptins diverge in their pharmacodynamic and pharmacokinetic properties, which might be clinically relevant for some patients (9;96). The peptide mimetic compounds vilda-, saxa and teneligliptin were identified by replacement experiments of peptide-based substrates, whereas the non-peptide mimetic compounds sita, alo- and linagliptin were derived from initially found inhibitors of random screenings. The diverse chemical structures also explain the unique binding modes of the inhibitors to DPP4 (10).

The six inhibitors have been classified into 3 classes depending on their different binding modes in the DPP4 active center (10). Class one contains vilda- and saxagliptin which only bind to the S1 and S2 subsites, and form a covalent bond with the nitrile group of their cyanopyrrolidine moiety and Ser630 of DPP4. Saxagliptin has a 5-fold higher activity in blocking DPP4 than vildagliptin. Group 2 contains alo- and linagliptin, which also interact with the S1' subsite or even in case of linagliptin with the S2' subsite. The uracil rings of both gliptins induce a conformational change in the Tyr547 of the S1' subsite. Because of the additional interaction of linagliptin with S2' subsite it has a 8-fold higher activity than alogliptin. The third class has the highest inhibitory function towards DPP4 because both sita-

as well as teneligliptin interact with the S2 extensive subsite of the DPP4 active center, and an increasing number of interactions seems to increase the potency of the gliptin (10). Teneligliptin which is only approved for T2DM treatment in the Japanese and Korean market so far, also has a unique structure characterized by a J-shape and an anchor lock domain, which explains the strong inhibitory function and the low IC₅₀ value of this drug (for review see (97)). The binding of the DPP4 S2 extensive subsite of some inhibitors also guarantees a high specificity towards DPP4 since other close-related peptidases like DPP8, DPP9 and FAP lack this subsite. All DPP4-inhibitors have in common that they build salt bridges with Glu-residues in the S2 subsite (10). At least for sitagliptin it is also known, that it lowers the level of free fatty acids (FFA) and thereby also comprises insulin sensitizing properties (98). Furthermore, sitagliptin was shown to have potent anti-

inflammatory properties by suppressing expression of pro-inflammatory genes in mouse and humans (98;99). In patients with renal impairment, which is a very common complication of T2DM, sitagliptin is more suitable than sulphonylureas (100).

Although some authors claim that DPP4-inhibitors are only beneficial in early stages of diabetes, this could be rebutted by the work of Kumar and Gupta (101). They could show beneficial effects of three gliptins (sita-, saxa- and vildagliptin) in lowering HbA1c also in patients with longstanding T2DM for more than 10 years. Thus, DPP4 inhibition also plays an important role irrespective of the duration of diabetes.

What has to be mentioned in respect of the beneficial roles of DPP4-inhibitors is that more and more studies about their beneficial pleiotropic effects are upcoming, which is also discussed in the following section of this review dealing

Table 1 Summarized properties of gliptins

Inhibitor	Approved since	Binding mode	Kind of inhibition	Route of excretion	IC ₅₀ value	Reference
Sitagliptin	2006 FDA	S1, S2, and S2 extensive subsites	Competitive inhibition	Mostly renal route	19 nM	(10, 98–100)
Vildagliptin	2007 European medicines agency	Only S1 and S2 subsite	Substrate–enzyme blocker	Mostly renal route	62 nM	(10, 209)
Saxagliptin	2009 FDA	Only S1 and S2 subsite	Substrate–enzyme blocker	Mostly renal route	50 nM	(10, 209)
Linagliptin	2011 FDA	S1, S2, and S1' subsites	–	Through biliary route	1 nM	(10)
Alogliptin	2013 FDA	S1, S2, and S1' subsites	Competitive inhibition	Mostly renal route	24 nM	(8, 10)
Teneligliptin	2012 Japan 2014 Korea	S1, S2, and S2 extensive subsites	Very potent because of unique anchor- lock domain and J-shape of molecule	Mostly renal route	0.37 nM	(97)

with different organs. There are reports that gliptins themselves have effects on lipid profile and blood pressure as well as on inflammatory processes (102). In addition to the incretins there are some DPP4 substrates, like SDF1 α , which might explain potential cardioprotective effects which are discussed for gliptins. However, cardiovascular outcomes are still widely debated and controversially evidenced. Ongoing long-term studies will further shed light on the respective role of DPP4i beyond glucose homeostasis. Furthermore one has to keep in mind that also DPP4 has direct effects independent of its enzymatic activity, like activation of downstream signaling events upon receptor binding, which are not well understood so far. Which role DPP4 inhibition plays on T2D relevant organs/comorbidities will be the topic of the following sections.

Alternative modes of DPP4 inhibition

Very recently Pang and colleagues published a different strategy to inhibit DPP4 activity. They used DPP4-targeted immune therapy by vaccines in a C57BL/6J mouse model and were able to show comparable effects like in treatments with gliptins regarding GLP-1 plasma levels and postprandial glucose excursion and insulin sensitivity in HFD fed mice. Furthermore they observed no side effects on immune cell activation by the DPP4 vaccine. An advantage of this

method is the long lasting effect of the vaccine in the mouse model, which could, if transferable to human patients, be a convenient alternative to the daily intake of gliptins (103). Further research in developing alternatives towards Gliptins especially for long-acting medications would be an interesting new approach to improve life-style of patients.

Incretin-Based Therapies: Comparing DPP4i and GLP-1 Analogs

It is well accepted that incretin-based therapies are able to lower blood glucose levels and are therefore a treatment option for T2DM. There are mainly two approaches to target the incretin system (1) via inhibiting the enzymatic action of DPP4 and thereby upregulating GLP-1 levels physiologically and (2) via increasing GLP-1 levels pharmacologically. While GLP-1 receptor agonists (GLP-1-RA) directly target GLP-1, GLP-1-independent effects are also possible with the use of DPP4 inhibitors (DPP4i). These drugs might also affect the level of other DPP4 substrates and might therefore have a more complex mode of action. However, there have been a lot of attempts to compare the effects of GLP-1-RA versus DPP4i in clinical studies. The results of these head-to-head comparisons are summarized in many current reviews (110–114). Most of these comparative studies agree that GLP-1 analogs are more effective in respect of glycemic control. Both incretin-based therapies are equally potent in lowering blood pressure and total cholesterol (110). Furthermore, both have the advantage of low incidence of hypoglycemia (110, 111). The results for body-weight lowering effects of DPP4i are heterogeneous throughout the studies (113), whereas beneficial effects on body-weight are well accepted for GLP-1-RA (110–112, 114). Therefore, some authors tend to prefer GLP-1-RA over the use of DPP4i (112). However, one should be aware of the fact, that GLP-1-RA have a higher incidence of gastrointestinal adverse events like nausea (110, 112, 114), which might be disadvantageous for elderly people who may be more prone to these side effects (114). Furthermore,

there are reports that DPP4i might also have cardio-protective effects (113), which will also shortly be discussed in section “Effect of DPP4 Inhibition on the Cardiovascular System” of this review. Despite the clear beneficial effects of incretin-based therapies, there are also concerns reported in respect of the risk for long-term complications like pancreatitis (115). These potential risks might, however, outweigh the benefits. These controversial discussions are well summarized by the reviews of Nauck and Butler (115, 116). To really assess which medication is of more importance always depends on the special patient characteristic.

Impact of DPP4 on T2DM relevant organs and associated comorbidities

DPP4-inhibitors exert glucose regulatory actions by prolonging the effects of GLP-1 and GIP, ultimately increasing glucose-mediated insulin secretion and suppressing glucagon secretion (104). Beside the glucose-lowering properties of DPP4-inhibitors, emerging evidence suggests that incretin-based therapies may also have a positive impact on inflammation, cardiovascular and hepatic health, sleep, and the central nervous system (105). However, the underlying mechanisms of these effects cannot be fully explained by lower blood glucose levels or increased GLP-1 bioavailability or signaling, and has to be further elucidated. Thus, the next section is focused on the role of DPP4 action in T2DM relevant organs and associated comorbidities.

Adipose Tissue

Adipose tissue is the primary storage organ for excess energy. While the role of adipose tissue as a central source of energy has been recognized for centuries, in the past decade it has become increasingly clear that adipose tissue also displays characteristics of an endocrine organ releasing a number of adipose tissue-specific factors, known as adipokines. During the progression of obesity, the ability of adipocytes to function as endocrine cells and to secrete multiple biologically active proteins is affected (106). Thus, adipose tissue has been shown to be a central driver of T2DM progression, establishing and maintaining a chronic state of low-level inflammation (107).

DPP4 expression and release within adipose tissue

Recently, we showed that DPP4 is highly expressed in human primary adipocytes (4). Furthermore, DPP4 expression in adipose tissue is increased in obese compared to lean individuals in both subcutaneous and visceral adipose tissue (4;5). Interestingly, visceral fat of obese patients exhibits the highest DPP4 level. According to the increased expression, we could identify sDPP4 as a novel adipokine released from primary human adipocytes. *In vitro*, the DPP4 release increased substantially during fat cell differentiation, and comparison with preadipocytes and adipose tissue macrophages showed that adipocytes most likely represent the major source of DPP4 released from the intact organ to the circulation. Furthermore, the release of sDPP4 was elevated in adipose tissue explants of obese patients compared to lean controls and correlates with various classical markers of the metabolic syndrome, namely BMI, waist

circumference, plasma triglycerides, and HOMA as an index of insulin resistance, as well as with fat cell volume and the adipokine leptin (4;5).

How DPP4 expression affects adipocyte homeostasis can only be speculated. DPP4 might be involved in adipose tissue lipolysis. DPP4 recruits ADA, a monomeric enzyme catalyzing deamination of adenosine to inosine and ammonia (108;109). It has been shown that DPP4-bound ADA has a 1000-fold greater activity than free ADA (110), which in turn may modulate the well established antilipolytic effects of adenosine. Moreover, DPP4 is a strong inhibitor of the antilipolytic activity of neuropeptide Y (NPY) (76), which is one of the best peptide substrates of the enzyme (89). In this regard, Rosmaninho-Salgado and colleagues demonstrated that DPP4 stimulates lipid accumulation and PPAR- γ expression through cleavage of NPY suggesting that sDPP4 might stimulate adipocyte differentiation (77). However it is noteworthy that the authors of this study were using tremendously high and non-physiological concentrations of sDPP4. On the contrary, a recent published study showed that DPP4 expression was strongly up-regulated during adipocyte dedifferentiation *in vitro*. Hence, the authors concluded that DPP4 might be a major component in adipose tissue remodeling and cell plasticity (111). Nevertheless, enhanced abundance of DPP4 within adipose tissue of obese subjects may be involved in adipose tissue remodeling and substantially augments the lipolytic activity of enlarged adipocytes (54in press;55).

Moreover, dendritic cells and macrophages resident in visceral adipose depots exhibit an increased DPP4

expression in response to inflammation or in the obese state (28). Since it is known that DPP4 exerts immunomodulating properties, Zhong *et al.* showed that membrane bound DPP4 is co-localized with membrane bound ADA on human dendritic cells resulting in an increased T-cell proliferation (28). Thus, it can be speculated that DPP4 might also play an important role in the chronic low-grade inflammation taking place in obesity and T2DM.

Adipose tissue as a relevant source of circulating DPP4

Serum levels of sDPP4 are altered in many pathophysiologic conditions, including different types of cancer, allergic asthma, or hepatitis C (7). Our group was the first analyzing circulating sDPP4 in the context of obesity and the metabolic syndrome. DPP4 serum levels of morbidly obese men are elevated compared with lean controls and significantly correlated with BMI, the size of adipocytes in subcutaneous and visceral fat, and the adipocyte hormones adiponectin (negatively) and leptin. These data suggest that sDPP4 is related not only to increased body weight but also to other important parameters of adipose tissue physiology. In addition, sDPP4 release and serum concentration can be reversed to normal levels by surgery-induced weight loss (4). Thus, in obesity, both circulating levels of sDPP4 and sDPP4 release by adipose tissue are increased and correlate strongly with the metabolic syndrome but can be reduced to control levels by substantial weight loss. Thus, indicating that enlargement of visceral adipocytes in obesity may substantially contribute to the augmented level of circulating sDPP4 in obese patients.

Endocrine effects of soluble DPP4

Although there is clear evidence that increased circulating levels of sDPP4 are associated with hallmarks of obesity and type diabetes, such as whole-body insulin resistance, elevated BMI and adipocyte hypertrophy, there are only few studies investigating the endocrine effects of sDPP4. We were the first showing that DPP4 consistently impairs insulin signaling at the level of Akt in primary human adipocytes (4). Enzymatic activity of sDPP4 appears to be involved in this process; however, since this work was done *in vitro* it is most unlikely that the sDPP4-induced impairment of insulin action is due to an increased bioavailability of any DPP4 substrate. It might rather be that DPP4-inhibitors may also affect the binding properties of sDPP4 to its receptors, namely M6P/IGFII receptor (38) or PAR2 (39). For the latter, it is not only known that PAR2 signaling induces insulin resistance in adipocytes (112), but PAR2 might also be a substantial contributor to inflammatory and metabolic dysfunction (113). Although there is a hint that circulating sDPP4 itself might affect adipose tissue function, the exact mechanism has to be further investigated.

Impact of DPP4 inhibition on adipose tissue

To further investigate the role of DPP4 in adipose tissue, several studies with DPP4-inhibitors were conducted. Interestingly, the administration of the DPP4-inhibitor des-fluoro-sitagliptin ameliorates linoleic acid-induced adipose tissue hypertrophy in β -cell-specific glucokinase haploinsufficient mice, a model of non-obese T2DM (114). Moreover, des-fluoro-sitagliptin protects against linoleic acid-induced adipose tissue inflammation

illustrated by CD8⁺ T-cell infiltration. Due to the loss of GLP-1 receptors in adipose tissue the authors exclude the involvement of GLP-1 and claim that the observed effects are due to the huge variety of DPP4 substrates. Thus, DPP4 inhibition might have pleiotropic effects in adipose tissue. A similar outcome has been observed in C57BL/6 mice fed a high-fat diet. After linagliptin treatment a significantly lower expression of the macrophage marker F4/80 was found compared with vehicle treatment. In line with these data, the authors demonstrated an increased insulin sensitivity after linagliptin treatment suggesting that DPP4 and adipose tissue inflammation play a pivotal role in the induction of insulin resistance. In 3T3-L1 cells, a murine preadipocyte cell line, Rosmaninho-Salgado *et al.* demonstrated that the DPP4-inhibitor vildagliptin reduces lipid accumulation by inhibiting adipogenesis, without affecting lipolysis through NPY cleavage and subsequent NPY Y2 receptor activation (77).

With the recognition that adult humans also have brown adipose tissue, an organ with substantial capacity to dissipate energy, brown adipose tissue gained considerable interest as a novel target to treat or prevent obesity and its associated diseases. In 2013, the group around Shimasaki was the first reporting that des-fluoro-sitagliptin attenuated body adiposity, without affecting food intake, in C57BL/6 mice with diet-induced obesity (115). The increase in energy expenditure could be explained by enhanced levels of PPAR- α , PGC-1, and uncoupling protein-1 (UCP-1) in brown adipose tissue as well as elevated levels of proopiomelanocortin in the hypothalamus. The beneficial effects of

des-fluoro-sitagliptin on energy expenditure could only partly be ascribed to increased GLP-1 levels and have to be further validated. Shortly afterwards, Fukuda-Tsuru *et al.* could confirm these data in the same animal model by administration of teneligliptin (116). Moreover, in this study teneligliptin also reduces fat mass and suppresses high-fat diet-induced adipocyte hypertrophy.

Collectively, there is clear evidence that DPP4 expression and release by adipose tissue plays a key role in obesity and T2DM associated processes, such as inflammation, adipocyte hypertrophy and insulin resistance. However, the underlying mechanism of these beneficial effects is not fully understood and remains unclear in most of the publications.

Pancreatic islets

β -cells play a central role in the etiology of T2DM. Due to failure of β -cell sensitivity to glucose and loss of β -cell mass, insulin secretion of these cells is not sufficient to counter balance insulin resistance, finally leading to T2DM. Although DPP4-inhibitors are now widely used for glycemic control, many debates are ongoing about their exact mode of action and their beneficial effects on pancreatic β -cells.

Regulation of DPP4 expression within pancreatic islets

Interestingly, within the pancreatic islets DPP4 localization differs between species. Islets of rodents showed a near-exclusive expression of DPP4 in β -cells, with little expression in α -cells. In contrast, human and pig islets express DPP4 almost exclusively in α -cells (117;118). The species difference in the localization of DPP4 expression, and the possible

physiological consequence of that difference, is unclear. Moreover, in a recent published study it has been demonstrated that DPP4 activity was detectable in the conditioned medium of human islets suggesting that DPP4 is released from human islets as well (119). Under pathological conditions, islets of obese mice chronically fed a high-fat diet exhibit an increased DPP4 activity. The contrary was found in human islets from type 2 diabetic donors, showing a decreased DPP4 activity (118).

Impact of DPP4 inhibition on pancreatic islets

Accumulating *in vitro* and pre-clinical data show that DPP4 inhibition has beneficial effects on T2DM induced β -cell dysfunction and apoptosis. Omar and colleagues demonstrated that DPP4 is not only present and active in mouse and human islets, but inhibition of islet DPP4 activity also has a direct stimulatory effect on insulin secretion, which is GLP-1 dependent (118). The same effect could be observed with a two week des-fluoro-sitagliptin treatment leading to increased insulin exocytosis by β -cells from *db/db* diabetic mice (120). Furthermore, it could be shown that DPP4 inhibition is clearly associated with significantly increased β -cell mass and function in several models of T2DM (121-123). These beneficial effects were associated with the transcriptional activation of anti-apoptotic and pro-survival genes, as well as the suppression of pro-apoptotic genes in β -cells (124). Additionally, Shah and collaborators showed that the DPP4-inhibitor linagliptin protects isolated human islets from gluco-, lipo-, and cytokine-toxicity (119). Accordingly, Akarte *et al.* reported anti-oxidative properties of vildagliptin shown

by a dose-dependent decrease in nitric oxide concentrations in both serum and pancreatic homogenates of vildagliptin-treated diabetic rats (125).

Beside these pre-clinical and *in vitro* studies, only few is known about the beneficial effect of DPP4-inhibitors on β -cells in human. In the short-term, 12-weeks vildagliptin treatment leads to a small increase in the capacity for insulin secretion (126). Treatment with vildagliptin over a longer period of time could also confirm an increased β -cell function in humans as a result of improved sensitivity of β -cells to glucose (127;128). However, this effect was not maintained after washout period, indicating that this increased capacity was not a disease modifying effect on beta cell mass and/or function. In the SAVOR-TIMI 53 trial, which was originally performed to assess the cardiovascular safety of saxagliptin, Leibowitz and colleagues recently reported that DPP4 inhibition may attenuate the progression of diabetes (129). This was evidenced by a decreased requirement for intensification of treatment associated with better preservation of glycemic control, as well as better sustained β -cell function as reflected in the fasting HOMA-2 β during the 2-year follow up period.

The exact mechanism how DPP4-inhibitors augment insulin secretion and increase β -cell mass *in vitro* and *in vivo* is still not fully understood, since not all these effects could be explained by elevated GLP-1 level or improved glycemic control associated with less glucotoxicity.

Liver

Non-alcoholic fatty liver disease (NAFLD) describes a disorder with excessive

deposition of fat within the liver with increasing prevalence in parallel to obesity and diabetes, which are major risk factors for NAFLD (130). Indeed, NAFLD is now the most common cause of chronic liver disease (131) and is present in one quarter to one half of diabetes patients (132). In the obese state, elevated triglyceride degradation in adipose tissue causes an increased hepatic uptake of fatty acids leading to fat accumulation within the tissue. Furthermore, reactive oxygen species (ROS), produced during lipid oxidation, are assumed to induce hepatocyte death and inflammatory reactions. Liver cirrhosis can be defined as the end stage of chronic liver diseases and is caused by progressive fibrosis. This process is characterized by excessive accumulation of ECM and activated hepatic stellate cells (133;134) that ultimately results in nodular regeneration with loss of function (135).

Regulation of DPP4 expression in the liver

Although DPP4 exhibits a widespread organ distribution, the liver is one of the organs that highly expresses DPP4 (136). In the healthy human liver, intense staining for DPP4 was found in hepatic acinar zones 2 and 3, but not in zone 1. This heterogeneous lobular distribution suggests that DPP4 might be involved in the regulation of hepatic metabolism (137). Furthermore, mRNA expression levels of DPP4 were significantly increased in NAFLD livers compared to that in control livers (138). In accordance to that, DPP4 expression levels of NAFLD patients were negatively correlated with HOMA-IR and BMI, and positively correlated with total cholesterol levels, but not with alanine aminotransferase (ALT), lactate

dehydrogenase (LDH) or triglyceride levels. Moreover, under conditions of high glucose, DPP4 expression was increased in HepG2 cells. However, other nutritional conditions, such as high insulin or the presence of fatty acids and cholesterol did not affect DPP4 expression in these cells. Thus, the authors claim that enhanced DPP4 expression in NAFLD liver may rather be associated with insulin resistance than triglyceride accumulation, and may promote the progression of liver disease via subsequent deteriorations in glucose metabolism. How increased DPP4 expression might affect liver function is still unknown. There are only a few hints that DPP4 might play a role in fibronectin-mediated interaction of hepatocytes with extracellular matrix (2;36;139). Beside DPP4 expression, there is only indirect evidence that hepatocytes also release DPP4 to the circulation, which will be further discussed in the next section.

Serum level of DPP4 in liver disease

As previously discussed, hepatic DPP4 mRNA expression level in the livers is significantly higher in patients with NAFLD compared to healthy subjects (138). This up-regulation of hepatic DPP4 expression is thought to be responsible for elevated DPP4 serum level in patients with liver disease (140-142). In line with this observation, serum DPP4 activity can be correlated with hepatic steatosis and NAFLD grading (143). Similarly, in patients with NAFLD, DPP4 activity in serum correlates with markers of liver damage such as serum gamma-glutamyltranspeptidase and alanine aminotransferase levels, but do not correlate with fasting blood glucose levels and HbA1c values (143;144). Thus, hepatic DPP4 expression in NAFLD may be

directly associated with increased DPP4 serum level and may be involved in hepatic lipogenesis and liver injury.

Impact of DPP4 inhibition on liver function

Since DPP4-Inhibitors are widely used in clinical practice, this drug was also investigated as a potential new therapeutic strategy against the development of liver fibrosis and steatosis. Kaji and collaborators demonstrated that sitagliptin markedly inhibits liver fibrosis development in rats via suppression of hepatic stellate cell proliferation and collagen synthesis (145). These suppressive effects were associated with dephosphorylation of ERK1/2, p38 and Smad2/3 in the hepatic stellate cells. Additionally, hepatic steatosis could be prevented in several different animal models by DPP4-inhibition (114;146;147). Shirakawa and colleagues studied the effects of sitagliptin in glucokinase^{+/−} diabetic mice with diet-induced hepatic steatosis (114). Here, sitagliptin prevented fatty liver in both wild-type and glucokinase^{+/−} mice paralleled by decreased expression of sterol regulatory element-binding protein-1c, stearoyl-CoA desaturase-1, and fatty acid synthase, and increased expression of peroxisome proliferator-activated receptor- α in the liver. Furthermore, in a mouse model of non-alcoholic steatohepatitis further studies indicated that linagliptin improves insulin sensitivity and hepatic steatosis in mice with diet-induced obesity (148) and ameliorates liver inflammation (149). The underlying mechanism of these beneficial effects has been further investigated by Ohyama *et al.* in *ob/ob* mice (150). The novel DPP4-inhibitor MK-0626 attenuates hepatic steatosis by enhancing AMPK

activity, inhibiting hepatic lipogenic gene expression, increasing triglyceride secretion from liver, and elevating serum adiponectin levels.

Clinical data are very limited; however, several non-randomized trials conducted in small groups of diabetic patients demonstrated that DPP4-inhibitors improved the levels of liver transaminases and liver fat (151-153). Accordingly, Iwasaki *et al.* found a decrease in ballooning and nonalcoholic steatohepatitis scores in post-treatment liver biopsies (152;153). Recently, in a comprehensive retrospective review of 459 type 2 diabetic patients, treated with DPP4-inhibitors, it was shown that DPP4-inhibitors improved the abnormality of the liver transaminases AST and ALT independent of HbA1c and body weight (154). Again in the majority of publications the authors postulate that these beneficial actions were mediated through potentiation of direct GLP-1 actions on hepatocytes; however, it seems unlikely that hepatocytes express the canonical GLP-1 receptor (155).

In conclusion, accumulating studies indicate that DPP4-inhibitors are clinically useful for patients with T2DM accompanied by liver dysfunction based on fatty liver, and that DPP4 inhibition affects liver function regardless of diabetic status and obesity.

Cardiovascular system

Cardiovascular complications (CVD) are common in patients with T2DM and a major cause of mortality (156). Atherosclerosis is the dominant cause of CVD and usually develops many years before any clinical symptoms are manifest. The underlying pathogenesis of

atherosclerosis involves an imbalanced lipid metabolism and a maladaptive immune response entailing a chronic low-grade inflammation of the arterial wall. Endothelial cells and intimal smooth muscle cells represent the major cell types of the artery wall preserving vessel wall homeostasis. Together with leukocytes they are the major players in the development of this disease. Beside atherosclerosis, T2DM also exacerbates heart failure associated with diastolic heart failure and coronary microangiopathy (157-159).

Regulation of DPP4 expression and release in vascular cells

DPP4 is expressed in both microvascular endothelial cells of different human tissues, such as liver, spleen, lung, brain, heart (157;159), and in human vascular smooth muscle cells (3). Under conditions of high glucose, DPP4 expression and activity were increased in human glomerular endothelial cells (160). Additionally, in STZ-induced diabetic rats activity of membrane-bound DPP4 was increased, thereby reducing cardiac SDF-1 concentrations and causing impaired angiogenesis (161). Also hypoxia has been shown to regulate DPP4 expression in vascular cells. Regarding endothelial cells, there are conflicting data on the influence of hypoxia on DPP4 expression. In human microvascular endothelial cells as well as human umbilical vein endothelial cells, Eltzschig and colleagues showed that hypoxia increased DPP4 mRNA and protein level (162), whereas another study by Shigeta *et al.* observed a decreased protein level of DPP4 under hypoxic conditions in the same cells (161). However, in human vascular smooth muscle cells we observed an increased

DPP4 expression in response to hypoxia (3). In this particular study, we could also show that DPP4 is released from human vascular smooth muscle cells. However, only very little is known about the physiological role of the membrane bound DPP4 within the vasculature. There is only one study showing that DPP4 forms a complex with adenosine deaminase capable of degrading extracellular adenosine to inosine in endothelial cells. Increased inosine levels in turn are known to induce vasoconstriction due to mast cell degranulation (163).

Effect of DPP4 inhibition on the cardiovascular system

In several *in vitro* and pre-clinical studies DPP4-inhibitors have been shown to exert important protective effects on the cardiovascular system. In this regard, it has been shown that DPP4-inhibitors decrease myocardial infarct size, stabilize the cardiac electrophysiological state during myocardial ischemia, reduce ischemia/reperfusion injury, and prevent left ventricular remodeling following myocardial infarction (164;165). Additionally, DPP4-inhibitors also exert vascular protective properties, including anti-inflammatory and anti-atherosclerotic effects and the ability to induce vascular relaxation (166;167). To confirm cardiovascular safety or even protection of DPP4-inhibitors in humans, several cardiovascular outcome studies were conducted. However, several clinical trials, namely SAVOR-TIMI53, EXAMINE or VIVID in patients with established cardiovascular disease failed to confirm a cardio-protective effect (168-170). As sDPP4 is an adipokine upregulated in obesity and T2DM that triggers insulin resistance and metabolic complications

(4;5), it might be speculated that the beneficial effects of DPP4-inhibitors would be higher in those early phases of the metabolic disorders previous to the development of established cardiovascular disease.

However, whether these beneficial effects observed in pre-clinical settings are due to increased levels of different DPP4 substrates or inhibition of direct effects of DPP4 remains unclear and will be assessed in more detail in the following section.

DPP4 substrates: GLP-1 dependent effects of DPP4-inhibitors

Since several studies have identified a role for GLP-1 receptor (GLP1R) signaling in DPP4-dependent cardioprotection, it is suggested that GLP-1 itself has favorable cardiovascular effects. Indeed, mRNA transcripts of the GLP-1R have been detected in the heart of rodents (171;172) and humans (173). Furthermore, GLP-1R has also been localized to mouse aortic smooth muscle and endothelial cells, as well as monocytes and macrophages (174).

Regarding myocardial infarction and heart failure, pre-clinical studies have demonstrated that DPP4-deficient rats subjected to 45 minutes of ischemia with 2 hours or reperfusion exhibited cardioprotection illustrated by reduced infarct size, improved cardiac performance, and reduced levels of BNP compared to control rats (175). These beneficial effects could be partially reversed by co-administration of the GLP-1R antagonist exendin [9-39]. Accordingly, administration of exendin [9-39] reversed the sitagliptin-induced improvement in ventricular function in Sprague Dawley rats with transient cardiac ischemia (176). Additionally, in a

rat model of chronic heart failure, GLP-1 analogues were able to improve cardiac function and morphology, with a concomitant amelioration of hyperglycemia and hyperinsulinemia (177).

Regarding the vascular system, continuous infusion of the GLP-1 analogue exendin-4 reduced monocyte adhesion to aortic endothelial cells, associated with a reduction in atherosclerotic lesion size in non-diabetic C57BL/6 and *ApoE*^{-/-} mice. Furthermore, treatment for 1 h with exendin-4 reduced the expression of the pro-inflammatory cytokines TNF α and MCP-1 in response to LPS (174). In addition, exendin-4 stimulates proliferation of human coronary artery endothelial cells through endothelial nitric oxide synthase (eNOS)-, protein kinase A (PKA)- and PI3K/Akt-dependent pathways (178;179). Accordingly, in humans, preliminary data confirm the ability of GLP-1 to protect from high glucose-induced endothelial dysfunction in the post-meal phase (180). In a model of vascular injury, it has been shown that continuous infusion of exendin-4 reduces neointimal formation at 4 weeks after injury without altering body weight or various metabolic parameters (181). From *in vitro* studies, Goto *et al.* suggest that this effect was mediated by the ability of GLP-1 to suppress platelet derived growth factor (PDGF)-induced proliferation of vascular smooth muscle cells. In contrast, in a pre-clinical study combining HFD and STZ treatment in *ApoE*^{-/-} failed to detect evidence for GLP-1R-dependent reduction of lesion size in the thoracic or abdominal aorta (155). The authors discuss that the duration of treatment, the dose of the GLP-

1 agonist or the age of mice might be responsible for the lack of anti-atherogenic activity in this study.

However, in patients with heart failure, pilot studies also suggest cardio-protection by GLP-1 infusion (182;183). Accordingly, a large retrospective analysis indicates that patients treated with the GLP-1 analogue exenatide had a significant 20% reduction of CVD events compared with patients on other glucose-lowering agents (184). Nevertheless, studies showing cardiovascular protective effects of GLP-1 were carried out using either native GLP-1 or recombinant GLP-1 analogues at high concentrations or in a way that induced supraphysiological GLP-1 signaling. Considering that DPP4 inhibition restores GLP-1 signaling within the physiological range, beneficial effects of DPP4-inhibitors might be different to those of GLP-1 analogues.

DPP4 substrates: SDF-1- and BNP-dependent effects of DPP4-inhibitors

But beside GLP-1, there are further substrates of DPP4 which might play a role in the favorable cardiovascular effects of DPP4-inhibitors. Two of the most promising candidates are stromal derived factor (SDF)-1 α and brain natriuretic peptide (BNP). SDF-1 is a chemokine that promotes angiogenesis and attracts endothelial progenitor cells (EPC) by binding to its receptor C-X-C motif chemokine receptor type 4 (CXCR4). EPC are derived from the bone marrow and are known to promote vascular repair and neoangiogenesis. When vascular damage occurs, local growth factors and cytokines signal the bone marrow to release EPC targeted to the injured sites. EPC then differentiate into mature endothelial cells and assist in the reconstruction of the

vasculature (185). In mice, genetic deletion or pharmacologic inhibition of DPP4 is able to increase the homing of CXCR4+ EPC at sites of myocardial damage, resulting in a reduced cardiac remodeling and improved heart function and survival (186). In a human study, Fadini *et al.* demonstrated that type 2 diabetic patients receiving a 4 week course of therapy with the DPP4-inhibitor sitagliptin show increased SDF-1 α plasma concentrations and circulating EPC levels (185). Additionally, SDF-1 engineered to be resistant to DPP4 cleavage, and delivered by nanofibers, improves blood flow in a model of peripheral artery disease (187). Collectively, these studies implicate a rationale to use DPP4-inhibitors for vascular repair through stimulation of EPC and neovascularization. BNP, another substrate of DPP4, plays an important role in regulating body fluid homeostasis and vascular tone through binding and subsequent activation of the cGMP- coupled natriuretic peptide receptor type A (NPR-A) (188). BNP is secreted predominantly by ventricular cardiomyocytes in response to increased wall stress. Thus, elevated BNP is a sensitive marker of heart failure and appears to play a role in cardiac remodeling and healing after acute myocardial infarction (189-191). DPP4 cleavage of the physiologically active BNP(1-32) to BNP(3-32) effectively lowers plasma cGMP levels, reduces diuresis and natriuresis, and inhibits vasodilatation (83;188).

Endocrine effects of soluble DPP4 on cardiovascular homeostasis

Although it is well established that serum levels of sDPP4 are altered in several pathological conditions and that sDPP4 is released from vascular cells, only a minor part of research has focused on potential endocrine effects of this proteolytic enzyme.

Considering that DPP4 is discussed in immunomodulation, it might be speculated that the inhibition of DPP4 modulates responses occurring within early or late atherosclerotic lesions. In low-density lipoprotein receptor-deficient (LDLR-/-) mice, Shah *et al.* could demonstrate that exogenously injected DPP4 increases monocyte migration *in vivo* (167). Although these pro-migratory properties of DPP4 could be completely inhibited by sitagliptin, the underlying mechanism of these effects remains unclear. Moreover, the combined treatment of sDPP4 and lipopolysaccharide (LPS) leads to increased expression and secretion of the pro-inflammatory cytokines TNF α and IL-6. This up-regulation was achieved by elevated levels of ERK, c-Fos, NF- κ B p65, NF- κ B p50, and CUX1, all factors known to bind to the promotor of TNF α and IL-6 (167). In accordance to that, Ikushima and collaborators observed that sDPP4 binds to the M6P/IGF-IIR resulting in enhanced transendothelial T cell migration (192). In a further study, sDPP4 binding to M6P/IGF-IIR leads to elevated ROS levels in HUVECs. In both studies, binding of DPP4 to this particular receptor was completely prevented by a DPP4-inhibitor (193).

In human vascular smooth muscle cells, we could show that sDPP4 activates the MAPK and NF- κ B signaling cascade resulting in pro-atherogenic changes in human vascular smooth muscle cells illustrated by an increased proliferation, the induction of iNOS and elevated expression and secretion of pro-inflammatory cytokines (39). Additionally, we observed that all these detrimental effects of sDPP4 were PAR2 mediated,

on vascular function illustrated by vascular reactivity of murine mesenteric arteries (194). sDPP4 impaired the endothelium-dependent relaxation to acetylcholine in a concentration-dependent manner by up to 75%, without modifying endothelium-independent relaxation to sodium nitroprusside. Again enzymatic activity of DPP4 appears to be involved in this process. Similarly, the cyclooxygenase inhibitor indomethacin

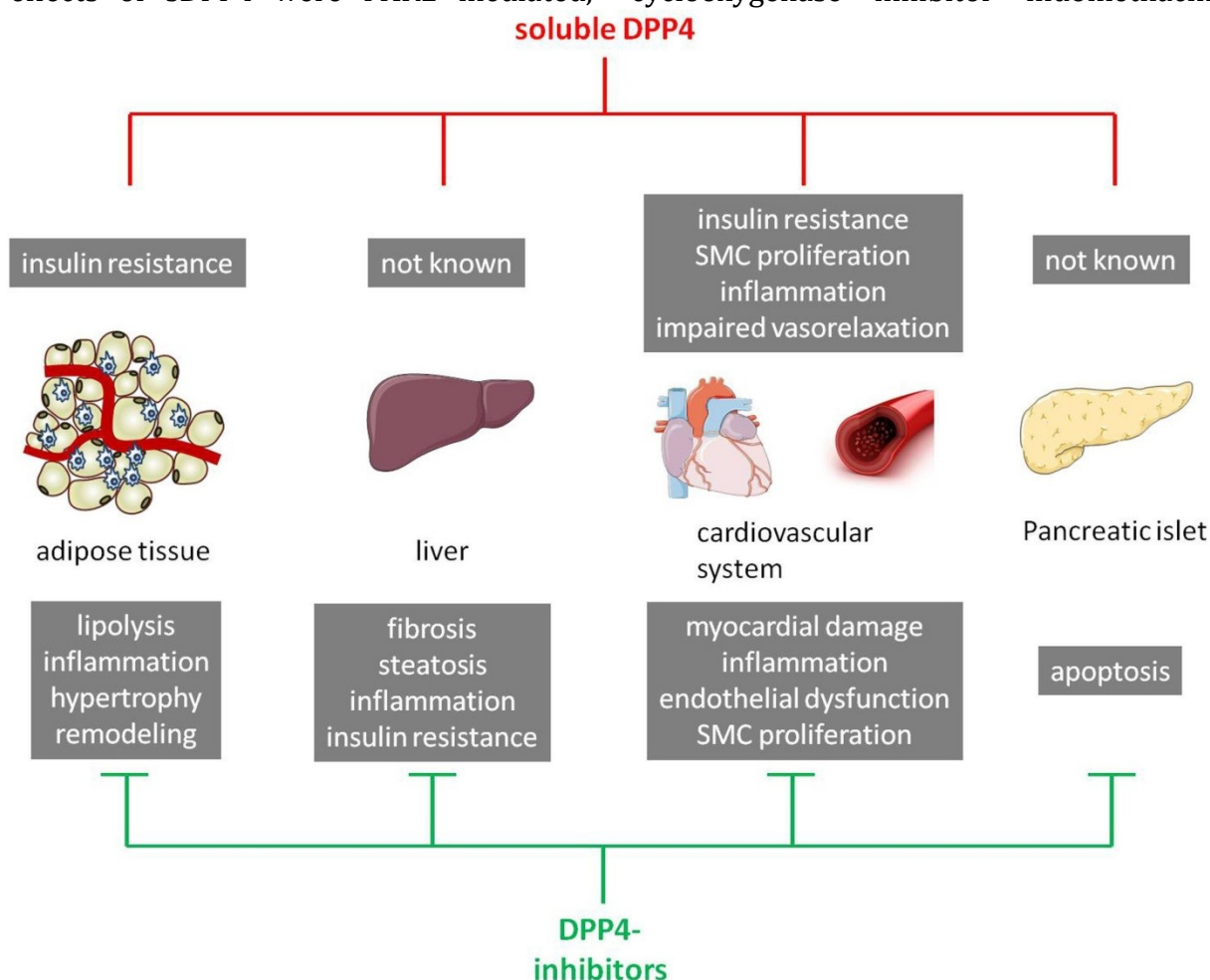


FIGURE 2 | Schematic overview of the impact of soluble DPP4 and DPP4 inhibitors on T2DM-relevant organs/tissues. In the upper panel, direct effects of soluble DPP4 (in red) on different organs/tissues are presented (gray boxes). The lower panel shows known effects of DPP4 inhibitors (in green) in these particular organs/tissues (gray boxes). SMC, smooth muscle cells.

since both a PAR2 antagonist and PAR2 silencing completely prevented the sDPP4-induced effects. In collaboration with the group of Sánchez-Ferrer we further showed that sDPP4 exhibits direct effects

and the thromboxane A₂ receptor antagonist SQ29548 abrogated the impairing action of DPP4. These data suggest that DPP-4 directly impairs endothelium-dependent relaxation

through a mechanism that involves cyclooxygenase activation, and likely the release of a vasoconstrictor prostanoid. Since sDPP4 has been reported not only to contribute to monocyte migration, and macrophage-mediated inflammatory reactions, but also stimulates proliferation of human coronary artery smooth muscle cells as well as impairs endothelium-dependent vasorelaxation, it might be speculated that sDPP4 itself acts as a risk factor for atherosclerosis.

Collectively, this section emphasizes that both membrane-bound and sDPP4 and its inhibition are not only playing an important role in glucose homeostasis, but also in several other processes and organs involved in the pathogenesis of T2DM (Fig. 2). This supports the notion that DPP4 exhibits pleiotropic properties that are not fully understood so far and have to be further elucidated in the future.

Conclusion

DPP4, originally identified as an enzyme nearly 50 years ago, has now been recognised to exert pleiotropic functions with substantial impact for a variety of diseases. The complexity of DPP4 action stems from i) a long list of substrates cleaved by the enzyme including hormones, growth factors, and cytokines, ii) an additional function of this protein being a binding partner at the surface of different cells, specifically immune cells, and iii) the recent discovery that DPP4 is an adipokine with different endocrine functions. Thus, an integrated view on this molecule is required to more precisely understand its impact for metabolic diseases like type 2 diabetes. For this disease, DPP4 inhibition has gained substantial interest, mostly related to the

DPP4 substrate GLP-1. As shown here, other substrates like SDF-1 and BNP should also be taken into account and may help to better understand the therapeutic potential of DPP4 inhibitors. In this context, the direct effects of DPP4 inhibitors require to be assessed in more detail, and several aspects like the cardio-protective function of DPP4 inhibition remains controversial. Finally, soluble DPP4 is emerging as a new research line, putting this molecule to the list of adipocytokines with pro-inflammatory and proliferative function. Combining the accumulated knowledge on DPP4 will lead to an improved understanding of its impact for health and disease.

Acknowledgements

This work was supported by the Ministerium für Wissenschaft und Forschung des Landes Nordrhein-Westfalen (Ministry of Science and Research of the State of North Rhine-Westphalia), and the Bundesministerium für Gesundheit (Federal Ministry of Health).

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2.2. STUDY 2: SHEDDING OF DPP4 IS MEDIATED BY MMPs

SHEDDING OF DIPEPTIDYL PEPTIDASE 4 IS MEDIATED BY METALLOPROTEASES AND UP-REGULATED BY HYPOXIA IN HUMAN ADIPOCYTES AND SMOOTH MUSCLE CELLS

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Published in: FEBS Lett. 2014 Nov 3;588(21):3870-7.

Key words: CD26/DPP4, hypoxia, non-classical secretion, proteases

Abstract

Dipeptidyl peptidase 4 is an important drug target for diabetes and a novel adipokine. However, it is unknown how soluble DPP4 (sDPP4) is cleaved from the cell membrane and released into the circulation. We show here that MMP1, MMP2 and MMP14 are involved in DPP4 shedding from human vascular smooth muscle cells (SMC) and MMP9 from adipocytes. Hypoxia increased DPP4 shedding from SMC which is associated with increased mRNA expression of MMP1. Our data suggest that constitutive as well as hypoxia-induced DPP4 shedding occurs due to a complex interplay between different MMPs in cell type-specific manner.

Introduction

Dipeptidyl peptidase 4 (DPP4) is a glycoprotein of 110 kDa, which is ubiquitously expressed on different cell types. The extracellular part of this type II cell surface protein is substantially glycosylated, which plays an important role in the interaction with different proteins (1). As an exopeptidase of the serine protease type, DPP4 cleaves numerous substrates at the penultimate position and thereby mostly inactivates them. Among these are peptides (e.g. stromal cell-derived factor 1 alpha (SDF1 α), eotaxin) and cytokines (monocyte chemoattractant protein-1 (MCP-1), interleukin 2 (IL-2)) as well as the incretin hormones (1). The incretin hormones glucagon-like peptide 1 (GLP-1) and glucose-dependent insulinotropic polypeptide (GIP) are major regulators of the postprandial insulin release (2). Therefore gliptins, a class of specific DPP4 inhibitors, are now widely used as a monotherapy or combination therapy for type 2 diabetes. By inhibition of DPP4 activity, these drugs prolong the half-life of GLP-1 and GIP which then stimulate pancreatic insulin secretion, suppress glucagon production and thereby contribute to an improved glycemic control (2;3).

DPP4 is not only present on the surface of cells, but can also be found in the circulation (4). By comprehensive proteomic profiling of the adipocyte secretome, we could identify soluble DPP4 (sDPP4) as a novel adipokine, with an upregulated release throughout the differentiation of adipocytes (5;6). We confirmed that mature adipocytes in comparison to macrophages and preadipocytes are a major source of DPP4

(5). Elevated serum levels of DPP4 were found in obese patients and correlate with the size of adipocytes and risk factors for the metabolic syndrome.

It has been reported, that DPP4 as a type II transmembrane protein is cleaved of the cell membrane in a process called shedding (7). The nature of enzymes contributing to the shedding of DPP4 and the regulation of this process is largely unknown. The aims of our study were to elucidate the underlying shedding mechanism and to explore the regulation of sDPP4 release *in vitro*. We show here for the first time that members of the metalloprotease family are involved in the release of sDPP4 from different primary human cells.

Material and methods

Material

Complete protease inhibitor (04693116001), and PhosStop phosphatase (04906837001) inhibitor cocktail were provided by Roche. Reagents for SDS-PAGE were supplied by Amersham Pharmacia Biotech and by Sigma. DPP4 rabbit polyclonal antibody (H00001803-D01P) was obtained from Abnova. Beta actin mouse antibody (ab6276) was supplied by Abcam. HRP-conjugated goat anti-rabbit (W4011) and goat anti-mouse (W4021) IgG antibodies were purchased from Promega.

Collagenase NB4 (17465.02) was obtained from Serva. FCS (10270-106), Dulbecco's modified Eagles/HAM F12 (DMEM/F12) medium (42400-010), α -modified Eagle's (α MEM) medium (11900-016) and Ham's F-12 medium (21700-026) was supplied by Gibco (Invitrogen). Troglitazone was obtained from Sigma Aldrich.

The Protease inhibitors AEBSF (ALX-270-022), E64 (ALX-260-007) were dissolved in water. BB-94 (196440), MMP9 Inhibitor I (444278) and MMP2 Inhibitor III (444288) were purchased from Calbiochem and dissolved in sterile DMSO. Human Protease Array Kit (ARY021) was obtained from R&D Systems.

Adipocyte isolation and culture

Preadipocytes of human subcutaneous adipose tissue were obtained from lean or moderately overweight subjects undergoing plastic surgery. Isolation was performed as previously described (8). Cells from up to passage 4 were grown to confluence in Dulbecco's modified Eagle's medium/Ham's F12 (DMEM/F12) supplemented with 10% FCS with medium change every 2-3 days. Passaging of the preadipocytes was performed according to Skurk et al.(9). Differentiation was started by adding 5 μ mol/L troglitazone for 3 days to adipocyte differentiation medium (DMEM/F12, 33 μ mol/l biotin, 17 μ mol/l d-panthothenic-acid, 66 nM insulin, 1 nM triiodo-l-thyronine, 100 nM cortisol, 10 μ g/ml apo-transferrin, 50 μ g/ μ l gentamycin, 15 mmol/l HEPES, 14 nmol/l NaHCO₃, pH 7.4) as described previously (5). After 14 days cells were treated with the indicated substances diluted in α -modified DMEM and incubated for the indicated periods.

Smooth muscle cell culture

Primary human smooth muscle cells (SMC) from three different donors (Caucasian, one male, two females) were supplied as proliferating cells from Lonza, TebuBio and PromoCell and kept in culture according to the manufacturer's protocol. For all experiments subconfluent cells of passage

three were used. SMC were characterized by morphologic criteria and by immunostaining with smooth muscle α -actin. For the experiments 100.000 cells/mL were seeded and grown for 24 hours in Growth medium (Promocell) with appropriate supplements. After washing with PBS and serum starvation for 24 hours cells were treated as indicated.

Hypoxia

For hypoxic experiments, cells were exposed to 1% O₂ supplemented with 5% CO₂ and respective concentrations of nitrogen in an Xvivo hypoxia chamber system (Biospherix) for 24 or 48 hours.

ELISA

DPP4 release to the cell culture medium was measured by human DPP4 DuoSet ELISA (R&D Systems, DY1180) according to the manufacturer's instructions.

Silencing of target genes

SMC were seeded in 6-well plates and grown until 60-80% confluence. Silencing experiments were performed by using 40 nM FlexiTube siRNA (Qiagen, MMP1 (SI03021802), MMP14 (SI03648841)) and 12 μ L HiPerfect (Qiagen, 301705) according to the manufacturers' instructions. At day 10-12 of differentiation adipocytes were treated with 40 nM of the respective siRNA and 9 μ L of HiPerfect. Optimal transfection conditions were tested by separate titration experiments. To control for unspecific effects, control cells were treated with AllStars Negative Control siRNA (QIAGEN, 1027280). After 24 hours mRNA was isolated to check for silencing efficiency. Supernatants were collected after 24 or 48 hours respectively.

qRT-PCR

Total RNA was isolated and reverse transcribed using the RNeasy Mini Kit (Qiagen, 74106) and Omniscript Reverse Transcription kit (Qiagen, 205113) according to the manufacturer's instructions. Gene expression was determined by quantitative real-time PCR (qRT PCR) using QuantiTect primer assays (Qiagen, ACTB, QT00057428, QT00001533, QT00040040, QT00088396, QT00014581, QT00055580) and GoTaq qPCR Master Mix (Promega, A6002) with 0.04-0.4 ng of generated cDNA on a Step One Plus Cyclor (Applied Biosystems). Beta-actin was used as a reference gene and expression levels of

investigated genes were normalized to beta-actin. Gene expression was analyzed via the $\Delta\Delta C_t$ method and compared with the designated control.

Statistical analysis

Data are expressed as mean \pm SEM. Unpaired two-tailed Student's *t* test or one-way ANOVA (post hoc test: Bonferroni's multiple comparison test) were used to determine statistical significance. All statistical analysis was done using Prism (GraphPad, La Jolla, CA, USA) considering a P value of less than 0.05 as statistically significant. Corresponding significance levels are indicated in the figures.

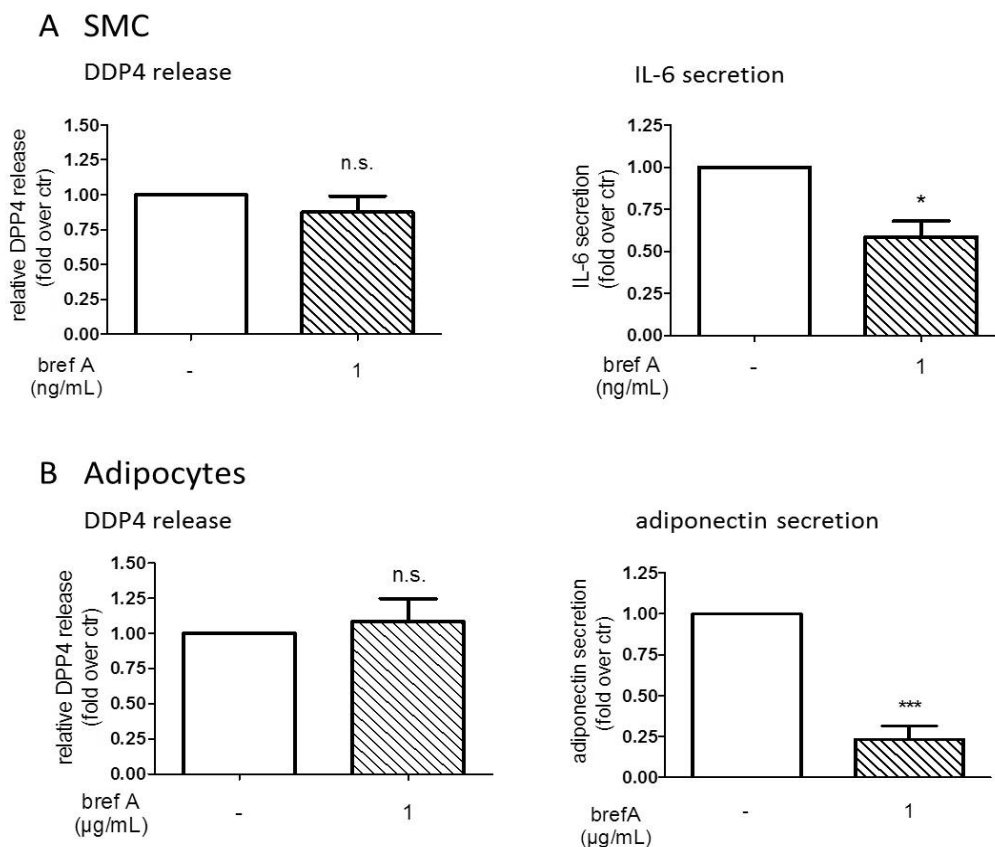


Fig. 1: Influence of brefA treatment on sDPP4 release in SMC (A) and adipocytes (B). Cells were treated for 24 hours with indicated concentrations of bref A. sDPP4 release and IL-6 or adiponectin secretion respectively to the culture medium was measured by ELISA. Data are mean values \pm SEM, n = 3-4; *P < 0.05, ***P < 0.001 vs. non-treated control; n.s. not significant; brefA, brefeldin A

Results

sDPP4 release is insensitive to brefeldin A treatment

In accordance with previously published data on sDPP4 release from skeletal muscle cells (10), sDPP4 release did not follow the classical ER/Golgi-dependant pathway in SMC and adipocytes, because it was insensitive to brefeldin A (bref A) treatment (Fig.1A, B). The applied concentrations of bref A were effective in blocking IL-6 secretion from SMC (Fig.1 A) and adiponectin secretion from adipocytes (Fig 1B).

Protease profile differs between SMC and adipocytes

To find out what types of proteases are released from different cell types and if there is a difference in the release profile of proteases, we used supernatants of

Array. This array enables us to assess the release of 34 different proteases of the four main types of proteases, namely matrix metalloproteases (MMP), serine proteases, cysteine proteases and aspartyl proteases. A huge panel of proteases spotted on this membrane belongs to the Cathepsins, which are serine, cysteine or aspartyl proteases. The comparison of different members of the Cathepsin family showed, that the detectable subtypes were more or less identical in the different cell types (Data not shown). In SMC, MMP1 and MMP3 signals were very prominent (Fig. 2A), whereas in adipocytes MMP2 and MMP9 signals were the strongest for all MMPs tested in the array (Fig. 2 B).

sDPP4 release can be reduced by general broad spectrum protease inhibitors

To identify the proteolytic enzymes

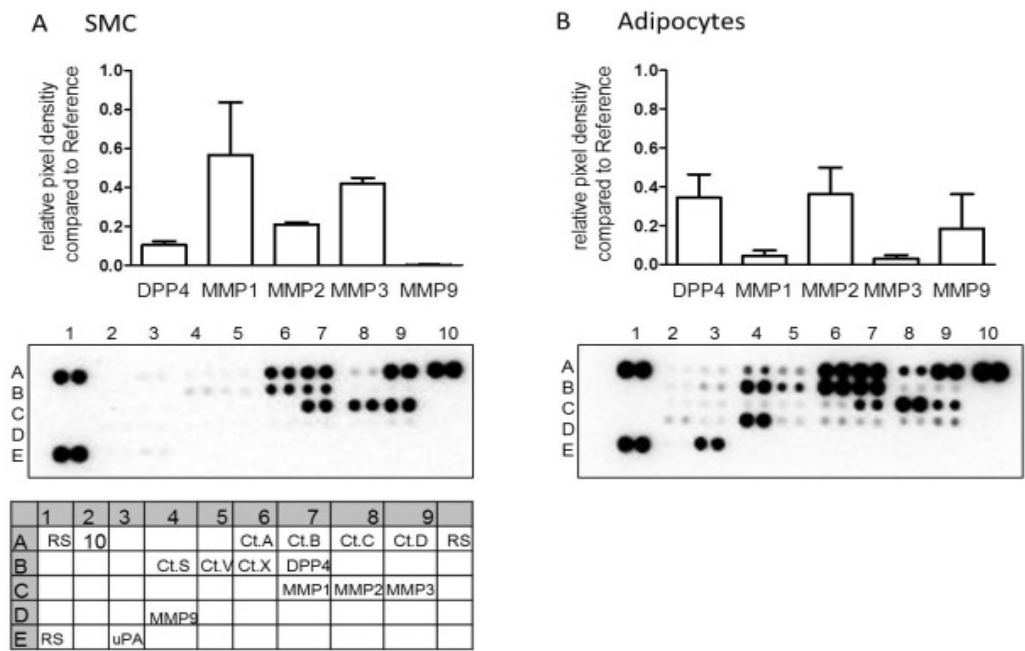


Fig. 2: Supernatants from SMC (A) and adipocytes (B) under control conditions were used to perform human Protease Profiler array. Data are depicted as relative pixel density compared to the reference spots. Representative arrays are presented and labeled with a grid pattern to identify corresponding spots. Data are mean values \pm SEM, n = 2; RS reference spot; Ct, cathepsin; uPA, urokinase-type plasminogen activator.

adipocytes and SMC in a Protease Profiler involved in the DPP4 shedding, different

classes of protease inhibitors were screened for their ability to block sDPP4 release. In SMC, sDPP4 release was impaired by the general broad spectrum MMP inhibitor BB-94, the general cysteine protease inhibitor E64 and the general serine protease inhibitor AEBSF to the same extent (Fig.3 A). To elucidate if a combination of these inhibitors could further diminish sDPP4 release, E64 and AEBSF, E64 and BB-94 as well as AEBSF and BB-94 were combined. None of these combinations showed additive effects on sDPP4 release (Fig. 3B). Furthermore, none

In adipocytes, only BB-94 showed a significant effect on sDPP4 release (Fig. 3 A). In the combination of the different classes of inhibitors no additive effects were observed (Fig. 3B). The protein expression of DPP4 remained unchanged after treatment with the different classes of protease inhibitors (data not shown).

sDPP4 release is mediated by metalloproteases

To correlate the shown effects of the general MMP inhibitor to a subset of MMPs, specific inhibitors or gene silencing were used. The IC₅₀ values of BB-94 are lowest

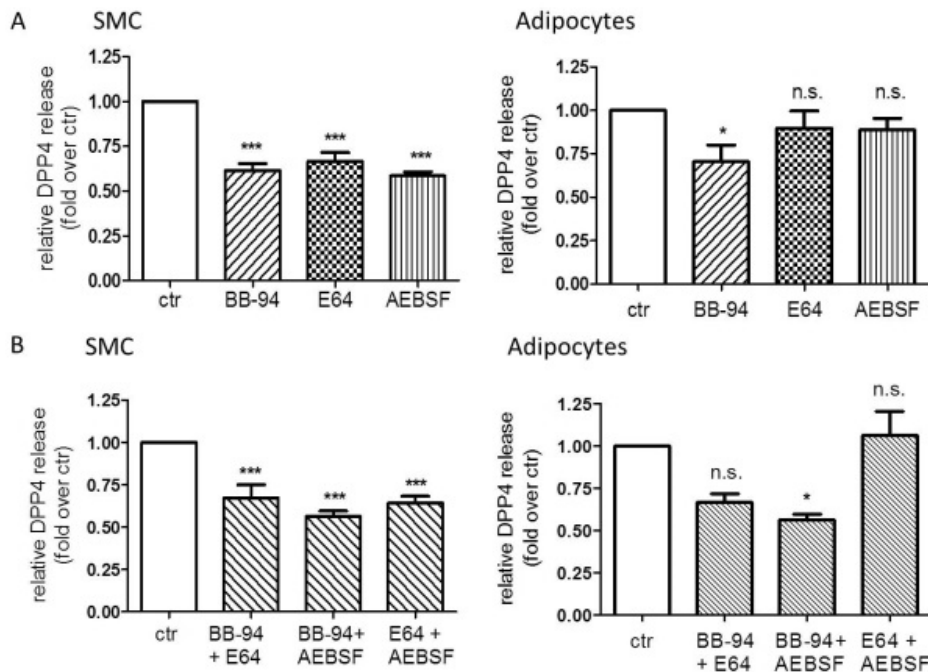


Fig 3: sDPP4 release after stimulation with different classes of Protease inhibitors in SMC and adipocytes. A: sDPP4 after treatment with 50 μ M BB-94, 20 μ M E64 and 20 μ M AEBSF for 24 hours. sDPP4 release was measured by ELISA. Data were normalized to the respective control and are shown as fold over control. Data are mean values \pm SEM, $n > 3$, *** $P < 0.001$ vs. respective control. B: sDPP4 after combined treatment with 20 μ M E64, 20 μ M AEBSF and 20 μ M BB-94 as depicted for 24 hours. Data are mean values \pm SEM, $n > 5$, *** $P < 0.001$ vs. respective control; n.s., not significant; ctr, control

of the treatments affected DPP4 protein expression (data not shown).

for MMP14 (2 nM), MMP1 (3 nM), MMP2 and MMP9 (4 nM) and some of these MMPs are elevated in mouse models of obesity (11;12). To deduce our findings with BB-94 to a specific MMP, we used specific inhibitors if available or gene silencing if no specific inhibitors could be used. Expression of the respective MMP could be reduced by about 70 to 80 % using specific siRNAs (Supl. Fig.1). In SMC, inhibition of MMP2 and silencing of MMP1 and MMP14 showed the most prominent effects on sDPP4 release, which was blocked by 20-30%, respectively (Fig. 4A). Inhibition of MMP9 in SMC showed only a slight effect on sDPP4 release (Fig. 4A). In contrast to SMC, MMP2 inhibition did not affect sDPP4 release in adipocytes, but MMP9 inhibition significantly reduced DPP4 shedding (Fig.

4B). Silencing of MMP1 or MMP14 in adipocytes had no effect on DPP4 shedding (Fig. 4B).

Hypoxia increases DPP4 shedding from SMC

To test whether lower oxygen levels can influence DPP4 shedding, SMC were incubated in an Xvivo hypoxia chamber system at 1% and 21% O₂ for 24 or 48 hours. After 24 hours as well as after 48 hours sDPP4 release was upregulated between 40 and 50%, respectively (Fig. 5A). However, DPP4 mRNA levels were not significantly elevated compared to normoxic conditions (Fig. 5B).

In addition to DPP4 shedding, mRNA expression of selected MMPs was tested after challenging of the SMC with 1% O₂. The most prominent effect of hypoxia could be shown for the expression of MMP1,

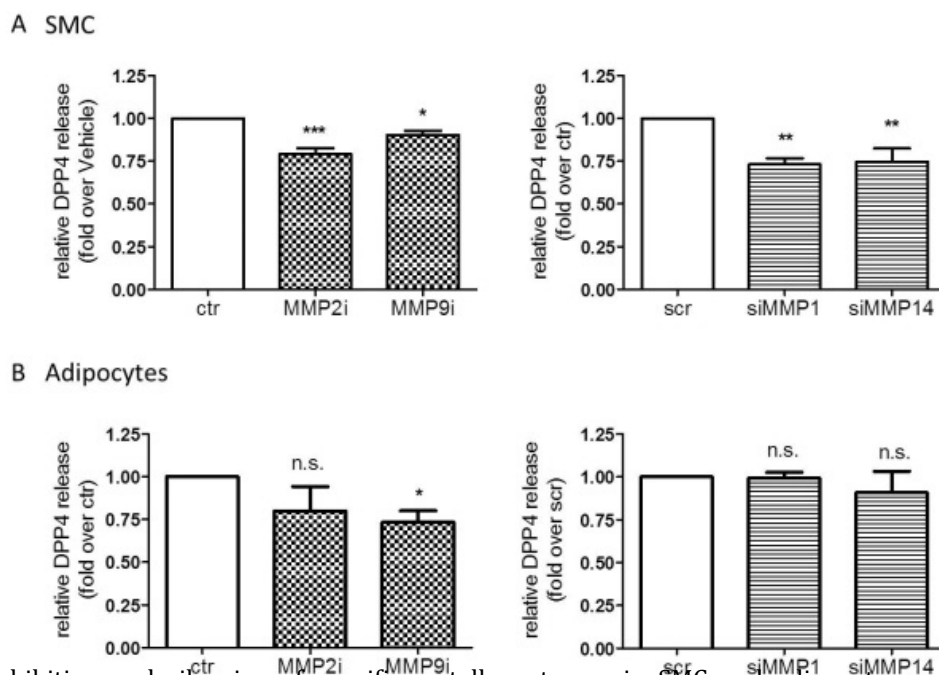


Fig. 4: Inhibition and silencing of specific metalloproteases in SMC and adipocytes partially prevented sDPP4 release. Treatment of SMC (A) and adipocytes (B) with specific MMP2 and MMP9 inhibitors in the indicated concentrations for 24 hours or with 40 nM MMP1 siRNA and 40 nM MMP14 siRNA respectively or with 40 nM scrambled siRNA for 48 hours. sDPP4 release is measured by ELISA. Data are presented as fold over respective control. Data are mean values \pm SEM, $n = 4-5$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ vs. respective control; n.s., not significant; ctr, control; scr, scrambled

which was upregulated more than 3-times by hypoxia-treatment after 48 hours in SMC. Even after 24 hours, mRNA levels increased 2-fold in the hypoxic situation (Fig 5C). MMP9 mRNA expression showed at least a 1.5-fold increase in this setting (Fig. 5C). A slight but significant increase was also detected after 48 hours for the expression of ADAM17/TACE (Fig. 5C). In contrast, expression of MMP2 and MMP14 remained comparable to normoxic conditions (Data not shown). Additional protease arrays were performed using supernatants from SMC cultured under hypoxic and normoxic conditions.

Protease array results confirmed that hypoxia increased relative sDPP4 release and indicate that the increased expression of MMP1 mRNA is paralleled by increased MMP1 release (Data not shown).

Discussion

DPP4 is a type II transmembrane glycoprotein that is released from the membrane in a non-classical secretion mechanism. This is evidenced by insensitivity to brefeldin A treatment and the lack of a cleavable signal sequence at the N-terminus (13;14). Type II single-pass transmembrane proteins possess a signal anchor sequence which is positioned

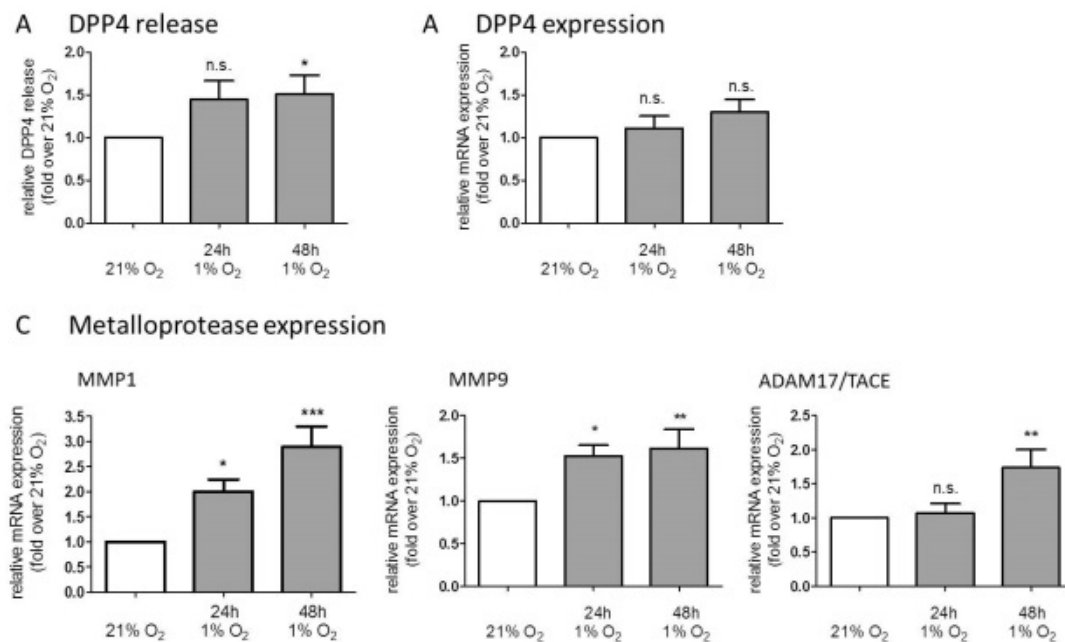


Fig 5: Influence of hypoxia on sDPP4 release and mRNA expression of selected genes in SMC. A: SMC were cultivated in parallel under normoxic (21% O₂) and under hypoxic (1% O₂) conditions for 24 and 48 hours. DPP4 release to the culture medium was measured by ELISA. Data are depicted as fold over normoxic control. Data are mean values \pm SEM, $n = 7$, * $P < 0.05$ vs. normoxic control. B: DPP4 mRNA expression from the above mentioned treatment was measured by qRT PCR. Data were normalized to the mRNA expression level of actin and expressed relative to the normoxic control. Data are mean values \pm SEM, $n = 7$. C: MMP1, MMP9 and ADAM17/TACE mRNA expression from the above mentioned treatment was measured by qRT PCR using specific primer sets for the indicated targets. Data were normalized to the mRNA expression level of actin and expressed relative to the normoxic control. Data are mean values \pm SEM, $n > 4$, * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$ vs. normoxic control. Grey bars indicate treatment with 1% O₂; n.s., not significant

within the membrane-spanning domain and which targets these proteins to the rough endoplasmatic reticulum. But in contrast to a classical secreted protein, the signal for the peptidase which cleaves off the signal sequence is missing (15). We were able to confirm, that DPP4 is insensitive to brefeldin A treatment not only in skeletal muscle cells (10), but also in SMC and adipocytes. Endogenous proteolytic release of transmembrane proteins is limited to type I or type II transmembrane proteins. This occurs by post-translational hydrolysis, the so called shedding (7). Bioinformatic analysis with Secretome 2.0 predicted DPP4 as non-classically secreted protein with a score of 0.719 (exceeding the threshold of 0.5). The cleavage of sDPP4 most likely occurs in the spacer region spanning amino acid 29 to 39 of the full length DPP4 according to the protein annotation at UniProt. However, the responsible enzymes are unknown so far.

Our data suggest that various types of proteases are able to induce sDPP4 release, because DPP4 shedding was significantly reduced by general serine-(AEBSF), cysteine-(E64) and metalloprotease (BB-94) inhibitors in SMC. Because combined treatment with the effective broad spectrum protease inhibitors lead to no additive effects we speculate, that in case of sDPP4 release a proteolytic cascade which Our results suggest that MMP1, MMP2 and MMP14 play a role in constitutive DPP4 shedding in SMC. One may keep in mind that MMP14 is able to activate MMP2 (17) and therefore might not only directly contribute to DPP4 shedding *in vitro*. Proteome profiler array data confirmed that MMP2 and MMP1 are released by SMC, whereas MMP9 was below the detection level in the supernatants of unstimulated

involves cathepsins and MMPs could be supposed. This goes in line with the rather complex activation of MMPs. MMPs belong to the family of zinc-dependent enzymes which are synthesized as an inactive proenzyme released into the extracellular space. Propeptides of MMPs are covalently bound to the zinc ion in the active center of these enzymes and thereby suppress the enzymatic activity until the propeptide is cleaved off (16). Different factors are able to activate MMPs like urokinase-type plasminogen activator (uPA), coagulation factors, phorbol esters or cytokines (16). But even MMPs can activate each other, which is known in case of MMP2 activation by MMP14 (17) or MMP9 activation by MMP2 and MMP3 (18). Also serine proteases like plasmin and kallikreins or cysteine proteases like Cathepsin G were shown to directly activate MMP1, MMP2 and MMP9 *in vitro* or *in vivo* (19).

For MMP2, MMP9 and MMP14 it has already been reported, that their expression levels are elevated in obese mice (11;12). Furthermore MMP1, MMP2, MMP9 and MMP14 play a role in the shedding of a large variety of substrates (20-24). These studies also emphasize that one MMP can shed several substrates and shedding of a specific target might not be limited to a specific MMP, but is a rather complex interplay between different enzymes.

SMC. Although also MMP3 was released from SMC, we did not further investigate this MMP due to the following reasons. First, MMP3 is described as a protective MMP in the context of atherosclerosis and it is not clear if this MMP is involved in shedding processes (25;26). Furthermore the IC₅₀ of BB-94 for MMP3 is significantly higher in comparison to the other candidates. In adipocytes only the specific

inhibition of MMP9 could decrease DPP4 shedding, whereas MMP2 inhibition, MMP1 or MMP14 silencing respectively showed no effect. MMP1, MMP2 and MMP9 were detectable in the unstimulated supernatants of adipocytes. This result suggests, that constitutive DPP4 shedding is cell-type specific. None of the investigated mechanisms to block MMPs were able to reduce DPP4 release below 50%, which indicates, that DPP4 shedding is not only regulated by a single MMP.

We were able to demonstrate that low oxygen levels of 1% O₂ increase DPP4 shedding in SMC. In developing lesions during atherogenesis the oxygen supply is often exhausted, which is partly due to the highly oxygen-consuming foam cells and the relatively low diffusion rate of oxygen through the cell environment (27). This can result in severe hypoxia (< 1% O₂) in some areas. Hypoxia affects transcription of genes, which are for example responsible for matrix remodeling (28). For some MMPs like MMP1 and MMP9, it is already known that hypoxia stimulates their release and expression (29;30). In our setting, we were able to show an increased expression of MMP1, MMP9 and ADAM17/TACE under low oxygen supply. MMP1 release was relatively high in SMC compared to other MMPs, whereas it was relatively low in adipocytes. Therefore, MMP1 might be an important player in DPP4 shedding both under normoxic and particularly under hypoxic conditions in SMC. Though MMP9 mRNA expression is also upregulated due to hypoxia, this MMP could only play a minor role in DPP4 shedding in SMC, because it is barely detectable in supernatants of these cells compared to supernatants from adipocytes

as shown by the Protease Array Analysis. Furthermore, MMP9 inhibition had only a very slight effect on DPP4 shedding. MMP2, which showed an impact on sDPP4 release after treatment with a specific inhibitor, was not influenced by hypoxia. ADAM17/TACE, cannot be ruled out to be involved in DPP4 shedding. From the literature it is known that it is involved in the processing of different substrates despite its eponymous target TNF α (31). Although we were able to silence ADAM17/TACE in SMC using different siRNAs, we always observed a concomitant upregulation of MMP1 thus preventing us from clarifying the role of ADAM17/TACE in DPP4 shedding. As no specific ADAM17/TACE inhibitor is available, it is unfortunately impossible to further study ADAM17/TACE at the moment. In the end, DPP4 expression itself is not influenced by hypoxia which shows, that the increased release of sDPP4 is not due to a higher DPP4 expression, but seems to be mediated at the level of DPP4 processing. In adipocytes, we could already show that culture at 1% O₂ for 24 hours had no effect on DPP4 release (5).

Adipose tissue and immune cells are recognized sources of DPP4. Circulating DPP4 concentrations are not only higher in obese patients but also in various inflammatory diseases (4;32). In a previous study, we were already able to show a significantly decreased DPP4 release from adipose tissue explants and in serum from obese patients who underwent bariatric surgery (5). MMP2 and MMP9 are key elements of extracellular matrix modulation in adipose tissue and both MMPs are significantly higher in serum of obese patients (33) and MMP2 is

significantly downregulated in serum of patients after bariatric surgery (34). High serum and mRNA expression levels of MMP1 and MMP9 are also associated with carotid atherosclerosis and plaque stability in patients (35-37). Accordingly, patients with a higher risk for cardiovascular disease are characterized by both higher circulating DPP4 and increased serum levels of MMP1 (38;39). *In vitro*, we have previously shown that sDPP4 in concentrations similar to circulating levels induces SMC proliferation (5). In parallel, sDPP4 induces inflammatory and stress pathways in vascular cells (40;41). Accordingly, sDPP4 generated in ischemic tissue or derived from perivascular and visceral adipose tissue might have similar effects *in vivo* (32;42). The multiple targets and functions of DPP4 and its inhibition by gliptins suggest that it could also play an important role beyond its effects on the incretin axis (43). As for the relation of DPP4 and potential shedding enzymes of DPP4 to obesity and atherosclerosis, it should be noted that only correlative data is available at the moment and no causal relationship can be established based on our current knowledge. In the future, research should focus on the molecular mechanisms of DPP4 shedding in the context of atherosclerosis and obesity

which might finally help to better understand the role of sDPP4 in physiological and pathophysiological conditions.

In conclusion, we could show that several MMPs are involved in the constitutive DPP4 shedding as well as under hypoxic conditions *in vitro*. Our data suggest, that not a single MMP is involved in sDPP4 release, but it is rather an interplay between different shedding enzymes in a cell type-specific manner.

Acknowledgement

This work was supported by the Ministry of Science and Research of the State of North Rhine-Westphalia (MIWF NRW) and the Federal Ministry of Health (BMG). This study was supported in part by a grant from the Deutsche Forschungsgemeinschaft (SE-1922 2-2), a grant from the German Diabetes Association (DDG) and a fellowship to HS from the European Foundation for the Study of Diabetes (EFSD).

We wish to thank the Dept. of Plastic Surgery, Florence-Nightingale-Hospital Düsseldorf, for support in obtaining adipose tissue samples. The technical assistance of Andrea Cramer, the scientific support from Dr. Nina Wronkowitz and the secretarial assistance of Birgit Hurow is gratefully acknowledged.

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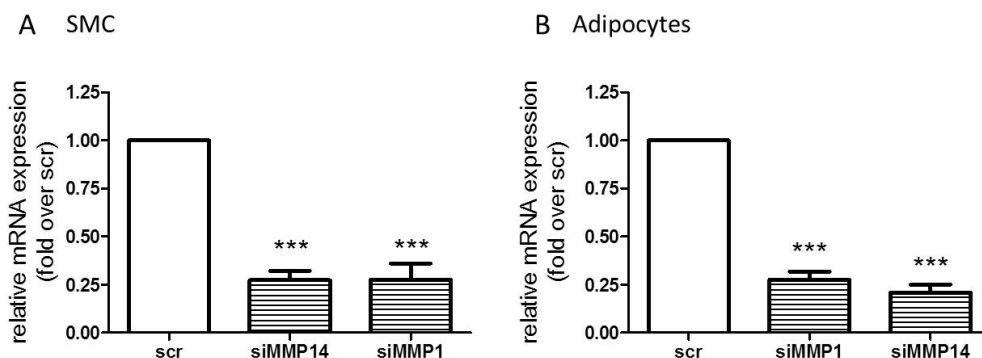
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Supl. Fig. 1: Silencing efficiency of siRNA in SMC (A) and adipocytes (B). Cells were treated with siRNA as described in Fig. 4. Expression of the depicted target gene was measured by qRT PCR. Data are presented as fold over scrambled siRNA. Data are mean values \pm SEM, n = 3, *** P < 0.001 vs. scr; n.s., not significant; ctr, control; scr, scrambled

2.3. STUDY 3: REDUCED DPP4 ACTIVITY IMPROVES INSULIN SIGNALING

REDUCED DPP4 ACTIVITY IMPROVES INSULIN SIGNALING IN PRIMARY HUMAN ADIPOCYTES

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Published in: Biochem Biophys Res Commun. 2016 Feb 10. pii: S0006-291X(16)30209-1. doi: 10.1016/j.bbrc.2016.02.019.

Keywords: DPP4, siRNA-mediated silencing, DPP4 inhibition, primary human adipocytes, insulin signaling

Abstract

DPP4 is a ubiquitously expressed cell surface protease which is also released to the circulation as soluble DPP4 (sDPP4). Recently, we identified DPP4 as a novel adipokine oversecreted in obesity and thus potentially linking obesity to the metabolic syndrome. Furthermore, sDPP4 impairs insulin signaling in an autocrine and paracrine fashion in different cell types. However, it is still unknown which functional role DPP4 might play in adipocytes. Therefore, primary human adipocytes were treated with a specific DPP4 siRNA. Adipocyte differentiation was not affected by DPP4 silencing. Interestingly, DPP4 reduction improved insulin responsiveness of adipocytes at the level of insulin receptor, protein kinase B (Akt) and Akt substrate of 160 kDa. To investigate whether the observed effects could be attributed to the enzymatic activity of DPP4, human adipocytes were treated with the DPP4 inhibitors sitagliptin and saxagliptin. Our data show that insulin-stimulated activation of Akt is augmented by DPP4 inhibitor treatment. Based on our previous observation that sDPP4 induces insulin resistance in adipocytes, and that adipose DPP4 levels are higher in obese insulin-resistant patients, we now suggest that the abundance of DPP4 might be a regulator of adipocyte insulin signaling.

Introduction

During obesity, adipose tissue (AT) expansion and a low-grade chronic inflammation occur, leading to an altered secretory profile in AT with a shift towards a more pro-inflammatory secretome (1). Although several studies confirmed that there is a link between dysregulated AT secretome and obesity-associated diseases like whole-body insulin resistance (IR) and type 2 diabetes mellitus (T2DM), the exact underlying molecular mechanisms remain mostly unknown. By comprehensive proteomic profiling of the adipocyte secretome our group identified novel adipokines including dipeptidylpeptidase 4 (DPP4). DPP4 is a serine protease, which was already discovered in 1966 by Hopsu-Havu and Glenner (2) and gained considerable interest because of its ability to cleave and thereby inactivate the incretin hormones, which are the main regulators of postprandial insulin secretion (3). Beyond this incretin-inactivation, DPP4 can cleave numerous substrates at the penultimate position and therefore alters the activity of cytokines or hormones (4;5). Furthermore, DPP4 is ubiquitously expressed on various cell types. It is able to interact with different binding partners and is thereby involved in signaling processes (5-8). DPP4 is not only a transmembrane protein, but is also released into the circulation as a fully functional enzyme by a process called shedding, which is regulated by matrix metalloproteases (MMP) (9). Therefore DPP4 is also able to act in a paracrine and endocrine way on different cells. DPP4 is upregulated in visceral versus subcutaneous adipose tissue (AT) and it is

higher in obese than in lean patients (10;11). Furthermore, insulin-resistant obese patients have elevated levels of circulating DPP4 (11). Since DPP4 is upregulated during differentiation of human *in vitro* cultured adipocytes, and its expression is higher in mature adipocytes than in preadipocytes or macrophages, the role of DPP4 in AT is especially interesting in the context of obesity (10).

We were able to show here for the first time that knock-down of DPP4 improves insulin signaling in adipocytes. This seems to be linked to the enzymatic function of DPP4. Taken together with our previously published observation that sDPP4 impairs insulin signaling in adipocytes (10) we postulate that DPP4 abundance might be a regulator of AT insulin signaling.

Material and methods

Material

Reagents for SDS-PAGE were supplied by Amersham Pharmacia Biotech and by Sigma. Antibodies were supplied as following: Adiponectin (Abcam, ab22554), DPP4 (abcam, ab129060), HSL (Cell signaling technologies, 4107), PPAR γ (CST, 2435), IRS-1 (upstate, 06-248), total Insulin receptor (Calbiochem, GR36), phospho-Insulinreceptor (Tyr1150/1151) (C.S.T., 3024), total Akt (CST, 9272), phospho-Akt (Ser473) (CST, 9271), total ERK (p42/44) (CST, 9102), phospho-ERK (Thr202/Tyr204) (CST, 9101), total NF κ B (CST, 8242), phospho-NF κ B (CST, 3033), phospho-AS160 (Thr642) (CST, 2997). Protein levels were normalized to beta-Actin protein levels (abcam, ab6276). HRP-conjugated goat anti-rabbit (W4011) and goat anti-mouse (W4021) IgG antibodies were purchased from Promega. Collagenase NB4 (17465.02) was obtained from Serva. FCS (10270-106), Dulbecco's modified Eagles/HAM F12 (DMEM/F12) medium (42400-010), α -modified Eagle's (α MEM) medium (11900-016) and Ham's F-12 medium (21700-026) were supplied by Gibco (Invitrogen). Troglitazone, IBMX (I5879_1G)

and Dexamethasone (D4902-25 mg) were obtained from Sigma Aldrich. Adipokine profiler arrays were supplied by R&D systems (ARY024).

Adipocyte isolation and culture

Subcutaneous adipose tissue was obtained from lean or moderately overweight women undergoing plastic surgery. Primary human adipocytes were isolated by collagenase digestion as previously described (12). Cells were proliferated and frozen after passage 1. Passaging of the preadipocytes was performed according to Skurk et al.(13). Frozen cells were seeded in basal medium (BM; DMEM/F12, 14 nmol/l NaHCO₃, 33 mmol/l biotin, and 17 mmol/l d-panthothenic-acid) supplemented with 10% FCS and 1% antibiotic-antimycotic-mix in six-well plates at a density of 70.000 cells per mL. One day prior to reaching confluence cells were silenced. 24h after silencing, differentiation was induced by adding an adipocyte differentiation medium (BM supplemented with 3% FCS, 100nM human insulin, 1μM Dexamethasone, 0,2mM IBMX, 0,25μM troglitazone and 0,5% gentamycin) which was used until day 7 of differentiation and was then changed to a maintenance medium (BM supplemented with 3% FCS, 100nM human insulin, 1μM Dexamethasone and 0,5% gentamycin) for additional 7 days. Medium was changed every 2-3 days. After 14 days, cells were treated with the indicated substances diluted in α-modified DMEM and incubated for the indicated periods.

Silencing

Frozen preadipocytes were seeded and cultured in 6-well-plates according to the above mentioned instructions. One day prior to reaching confluence (usually 4 days after seeding), silencing experiments were performed by using 20nM FlexiTube siRNA targeted against DPP4 (Qiagen Hs_DPP4_1 Cat. No: SI00030212) or 20nM AllStars Negative Control siRNA (Qiagen Cat No: 1027280) and 6μL HiPerfect (Qiagen, 301705) per well according to manufacturers' instructions. Optimal transfection conditions for high silencing efficiencies were elucidated by separate titration experiments. Silencing efficiency was assessed by qRT-PCR at different time-points during differentiation.

qRT-PCR

Total RNA was isolated and reverse transcribed using the RNeasy Mini Kit (Qiagen, 74106) and Omniscript Reverse Transcription kit (Qiagen, 205113) according to the manufacturer's instructions. Gene expression was determined by quantitative real-time PCR (qRT PCR) using QuantiTect primer assays (Qiagen) and QuantiTect SYBR Green PCR Kit (Qiagen, 204145) on a Step One Plus Cyclor (Applied Biosystems). Optimal cDNA amount for each primer was separately tested. Beta-actin was used as a reference gene and expression levels of investigated genes were normalized to beta-actin. Gene expression was analyzed via the ΔΔCt method and compared with the designated control.

Isolation of total protein

Total cellular proteins were isolated at the indicated time-points during adipocyte culture by aspirating the culture medium and washing with ice-cold PBS. The Kinexus lysis buffer consisted of 20mM MOPS, 2mM EGTA, 5mM EDTA and 1% Triton X-100. After pH was adjusted to 7.2 1mM DTT, 40μL Complete protease inhibitor cocktail (Roche, 04693116001) and 100μL PhosStop (Roche, 04906837001) per mL lysis buffer were freshly added and cells were scratched from the plates. After 1-2h overhead shaking at 4°C lysates were centrifuged for 15min at 4°C and 10.000 g. Protein amount was determined by using the QuickStart Bradford Protein Assay (Bio-Rad, 500-0205).

Western Blot

5 μg of the total cellular proteins were separated by SDS-PAGE using 10% horizontal gels. Proteins were transferred to a polyvinylidene difluoride membrane (Millipore) in a semidry blotting system. Membranes were blocked with 5% nonfat dry milk in TBS containing 0.1% Tween for 1-2 h at room temperature and probed with the indicated primary antibodies. After being washed, membranes were incubated with a secondary horseradish peroxidase (HRP)-coupled antibody and processed for enhanced chemiluminescence detection using Immobilon HRP substrate (Millipore). Signals were visualized and analyzed on a Bio-Rad VersaDoc 4000 MP work station.

ELISA

DPP4 release and adiponectin secretion to the cell culture medium were measured by human DuoSet

ELISA (R&D Systems, DY1180 and DY1065) according to the manufacturer's instructions. IL6 and MCP-1 secretion was measured by ELISA (Hözel Diagnostika 950030192 and 873030096) according to the manufacturer's instructions.

Oil Red O staining

After 14 days of differentiation and the indicated treatments, adipocytes were washed with PBS and fixed overnight with a solution containing 71% picric acid (vol/vol), 24% acetic acid (vol/vol), and 5% formaldehyde (wt/vol). Afterwards, cells were washed three times with PBS and lipids were subsequently stained with 0.3% Oil Red O (Sigma-Aldrich, O0625-25G) dissolved in 60% isopropanol for 10 min. The staining was quantified by dissolving Oil Red O with 100% isopropanol and measuring absorbance at 500 nm.

DPP4 activity assay

The efficiency of DPP4 inhibition in primary human adipocytes cultures was measured with the DPP-4 Activity Assay Kit (sigma Aldrich, MAK088-1KT) according to the manufacturers' instructions.

detected with a Tecan microplate reader (Infinite M200, Tecan).

Statistical analysis

Data are expressed as mean \pm SEM. Unpaired two-tailed Student's *t* test was used to determine statistical significance between selected pairs of treatments. All statistical analysis was done using Prism (GraphPad, La Jolla, CA, USA) considering a *P* value of less than 0.05 as statistically significant. Corresponding significance levels are indicated in the figures.

Results

siRNA-mediated silencing of DPP4 does not affect adipocyte differentiation

To elucidate the role of DPP4 within primary human adipocytes, DPP4 was silenced one day prior to the start of adipocyte differentiation via siRNA. DPP4 silencing was very stable at mRNA level until the end of differentiation, and also

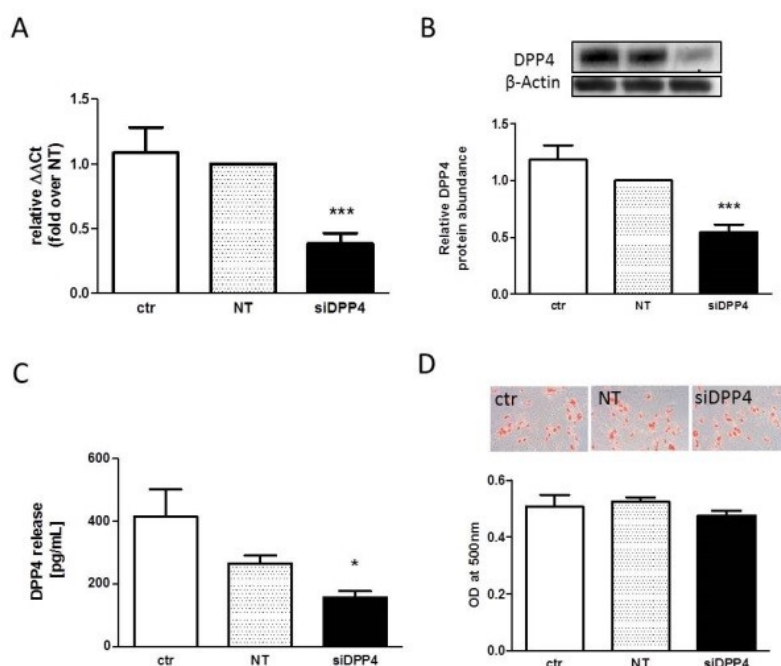


Fig. 1: Effect of siRNA-mediated silencing of DPP4 on primary human adipocyte differentiation. Human primary adipocytes were silenced one day prior to start of differentiation and silencing efficiency was validated on day 14 of differentiation on mRNA (A), protein (B) and release level (C). To assess accumulation of lipids an Oil Red staining was performed on day 14 of differentiation (D). Data are mean values \pm SEM, $n=3-4$, * $P < 0.05$, *** $P < 0.001$ vs. NT; Ctr control; NT non-target control siRNA; siDPP4 siRNA against DPP4; representative Western Blots for (B) are presented.

Undiluted supernatants of cells treated with vehicle (DMSO), saxagliptin or sitagliptin (100nM) were examined and the resulting fluorescent signal

resulted in significant down-regulation of DPP4 protein level and approximately 50%

Tab.1 Silencing does not affect the expression level of differentiation markers

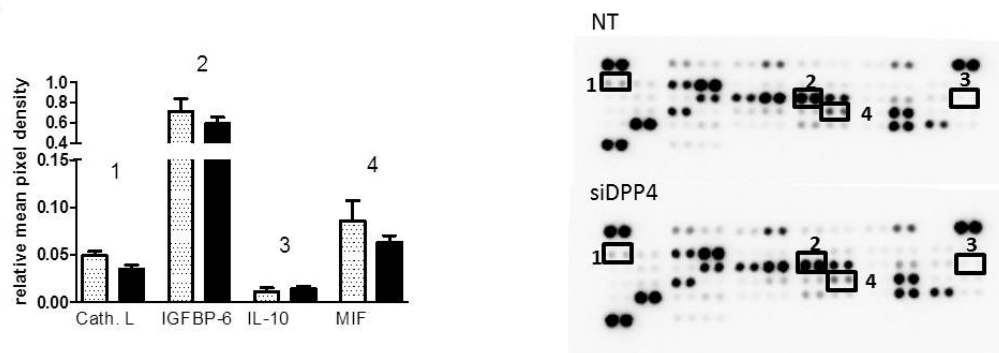
The level of protein or mRNA expression of the indicated markers on d14 of differentiation was assessed. Expression levels are presented in percent of non-target control siRNA on d14 of differentiation \pm SEM. n.d. not determined

Expression level on d14 in % of NT	adiponectin	PPAR γ	HSL	Glut4
mRNA	84 \pm 3.6	98.2 \pm 1.5	n.d.	71.9 \pm 9.6
protein	86.4 \pm 8.1	88.4 \pm 5.1	80.6 \pm 1.5	104.4 \pm 10.3

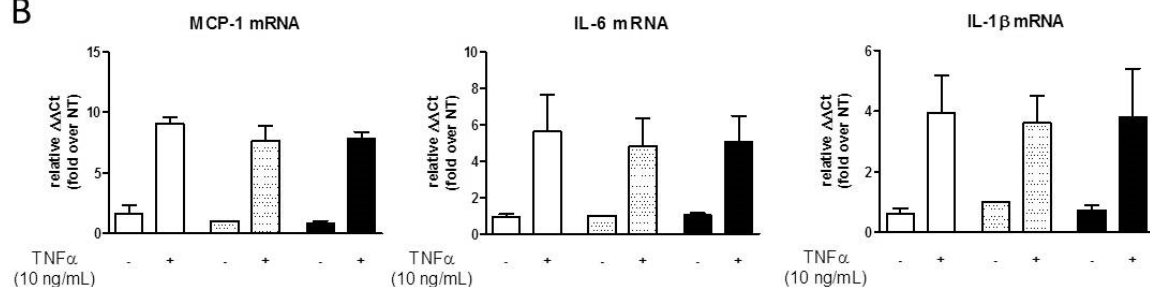
reduction of DPP4 release (Fig. 1A-C). To assess the impact of DPP4 silencing on

adipocyte differentiation, both expression of classical differentiation markers at mRNA

A



B



C

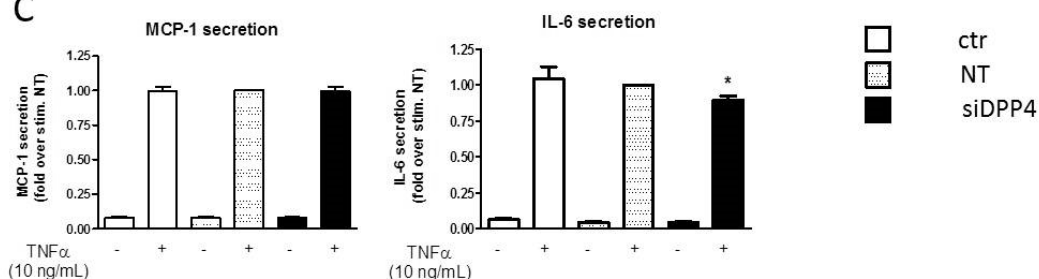


Fig. 2: Influence on secretory output or inflammation by DPP4 silencing. Supernatants of adipocytes on day 14 of differentiation were used to perform human adipokine profiler arrays (A). Data are depicted as relative pixel density normalized to the intensity of the reference spots. Representative arrays are presented and spots corresponding to the blot are highlighted. To assess whether inflammation induced by inflammatory stimuli differs between silenced and control cells mRNA expression (B) and secretion (C) of selected NF κ B target genes was assessed after 24h treatment with 10 ng/mL TNF α by qRT-PCR and ELISA. Data are mean values \pm SEM, n = 4-5, *P < 0.05 vs NT; Ctr control; NT non-target control siRNA; siDPP4 siRNA against DPP4;

and protein level (Tab. 1), as well as lipid droplet formation at the end of differentiation were analyzed (Fig. 1 D). None of these investigated parameters showed significant changes when compared to the non-target control siRNA (NT).

Dpp4 silencing does not affect adipocyte secretory function

To elaborate whether DPP4 silencing has an impact on the adipocyte secretome, adipokine profiler arrays were performed. Of the spotted adipokines, 31 adipokines could be detected in the adipocyte conditioned media. However none of the detected adipokines was significantly altered upon DPP4 silencing (Fig. 2A).

To analyze whether DPP4 knock-down has an effect on the responsiveness to inflammation, silenced cells were treated with the pro-inflammatory cytokine TNF α .

This stimulation of adipocytes resulted in a strong induction of NF κ B target genes MCP-1, IL-1 β and IL-6 at the level of mRNA expression (Fig 2B) as well as secretion (Fig 2C). After DPP4 silencing, a slight but significant reduction in TNF α -stimulated IL-6 secretion can be observed whereas MCP-1 levels remained unaltered (Fig 2C).

siRNA-mediated DPP4 silencing and DPP4 inhibition improves insulin signaling

An important functional parameter of adipocytes is the insulin sensitivity. To

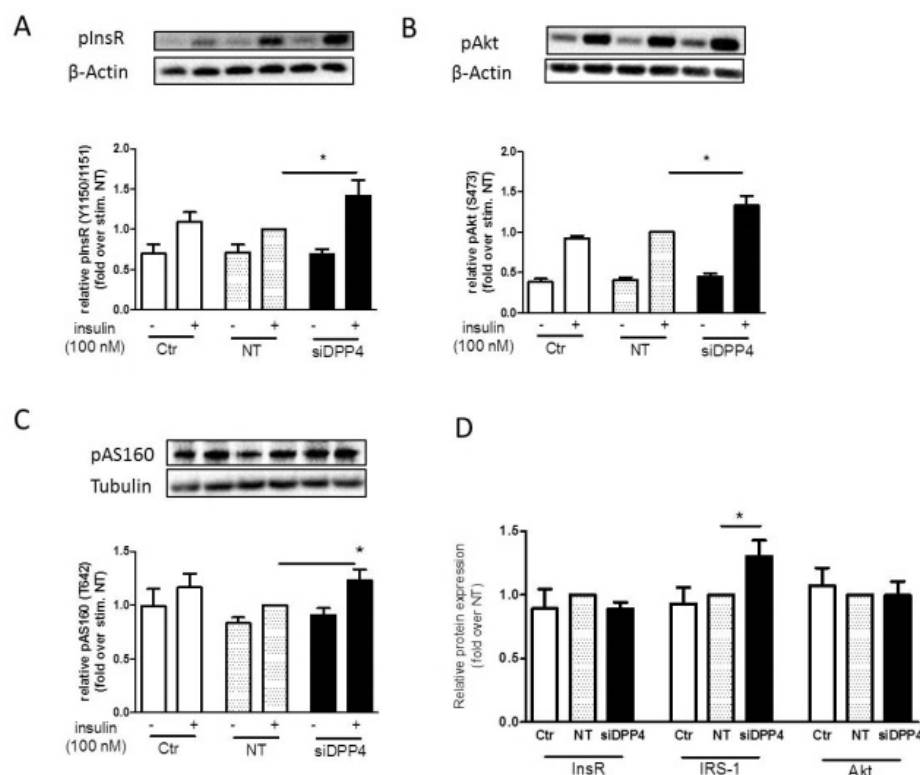


Fig. 3: Expression of proteins within the insulin signaling pathway after siRNA-mediated DPP4 silencing. On day 14 of differentiation, primary adipocytes were stimulated with 100 nM of insulin for 10 min and proteins of the insulin signaling cascade were analyzed by Western Blot. Levels of phospho InsR (A) phospho-Akt (B) and phospho-AS160 (C) were analyzed. Furthermore total protein levels of the unstimulated proteins were assessed (D). Data were normalized to the indicated housekeepers and are presented as fold over stimulated scr. Data are mean values \pm SEM, $n=7-9$; * $P < 0.05$ vs. NT; Ctr control; NT non-target control siRNA; siDPP4 siRNA against DPP4; representative Western Blots for are presented.

assess whether knock-down of DPP4 has a potential impact on this function we analyzed activation and expression of different proteins within the insulin signaling cascade.

We could observe a significant upregulation of insulin-stimulated insulin receptor (InsR), proteinkinase B (Akt) and Akt substrate of 160 kDa (AS160) phosphorylation (Fig 3 A-C) with most prominent effects at the receptor level. The basal phosphorylation levels of the investigated proteins remained unaltered. Interestingly, the total protein level of IRS-1 was significantly upregulated upon DPP4 silencing, whereas the total protein expression of the InsR and Akt were unaltered compared to control (Fig 3D).

To clarify if these effects could be explained by the enzymatic activity of DPP4, the well-established DPP4 inhibitors sitagliptin and saxagliptin were used to block DPP4 activity using *in vitro* differentiated mature adipocytes. Both inhibitors were able to almost completely block DPP4 activity measured in adipocyte supernatants (Fig 4A). In agreement with our silencing data,

we could observe a significantly increased insulin-stimulated Akt phosphorylation with both inhibitors (Fig 4B) by about 30%. Also in this setting total protein levels of Akt and InsR remained unaltered by the treatment (data not shown).

Discussion

During obesity which is a major health risk in Western society, AT expansion and inflammation lead to a dysregulated release of adipokines. Recently we were able to show that DPP4 is upregulated during obesity and might link this adipokine to the metabolic syndrome (10;11). However the role of DPP4 within AT and how it affects adipocyte function is not known so far.

From a study by Rosmaninho-Salgado and colleagues it could be speculated that sDPP4 might stimulate lipid accumulation and PPAR γ expression through degradation of neuropeptide Y (NPY), which is well-known for its anti-lipolytic activity (14). However, the concentrations of sDPP4 used in this study are beyond the physiological levels of sDPP4. Furthermore studies on the

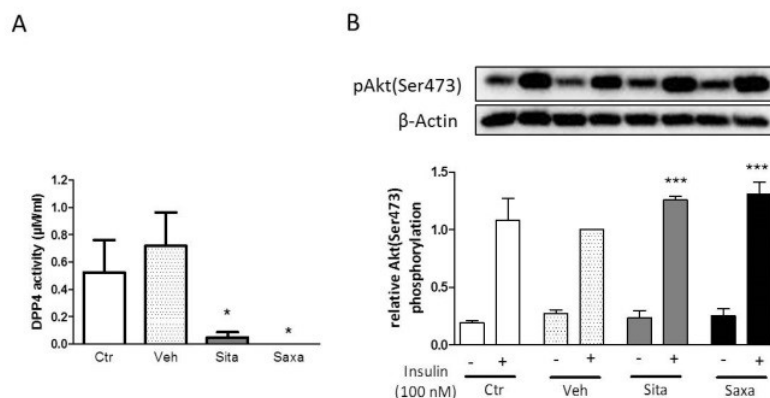


Fig. 4: Impact of DPP4i treatment on DPP4 activity and the level of Akt activation. Human primary adipocytes were incubated from day 10 of differentiation until day 14 of differentiation with 100 nM of the DPP4i sitagliptin or saxagliptin. On day 14 of differentiation, supernatants were collected and remaining DPP4 activity was measured with an activity assay (A). Furthermore cells were treated with 100 nM insulin for 10 min and insulin signaling was assessed by Western Blot. DMSO served as vehicle control. Representative blots for (B) are depicted. Data are mean values \pm SEM, $n=4$ * $P < 0.05$, *** $P < 0.001$ vs Veh; Ctrl control; Veh DMSO vehicle; Sita sitagliptin; Saxa saxagliptin

physiological role of DPP4 on adipocyte differentiation are missing. We could show here that DPP4 depletion by siRNA-mediated silencing does not affect adipocyte differentiation illustrated by differentiation markers such as adiponectin, PPAR γ or HSL and by amount of incorporated lipids determined by OilRed staining.

Recently, several groups observed beneficial anti-inflammatory effects of DPP4i. Cytokine production and mRNA expression of inflammatory markers like IL6 or TNF α could be reduced by DPP4i both *in vitro* (20;21) and *in vivo* (15;16;22). Although the adipokine array data indicate an unaltered secretory output from adipocytes after silencing, this could be misleading since DPP4 only clips its substrates at the penultimate position resulting in only slightly altered proteins, which might still be detectable by the spotted antibodies. This problem was extensively summarized in a recent review by Mulvihill and Drucker (6). However, our data indicate that DPP4 silencing seems not to primarily target adipocyte inflammation or secretory output.

Interestingly, DPP4 silencing mediates a prominent effect on insulin signaling in the adipocytes with reduced DPP4 being associated with improved signaling. This is in line with our previous observations that increasing DPP4 levels by addition of recombinant protein impairs insulin signaling in adipocytes (10). One point which could explain the improved responsiveness towards insulin in general is the elevated protein level of total IRS-1. Low levels of IRS-1 are often observed in T2D and higher amounts of IRS-1 protein are associated with improved insulin

signaling (23). However, how DPP4 affects IRS-1 protein level in the absence of insulin remains elusive and needs to be addressed in the future.

There are some other possible mechanisms by which DPP4 depletion might lead to insulin sensitizing in adipocytes. First, it seems plausible that the clipping of DPP4 substrates could influence insulin sensitivity. This could be either by altering the binding mode of the substrates to insulin target proteins and hence positively influence InsR responsiveness towards insulin. Or the altered activity of substrates could influence regulators of insulin signaling. In this scenario DPP4i would directly affect clipping of DPP4 substrates and therefore impair insulin signaling. Yet unidentified secreted factors and other mechanisms could potentially explain how reduced amount and activity of DPP4 improves insulin signaling. This needs to be further addressed in the future.

A second conceivable explanation despite affecting DPP4 substrates is that DPP4 and the insulin receptor could interact with each other and thereby DPP4 somehow reduces the activation of the insulin receptor. That the InsR is able to interact with other proteins which could alter its responsiveness towards insulin is well known. Glycoprotein-1, ectonucleotide pyrophosphatase/phosphodiesterase and alpha 2-HS glycoprotein were proposed as negative regulators, since they interact with the extracellular domain of the InsR and thereby negatively affect insulin binding (24;25). This mode of action is also conceivable in case of DPP4. A similar mechanism with opposite function is proposed for Gpc4 by Ussar and colleagues, who could show that both membrane-

bound as well as the free form of Gpc4 enhance insulin signaling (26). Gpc4 seems to interact with the InsR in the unstimulated state and upon insulin stimulation the receptor is unbound to Gpc4. In contrast to our results Gpc4 is also pro-adipogenic (26). Since we also observed sensitizing effects when DPP4 enzymatic activity is blocked (8), the binding of the inhibitor somehow seems to affect the binding of DPP4 to InsR and /or other partners. This could be because of a conformational change of DPP4 upon inhibitor binding which was proposed by Wronkowitz et al in case of the binding to protease activated receptor 2 (8). Another example that DPP4i treatment affects DPP4 interaction with binding partners is reported for Fibronectin as shown by Piazza et al (27).

In conclusion, we could show here for the first time that knock-down of DPP4 in human adipocytes leads to an improved insulin signaling response despite a similar rate of differentiation. This effect is at least partly mediated by DPP4 enzymatic activity. This finding is of importance since AT is a key source of DPP4 in obese patients and links obesity to the metabolic syndrome (10;11). Taken together with our previously published results on sDPP4 in adipocytes (10), the amount of DPP4 might be a regulator for insulin signaling in AT, especially in the obese state and might also open up new explanations for the beneficial effects of DPP4i on insulin sensitivity beyond the incretin hormones.

Acknowledgement

This work was supported by the Ministry of Science and Research of the State of North Rhine-Westphalia (MIWF NRW) and the Federal Ministry of Health (BMG). We wish to thank the Dept. of Plastic Surgery, Florence-Nightingale-Hospital Düsseldorf, for support in obtaining adipose tissue samples. The technical assistance of Andrea Cramer, the scientific support from Dr. Nina Wronkowitz and the secretarial assistance of Birgit Hurow is gratefully acknowledged.

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2.4. STUDY 4: IMPACT OF ADIPOSE TISSUE-SPECIFIC DPP4 DELETION

DPP4 DELETION IN ADIPOSE TISSUE IMPROVES HEPATIC INSULIN RESISTANCE IN DIET-INDUCED OBESITY

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Submitted to: Cell reports

Summary

Besides a therapeutic target for type 2 diabetes, dipeptidyl peptidase 4 (DPP4) is an adipokine potentially linked to human obesity. The role of adipose tissue (AT)-derived DPP4 was explored generating an AT-specific KO mouse (AT-DPP4-KO). Under high fat diet (HFD), AT-DPP4-KO displayed reduced circulating DPP4, proving AT as a relevant source. Independently of glucose-stimulated incretin hormones, glucose tolerance and suppression of endogenous glucose production were improved. AT-DPP4-KO displayed smaller adipocytes, increased M2 macrophages and decreased AT fibrosis. IGF binding protein 3 (IGFBP3) levels were lower in AT and serum, while free IGF1 was increased. In type 2 diabetes patients treated with the DPP4 inhibitor sitagliptin, both free IGF1 and free/total ratio increased. During HFD, lack of adipose DPP4 triggers beneficial remodeling and decreases production of IGFBP3, resulting in increased free IGF1 and improved glucose tolerance and hepatic insulin resistance, supporting a key role of DPP4 in obesity-related metabolic disorders.

Highlights

- AT-DPP4-KO is a novel model which demonstrates that AT is a major source of soluble DPP4 in obesity.
- Under HFD, AT-DPP4-KO mice display improved glucose tolerance and hepatic insulin resistance, independently of glucose-stimulated incretin hormones.
- Lack of adipose DPP4 triggers favorable AT remodeling during HFD with smaller adipocytes, reduced fibrosis and increased M2 macrophage-markers.
- IGF binding protein 3 (IGFBP3) levels were reduced in AT and serum of AT-DPP4-KO mice, resulting in increased free IGF1 potentially linked to the observed improved hepatic insulin resistance.
- Analogously, type 2 diabetes patients treated with the DPP4 inhibitor sitagliptin, displayed increased serum levels of free IGF1 and free/total IGF ratio.
- Our model underpins a key role of DPP4 in obesity-related metabolic disorders.

Introduction

Obesity is reaching an epidemic dimension nowadays (Ng et al., 2014) and is intimately related to the development of insulin resistance (Wellen and Hotamisligil, 2003), characterized by decreased insulin-stimulated glucose uptake in muscle (DeFronzo and Tripathy, 2009) and adipose tissue (AT) (Guilherme et al., 2008), as well as by impaired insulin-mediated suppression of endogenous (hepatic) glucose production (EGP) (Perry et al., 2014). Consequently, obesity represents a major risk factor for type 2 diabetes (Hardy et al., 2012). In search for the mechanisms underlying these diseases, AT has been recognized as an important endocrine organ releasing very diverse bioactive factors named adipokines (Romacho et al., 2014). By an in-depth proteomic profiling of the secretome of primary human adipocytes, we identified dipeptidyl peptidase 4 (DPP4) as an adipokine (Lehr et al., 2012). DPP4 is a ubiquitous transmembrane glycoprotein and exoprotease which cleaves N-terminal dipeptides from a wide range of substrates including growth factors, neuropeptides and chemokines (Yazbeck et al., 2009). Of note, DPP4 also cleaves and inactivates the members of the incretin hormone family glucagon-like peptide-1 (GLP-1) and gastric inhibitory polypeptide (GIP), which account for approximately up to 70% of postprandial insulin secretion (Nauck et al., 1986). Thus, DPP4 inhibitors are currently used as glucose-lowering agents to prolong the insulinotropic effect of incretins in type 2 diabetes. Besides its enzymatic activity,

DPP4 was originally identified as the CD26 antigen in lymphocytes involved in T cell activation (Fleischer, 1994). Both, the abundance of the membrane-bound form and the activity of circulating soluble DPP4 are altered in a variety of inflammatory diseases, metabolic syndrome and diabetes mellitus (Rohrborn et al., 2015). Although a fraction of soluble DPP4 most likely originates from immune cells (Cordero et al., 2009), the major source of circulating DPP4 remains unknown.

In vitro, DPP4 knockdown and pharmacological inhibition in human adipocytes improved insulin signaling without affecting adipogenesis (Rohrborn et al., 2016). Studies in animals show that circulating DPP4 activity is higher in C57/BL6 mice under high fat diet (HFD) (Nistala et al., 2014) and in ob/ob mice (Ruter et al., 2004). On the contrary, genetic DPP4 deletion in Fischer rats and congenital DPP4 depletion in Dark Agouti rats resulted in improved glucose tolerance under HFD (Frerker et al., 2009; Yasuda et al., 2002). Furthermore, whole body DPP4 knockout (KO) mice display improved glucose tolerance, increased GLP-1 levels and prevented insulin resistance during HFD (Conarello et al., 2003; Marguet et al., 2000). We previously identified DPP4 as an adipokine that may be a missing link between increased AT mass in obesity and obesity-associated metabolic diseases. Since previous studies suggested that DPP4 may affect AT adipogenesis, inflammation and insulin sensitivity (Rohrborn et al., 2015), we aimed to explore the role of DPP4 within AT in the context of metabolic diseases. However, DPP4 pharmacological

inhibition and genetic deletion affect both central regulation of food intake and energy expenditure. Therefore, we have generated an AT specific DPP4 KO mouse (AT-DPP4-KO) in order to characterize the impact of AT-derived DPP4 in obesity.

Results

The AT-DPP4-KO mouse model

Cre expression was only detectable in mature adipocytes from KO animals (Fig 1A), where DPP4 protein levels were significantly reduced by up to 65 % (Fig. 1B) with unaltered DPP4 expression in the stromal vascular fraction (SVF) within AT (Fig. 1C). DPP4 protein levels in immune cells isolated by peritoneal lavage from AT-DPP4-KO mice remained similar to WT mice (Fig. 1D). This specific AT KO resulted in significantly lower serum DPP4 in KO animals on HFD (Fig 1E). As DPP4 KO was restricted to AT, we did not observe differences in incretin levels. Circulating active GLP-1 and GIP were similar between the genotypes both in basal conditions and after 15 min oral glucose load (Suppl. fig. 1). To further prove the specificity of our animal model we explored DPP4 enzymatic activity in different organs and tissues such as liver, pancreas, kidney, lung, heart, spleen, brain, ingWAT, epiWAT and BAT. DPP4 was only decreased in WAT and BAT (Fig. 1F).

Lack of DPP4 in AT improves glucose tolerance in mice under HFD in spite of increased body weight

After 24 weeks of HFD, AT-DPP4-KO mice gained more body weight compared to WT (41.9 ± 3.6 g vs. 56.7 ± 4.3 g; Fig. 2A). This

was paralleled by an increase in fat and lean mass (Suppl.Fig. 1A-B). Analogously, the genotype did not affect EE (volume of oxygen consumed ($\text{VO}_2/\text{kg}^{0.75}/\text{h}$), respiratory quotient (RQ) and SPA (Suppl. Fig. 2 A-C). These differences in body weight, fat and lean mass were not due to differences in food intake normalized to body weight (Suppl. Fig. 2d). Body length was similar in both genotypes (Suppl. Fig. 2E). Furthermore, BAT mass and RQ was not affected by the genotype (Suppl. Fig. 2B).

During the oral glucose tolerance test, plasma glucose was lower during the first 60 minutes in KO animals compared to the diet-matched controls (Fig. 2B-C), while plasma insulin levels were significantly increased during the initial 30 minutes (Fig. 2D). HOMA-IR index was significantly lower in KO mice after 24 weeks HFD (Fig. 2E). The hyperinsulinemic-euglycemic clamps revealed increased suppression of endogenous glucose production (EGP) in KO animals after HFD (Fig. 2F). Whole body glucose disposal rate (Rd) and NEFA suppression were not different from WT (Suppl Fig. 3), indicating that AT-DPP4-KO mice exhibit selective improvement of hepatic insulin sensitivity upon HFD. Of note, circulating DPP4 levels correlated negatively with hepatic insulin sensitivity, as assessed from suppression of EGP in WT animals (Fig 2G). Under chow diet, insulin sensitivity in AT-DPP4-KO mice was not different from KO.

Liver lipid content as assessed histologically (Supl. Fig 4A) or colorimetrically after extraction (Supl. Fig 4B) did not differ between the WT and KO animals. The KO animals under HFD had similar plasma triglycerides (Suppl. Fig. 4D) but significantly reduced cholesterol

plasma levels compared to their matched WT controls (Suppl. Fig. 4C).

DPP4 deletion in AT promotes remodeling

The 24-week HFD resulted in alterations of the morphology of epiWAT in both genotypes. Within the HFD group, the KO mice displayed a marked shift in the adipocyte size distribution towards smaller adipocytes in epiWAT (Fig. 3A). A comparison between AT-DPP4-KO animals and WT animals under HFD showed decreased mean adipocyte size in AT-DPP4-KO mice (Fig. 3B). Adipocyte size was positively correlated with circulating DPP4 levels (Fig. 3C), as previously shown for humans (Sell et al., 2013). In order to determine if the changes observed in adipocyte size were related to fibrosis, we investigated the expression of several fibrosis markers, namely *Col1A1*, *Col3A1* and *Col6A6*. All fibrosis markers were reduced in the epiWAT of KO animals (Fig. 3D-F). Adipocyte size was also substantially reduced in the ingWAT of KO under HFD and circulating DPP4 levels significantly correlated with adipocyte size in this depot (Suppl. Fig. 5C). However, the lack of DPP4 in adipocytes did not affect the expression of fibrosis markers in the subcutaneous fat depot (Suppl. Fig. 5D-F).

Since AT inflammation is involved in the development of insulin resistance, we also assessed macrophage infiltration in AT and the expression of the M2 anti-inflammatory macrophage markers vs. M1 pro-inflammatory markers. Crown-like structures (CLS) are formed as a result of macrophages infiltrating into AT to reabsorb dead adipocytes. Macrophage infiltration within AT was analyzed by counting galectin-3 positive CLS. Under HFD, the KO animals displayed significantly increased number of CLS only

in the epiWAT (Fig 3G-H). In line with this observation, in the epiWAT, M1 pro-inflammatory markers IL-6 and chemokine (C-C Motif) ligand 2 (CCL2) were significantly increased in KO mice compared to WT animals under HFD (Fig. 3i). On the other hand, the anti-inflammatory M2 macrophage markers mannose receptor 1 (*Mrc1*) and interleukin (IL)-10 were also significantly upregulated in KO animals under HFD (Fig. 3j). Regarding the subcutaneous depot an increase of the M1 marker galectin-3 was observed although no differences in CLS were found in this depot (Suppl. Fig. 6A-B). Markers of adipogenesis such as adiponectin, PPAR γ and GLUT4 were simultaneously increased in epiWAT (Fig. 3l) but remained unaltered in ingWAT (Suppl. Fig. 6D).

DPP4 deletion results in reduced circulating IGFBP3 and increased free IGF1 levels

In order to characterize how the lack of DPP4 in adipocytes affects adipokine release, we screened the adipokine profile in conditioned medium (CM) obtained from AT explants of animals after 24 weeks of HFD (data not shown) and gained preliminary evidence that IGFBP3 was a factor downregulated in the CM from epiWAT of KO animals. We observed that IGFBP3 release was reduced in the CM from explants of epiWAT of KO animals under HFD in parallel to reduced IGFBP3 gene expression (Fig. 4A-B). This was paralleled by reduced circulating levels in the KO animals which underwent HFD (Fig. 4C). Furthermore, KO animals after HFD displayed increased free IGF1

circulating levels (Fig. 4D), although no changes were observed among total IGF1 levels (Fig. 4E).

IGFBP3 impairs insulin signaling and insulin-stimulated suppression of glucose production in HepG2 cells

In order to further study the effects IGFBP3 on insulin sensitivity in hepatocytes, HepG2 cells were treated with growing concentrations of IGFBP3, which resulted in increasing impairment of insulin-stimulated Akt phosphorylation at Thr308 but not at Ser473 (Fig. 5A). IGFBP3 (300 ng/ml) reduced insulin stimulated Akt phosphorylation at Thr308 by approximately 20% (Fig. 5B) while Akt phosphorylation at Ser473 remained unaltered (Fig. 5C). Finally, IGFBP3 (300 ng/ml and 1 µg/ml) resulted in complete abrogation of insulin-stimulated suppression of glucose production by hepatocytes (Fig. 5D).

DPP4 inhibition in patients with type 2 diabetes increases free IGF1 circulating concentrations

IGFBP3, free IGF1, total IGF1, DPP4 protein and DPP4 activity were measured in serum samples obtained from recent onset metformin-treated type 2 diabetes patients with or without treatment with the DPP4 inhibitor sitagliptin. Both groups of patients had comparable anthropometric and metabolic parameters. However, patients on sitagliptin treatment displayed significantly lower DPP4 activity in serum with comparable amounts of DPP4 protein in circulation (Table 1). Circulating IGFBP3 concentrations were similar in both groups (Fig. 6A). However, patients treated with sitagliptin had significantly higher serum levels of free IGF1 and total

IGF1 (Fig. 6B-C). In addition, the free IGF1/total IGF1 ratio was higher in patients receiving sitagliptin (Fig. 6D). Total IGF1 correlated positively with free IGF1 ($r=0.50$, $p=0.0002$) and negatively with hs-CRP ($r=-0.31$, $p=0.02$). The free IGF1/total IGF1 ratio declined with aging ($r=0.30$, $p=0.04$). Of note, IGFBP3 correlated with cholesterol ($r=0.56$, $p<0.0001$), LDL-cholesterol ($r=0.45$, $p=0.001$), serum triglycerides ($r=0.44$, $p=0.002$) and γ GT ($r=0.31$, $p=0.03$). DPP4 was positively related to liver transaminases (ALT $r=0.54$, $p<0.0001$; AST $r=0.40$, $p=0.004$; γ GT $r=0.40$, $p=0.004$).

Discussion

The novel mouse model of adipose-specific knockout of DPP4-KO demonstrates that AT is a major source of circulating DPP4 in obesity neither affecting basal nor glucose-stimulated incretin hormone secretion. When fed a HFD, AT-DPP4-KO mice display improved glucose tolerance and hepatic insulin resistance. DPP4 depletion affects AT itself through a favorable remodeling during HFD with smaller adipocytes, reduced fibrosis and increased M2 macrophage-mediated inflammation.

Our group has previously provided the first evidence for DPP4 being an adipokine (Lamers et al., 2011) and demonstrated that DPP4 is upregulated in human obesity and the metabolic syndrome (Sell et al., 2013). AT-DPP4-KO mice prove that AT is an important source of circulating DPP4 in the obese state. Here, we provide the first comparison of DPP4 enzymatic activity in AT in relation to other organs such as the liver, pancreas or the kidney, which may represent sources of circulating DPP4 (Hildebrandt

et al., 1991; Kirino et al., 2009; Shinjo et al., 2015). Of note, except from liver, all other tested tissues are probably only minor contributors to circulating DPP4 due to their relative low mass compared to enlarged AT. The tissue specificity of our model compared to previously described global DPP4 KO models (Conarello et al., 2003; Marguet et al., 2000) allows us to detect the impact of DPP4 deletion within AT and dissect these effects from incretin-mediated actions, since GIP and active GLP-1 did not differ among the genotypes. Therefore, the effects of DPP4 deletion in AT under HFD on body composition, glucose tolerance and hepatic insulin sensitivity occur independent of the incretin system which is not affected by adipose KO of DPP4. In global DPP4 KO mice, active GLP-1 and insulin are significantly increased after an oral glucose load (Marguet et al., 2000). Furthermore, global KO mice display significantly lower food intake resulting in almost complete resistance to diet-induced obesity (Conarello et al., 2003). But not only food intake is responsible for this resistance to HFD, as demonstrated by pair feeding experiments, global KO mice are also characterized by higher oxygen consumption and increased expression of UCP-1 in BAT. Thus, central effects of global DPP4 KO on food intake and increased BAT activity can be attributed to DPP4 depletion in combination with a boosted incretin system. DPP4 ablation only in AT did not affect food intake nor oxygen consumption and occurred without affecting the incretin system which makes our novel model

independent from central effects of DPP4 and incretin actions.

AT-DPP4-KO mice display improved glucose tolerance under HFD compared to controls despite higher body weight and fat mass. Furthermore, insulin secretion in the initial phase of oGTTs and HOMA-IR was improved in AT-DPP4 KO mice on HFD compared to WT mice. In fact, deletion of DPP4 in AT seems to play a role specifically for hepatic insulin sensitivity. Compared to WT mice on HFD, AT-DPP4-KO mice displayed significantly increased insulin-mediated suppression of EGP, but no difference in basal EGP, insulin-mediated suppression of NEFA and insulin-stimulated whole body glucose disposal. These data indicate that improved insulin action in the liver is the key metabolic feature of AT-DPP4-KO mice on HFD. Impaired insulin-mediated suppression of EGP is an early feature of insulin resistant states and determines the progression to impaired glucose metabolism in obese humans (Ter Horst et al., 2016). Abnormal suppression of EGP further contributes to hyperglycemia in type 2 diabetes mellitus (Mittelman et al., 1997). One may speculate that DPP4 overexpression could contribute to the pathogenesis of hepatic insulin resistance and type 2 diabetes and that its deletion in AT may therefore delay the development of type 2 diabetes. The mechanism by which AT-DPP4-KO affects hepatic insulin sensitivity is still unknown. We can exclude a contribution of NEFA and circulating adiponectin (data not shown) as these parameters were not affected by the KO, while IGFBP3 and IGF1 may be the mediators for improved hepatic insulin

sensitivity. Release from AT and circulating levels of IGFBP3 were reduced in KO mice under HFD. In addition to decreased IGFBP3, free IGF1 was specifically increased in serum of KO mice under HFD. IGFBP3 is one of the main circulating IGFBP species found in serum and binds approximately 90% of circulating IGF1 (Jogie-Brahim et al., 2009). Both IGFBP3 and IGF1 are increased in patients with impaired glucose tolerance and type 2 diabetes (Kim and Lee, 2015). Additionally, IGFBP3 overexpression in transgenic mice impairs insulin secretion resulting in fasting hyperglycemia, impaired glucose tolerance, and insulin resistance (Nguyen et al., 2011; Silha et al., 2002). Differently, whole body KO of IGFBP3 results in a complex metabolic phenotype with higher body growth and weight due to increased growth hormone concentrations and decreased resting metabolic rate compared to controls (Yamada et al., 2010). Furthermore, IGFBP3 KO animals display increased basal glucose turnover but preserved insulin sensitivity and reduced WAT mass. However, it should be noted that complete absence of IGFBP3 is not comparable with our model where IGFBP3 is only reduced, total IGF1 unaltered and animal growth normal. In our KO model, reduced IGFBP3 levels occur in parallel to higher free IGF1 which is known to suppress hepatic glucose production (Laager et al., 1993). Alternatively, IGFBP3 could also regulate hepatic glucose production independently from IGF1 as previously shown (Muzumdar et al., 2006). In fact, surface association of IGFBP3 on hepatocytes has been demonstrated by immunohistochemistry (Hallak et al., 2002). Furthermore, treatment of

adipocytes with IGFBP3 resulted in impaired insulin signaling and reduced insulin-stimulated glucose uptake (Chan et al., 2005). Here, we also provide evidence that IGFBP3 also impairs insulin signaling and insulin-stimulated suppression of glucose production by hepatocytes. In this study, reduced IGFBP3 levels could therefore contribute to improved hepatic insulin sensitivity in two different ways, first by regulating the bioavailability of IGF1 in the form of increased free IGF1, and second by direct hepatic effects of IGFBP3 independent of IGF1. Taken together, we propose that the reduced release of IGFBP3 from visceral AT might mediate a protective crosstalk between AT and liver in AT-DPP4-KO mice on HFD.

Adipocyte size, a surrogate marker of insulin resistance (Cotillard et al., 2014), was reduced in both subcutaneous and visceral fat of AT-DPP4-KO mice on HFD. Our results are in line with our previous report in humans, where circulating DPP4 positively correlated with adipocyte size (Sell et al., 2013). In diet-induced obesity, DPP4 inhibitors have been proven to reduce adipocyte size (Chae et al., 2015). However, solely in the epiWAT of KO mice under HFD, we observed a trend towards increased markers of adipogenesis potentially suggesting hyperplasia. This is in line with our findings reported in human subcutaneous adipocytes, where DPP4 knockdown did not affect adipogenesis (Rohrborn et al., 2016). We discarded AT fibrosis as the cause of the reduced adipocyte size. Thus, fibrosis was also solely reduced in epiWAT from AT-DPP4-KO mice under HFD. Since AT fibrosis has been linked to insulin resistance (Sun et al., 2013), we hypothesize that reduced fibrosis in visceral fat may represent an

additional mechanism for DPP4 deficiency to promote a protective remodeling in AT during diet-induced obesity. Although chronic inflammation in AT links obesity to its complications, there is growing evidence that pro-inflammatory signaling is a prerequisite for AT remodeling and expansion (Wernstedt et al., 2014). We employed galectin-3 to quantify CLS in AT, which besides being a M1 macrophage marker, has been recently proposed as an indicator of phagocytosis of apoptotic cells (MacKinnon et al., 2008). Thus, galectin-3 KO mice exhibit impaired expansion of AT under diet-induced obesity resulting in increased hyperglycemia and glucose intolerance under HFD (Darrow and Shohet, 2015). Therefore, increased galectin-3 positive macrophages in epiWAT from KO mice may contribute to a beneficial AT expansion under HFD. As mentioned, IGFBP3 levels were reduced in both CM from epiWAT and serum from KO animals. IGFBP3 deletion has been shown to improve differentiation in adipocytes via direct interaction with PPAR γ , while both administration of exogenous IGFBP3 and overexpression inhibits adipogenesis in 3T3-L1 (Jogie-Brahim et al., 2009). Therefore, we propose that reduced IGFBP3 levels in AT-DPP4 KO mice promotes a beneficial remodeling during HFD, characterized by reduced hypertrophy, fibrosis and inflammation while adipogenesis is increased.

Of note, also in humans with type 2 diabetes DPP4 inhibition increases free and total IGF1 concentrations in serum. Although not directly comparable to our mouse model, where circulating DPP4 is reduced and incretin levels unaltered,

these data provide additional evidence for a link between DPP4 and the IGF1/IGFBP3 axis. Recombinant IGF1 and combinations of recombinant IGF1 with IGFBP3 have been previously discussed as treatment options for type 2 diabetes (Ranke, 2005). However, the long term potential of this therapy has not been further developed due to various side effects and the association of very high IGF1 levels with prostate and breast cancer (Renehan et al., 2004). Nevertheless, IGF1 has been reported to exert vasoprotective effects not only in type 2 diabetes (Ezzat et al., 2008) and lower IGF1 serum concentrations are associated with diabetes (Teppala and Shankar, 2010). Since pharmacological interventions increasing circulating IGF1 have not been reported so far, the observed increase in serum free IGF1 and total IGF1 exerted by the DPP4 inhibitor sitagliptin may represent a novel therapeutic target in type 2 diabetes. It can be speculated that increased IGF1 concentrations could be linked to altered hepatic glucose production in patients treated with DPP4 inhibitors. In fact, sitagliptin improves the suppression of EGP in dogs (Edgerton et al., 2009) and in humans (Muscelli et al., 2012). Also vildagliptin triggers a better suppression of EGP (Balas et al., 2007) or lower basal EGP in patients (Vella et al., 2007).

Future studies will help to clarify how DPP4 deletion in AT can be translated into a therapeutic tool in metabolic diseases. This is of special interest in the case of obese type 2 diabetic patients which are currently treated with DPP4 inhibitors. How exactly DPP4 inhibitors

might also affect AT biology and hepatic insulin sensitivity in addition to their incretin-mediated effects remains fully unexplored. Since DPP4 is an adipokine upregulated in adipose tissue in obesity both in human and rodents, AT arises as an important and novel source of DPP4 and as a new therapeutic target for DPP4 inhibitors.

Experimental procedures

Materials

Reagents for SDS-PAGE were supplied by GE Healthcare (Freiburg, Germany) and Sigma-Aldrich (Munich, Germany). Antibodies against murine DPP4, CD11b and β -actin were supplied from Abcam (Cambridge, U.K.) and pAkt Ser473 and Thr308 from New England Biolabs (Frankfurt, Germany). Horseradish peroxidase (HRP)-conjugated goat anti-rabbit and goat anti-mouse IgG anti-bodies were supplied by Promega (Mannheim, Germany). Complete protease inhibitor cocktail and PhosStop phosphatase inhibitor cocktail were provided by Roche (Mannheim, Germany). Unless stated elsewhere, all reagents were purchased from Sigma-Aldrich.

Mouse model

The adipose-specific DPP4 knockout (AT-DPP4-KO) mice have been generated by a Cre-lox strategy based on deletion of exons 1 and 2 of the DPP4 gene and crossbreeding with B6.Cg-Tg(Fabp4 cre)1Rev/J mice (Jackson Laboratories), expressing Cre-recombinase under the control of the Fabp4 promoter. Genetic deletion of DPP4 was confirmed at the DNA level by gel electrophoresis and also at the RNA and protein level by real-time PCR and Western blotting.

C57BL/6J floxed mice and adipose-specific DPP4 knockout male mice were housed in mixed groups of maximum 5 animals per cage under a light/dark cycle (12 h/12 h), in a temperature controlled room (22 °C) with standard food and water *ad libitum*. At 12 weeks of age animals were randomly allocated to standard chow diet or HFD (60% fat; Research diets D12492) for 24 weeks. All procedures followed the principles outlined in the European Commission Council Directive for the care and use of laboratory animals (86/609/EEC). Animal experiments were approved by the Ethics

Committee of the State Agency for Nature, Environment and Consumer Protection (LANUV, North Rhine-Westphalia, Germany) and conducted at the animal facility of the German Diabetes Center.

DPP4 activity in serum, organs and tissues

DPP4 activity was measured with a fluorometric kit from Sigma Aldrich. 10 μ l of serum was assayed as detailed by the manufacturer. 10 mg of frozen tissues were homogenized in cold assay buffer. Following homogenization, the samples were centrifuged at 13000 rpm for 15 min at 4°C. The resulting supernatants were collected, diluted 1:10 and were immediately used for DPP4 activity fluorometric assay following manufacturer's instructions. The resulting fluorescent signal was detected with a microplate reader (Infinite M200, Tecan). DPP4 enzymatic activity in each tissue was expressed as the amount of cleaved AMC per minute per total tissue (μ U/ tissue) at 37°C.

Western blot

5 μ g of proteins were separated by SDS-PAGE using 10% horizontal gels. The proteins were then transferred to a polyvinylidene difluoride membrane (Millipore) in a semidry blotting system. Membranes were blocked with 5% nonfat dry milk in TBS containing 0.1% Tween for 1 h at room temperature and later incubated with the indicated primary antibodies. After washing with TBST, membranes were incubated with a secondary horseradish peroxidase (HRP)-coupled antibody and processed for chemiluminescence detection using Immobilon HRP substrate (Millipore). Signals were visualized and analyzed on a Bio-Rad VersaDoc 4000 MP work station.

Peritoneal lavage

Mice were sacrificed by cervical dislocation and the peritoneum was flushed with cold PBS with 5% FCS in order to harvest peritoneal cells. The resulting peritoneal lavage was resuspended in 0.4 ml MACS buffer (1 \times PBS, 2% FCS, 5 mM EDTA). For Western blot analysis about 3 \times 10⁶ cells were resuspended in lysis buffer and stained with anti-CD11b (ab53187 Abcam) or a DPP4 antibody.

Body composition

Longitudinal changes in body composition of all animals were assessed using quantitative nuclear magnetic resonance imaging (Whole Body Composition Analyzer; Echo MRI, Texas, USA).

Body composition was measured at the beginning of the diet and at every 4 weeks.

Hyperinsulinemic-euglycemic clamp test

At 4-6 days before the clamp, an indwelling silicon catheter (Silastic Laboratory Tubing, Dow Corning, Midland, MI) was placed in the right-side jugular vein of the animals under isoflurane anesthesia (CP Pharma, Burgdorf, Germany), as previously described (Jelenik et al., 2014). After recovering from surgery, the mice were fasted during the 6 h prior to the clamp, with free access to drinking water. In order to assess basal glucose disposal, D-[6,6-²H₂]glucose (98% enriched) (Cambridge Isotope Laboratories, Andover, MA) was infused at a rate of 4 μmol/kg/min for 120 min. The hyperinsulinemic-euglycemic clamp was performed with a primed (40 mU/kg), continuous infusion of insulin (10 mU/kg/min) (Huminsulin; Lilly, Giessen, Germany) for 180 min. Euglycemia was maintained by periodically adjusting a variable 20% glucose infusate. D-[6,6-²H₂] glucose was co-infused together with insulin (0.4 μmol/kg/min) and variable glucose infusion to obtain stable tracer concentrations during varying glucose infusion rates (GIR expressed as “mg glucose/ (kg body weight x minute)). Blood samples were taken at 10 min intervals during the basal period and during the last 30 min of the hyperinsulinemic-euglycemic clamps. After the clamps, mice were exsanguinated through cervical incision and killed by cervical dislocation, serum and organs were collected for future analysis.

Glucose tolerance tests

For oral glucose tolerance tests (oGTT), a glucose solution (2 g/kg body weight, 40% solution in 0.9% wt/vol. NaCl) was given by gavage into 16 h fasted animals. Tail blood glucose levels were measured with a glucometer (Free Style Precision Abbot, Wiesbaden, Germany) at 0, 15, 30, 45, 60, and 120 minutes after gavage.

Adipose tissue immunohistochemistry analysis

Pieces of AT were collected from WT and AT-DPP4-KO mice after 24 weeks of HFD or chow diet. The tissues were fixed in 10% formalin and then dehydrated in ethanol followed by paraffin embedding. A total of 200 adipocytes from 3

different levels of the tissue (100 μm distance between levels) were analyzed per animal and depot, respectively.

a) Adipocyte size

Adipocyte area was measured by a blinded observer at a 10-fold magnification with Cellsense software (Olympus SIS). Adipocyte sizes were clustered in corresponding cell size groups and represented as percentage of cells in each size class.

b) Crown-like structures (CLS)

10-μm dewaxed serial sections were incubated with anti-mouse Mac-2/galectin-3 (Cedarlane Laboratories, Canada) followed by incubation with a biotinylated HRP-conjugated secondary antibody goat anti-rat IgG (Mac-2/galectin-3; Vector Laboratories; Burlingame, CA, USA). Histochemical reactions were performed using Vector's Vectastain ABC Kit and diaminobenzidine as substrate. Sections were counterstained with hematoxylin-eosin and mounted in coverslips. CLS structures per 1000 cells were counted by a blinded observer with Image J software in microphotographs obtained at a 40-fold magnification.

Generation of conditioned media from AT explants

Explants from ingWAT and epiWAT from animals fed HFD for 24 weeks were collected in sterile cold PBS. Connective tissue and vessels were removed and fat pads were cut into pieces of 10 mg. After three times washing and centrifugation in fresh PBS supplemented with an antibiotic and antimycotic mix (Life Technologies) explants were weighted and 100 mg of adipose tissue were incubated in low-glucose DMEM smooth muscle cell growth medium (PromoCell, Heidelberg, Germany) supplemented with 50 mg/ml gentamycin for 24h at 37°C and 5%CO₂ to generate 1 ml conditioned medium.

Real-time quantitative PCR (RT-qPCR).

Total RNA was extracted from frozen tissue samples using TRIzol Reagent (Ambion Life Technologies, Darmstadt, Germany) and RNeasy purification kit (Qiagen, Hilden, Germany) and cDNA was transcribed using 1 μg of total RNA (Omniscript reverse transcription kit, Qiagen).

qPCR was performed using QuantiFast SYBR Green PCR kit (Qiagen). mRNA expression was measured by RT-qPCR with a Step One Plus Real-Time PCR System (AB Applied Biosystems). Values were normalized to the concentration of the housekeeping gene 18S in each sample. mRNA expression was measured in epiWAT and ingWAT from WT and AT-DPP4-KO mice as previously described (Schmittgen and Livak, 2008). The following predesigned primers were used: *Mm_Dpp4_1_SG*, *Mm_Ill10_1_SG*, *Mm_Adipoq_1_SG*, *Mm_Ccl2_1_SG*, *Mm_Il6_1_SG*, *Mm_Col1a1_1_SG*, *Mm_Col3a1_2_SG*, *Mm_Col6a6_1_SG*, *Mm_Lgals_3_SG*, *Mm_Loxl1_2_SG*, *Mm_Mrc_1_SG*, *Mm_Pparg_1_SG*, *Mm_Slc2a4_1_SG*, *Mm_Tnf_1_SG* (Applied Biosystems). Customized primers were purchased from Eurofins and had the following sequences *Cre fwd*: GATTCGACCAGGTTTCGTTC *Cre rev*: GCTAACCAGCGTTTTTCGT. *UCP-1 rev*: CTTTGCCTCACTCAGGAT; *UCP-1 fwd*: ACTGCCACACCTCCAGTC

Hormone and biochemical assays

Plasma insulin was measured with a mouse insulin ELISA immunoassay (Mercodia, Uppsala, Sweden). Mouse DPP4 (Boster), IGBP3, total IGF1 (R&D systems) and free IGF1 (abcam, United Kingdom) were measured by ELISA. Human IGFBP3, free and total IGF1 were measured using ELISA kits from R&D Systems. Human DPP4 was monitored by ELISA (Abnova).

HepG2 culture and glucose production assay

HepG2 cells were obtained from ATCC to study hepatocytes and checked for mycoplasma contamination. Cells were cultured in RPMI 1640 medium (Invitrogen) supplemented with 10% fetal bovine serum (Gibco), 1x Antibiotic-Antimycotic mix (Gibco). Cells were maintained at 37 °C with humidified air and CO₂ (5%). At subconfluence, cells were treated with 300 ng/ml human recombinant IGFBP3 (Biotechne) for 18 h. Cells were washed two times with PBS to remove glucose and incubated for 3 h in glucose production medium (glucose- and phenol red-free DMEM, 20 mM sodium lactate, 2 mM sodium pyruvate) in the presence or absence of 100 nM insulin (Sigma) during 10 min. A quantity of 150 µl of medium was sampled for measurement of glucose concentration using a colorimetric glucose assay kit (Sigma). Glucose concentration was normalized with cellular protein concentration.

Patients

The study was approved by the ethics committee of the Heinrich Heine University Düsseldorf and was conducted in accordance with the Declaration of Helsinki. All participants provided a written informed consent. All patients were participants of the prospective German Diabetes Study (GDS), which evaluates the long-term course of diabetes (Szendroedi et al., 2016). Inclusion criteria for entry into the GDS were type 2 diabetes, known diabetes duration ≤1 year, and 18–69 years of age. Exclusion criteria were: secondary diabetes, pregnancy, severe diseases (cancer), psychiatric disorders, immunosuppressive therapy and limited cooperation ability. Fasting serum samples were obtained from patients treated with sitagliptin in addition to metformin (n=17) and patients treated only with metformin (n=33) matched for age, body mass index (BMI) and sex.

Statistics

Statistical analysis was performed with the GraphPad Prism software (La Jolla, CA, USA). *p* values were calculated using the two-tailed Student's *t*-test. For statistical comparisons between experimental groups, two-way ANOVA was used, followed by Bonferroni *post hoc* test. A *p* value below 0.05 was considered statistically significant. Data are shown as the mean ± S.E.M or mean ± S.D if specified. Normal distribution and equal variances were tested for each analysis. Animals were randomly allocated to the different diets and at least three animals were included in each experimental group. Groups size was calculated by Simple Interactive Statistical Analysis.

Acknowledgments

The authors thank Alexander Strom from the Institute for Clinical Diabetology, German Diabetes Center, Düsseldorf, for his help and technical advice. The secretarial assistance of Birgit Hurow and the technical help of Andrea Cramer, Waltraud Paßlack and Kay Jeruschke are gratefully acknowledged. We would also like to thank Pavel Bobrov for matching of the patients. This work was supported by the German Federal Ministry of Health

(Germany) and the Ministry of Innovation, Science, and Research of the State North Rhine-Westphalia (Germany), an EFSD-MSD grant, the Commission of the European Communities (Collaborative Project ADAPT, Contract No. HEALTH-F2-2008-201100), the Helmholtz Alliance to Universities: Imaging and Curing Environmental Metabolic Diseases (ICEMED), the German Research Foundation (DFG, SFB 1116), German Diabetes Association (DDG), Schmutzler Stiftung and the German Center for Diabetes Research (DZD e.V.). TR was the recipient of a Marie Curie Intra-European Fellowship (2012-IEF- 328793ADDIO).

Author contributions

TR wrote the manuscript; TR, HS, MR and JE designed experiments; TR, HS, DR and II performed experiments; TRC collaborated in setting oGTT and performed the analysis of the data of the metabolic cages; TJ performed hyperinsulinemic-euglycemic clamps; TR, HS, DR, II, TRC, TJ, HA-H, JE and MR discussed the manuscript, SH performed Luminex experiments, JW trained for immunohistochemistry.

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Table 1

Antropometric and clinical data obtained from type 2 diabetic patients treated with metformin alone or in combination with sitagliptin.

	Metformin	Metformin + Sitagliptin
n (male/female)	33 (25/8)	17 (13/4)
Age (years)	52 ± 11	52 ± 12
BMI (kg/m ²)	29.0 ± 4.3	28.3 ± 4.5
Waist circumference (cm)	110 ± 11	96 ± 13
WHR	0.96 ± 0.06	0.93 ± 0.08
M-value (mg/kg*min)	6.18 ± 2.11	6.65 ± 2.53
Fasting blood glucose (mg/dl)	127 ± 25	140 ± 36
Fasting insulin (mU/L)	14.8 ± 6.6	12.8 ± 7.2
C-peptide (ng/ml)	3.07 ± 1.05	2.79 ± 1.02
HbA1c (%)	6.56 ± 1.04	6.42 ± 1.12

hs-CRP (mg/dl)	0.46 ± 0.64	0.25 ± 0.20
Triglyceride (mg/dl)	159 ± 98	131 ± 75
Cholesterol (mg/dl)	208 ± 46	199 ± 42
HDL-cholesterol (mg/dl)	46.6 ± 12.6	54.5 ± 15.8
LDL-cholesterol (mg/dl)	133 ± 39	122 ± 38
AST (U/L)	23.5 ± 9.3	24.0 ± 6.6
ALT (U/L)	32.4 ± 18.3	32.6 ± 19.5
γGT (U/L)	37.1 ± 27.1	33.7 ± 16.4
estimated glomerular filtration rate (ml/min*1.73m ²)	87.6 ± 15.2	90.7 ± 14.8
DPP4 activity (μU/ml)	1.03 ± 0.25	0.51 ± 0.16*
DPP4 protein (ng/ml)	314 ± 23	337 ± 31

BMI: Body mass Index, WHR: waist to hip ratio. Data expressed as mean ± SD, * $p < 0.05$ vs. patients treated with metformin alone.

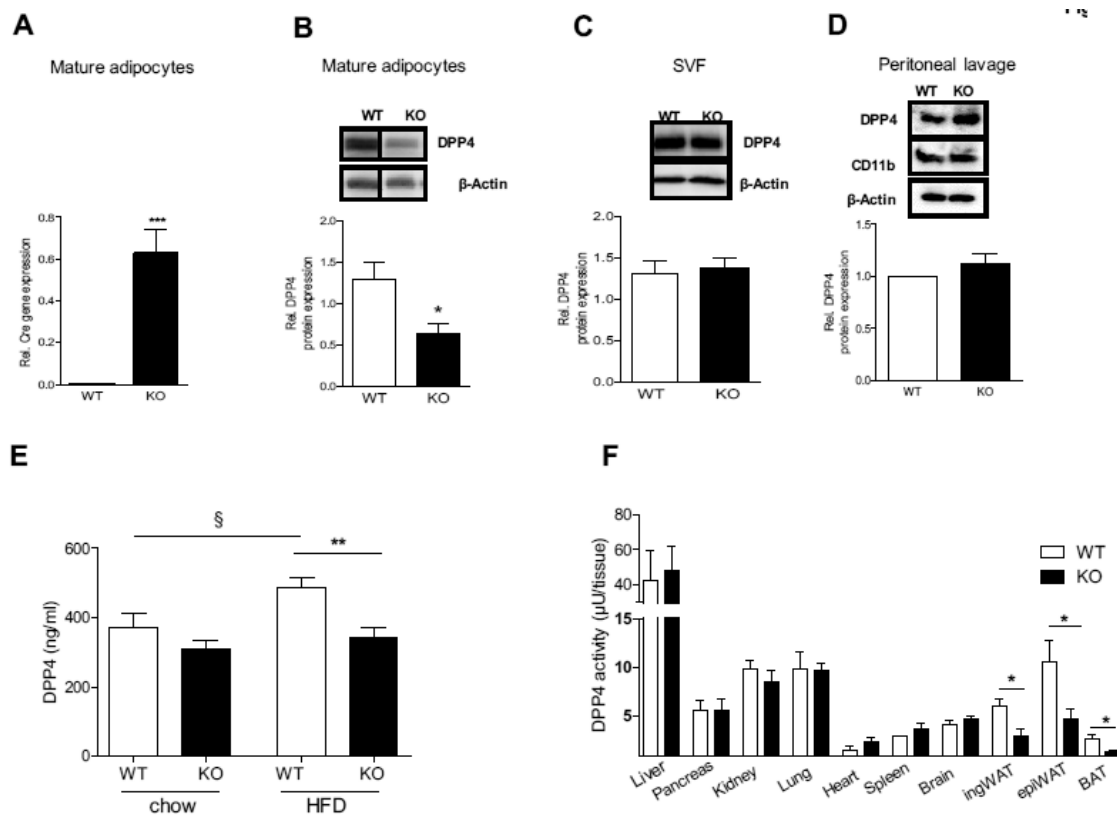


Figure 1. DPP4 deletion is restricted to adipocytes in AT-DPP4-KO mice. (A) Cre mRNA levels in mature adipocytes isolated from wild type (WT) or their corresponding DPP4 adipose tissue-specific

knockout littermates (KO) (n=12 animals per group). mRNA levels were normalized to 18S levels. **(B)** DPP4 protein levels in mature adipocytes and in stroma vascular fraction **(C)** isolated from the inguinal subcutaneous AT depot, from WT and KO animals (n=4-6 animals per group). Corresponding representative blots are shown on top. **(D)** DPP4 and CD11b expression in resident immune cells isolated from peritoneal lavage (n=3 animals per group). Corresponding representative blot is shown on top. **(E)** Fasting circulating DPP4 levels assessed by ELISA in WT and KO mice after 24 week of chow and HFD (n=11 animals per group in ND and n=22 animals per group in HFD). **(F)** DPP4 enzymatic activity in different tissues and organs (n=4 animals per group). Data expressed as mean \pm S.E.M. *** $p<0.001$; ** $p<0.01$; * $p<0.05$ vs. WT littermates on the same diet; § $p<0.05$ vs corresponding genotype on different diet.

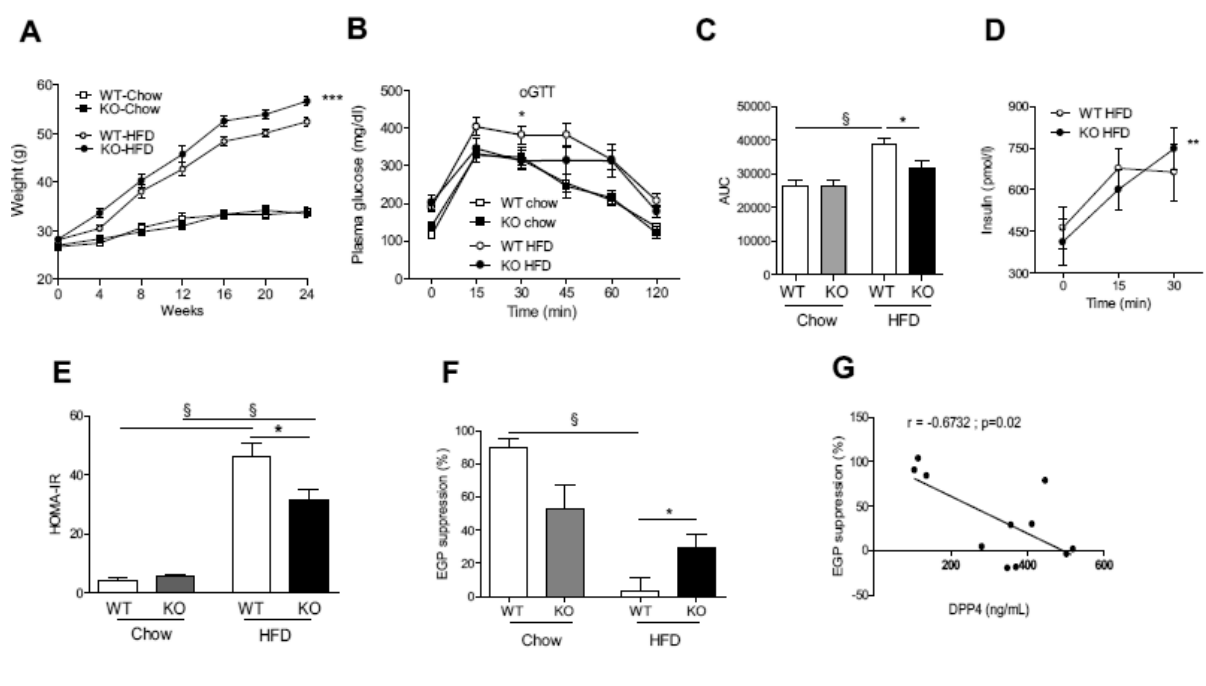


Figure 2. AT-DPP4-KO animals gain more body weight but display improved glucose tolerance and hepatic insulin sensitivity on HFD. **(A)** Body weight was assessed every 4 weeks during chow and HFD (n=11-16 animals per group on chow, n= 26-31 animals per group on HFD). Data expressed as mean \pm S.E.M. *** $p<0.01$ vs. diet-matched WT littermates. **(B)** oGTTs were performed after 18-20 weeks of chow or HFD (WT chow n=8; KO chow n=6; WT HFD n=9; KO HFD n=6). **(C)** Corresponding AUC of oGTT. **(D)** Plasma insulin levels at 0, 15 and 30 minutes after glucose gavage (2 mg/g body weight) (WT HFD n=9; KO HFD n=7). **(E)** HOMA-IR after 24 weeks of dietary intervention (WT chow n=7; KO chow n=7; WT HFD n=17, KO HFD n=15). **(F)** Percentage of suppression of endogenous glucose production (EGP) during hyperinsulinemic-euglycemic clamps, after 22 weeks of dietary intervention (WT chow n=4; KO chow n=9; WT HFD n=7; KO HFD n=9). **(G)** Correlation between EGP suppression and DPP4 circulating levels (WT chow n=4; WT HFD n=7). Data expressed as mean \pm S.E.M. * $p<0.05$; ** $p<0.01$; *** $p<0.001$ vs. WT littermates on the same diet, § $p<0.05$ vs corresponding genotype on different diet.

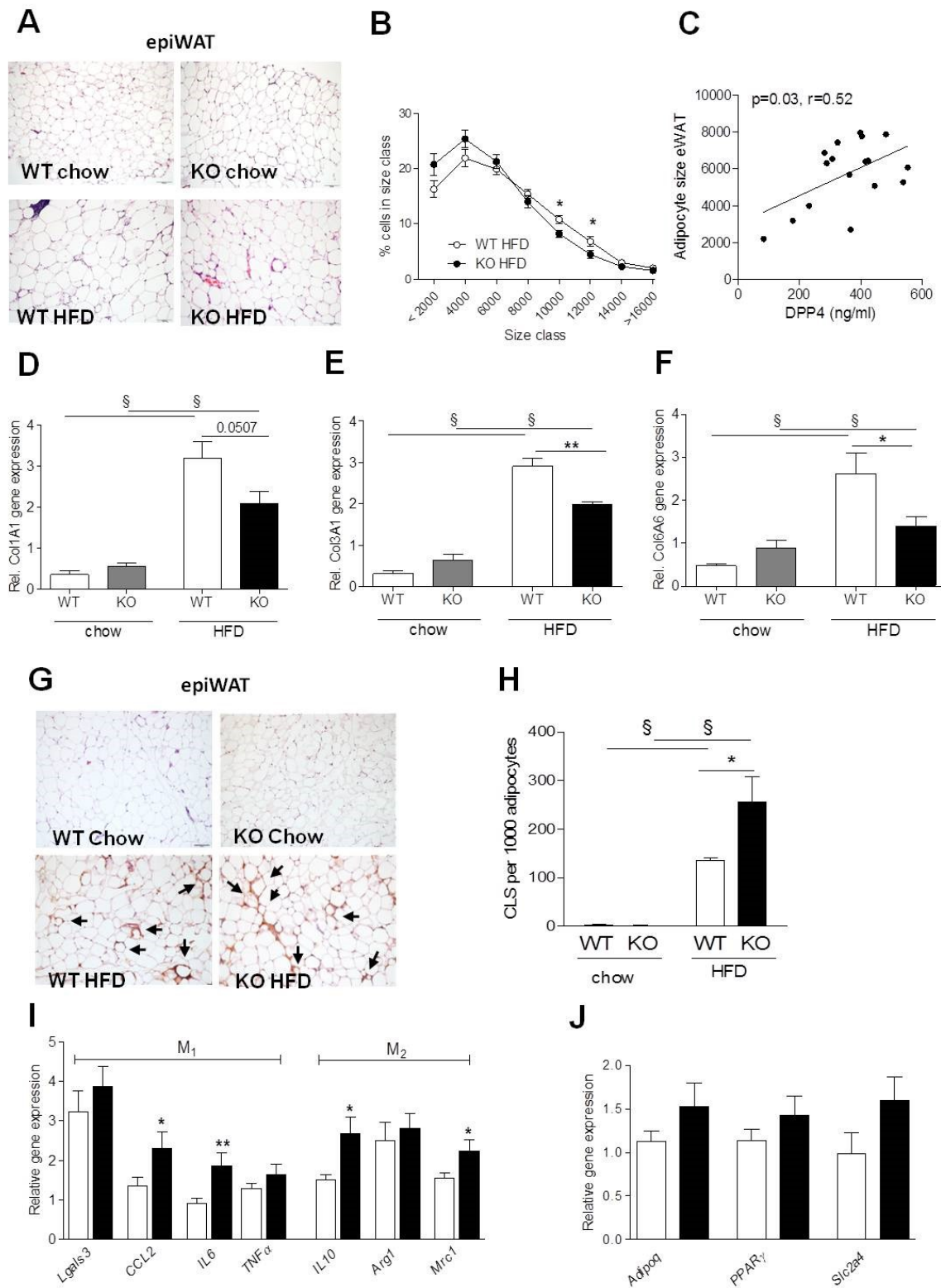


Figure 3. Adipocyte morphology, fibrosis markers and galectin-3 positive macrophage infiltration in epiWAT. (A) Representative microphotographs of hematoxylin-eosin stained adipocytes from epiWAT obtained from WT and KO animals after 24 weeks under chow or HFD. (B) Percentage of cells per adipocyte size class (μm^2) in epiWAT obtained from WT and KO animals after 24 weeks under chow or

HFD (WT HFD n=16; KO HFD n=16). (C) Correlation between adipocyte size and DPP4 circulating levels (n=33). mRNA levels of the fibrosis markers collagen 1A1 (D), collagen 3A1 (E) and collagen 6A6 (F), respectively (n=5-8 animals per group). (G) Representative microphotographs of immunohistochemistry staining for galectin-3, showing CLS in epiWAT. (H) Number of CLS per every 1000 adipocytes calculated after 24 weeks of dietary intervention (WT chow n=4; KO chow n=4; WT HFD n=7; KO HFD n=6). (I) mRNA levels of M1 macrophage markers: Lgals3, CCL2, IL-6, TNF- α , and M2 macrophage markers: IL-10, Arg10 and Mrc1 in epiWAT from WT and KO animals after 24 weeks of HFD (WT HFD n= 24; KO HFD n=25). (J) mRNA levels of the adipogenic markers: adiponectin, PPAR γ (WT HFD n=24; KO HFD n=25) and GLUT4 (WT HFD n=6; KO HFD n=6). Data are expressed as \pm S.E.M. * $p<0.05$; ** $p<0.01$ vs. WT littermates under HFD. All mRNA levels normalized to 18S.

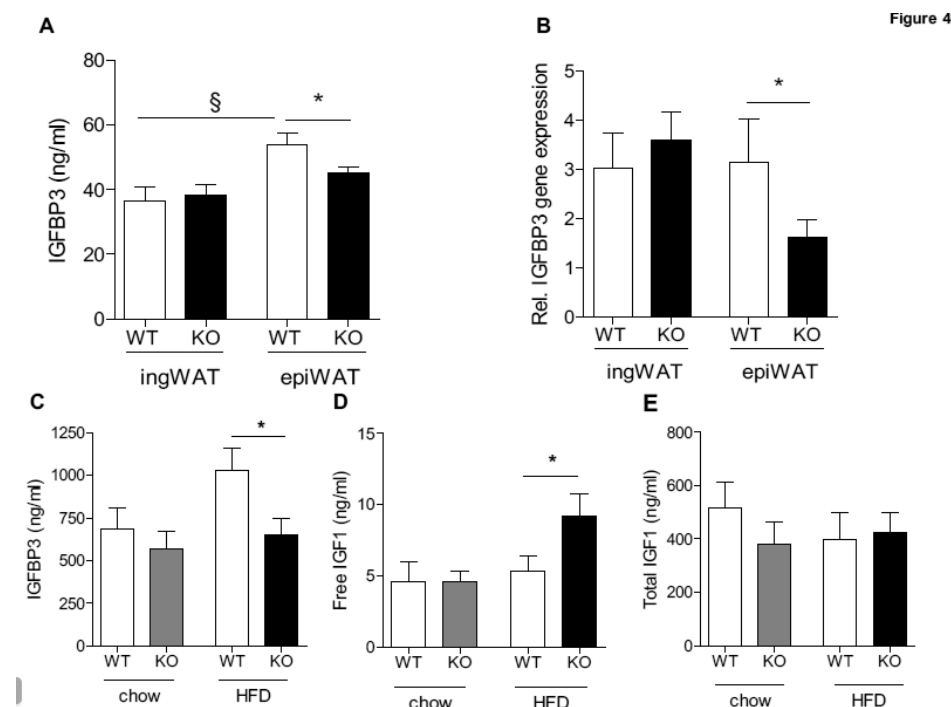


Figure 4. IGFBP3 is downregulated in epiWAT from KO animals under HFD and reduced in serum in parallel to increased concentrations of free IGF1. (A) IGFBP3 levels in CM from explants obtained from ingWAT or epiWAT isolated from WT and KO animals after 24 weeks on HFD (ingWAT: WT HFD n=3, KO HFD n=7; epiWAT: WT HFD n=3; KO HFD n=6). (B) mRNA levels of IGFBP3 in ingWAT and epiWAT of animals on HFD (ingWAT: WT HFD n=6, KO HFD n=6; epiWAT: WT HFD n=5; KO HFD n=6). (C) Plasma IGFBP3 levels in WT and KO animals after 24 weeks dietary intervention (WT chow n=14; KO chow n=13; WT HFD n=8; KO HFD n=18). (D) Plasma free IGF1 levels in WT and KO animals after 24 weeks dietary intervention (WT chow n=7; KO chow n=11; WT HFD n=16; KO HFD n=19). (E) Plasma total IGF1 levels in WT and KO animals after 24 weeks dietary intervention (WT chow n=8; KO chow n=11; WT HFD n=14; KO HFD n=18). Data are expressed as \pm S.E.M. * $p<0.05$; vs. WT littermates on HFD, § $p<0.05$ vs different fat depot in corresponding genotype.

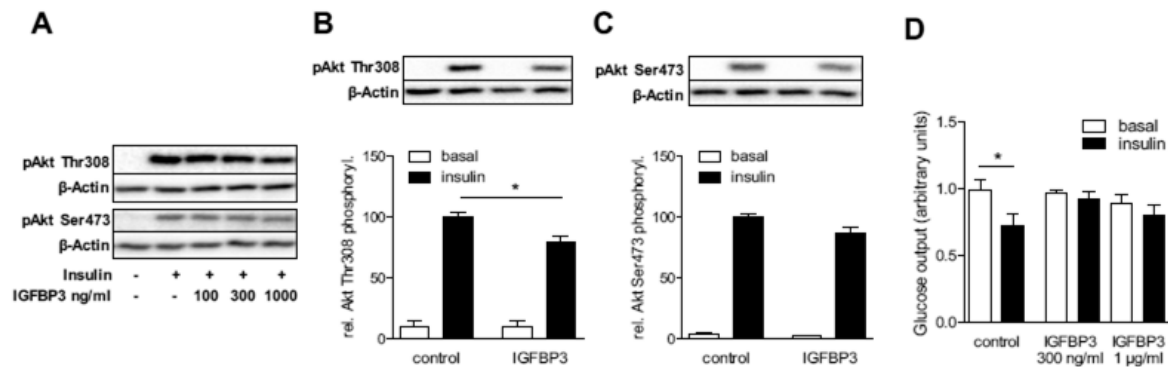


Figure 5. IGFBP3 impairs insulin signaling and insulin-induced suppression of glucose production in HepG2 cells. (A) HepG2 cells were treated with 100-1000 ng/ml IGFBP3 for 18 h and stimulated with 100 nM insulin for 10 min. Representative Western Blots are presented. (B-C) HepG2 cells were treated with 300 ng/ml IGFBP3 for 18 h and stimulated with 100 nM insulin for 10 min. Data are expressed as \pm S.E.M (n=4). $*p<0.05$; vs. insulin-stimulated control. Representative Western Blots are presented. (D) HepG2 cells were treated with IGFBP3 for 18 h and glucose production was measured as detailed in Materials and Methods. Forskolin was used as a positive control and induced glucose production (from 1.0 ± 0.1 to 1.9 ± 0.7 , $p=0.01$). Data are expressed as \pm S.E.M (n = 4). $*p<0.05$; vs. basal control.

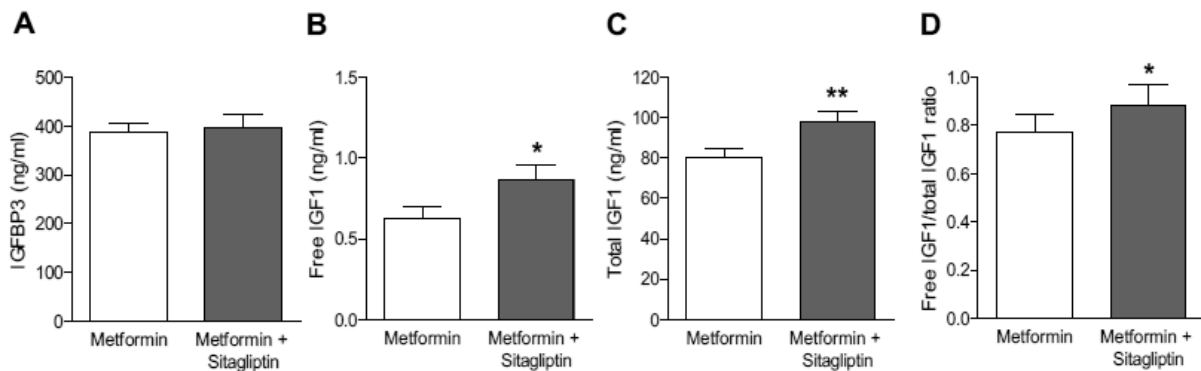
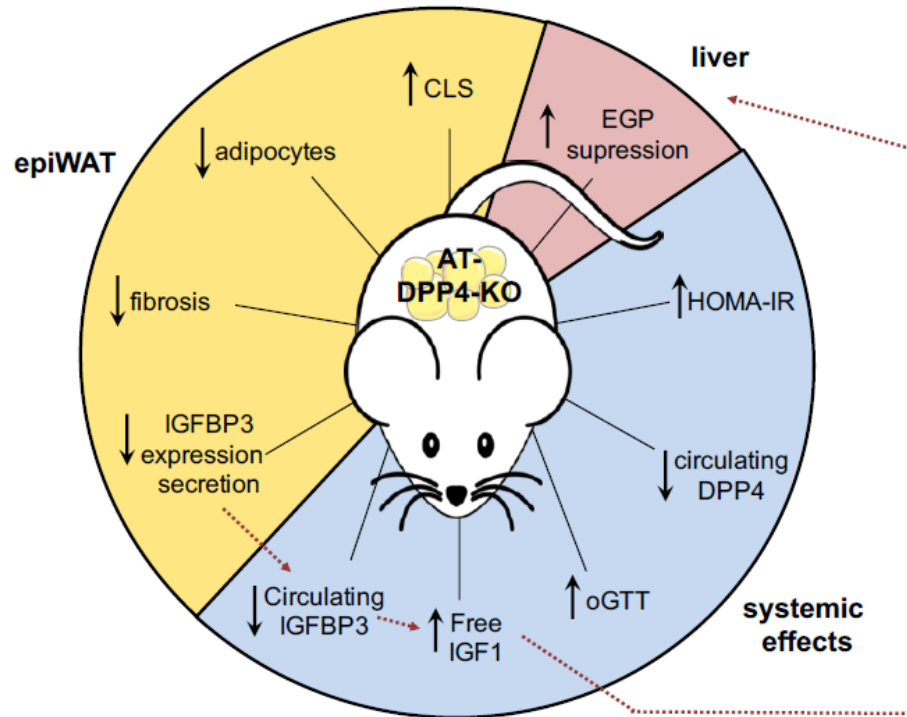


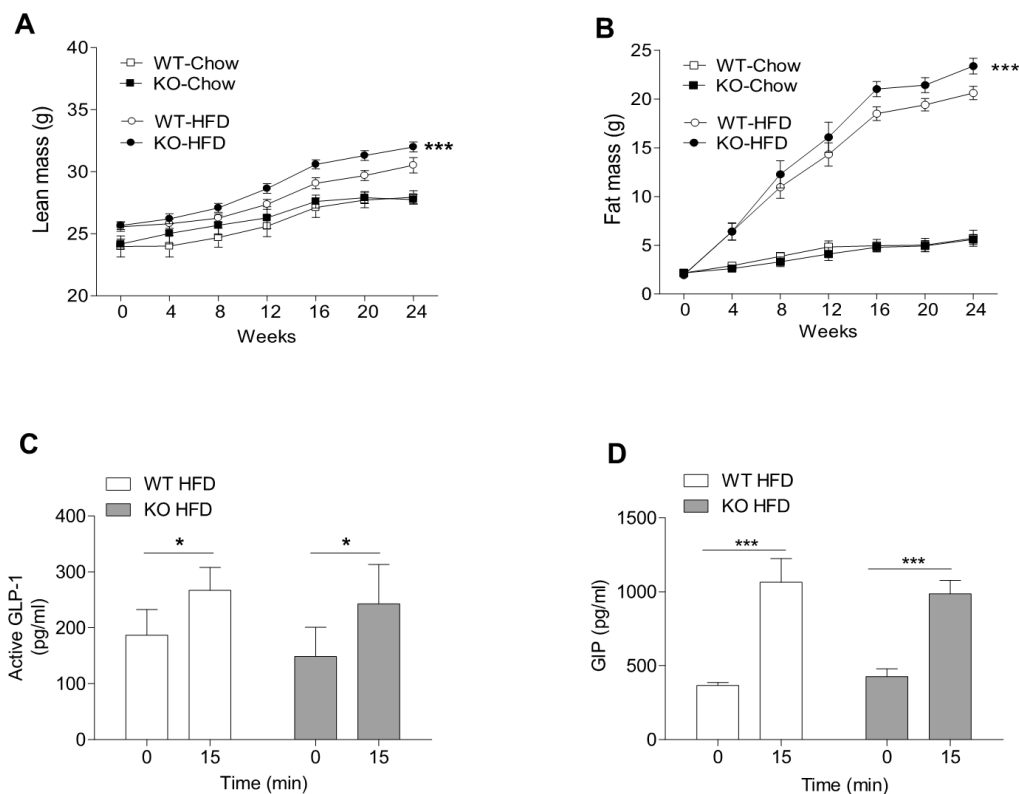
Figure 6. Type 2 diabetic patients treated with metformin alone or in combination with sitagliptin are characterized by increased serum free IGF1, serum total IGF1 and free IGF1/total IGF1 ratio compared to patients with type 2 diabetes treated with metformin alone. IGFBP3 (A), free IGF1 (B) and total IGF1 (C) were measured by ELISA. Free IGF1/total IGF1 ratio was calculated. $*p<0.05$; $**p<0.01$ vs. patients treated with metformin alone



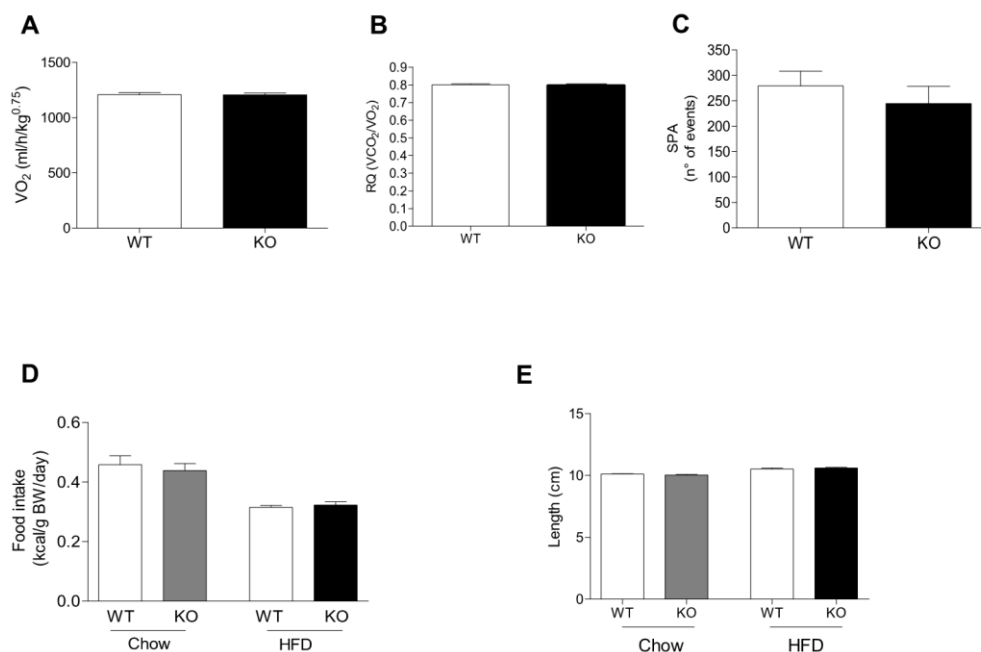
Supplemental Information

DPP4 deletion in adipose tissue improves hepatic insulin resistance in diet-induced obesity

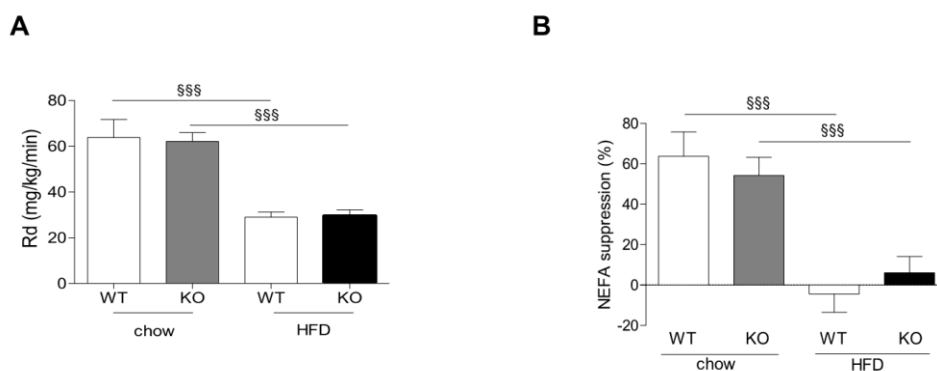
Tania Romacho, Henrike Sell, Ira Indrakusuma, Diana Roehrborn, Tamara R. Castañeda, Tomas Jelenik, Sonja Hartwig, Jürgen Weiß, Hadi Al-Hasani, Michael Roden, Jürgen Eckel.



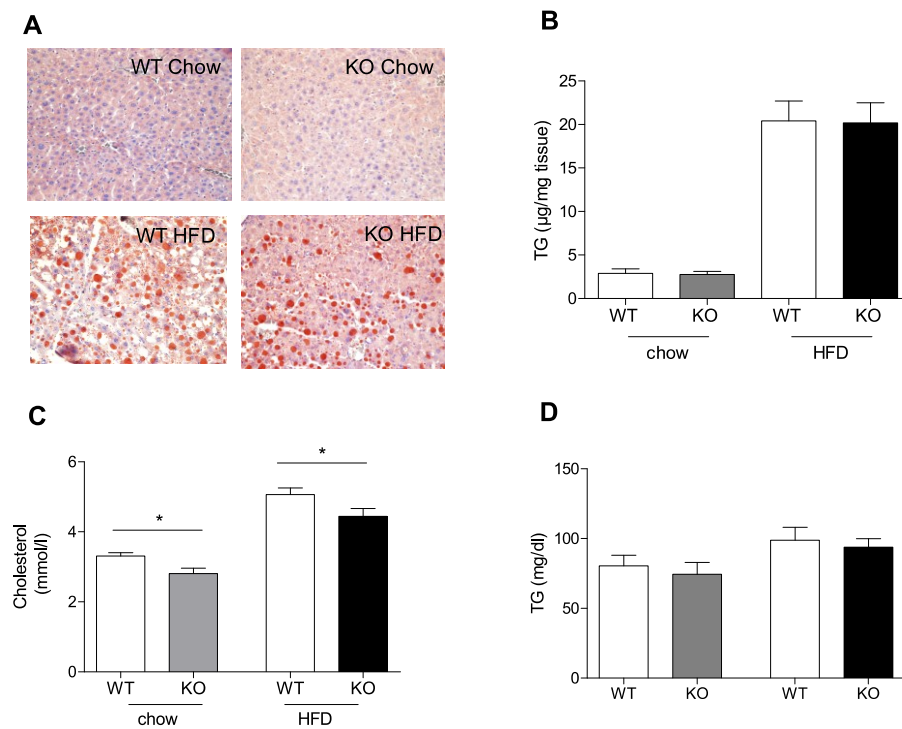
Supplementary Figure 1. Increased lean and fat mass but unaltered plasma incretins in AT-DPP4-KO animals under HFD. Lean mass (A) and fat mass (B) was assessed every 4 weeks during dietary intervention (n=11-16 animals per group on chow, n= 26-31 animals per group on HFD). Data expressed as mean \pm S.E.M. *** $p < 0.01$ vs. vs. diet-matched WT littermates. Plasma active GLP-1 (C) and GIP (D) levels at 0 and 15 min after glucose gavage (2mg/g body weight) in animals at week 20 of HFD (WT HFD n=4; KO HFD n=4-5). * $p < 0.05$; *** $p < 0.001$ vs. levels at time 0.



Supplementary Figure 2. Metabolic phenotyping of AT-DPP4-KO mice. Measurements were carried out for 4 days (48 h adaptation + 48h follow up) at week 20 after dietary intervention. **(A)** Energy expenditure corrected per body surface (WT HFD n=19; KO HFD n=16). **(B)** Respiratory quotient (RQ; WT HFD n=15; KO HFD n=13) **(c)** Spontaneous physical activity (SPA; WT HFD n=20; KO HFD n= 18. **(C)** Daily food intake (WT HFD n=23; KO HFD n=21) **(D)** Nose-tail length was measured in isoflurane-anesthetised animals at week 30 of age (WT chow n=8; KO chow n=8; WT HFD n=14; KO HFD n=14). Data are expressed as mean \pm S.E.M.

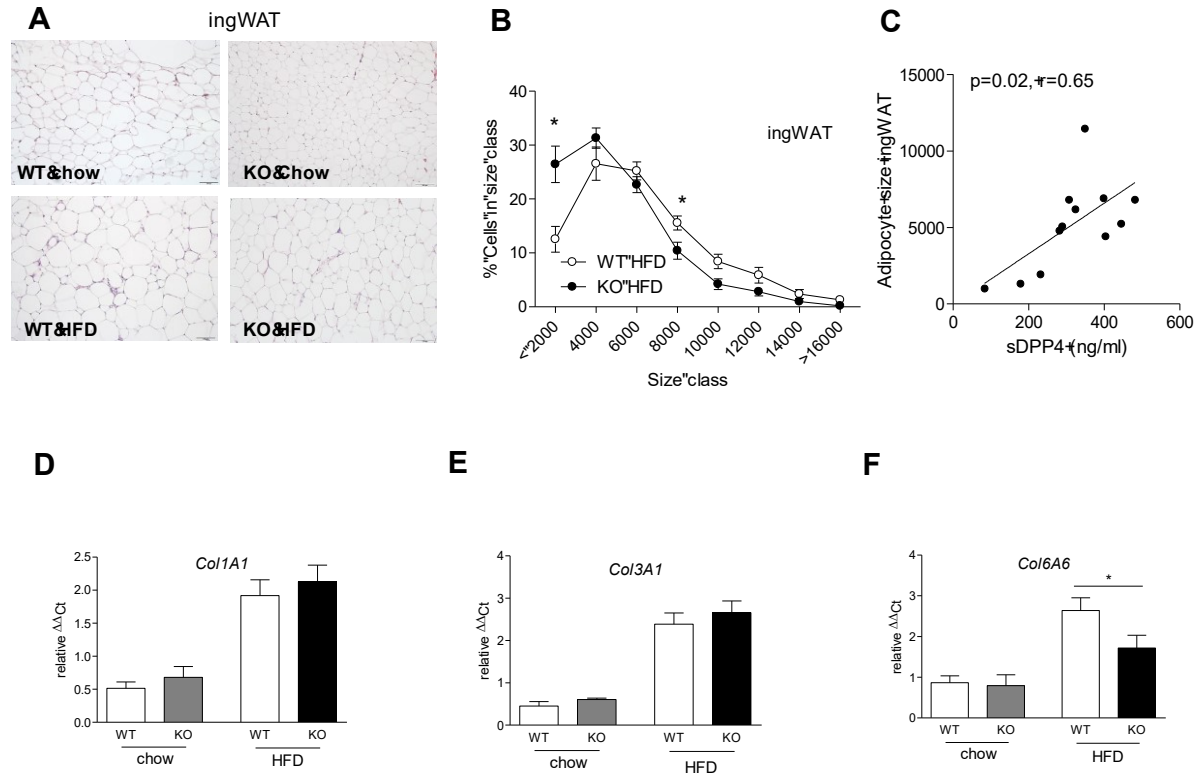


Supplementary Figure 3. Insulin sensitivity *in vivo*. Hyperinsulinemic-euglycemic clamps were performed after 22 weeks of dietary intervention. **(A)** Glucose disposal rate (Rd) and **(B)** suppression of non-esterified fatty acids (NEFA) were assessed (WT chow n=4; KO chow n= 9; WT HFD n= 7; KO HFD n=9). Data are expressed as mean \pm S.E.M. $§§§p<0.001$ vs. same genotype under chow diet.

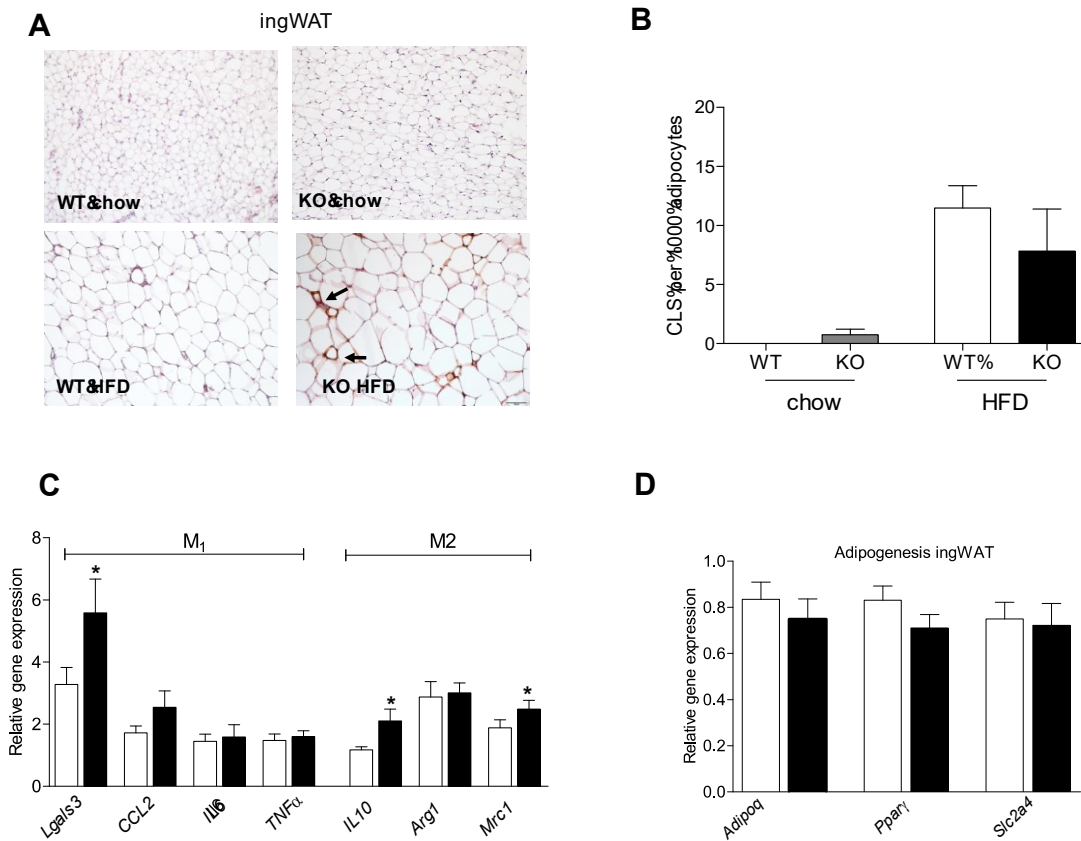


Supplementary Figure 4. Lipidic profile and hepatic steatosis in AT-DPP4-KO mice.

(A) Representative microphotographs of Oil Red-stained liver sections adipocytes from WT and KO animals under chow or HFD. (B) Hepatic triglyceride content in WT and KO animals under HFD for 24 weeks (WT chow n=7; KO chow n=8; WT HFD n=8; KO HFD n=11). (C) Plasma cholesterol and triglycerides (D) in WT and KO animals under chow or HFD for 24 weeks (WT chow n=8; KO chow n=8; WT HFD n= 14; KO HFD n=14). * $p < 0.05$ vs. matched-WT littermates under same diet.



Supplementary Figure 5. Improved adipose tissue remodeling in ingWAT. (A) Representative microphotographs of hematoxylin-eosin stained adipocytes from WT and KO animals under chow or HFD. (B) Percentage of cells per adipocyte size class (μm²) in ingWAT obtained from WT and KO animals after 24 weeks under chow or HFD (WT HFD n=11; KO HFD n=11). (C) Correlation between adipocyte size and DPP4 circulating levels in WT animals (n=33). Expression of the fibrosis markers collagen 1A1 (D), collagen 3A1 (E) and collagen 6A6 (F) (WT chow n=5-6; KO chow n=6-8, WT HFD n=6; KO HFD n=6). mRNA levels were normalized to 18S. Data are expressed as mean ± S.E.M. **p*<0.05 HFD-matched littermates. **p*<0.05 vs. matched-WT littermates under same diet.



Supplementary Figure 6. Macrophage infiltration in ingWAT. (A) Representative microphotographs of immunohistochemistry staining for galectin-3, showing crown-like structures (CLS) in epiWAT. (B) Number of CLS per every 1000 adipocytes was calculated by a blind observer in WT and KO under chow or HFD after 24 weeks of dietary intervention. (C) mRNA levels of M1 macrophage markers: Lgals3, CCL2, IL-6, TNF- α (WT HFD n=21-24; KO HFD n=15-24) and M2 macrophage markers: IL-10, Arg1 and Mrc1 (WT HFD 12-18; KO HFD n=16 animals) in epiWAT from WT and KO animals after 24 weeks of HFD. (D) mRNA levels of the adipogenic markers: adiponectin, PPAR γ and GLUT4 (WT HFD n=8; KO HFD n=7 animals). mRNA levels were normalized to 18S. Data are expressed as mean \pm S.E.M. * $p < 0.05$ vs. matched WT littermates under HFD.

EXPERIMENTAL PROCEDURES

Energy balance

Age-matched AT-DPP4-KO and WT control mice were singly housed in an indirect calorimetry system (TSE Phenomaster system, Bad Homburg, Germany) for four light/dark cycles (12 h/12h), at week 20 of dietary intervention. After an adaptation period of 48 h, the data obtained during the last 2 light/dark cycles were used to quantify spontaneous physical activity (SPA), energy expenditure (EE; ml/h/kg^{0.75}) and the respiratory quotient (RQ, VCO₂/VO₂), as previously described (Castaneda et al., 2011). Measurements of food intake were taken manually every day in the morning.

Hormone and biochemical assays

Total GIP and GLP-1 were measured with a DuoPlex assay (BioRad, Hercules, California). Active GLP-1 was measured with a Singleplex kit (Millipore, Billerica, California).

Cholesterol and triglycerides were obtained by standard peroxidase-based clinical assays (ErbaLachema, Czech Republic). Non-esterified fatty acids were quantified using colorimetric assay (NEFA C; Wako, Neuss, Germany).

Liver fat content

Livers were dissected and fixed in 10% formalin, and then dehydrated in ethanol followed by cryopreservation and further sectioning for oil red O stainings. Representative images from at least 5 animals per group were taken with a Leica DM6000 B microscope (Jelenik et al., 2014).

Triglycerides content in liver was assessed by a colorimetric kit (RANDOX) and normalized per protein content as estimated by BCA (Thermo) (Baumeier et al., 2015).

Statistics

Statistical analysis was performed with the GraphPad Prism software (La Jolla, CA, USA). *p* values were calculated using the two-tailed Student's *t*-test. For statistical comparisons between experimental groups, two-way ANOVA was used, followed by Bonferroni *post hoc* test. A *p* value below 0.05 was considered statistically significant. Data are shown as the mean ± S.E.M or mean ± S.D if specified. Normal distribution and equal variances were tested for each analysis. Animals were randomly allocated to the different diets and at least three animals were included in each experimental group. Groups size was calculated by Simple Interactive Statistical Analysis.

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Castañeda, T.R., Nogueiras, R., Muller, T.D., Krishna, R., Grant, E., Jones, A., Ottaway, N., Ananthakrishnan, G., Pfluger, P.T., Chaudhary, N., et al. (2011). Decreased glucose tolerance and plasma adiponectin:resistin ratio in a mouse model of post-traumatic stress disorder. *Diabetologia* 54, 900-909.

Jelenik, T., Sequaris, G., Kaul, K., Ouwens, D.M., Phielix, E., Kotzka, J., Knebel, B., Weiss, J., Reinbeck, A.L., Janke, L., et al. (2014). Tissue-specific differences in the development of insulin resistance in a mouse model for type 1 diabetes. *Diabetes* 63, 3856-3867.

2.5. AUTHOR CONTRIBUTIONS

„DPP4 in Diabetes“

Röhrborn D, Wronkowitz N, Eckel J

Front Immunol. 2015 Jul 27;6:386. doi: 10.3389/fimmu.2015.00386.

Total contribution:	53%
Conceived/designed experiments:	-
Performed experiments:	-
Analysed data:	-
Contribution to discussion:	50%
Wrote manuscript:	50%
Reviewed/edited manuscript:	60%
Author:	1 st

„Shedding of dipeptidyl peptidase 4 is mediated by metalloproteases and up-regulated by hypoxia in human adipocytes and smooth muscle cells“

Röhrborn D, Eckel J, Sell H.

FEBS Lett. 2014 Nov 3;588(21):3870-7. doi: 10.1016/j.febslet.2014.08.029. Epub 2014 Sep 12.

Total contribution:	90%
Conceived/designed experiments:	80%
Performed experiments:	100%
Analysed data:	100%
Contribution to discussion:	80%
Wrote manuscript:	100%
Reviewed/edited manuscript:	80%
Author:	1 st
Impact factor:	3,169

„Reduced DPP4 activity improves insulin signaling in primary human adipocytes“

Röhrborn D, Brückner J, Sell H, Eckel J.

Biochem Biophys Res Commun. 2016 Mar 11;471(3):348-54. doi:10.1016/j.bbrc.2016.02.019

Total contribution:	91%
Conceived/designed experiments:	90%

Performed experiments:	90%
Analysed data:	90%
Contribution to discussion:	85%
Wrote manuscript:	100%
Reviewed/edited manuscript:	90%
Author:	1 st
Impact factor:	2,297

„ DPP4 deletion in adipose tissue improves hepatic insulin resistance in diet-induced obesity “ Tania Romacho , Henrike Sell , Ira Indrakusuma, Diana Roehrborn, Tamara R. Castañeda, Tomas Jelenik, Sonja Hartwig, Jürgen Weiß, Hadi Al-Hasani, Michael Roden, Jürgen Eckel”

Submitted to Cell Reports

Total contribution:	22%
Conceived/designed experiments:	20%
Performed experiments:	30%
Analysed data:	30%
Contribution to discussion:	30%
Wrote manuscript:	10%
Reviewed/edited manuscript:	10%
Author:	2 nd
Impact factor:	7.870

3. DISCUSSION

3.1. RELEASE OF SOLUBLE DPP4

3.1.1. MECHANISM AND REGULATION OF DPP4 RELEASE

Additionally to being expressed as a membrane-located protease, DPP4 is also found in high amounts in the circulation with full enzymatic potential (211). However, controverse reports about the mechanism of release can be found in the literature. On the one hand, some researchers found DPP4 in granules or secretory lysosomes (212), whereas, on the other hand, Andrieu et al proposed an active cleavage mechanism from the cell surface (213). I was able to show that DPP4 release is not mediated through the classical ER/Golgi-dependent release mechanism, since *in vitro* cultured primary human adipocytes and human SMC are insensitive to brefeldin A treatment. This also supports an earlier finding of our group, where DPP4 release from SkMc is also insensitive to brefeldin A treatment (108). Since DPP4 belongs to the group of type II transmembrane proteins and endogenous proteolytic release is limited to type I or type II transmembrane proteins, it is very likely, that DPP4 is released via this mechanism. This post-translational hydrolysis mechanism is called shedding (100).

By using different broad spectrum protease inhibitors, I found out, that various types of proteases are involved in DPP4 release. Especially in human adipocytes only with the broad spectrum metalloprotease inhibitor batimastat significant differences could be observed, meaning that at least in this cell type MMPs are the major sheddases for DPP4. Although I saw significant changes of DPP4 release with broad spectrum inhibitors against serine-, cysteine- and metalloproteases, I could not see additive effects of these inhibitors on DPP4 shedding. Analysis of supernatants from SMC and adipocytes revealed a relatively high release of certain MMPs and cathepsins in a cell-type specific manner. It is well-known that activation of MMPs is rather complex. MMPs are released into the extracellular space as inactive proenzymes. Only upon cleavage of the propeptides, which block the active center of the MMPs, they become active (214). Interestingly a lot of different factors are able to activate MMPs. In addition to serine proteases like plasmin and kallikreins, also cysteine proteases like cathepsin G are able

to activate MMPs (215). Furthermore, MMPs are also able to activate one another, as it is reported in case of MMP2 activation via MMP14 (216), or MMP9 activation via MMP2 or MMP3 (217). Therefore, I postulate that DPP4 shedding involves a catalytic cascade which involves MMPs and cathepsins. The fact that some MMPs are reported to be dysregulated in obesity further supports the involvement of these MMPs in DPP4 shedding, since it is known that DPP4 release is higher under obese conditions (186). Especially in case of MMP2, MMP9 and MMP14, levels are upregulated in obese mice (218;219). Particularly in AT, MMPs play an important role in tissue remodeling, which is necessary to keep up normal AT function during expansion of this tissue in obesity (37). In this work I was able to show that MMP1, MMP2 and MMP14 seem to be involved in constitutive DPP4 shedding from SMC, whereas in adipocytes, only specific inhibition of MMP9 resulted in a decreased DPP4 shedding. All of these four candidates are known to be involved in the shedding of various substrates (220-224). This also underpins the complex interplay of different enzymes in the shedding process, since one MMP is not limited to a specific target and one target might be released by several MMPs depending on experimental conditions or investigated cell-type.

In addition to elucidating the mechanism how DPP4 is released, it is also of great importance to understand how this release is regulated in order to understand the dysregulation of DPP4 under physiopathologic conditions like T2DM. DPP4 serum levels are elevated in obese subjects and can be reduced to normal levels after bariatric surgery (185). Furthermore, DPP4 serum levels and release from AT is elevated in patients with diagnosed metabolic syndrome (185). The most obvious regulator of DPP4 in the context of T2DM seems to be glucose levels. Therefore several groups addressed the impact of high and low glucose levels on DPP4 *in vitro* (225;226) and *in vivo* (225). However, the results are rather controversial and dependent on the investigated cell type. In Caco-2 cells, which are a model resembling the enterocytes lining the small intestine (227), high glucose levels inhibited DPP4 gene expression and DPP4 activity which seems to be mediated by HNF-1 α (226). Das et al reported lower intracellular DPP4 content and release under high glucose conditions in differentiated 3T3-L1 cells, which is regulated at the transcriptional level (225). However, this is only true in non-diabetic conditions, whereas when they induced diabetic conditions by streptozotocin treatment, no decrease of DPP4 was observed (225). Furthermore, it is quite interesting that the authors only observed a positive correlation of DPP4 levels and blood glucose later than 4 weeks of high-fat diet feeding. So they postulated that in the physiological

state DPP4 is negatively regulated by high glucose levels, thereby generating more active incretins, which improve glucose disposal. This regulation is lost in T2DM, where a reduced glucose uptake into adipocytes occurs. Therefore in adipocytes, isolated from diabetic, streptozotocin-treated animals, the conditions reflect low glucose levels and DPP4 is upregulated (225). However, I found no regulation of DPP4 release in human SMC by high glucose levels (Fig. 4). This might be either due to the fact that Das and coworkers used a cell-line for their experiments whereas I used primary cells or due to the difference between mice and human.

During the development of obesity, alterations in the secretory profile of AT towards more pro-inflammatory cytokines occur. This also leads to an elevated number of classically activated M1 macrophages either via recruiting them from the circulation or via a phenotypic switch from M2 to M1 macrophages (228). So another plausible mechanism of DPP4 regulation might be the induction via cytokines present during the local chronic low-grade inflammation of AT. Indeed, Das et al were able to show that TNF α markedly increased DPP4 release from *in vitro* cultured 3T3-L1 cells. This seems to be mediated at the release level since neither mRNA nor intracellular DPP4 levels are affected (225). Furthermore, TNF α -induced DPP4 shedding seems to be uncoupled from glucose levels, meaning that inflammation is an independent regulator of DPP4 release from adipocytes (225). This observation is in accordance with our previously published data on primary human adipocytes, where we also see an induction of DPP4 release by TNF α (185). This regulation seems to be independent of the source of adipocytes, whether mouse or human. However, when I repeated this experiment in SMC I saw no regulation of DPP4 release by TNF α (Fig 4), which points towards an adipocyte specific mode of DPP4 regulation. Therefore, induction of DPP4 release seems to be cell type specific and TNF α -induced DPP4 release might be limited to adipocytes underlining the role of adipose tissue inflammation in the development of obesity. Bauvois and colleagues were also able to show that interferon γ (IFN γ) is able to induce DPP4 gene expression in B lymphatic leukemia cells by increasing tyrosine phosphorylation of Stat1 α . Stat1 α is thereby able to accumulate in the nucleus and binds to GAS response elements in the promoter region of DPP4, leading to an upregulation in mRNA expression (229). In my case, IFN γ had no influence on DPP4 release neither from

human primary adipocytes nor human SMC (Fig 4), which might be due to the difference in the used cell types.

While increasing in size during obese AT expansion, adipocytes reach a critical size for oxygen diffusion at some point (42). Whereas efficient oxygen diffusion only occurs approximately 100µm apart from blood vessels, adipocytes can increase to around 180µm in diameter (230). So at some point hypoxia occurs within AT, leading to an altered gene expression. We were able to show in adipocytes which were differentiated at 10% as well as 5% O₂ significantly upregulated DPP4 expression and release (231), whereas 1% O₂ for 24h seems to have no effect on DPP4 release from adipocytes (185). In SMC, 1% O₂ significantly increases DPP4 release after 24h and 48h. However, this seems to be independent from Hif-1α binding to the promoter region of DPP4, since mRNA levels are unaffected. Hypoxia seems to rather influence sheddase levels or activity since I could show increased mRNA levels of MMP1 and MMP9 in SMC .

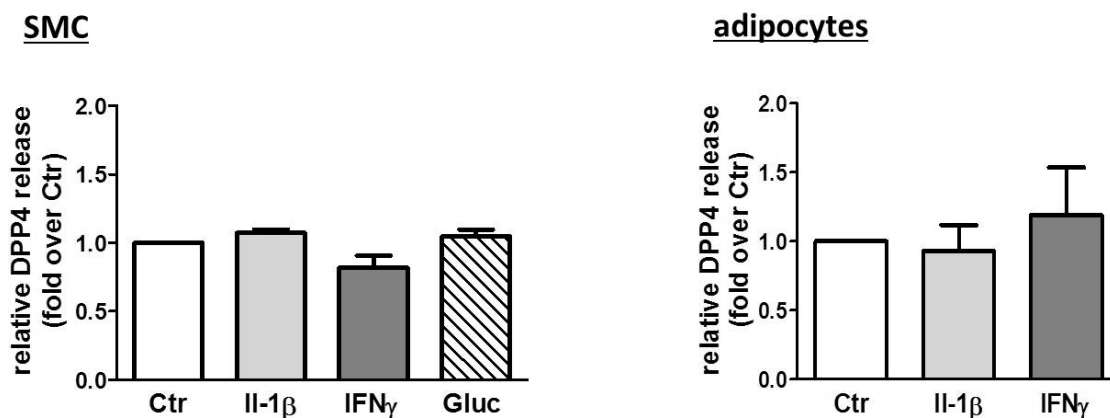


FIGURE 4 REGULATION OF DPP4 RELEASE.

Human SMC and differentiated adipocytes were cultured *in vitro* and treated with 100ng/mL IL-1β or IFNγ, as well as 20mM glucose respectively for 24h. Supernatants were collected and DPP4 release was monitored via DuoSet DPP4 ELISA from R&D systems (DY1180). Assays were performed according to manufacturers instructions. Data are depicted as mean ±SEM n=3-4; Ctr control; Gluc glucose.

3.1.2. IMPACT OF SOLUBLE DPP4 ON THE PHYSIOLOGY OF DIFFERENT CELLS

To date not much is known regarding the impact of soluble DPP4 on the physiology of different cells, and most studies published so far have concentrated on the effects of DPP4 inhibitors. However, the knowledge on how DPP4 is released and how this release is regulated helps to understand the role of circulating DPP4 independent from its

source. Most of the studies on DPP4 inhibitors have attributed the effects to an impact on the incretin axis. However, there are also direct effects of sDPP4 independent of GLP-1. We were the first to show that soluble DPP4 impairs insulin signaling in different cell types namely SkMc, SMC and adipocytes on the level of Akt activation (185). Furthermore sDPP4 induces SMC proliferation and migration (158). Ishibashi and coworkers showed that sDPP4 elevates reactive oxygen species (ROS) production and receptor for advanced glycation end-products (RAGE) expression in endothelial cells (EC) (232). Upon binding to mannose-6-phosphat/insulin-like growth factor-II receptor (M6P/IGF-IIR) sDPP4 potentiates the effects of advanced glycation end products in EC, which was prevented by the DPP4i linagliptin. Our group also pointed out, that circulating sDPP4 might be involved in the progression of atherosclerosis, since it initiates stress and inflammatory signaling cascades in SMC and elevates the release of inflammatory cytokines like IL-6 and MCP-1 (184). The observed effects could be prevented by DPP4i and seem to be mediated through the PAR2 receptor (184). These observations might also help to understand the beneficial effects of DPP4i on the cardiovascular system and further strengthen the role of DPP4 beyond the incretin axis (233). These data are also supported by another study, where Ervinna and colleagues could show an increased ERK1/2 activation in rat SMC after short-term treatment with sDPP4, which was partially blocked by DPP4i (234). Very recently, we were also able to show that sDPP4 triggers thromboxan release from endothelial cells through a PAR2-mediated pathway (235). Since thromboxan acts as a vasoconstrictor prostanoid, sDPP4 impairs endothelium-dependent relaxation. Thereby we were able to show that sDPP4 is a direct mediator of endothelial dysfunction. All these data indicate that dysregulated DPP4 release, as it occurs during the development of obesity, has an impact on distinct target tissues in a para- or endocrine way, like e.g. acting on the vascular wall and inducing inflammation in this setting.

3.2. ADIPOSE TISSUE-DERIVED DPP4

3.2.1. ROLE OF DPP4 WITHIN ADIPOSE TISSUE

3.2.1.1. DPP4 AND AT REMODELING

Our group already described DPP4 as an adipokine in 2011 (185) and we were able to show that especially during obesity and in T2DM DPP4 levels are upregulated (186). This observation points towards an important role of AT in systemic levels of DPP4, but the knowledge about the role of DPP4 within AT is very limited. Therefore, one aim of this thesis was to elucidate the role of AT-derived DPP4 during the development of obesity by a unique AT-specific KO mouse model. Furthermore, it was aimed to dissect the role of DPP4 in AT by *in vitro* silencing of DPP4 or treatment with well characterized DPP4 inhibitors of primary human adipocytes.

We were already able to show that DPP4 levels positively correlate with adipocyte diameter in human biopsies (185). This correlation could also be shown in the investigated mice. Furthermore, a size shift towards more small adipocytes and less big adipocytes was observed in KO animals under HFD feeding. It can be speculated that adipocyte size could be related to enzymatic activity of DPP4, since adipocyte size is reduced upon DPP4 inhibitor treatment in animal models with diet-induced obesity (DIO) (236). However, the authors also observed metabolic alterations in white AT which is paralleled by increased energy expenditure. This was not the case in the AT specific KO model and seems to be due to the systemic impact of orally applied DPP4i. Recently, it was also reported that DPP4 might be involved in dedifferentiation of mature adipocytes, since expression of MMP1, FAP and DPP4 was upregulated during a dedifferentiation protocol. Furthermore, this altered expression leads to an upregulation of inflammatory markers like IL-6 and IL-8 (237). However, no evidence for alterations in dedifferentiation was found in AT specific KO mouse model.

The occurrence of smaller adipocytes in AT can also be explained by increased AT fibrosis, which increases the stiffness of this tissue and is upregulated during obesity. That means that due to AT fibrosis the adipocytes are not able to further increase their size by lipid uptake (238). Fibrosis seems to be a key factor for stimulating local inflammatory responses with upregulated levels of lysyl oxidase (LOX) and collagens I and III, as was shown by a degradation-resistant overexpression model of HIF-1 α in AT (68). The size of the adipocytes is not further increasing since the ECM is unable to remodel and accommodate the need for increased adipocyte size due to higher lipid accumulation. The ECM is translating adipocyte stress into a pro-inflammatory signal with fibrosis being a key hallmark of metabolically dysfunctional AT (64). Khan and coworkers showed upon crossing a Col6a1-deficient mouse into the ob/ob background that hypertrophy per se is not sufficient to induce an inflammatory response (238). So

reducing collagen VI improved metabolic parameters and glucose tolerance, increased survival rates and reduced CLS in AT (238). In this thesis in the KO model, Col6a6 and Col3a1 were significantly downregulated under HFD compared to their WT littermates. This observation further strengthens the hypothesis that DPP4 depletion in AT leads to a beneficial AT remodeling.

DPP4 levels also negatively correlate with adiponectin levels in humans (185) as well as in AT specific DPP4 KO mouse model. However, no significant changes in adipogenesis markers within AT were observed neither in chow nor in HFD challenged animals. Furthermore, no differences in the differentiation of *in vitro* cultured human adipocytes with reduced DPP4 content in respect of lipid droplet accumulation or expression of differentiation markers (Fig. 5) were found. In conclusion, the observed data indicate that DPP4 seems to play no critical role in adipocyte differentiation per se.

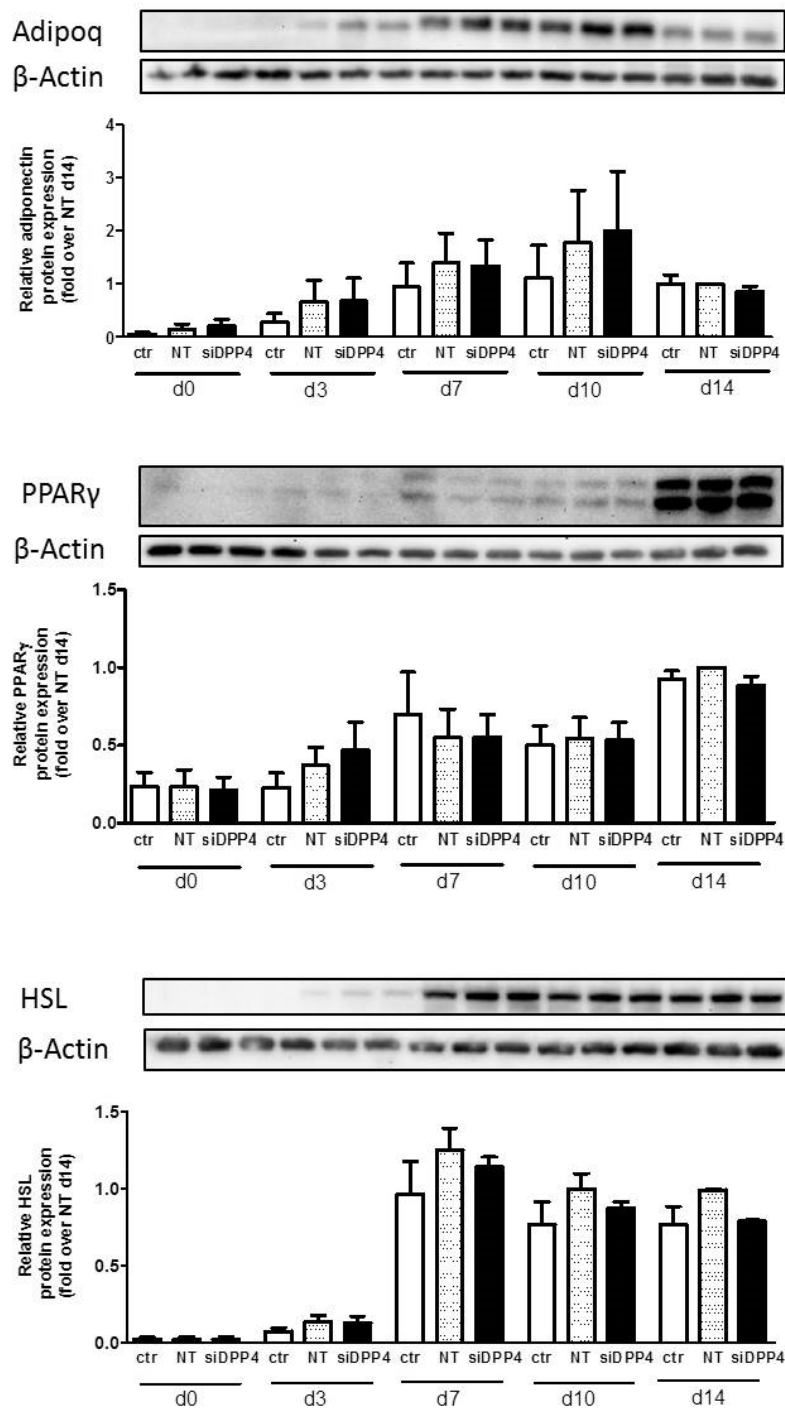


FIGURE 5: EFFECT OF siRNA-MEDIATED SILENCING OF DPP4 ON ADIPOCYTE DIFFERENTIATION.

Protein expression of differentiation markers was assessed after siRNA-mediated silencing of DPP4 via Western Blot analysis. Data are expressed as mean \pm SEM, n =4. Ctr control; NT non-target siRNA, siDPP4 DPP4-specific siRNA

3.2.1.2. DPP4 AND ITS ROLE IN AT MACROPHAGE PHENOTYPE AND INFLAMMATION

Macrophages and other immune cells also play an important role in normal AT function. During obesity the number of pro-inflammatory M1 macrophages is increasing via recruitment of novel macrophages and via a phenotypic switch from resident anti-inflammatory M2 macrophages (37). The expression of M1 macrophage markers compared to M2 markers is markedly increased in obese T2DM patients (239). Co-culture experiments of macrophages and adipocytes showed that the production of pro-inflammatory cytokines and FFA creates a paracrine vicious cycle with further upregulated release of macrophage-attracting cytokines (240). M2 polarized macrophages may help to preserve normal adipocyte function. Patsouris and colleagues were able to show that a specific ablation of CD11c⁺ macrophages leads to a normalization of systemic insulin sensitivity (241). Improving the imbalance between M1 and M2 macrophages within AT might be a novel strategy to treat or prevent obesity-induced disorders by improving insulin sensitivity (242;243). To preserve adequate adipocyte function and insulin action during obesity it may be fruitful to identify novel factors that retain M2 polarisation or trigger a phenotypic switch from M1 towards M2 macrophages. In the adipose-specific DPP4 KO model both in VAT and SAT a significant upregulation of the M2 macrophage markers IL-10 and mannose receptor, C type 1 (Mrc1) was observed in HFD compared to wildtype. However, I also saw an upregulation of pro-inflammatory markers like IL-6 and MCP-1 and a higher number of crown-like structures (CLS) in VAT. It should be noted that inflammation might be beneficial for normal adipocyte function to some extent and that macrophages could help to remove necrotic adipocytes by surrounding them in CLS (85). Acute inflammation of white AT in contrast to chronic inflammation seems to sustain healthy AT expansion and prevents lipotoxicity and chronic inflammation (244). The AT specific DPP4 KO model at least partially fulfills the definition of healthy AT expansion characterized by enlargement of fat pad mass due to accumulation of smaller mature adipocytes, recruitment of macrophages in an appropriate ratio (M2 vs M1) and a minimal induction of ECM and inflammation (64). The notion that DPP4 might somehow be involved in inflammatory processes is also supported by studies on DPP4i. Shinjo and colleagues for example could show a weak but significant reduction in LPS- or TNF α -

induced expression of IL-6 and MCP-1 in 3T3-L1 cells (245). In the *in vitro* model of DPP4 depletion in primary human adipocytes I could observe no marked effects on TNF α -induced inflammation in respect of NF κ B activation or expression and release of inflammatory markers. This difference might be due to the lack of interaction between adipocytes and macrophages as present in whole AT or it might reflect the difference of primary human cells vs. a mouse cell line as it was used in the study of Shinjo.

3.2.1.3. DPP4 AND ALTERATIONS IN AT SECRETOME

In addition to alterations in AT composition with respect to immune cell phenotype and remodeling of AT during obesity, another feature is the alteration of the AT secretome. Already in 2011, Xu and colleagues provided first evidence that DPP4 inhibition regulates adipokine secretion (246). DPP4 as an exopeptidase is able to inactivate cytokines secreted within AT or to generate novel bioactive compounds upon cleavage. Theoretically, it has a broad substrate specificity and can act on numerous different targets which might be involved in the progression or severity of obesity-associated diseases (107). However, as extensively reviewed by Mulvihill and Drucker it turned out to be very difficult to identify physiological targets of DPP4 (187). One reason is limitations in assay sensitivity making it rather difficult to differentiate between intact vs. cleaved substrates *in vivo*. Furthermore, there are no KO mouse models established or selective antagonists available for most of the potential physiological targets (187). I aimed to elucidate the role of siRNA-mediated DPP4 silencing on adipocyte secretome *in vitro* by the use of adipokine profiler arrays. I could observe no significant changes in the secretome of primary human adipocytes and very high donor variability. On the one hand it could mean, that DPP4 reduction plays no key role in secretion of the investigated adipokines, but it might on the other hand also mean that the assay is not sensitive enough to find changes in cleaved vs. intact peptides. Depending on where the spotted antibodies bind their substrates it is conceivable that also the cleaved forms are still recognized. In addition, it might be speculated that the ratio of cleaved versus intact substrates of DPP4 seems not to affect overall release of these factors. In conclusion, with the obtained data, the possibility that DPP4 alters the secretory output of adipocytes can not completely be ruled out. In the AT-specific KO mouse model significant changes in the secretion level of resistin and insulin-like growth factor binding protein 3 (IGFBP-3) from AT biopsies were found. The difference towards using human primary cells is that the secretome of the whole AT is obtained by the use of

biopsies in a more physiological setting. But this might also be a disadvantage since one can't ascribe the changes in the secretome directly to the adipocytes. It might as well be a change in the secretome of immune cells via cross-talk to adipocytes.

3.2.1.4. DPP4 AND AT FUNCTION

AT accounts for approximately 10% of postprandial glucose disposal. Therefore, insulin sensitivity is an important feature of normal adipocyte function. We were able to previously show that sDPP4 directly impairs insulin-stimulated Akt phosphorylation in human adipocytes (185). Furthermore, circulating DPP4 levels are significantly higher in obese individuals with insulin resistance than in their insulin sensitive counterparts (186). Upon siRNA-mediated silencing, I could show improved insulin signaling on the level of insulin receptor (InsR), proteinkinase b (Akt) as well as akt-substrate of 160kDa (AS160) phosphorylation. This phenomenon might be due to elevated basal levels of insulin receptor substrate 1 (IRS-1). However, it is also possible that DPP4 and the InsR interact with each other, either directly upon binding or indirectly via a substrate of DPP4. It has already been reported that the InsR is able to interact with different molecules which alter the responsiveness towards insulin in a positive (247) or negative way (248;249). The effects of DPP4 on insulin signaling seem to be partially mediated through DPP4 enzymatic activity since upon DPP4 inhibition via sitagliptin or saxagliptin treatment I found a consistent upregulation of Akt phosphorylation. It was also shown that deleterious effects of recombinant sDPP4 on insulin signaling are prevented upon DPP4 inhibitor treatment (185). These results might point towards an involvement of DPP4 substrates, which might be present at higher levels due to DPP4 ablation. These substrates might thereby be able to improve insulin signaling. On the other hand, it is also possible that the seen effects of DPP4i might be mediated by a conformational change of DPP4 upon inhibitor binding. The conformational change may result in an inability to impair InsR responsiveness towards insulin. This mechanism was proposed in case of DPP4 activation of PAR2 which results in a downstream signaling event. The activation of downstream signaling pathways was abrogated upon DPP4i treatment (184). Also the binding of DPP4 to other partners can be altered upon DPP4i treatment, as it is the case for fibronectin (250).

DPP4 might also be a regulator of lipolysis since it could be shown that NPY is regulated by AT-derived DPP4 (251). Furthermore, this study revealed an augmented antilipolytic effect of NPY via DPP4i treatment. DPP4 might also regulate lipolysis through ADA interaction and alteration in adenosine levels. It is well known that adenosine levels affect lipolysis (252). However, I could observe no effects of siRNA-mediated silencing on adipocyte lipolysis (Fig. 6), neither on basal glycerol release nor on isoproterenol-stimulated lipolysis. Furthermore, the suppression of lipolysis via insulin was unaffected upon DPP4 silencing. In contrast to my approach, Kos and colleagues directly applied recombinant human NPY with or without DPP4 inhibitor on adipocytes (251). NPY is mainly produced in the brain and reaches adipose tissue via the blood stream (253). It is well known that NPY inhibits lipolysis in human AT (254). Upon treatment of adipocytes with recombinant NPY directly, Kos and colleagues rather mimick a cross-talk scenario of hypothalamus and AT which is not the case in my model (251). Therefore it is not possible to elucidate the role of DPP4 inhibition on adipocyte lipolysis directly. In addition to that Kos et al directly isolated mature adipocytes whereas in this thesis I differentiated isolated preadipocytes *in vitro*. Furthermore, it might be possible that the concentrations of insulin and isoproterenol I used in the study are not optimal to observe differences in glycerol release. To finally evaluate the role of DPP4 inhibition on lipolysis further experiments are necessary.

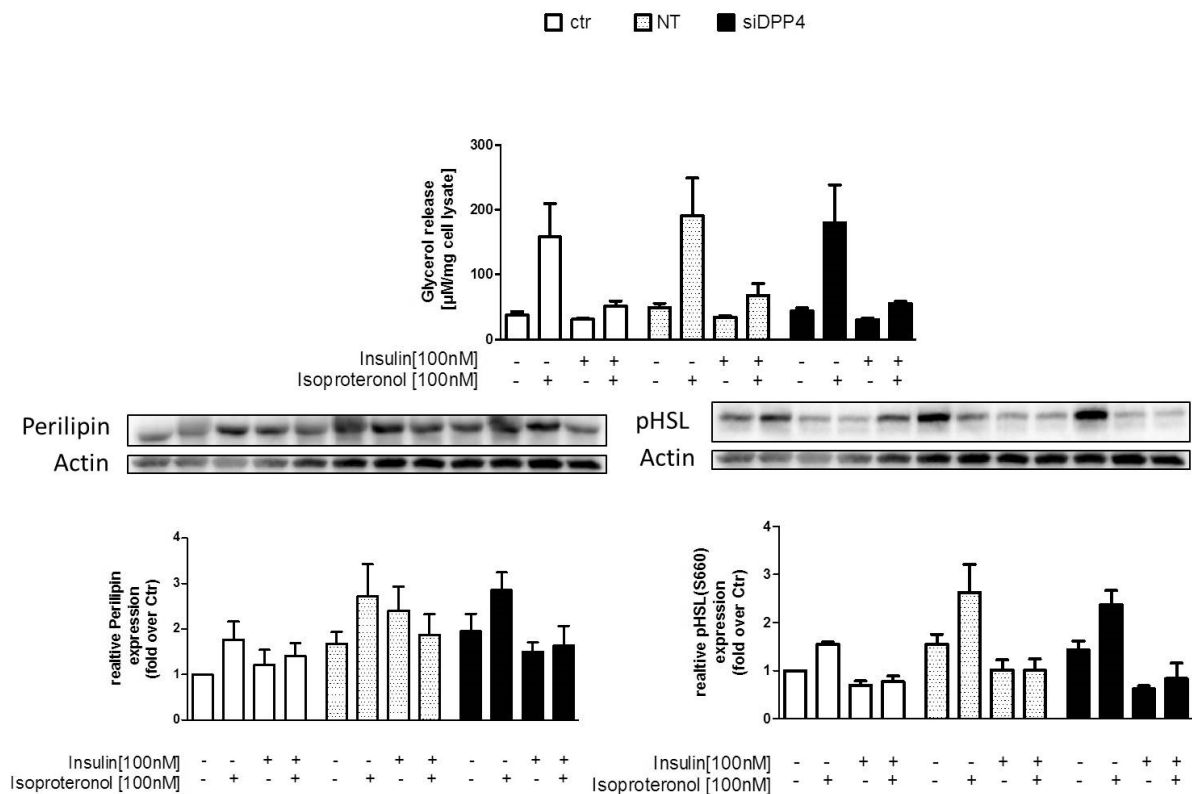


FIGURE 6: IMPACT OF siRNA-MEDIATED DPP4 SILENCING ON LIPOLYSIS.

In vitro differentiated adipocytes were stimulated with 100nM insulin or isoproterenol as indicated and glycerol release to the cell culture medium was measured as well as intracellular protein expression of key mediators of lipolysis. Data are expressed as mean \pm SEM. n=4. Ctr control; NT non-target siRNA; siDPP4 DPP4-specific siRNA

3.2.2. SYSTEMIC ROLE OF AT-DERIVED DPP4

3.2.2.1. SOURCE OF CIRCULATING DPP4

DPP4 is ubiquitously expressed on numerous cell types so that the main source of circulating DPP4 is difficult to define. In the AT-specific DPP4-KO mouse model it was shown, that DPP4 activity is very high in liver, AT, kidney and lung. Although it looks as if liver has the highest DPP4 activity in chow animal, one has to keep in mind that only DPP4 activity in two white AT depots and in one brown AT depot has been measured. There are many more AT depots within the body whose contribution to DPP4 activity could not be assessed. Furthermore, the measured activities of the three AT depots put together already display half the activity measured in the liver. During the progression

of obesity mice mainly gain fat mass and the body composition is shifted towards almost 50% fat content after 24 weeks of HFD challenge in contrast to around 20% fat mass in animals fed with a chow diet. Therefore, AT might especially contribute to DPP4 circulating levels in the obese state. Circulating levels of DPP4 are significantly higher in WT-HFD mice in comparison to their littermates on chow diet. The serum level of DPP4 is lower in AT-specific KO animals irrespective of the diet but only reaches significance in HFD animals. This shows that the increase of DPP4 circulating levels is mainly coming from AT during the progression of obesity and also proves that the mouse model has a systemic impact on DPP4 levels.

3.2.2.2. THE ROLE OF DPP4 ON METABOLIC PARAMETERS AND BODY WEIGHT

To date there have only been studies on whole body KO mice (208;209). DPP4 serum levels in homozygous KO mice are below detection level and thus levels of the incretin hormone GLP-1 are significantly upregulated (208). In the whole body KO animals, an improved glucose tolerance and a protection from DIO and IR were observed (208;209). In line with these data, AT specific DPP4 KO mice on HFD showed an improved glucose tolerance in an oral glucose tolerance test, which might be due to alleviated incretin action and thus pointing towards an involvement of the incretin system. However, no difference in the level of active GLP-1 or GIP was observed in the circulation in the AT specific KO mouse. So one can speculate that the improvements on glucose tolerance observed in the generated mouse model might be independent from the incretin system. No differences in systemic insulin sensitivity or glucose tolerance have been observed after bypassing the incretin system by hyperinsulinemic-euglycemic clamps or intraperitoneal glucose / insulin tolerance tests. Interestingly, KO animals showed even significantly elevated body weight under HFD and thus opposing the data in the total KO mice. The authors observed a significantly lower body weight under HFD which is due to an effect of the KO on food intake and body length (209). This also shows one of the disadvantages of the whole body KO, since the seen beneficial effects on insulin sensitivity and AT phenotype can not directly be addressed to lower DPP4 levels, but might rather be due to the lower body weight per se. It is well known that DPP4 serves as a central regulator of satiety upon regulating food intake. NPY is one of the physiological substrates of DPP4, which was shown to have an altered receptor affinity in rats with DPP4 loss-of-function mutation thus altering food intake and feeding motivation (255;256). In the AT-specific KO model, effects on the central regulation of

food intake can be excluded and no differences in food intake have been observed. Data on clinical use of DPP4 inhibitors have repeatedly shown, that they act weight neutral (257). Therefore the impact of DPP4 on body weight seems rather complex and might be dependent on the primary organ targeted by the DPP4 inhibition.

3.2.2.3. AT-DERIVED DPP4 AND LIVER FUNCTION

It is well known that elevated serum levels of DPP4 are associated with various liver diseases like liver cirrhosis (258), hepatitis C infection (259) and NAFLD (260). Recently it could also be shown that in the diabetic and/or obese state circulating levels of DPP4 are associated with apoptosis and liver fibrosis (261). Therefore, one of the most important targets for circulating DPP4 might be the liver. Interestingly, a significant difference in endogenous glucose production (EGP) was observed in the generated mouse model in KO animals under HFD challenge. Especially during fasting, glucose is removed from the circulation in a constant rate and therefore, EGP by the liver is necessary to counteract the disappearance of glucose (262). As a key regulatory hormone for glucose disposal insulin immediately post-feeding removes glucose from the circulation upon triggering glucose uptake into SkMc and AT. Furthermore, it directly suppresses EGP in the liver. EGP is also suppressed indirectly via suppression of glucagon production in the pancreas (262). Therefore, EGP is a key diagnostic parameter of hepatic insulin sensitivity. During the development of T2DM, insulin action is impaired and effective glucose disposal is lowered (263). Under metabolically healthy conditions, glucose and insulin are in tight cross-talk to promote glucose disposal and to suppress EGP, which is abrogated in T2DM (264). In the AT specific DPP4 KO mouse model, EGP suppression is significantly elevated in KO mice under HFD challenge. Although, it is still significantly different from the chow control group, this points towards a selective improvement in liver insulin sensitivity upon AT-specific DPP4 KO. DPP4 inhibitors have been shown to be beneficial for liver steatosis and fibrosis via different mechanisms. Sitagliptin treated rats showed improved liver function via suppression of stellate cell proliferation and collagen synthesis (265). Diet-induced liver steatosis in a β -cell-specific glucokinase haploinsufficient mouse model was prevented by des-fluoro-sitagliptin treatment via decreasing the expression of e.g. SREBP-1c and

fatty acid synthase (FAS) (266). In AT specific DPP4 KO mice, no significant differences in respect to lipid content within the liver were seen. Also circulating levels of triglyceride or FFA were unaltered. However, all these measurements were performed after 24 weeks of HFD challenge and it might well be that progression of steatosis is slower in KO animals thus preserving insulin sensitivity also for a longer period.

A key question arising from the observations is which factor is mediating the beneficial effect on EGP suppression. It is reported that DPP4 enzymatic inhibition via vildagliptin treatment also enhances EGP suppression in T2DM patients in comparison to placebo (267). So there are two possible explanations. Either lower DPP4 levels in the circulation are directly contributing to improved liver sensitivity or DPP4 substrates are altered and thus mediating the seen effect. Via adipokine profiler arrays it could be shown that resistin as well as IGFBP-3 were significantly lower in the secretome of biopsies generated from visceral AT of KO animals on HFD. In addition, IGFBP-3 levels turned out to be significantly reduced in the circulation while free IGF-1 levels are elevated in KO after HFD. Among circulating total IGF-1 levels there were no changes observed. These differences in circulating levels of IGFBP3 and free IGF-1 might have an impact on peripheral organs like the liver.

The IGF system comprises two IGFs, two IGF receptors and six IGF binding proteins. Upon linkage to IGF, the IGFBPs escape degradation and the transport through body compartments is facilitated (268). The most abundant IGFBP in human serum is IGFBP-3, which binds about 90% of the circulating IGFs without a clear preference for one IGF (269). Thereby IGFBPs lower the amount of free IGFs and thus may act anti-proliferative, anti-mitotic and pro-apoptotic (270). IGFBPs consist of three domains, whereupon the central region contains not only IGF binding domains but also binding domains for cells, acid labile subunit (ALS) and heparin (271;272). Thus, IGFBP-3 is also able to act in an IGF-independent way. *In vitro* studies could show IGFBP-3 receptors are present on the surface of different cells (273). Furthermore, IGFBP-3 can be internalized and, upon linkage with the retinoic acid receptor, is able to induce gene expression (274). It has been shown that IGFBP-3 is able to interact with the nuclear receptor PPAR γ , thus acting on the regulation of glucose and lipid metabolism (275). Several studies have shown that IGF-1 and IGFBP-3 are linked to the development of T2DM. Sesti and coworkers showed a positive correlation of endogenous IGF-1 levels and the degree of glucose intolerance in patients (276). The increased serum levels of IGF-1 might be counter-regulating the detrimental effects of IGFBP-3, since IGF-1 seems to be

acting in a protective way on insulin sensitivity. Higher production of IGF-1 seems to be a counterregulatory mechanism to combat the high levels of IGFBP-3 seen in T2DM. IGFBP-3 inhibits the biologic activity of IGF-1, contributing to less free IGF-1 and thereby increasing the risk of diabetes (277). Furthermore, IGF-1 is involved in lipid clearance from the circulation via increasing FFA uptake into adipocytes (278;279). Additionally, IGF-1 is able to suppress hepatic glucose production (280;281), thereby enhancing hepatic insulin sensitivity. An inverse correlation of serum IGFBP-3 and insulin sensitivity and an association of higher levels with BMI and fasting insulin further strengthens the detrimental role of IGFBP-3 in T2DM (282). This was also confirmed by *in vitro* studies in 3T3-L1 adipocytes, where IGFBP-3 induces IR via inhibition of insulin-stimulated Glut4 translocation and impaired glucose uptake (283). In this thesis it was shown, that IGFBP3-treated HepG2 cells display impaired insulin signaling and responsiveness towards insulin-stimulated glucose production. This is in line with the above mentioned studies in 3T3-L1 adipocytes and points towards a direct effect of IGFBP3 on liver physiology. In IGFBP-3 overexpressing mice it was shown that plasma IGFBP-3 levels mediate peripheral IR independent of IGF-1 (284). Furthermore, ER stress in the liver is associated with eIF2 α signaling via IGFBP-3. Transgenic mice, overexpressing a constitutively active regulatory subunit of the phosphatase that terminates ER stress-signaling by phospho-eIF2 α , showed higher hepatic mRNA expression and circulating levels of IGFBP-3, which are transducing the ER stress to peripheral organs like AT (285). Mass spectrometry analysis revealed that IGF-1 is a substrate of DPP4. Upon cleavage IGF-1 has a lowered receptor binding affinity, but an increased binding to IGFBP-3 than the full length form (286). However, treatment of pigs for 72h with sitagliptin and also treatment of healthy non-diabetic human subjects for 10 days revealed no impact on circulating levels of IGF-1 or IGFBP-3 (287;288). In this thesis serum levels of free IGF-1 and also total IGF-1 were increased in recent onset metformin-treated type 2 diabetes patients additionally treated with the DPP4i sitagliptin. This highlights how difficult it is to predict changes of DPP4i in downstream pathways.

Finally it seems plausible that the lowered IGFBP-3 release in the AT-specific KO mouse model may contribute to the selective hepatic insulin sensitizing effects first upon

increased free IGF-1 levels and second via directly mediating insulin sensitivity of hepatocytes. So in AT specific DPP4 KO mice under HFD, reduced release of IGFBP3 from visceral AT might contribute to a protective cross-talk between AT and liver. However, the concrete mechanism how DPP4 is linked to IGFBP-3 remains open and needs to be addressed in the future.

3.2.2.4. ADVANTAGE OF TISSUE-SPECIFIC KO APPROACHES

Another drawback of the whole body KO animals in addition to the already mentioned effect on feeding behaviour, is that the immune cells are also affected by the KO. Immune cell infiltration and activation is a crucial parameter of the progression of AT dysfunction during obesity. Furthermore, low DPP4 levels might also be contributing to chronic inflammatory diseases or cancer. Low circulating levels are e.g. associated with different types of cancer (105;289), rheumatoid arthritis (290) and chronic obstructive pulmonary disease (291). DPP4 is interacting with numerous binding partners and is thereby involved in various intracellular downstream signaling processes (107). Therefore the role of DPP4 within the body is multidimensional and tissue-specific KO approaches are more fruitful in dissecting the role of DPP4 in different organs. However, there are some concerns upcoming for the use of aP2 as AT-specific promoter, as used in this mouse model (162). For example, it has been reported that also macrophages are expressing aP2 and might thereby be affected by the KO. To rule out that the model affects DPP4 expression in macrophages, AT has been fractionated into mature adipocytes and the stroma-vascular fraction. The major cellular components of the stroma-vascular fraction are preadipocytes, immune cells and fibroblasts. No difference in DPP4 protein expression in WT or KO preparations was observed. Furthermore, it also has been confirmed that CD11c positive fractions from peritoneal lavage display no difference in DPP4 expression. Thereby, it could be ruled out that the KO affects macrophages and that the shown effects are overlapped by macrophage contribution.

3.3. DPP4 AS AN IMPORTANT ADIPOKINE IN THE CONTEXT OF OBESITY AND T2DM

As already highlighted before, DPP4 displays a wide-spread role in diabetes. This is mediated through its incretin-dependent, but also through its incretin-independent functions. Most of the so far published studies have allocated the beneficial effects of

DPP4i to prolonging the half-life of the incretin hormones like GLP-1 (190;205;292). However, more and more studies also revealed that DPP4 exerts its role in diabetes in an incretin-independent way for example via regulating T-cell activation directly (293) or indirectly via facilitating adenosine clearance upon ADA binding (294). Thereby DPP4 is involved in inflammation, which is a major contributor of IR and T2DM during the progression of obesity. But DPP4 may also exert GLP-1-independent effects via the regulation of other substrates (266;295). Furthermore, we confirmed that DPP4 plays a role in insulin signaling via impairing pAkt activation in an endocrine and paracrine manner (185). This was also supported by the fact that siRNA-mediated silencing or treatment with specific DPP4i improved insulin signaling in adipocytes as presented in this thesis. DPP4 also plays a role in glucose homeostasis via adenosine, which is involved in maintaining high efficiency of insulin signaling and insulin-stimulated glucose transport (181). Additionally, it could be shown by an AT-specific KO mouse approach that AT is one important contributor to circulating DPP4. Furthermore, elevated DPP4 release into the circulation, which is observed during HFD-feeding, is prevented in KO animals. Since DPP4 is an adipokine and AT mass is mainly expanding during obesity, it is important to understand the regulation and mechanism of DPP4 release. In this context I was able to show an involvement of MMPs in DPP4 shedding, which are known to be dysregulated in obesity (218;219). On the other way round, it is also reported that DPP4 itself mediates MMP activation (179). MMPs might also be the reason for the observed effects on healthy AT remodeling under HFD challenge. They could be one link of lowered fibrosis and the occurring adipocyte size shift and altered DPP4 levels within AT in obesity. The influence of DPP4 on the AT secretory output could be another mediating mechanism, since altered resistin and IGFBP-3 levels in KO animals under HFD were observed. DPP4 release could be regulated by inflammatory markers like TNF α , as well as metabolic parameters like insulin (185), both of which are important players in T2DM. Interestingly I could show that AT-derived DPP4 has a selective impact on hepatic insulin sensitivity most likely via regulating circulating levels of IGFBP3.

Although questions on the exact molecular mechanisms underlying these observations still remain open, I was able to highlight in this work the role of DPP4 in obesity especially beyond the incretin axis. Thereby, I contributed significantly to a better understanding of this complex molecule as summarized in Fig 7.

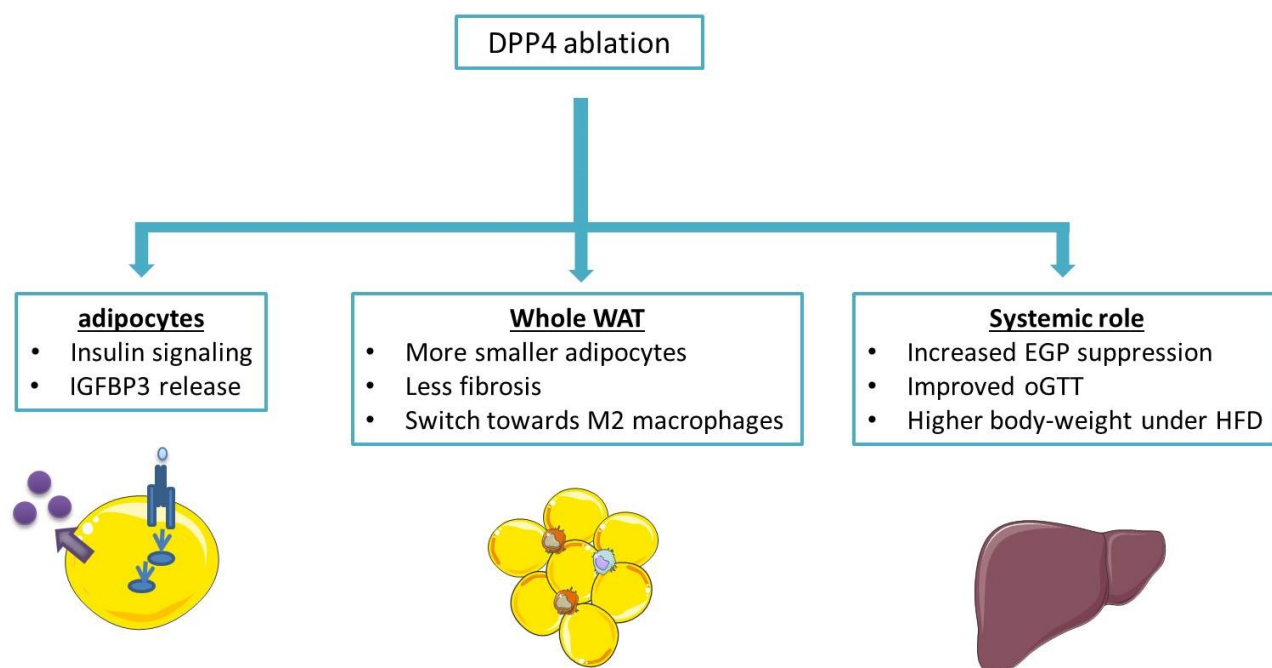


FIGURE 7: IMPACT OF DPP4 ABLATION.

The outcome of this thesis is summarized in this figure. Downregulation of DPP4 has been shown to have a beneficial effect on adipocytes themselves, AT in total as well as systemically via e.g. improving hepatic insulin sensitivity. IGFBP3 insulin-like growth factor binding protein 3; EGP endogenous glucose production; oGTT oral glucose tolerance test; HFD high fat diet

3.4. PERSPECTIVES

DPP4 is not only expressed as a cell surface protease, but is also released into the circulation. It is well known that circulating levels of DPP4 correlate with various obesity-associated complications like MetS (185;186), cardiovascular diseases (294), and cancer (105). However, the mechanism of DPP4 release and its regulation is mainly unknown. Therefore, the first objective of this thesis was to identify the sheddases and regulatory factors involved in DPP4 release from SMC and adipocytes. I confirmed that DPP4 release occurs through a non-classical secretory pathway. Constitutive as well as hypoxia-induced DPP4 shedding from SMC is mediated via MMPs like MMP1, MMP2 and MMP14. Furthermore, I could show that DPP4 release via MMPs is cell-type specific and involves MMP9 in adipocytes. I also confirmed that DPP4 shedding is a complex interplay between different shedding enzymes and might involve other unidentified factors, since I was only able to block DPP4 release by about 50% in the investigated cell types. A causal relationship between DPP4 and the involved shedding enzymes in obesity is lacking so far. Therefore, future research should focus on the molecular mechanisms to better understand the dysregulated release of sDPP4 in pathophysiological conditions.

Although we already described DPP4 as an adipokine potentially linking obesity to the MetS (185), it was unclear which role DPP4 plays within AT. The second objective of this work was to assess the role of DPP4 within adipocytes *in vitro* via siRNA-mediated silencing or the use of DPP4i. I demonstrated that DPP4 plays no central role in adipocyte differentiation or TNF α -induced inflammation. However, I provide clear evidence that reduction of DPP4 improves insulin signaling in adipocytes and seems to be at least partly mediated via its enzymatic activity. This is in line with previously published data where sDPP4 directly impairs insulin-stimulated Akt phosphorylation in adipocytes which could be prevented by DPP4i (185). However, the physiological role of DPP4 in adipocyte function downstream of AS160 phosphorylation remains elusive. Future studies should therefore investigate the impact of siRNA-mediated silencing on Glut4 translocation or glucose uptake in adipocytes. Furthermore, a role of DPP4 in altering the adipocyte secretome could not be ruled out by the generated data and needs

to be addressed in future experiments with assays bypassing the limitations of the used adipokine arrays.

Data on global DPP4 KO mice demonstrated a high impact of DPP4 on metabolic health (208;209). These results are difficult to interpret, because of the impaired food intake, the KO in every organ and most importantly also in immune cells. From the already published data we hypothesized that, especially during obesity, AT is a major source of sDPP4. The third objective of this thesis was to elucidate the role of AT-derived DPP4 during obesity on AT itself and in the cross-talk to other organs. In this thesis, a unique AT-specific KO mouse model was established which was challenged with HFD feeding for 24 weeks. It could be demonstrated that DPP4 depletion in AT plays a beneficial role in visceral AT remodeling under diet-induced obesity. This was mediated through elevated expression of M2 macrophage markers, lowered expression of fibrosis markers, and a shift towards smaller adipocytes. On the systemic level, it could be shown that DPP4 depletion, despite elevated body-weight, leads to an improved oral glucose tolerance and selective improvement of hepatic insulin sensitivity possibly in an incretin-independent way. Although, IGFBP-3 was suggested as a potential mediator of the seen effects, the molecular link between DPP4 and IGFBP-3 remains open and needs to be addressed by future experiments. Although IGFBP3 directly affects insulin signaling in HepG2 cells these experiments are only a hint for a potential interaction of IGFBP3 and liver. The exact underlying mechanism is still unknown and further experiments need to address the impact of IGFBP3 on liver cells. Additionally, *ex vivo* insulin signaling in the liver of AT specific DPP4 KO animals in comparison to control animals should be analysed in the future. It was also demonstrated that liver has a high impact on circulating active levels of sDPP4. So via a liver-specific KO approach the impact of sDPP4 derived from liver in the context of obesity should be addressed and compared to the AT-specific data.

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DANKSAGUNG

Ein großes Dankeschön möchte ich vor allem an Prof. Jürgen Eckel richten, für die Bereitstellung des Themas und viele sehr gute fachliche Diskussionen, die es mir ermöglicht haben, Ergebnisse auch aus neuen Blickwinkeln zu beurteilen. Außerdem vielen Dank für das entgegengebrachte Vertrauen und das fortwährende Interesse an meiner Arbeit. Dank der bereitgestellten finanziellen Mittel hatte ich die Möglichkeit Ideen im Labor umzusetzen und an nationalen und internationalen Kongressen teilzunehmen. All das lieferte wertvolle Beiträge zum Voranschreiten der Arbeit und hat mich nicht nur fachlich sondern auch persönlich reifen lassen.

Herrn Prof. Ulrich Rüther danke ich für die Übernahme des Korreferats und die Möglichkeit an den Arbeitsgruppen Seminaren teilzunehmen, die ich dank der angenehmen Atmosphäre immer in Erinnerung behalten werde. Vielen Dank auch für die anregenden Diskussionen, die mir oft neue Möglichkeiten eröffnet haben.

Ein ganz besonderer Dank gilt allen derzeitigen und ehemaligen Mitgliedern der AG Eckel, die einem auch aus den tiefsten Motivationslöchern herausgeholfen haben. Ein besonderer Dank gilt hier Henrike für die fachliche Betreuung, das Korrekturlesen der Arbeit und für anregende Diskussionen. Vielen Dank auch an Manu für ein immer offenes Ohr für Fragen zu Differenzierung. Vielen Dank an Kristin für das Einarbeiten in das qRT-PCR Geheimnis und für deine nette und unkomplizierte Art. Vielen Dank an Birgit für das Überwinden vieler bürokratischer Hürden und die netten privaten Gespräche. Ein Riesendank auch an Andrea, für die tatkräftige Unterstützung beim Präparieren und Aufziehen. Vielen Dank für gefühlte 100.000 bradforbs, die du immer ohne Murren übernommen hast. ;-) Ohne dich wäre ich verzweifelt! Und für die Hilfe bei Blots, die wie aus Zauberhand fertig zum Einlesen morgens bereit standen. :-) Auch vielen Dank für deine Lebensfreude mit der du uns alle oft angesteckt hast..

Danke an alle Doktoranden und Studenten für nette Mittagspläusche fernab vom Laboralltag, danke für unvergessliche Karnevalsbesuche und den ein oder anderen Weihnachtsmarktglühwein, sowie die Adrenalinkicks auf der Rheinkirmes und danke für die „Dönerstage“. ;-)

Danke an Ira, Thorsten und Sven für die nette Atmosphäre im Hamsterkäfig, für alle fachlichen und unfachlichen Gespräche. ;-) Danke für Kletterabende, gemeinsames Public viewing und die Geburtstagsfeiern. Dank euch verging die Zeit im Endeffekt doch wie im Flug.

Ein besonderer Dank gilt auch Nina, nicht nur für viele fachliche Hilfestellungen zu DPP4 und den Smoothies, sondern auch für ein immer offenes Ohr, für die netten Apfelpäuschen, die ich verdammt vermissen werde. Selbst ungeliebte Aufgaben wurden dank dir erträglich und lustig. Vielen Dank für die tolle Zusammenarbeit am „Monster-DPP4-Review“. Außerdem an dich und auch an Sven vielen Dank für die tollen privaten Abende und die tollen gemeinsamen Kongresszeiten! Ihr seid mir echt ans Herz gewachsen und habt mir die Zeit fernab von der Familie wahnsinnig erleichtert..

Abschließend bedanke ich mich von ganzem Herzen bei Mom und Paps, bei Franzi und Max für das Vertrauen, die liebevolle Unterstützung und ein immer offenes Ohr, wenn es mal wieder nicht so leicht war.. Die oft stundenlangen Telefonate haben mich stets aufgeheitert und wieder motiviert nach vorn zu schauen. Ich danke euch, dass ihr mir immer den Rücken gestärkt habt auch über die weite Distanz. Danke, dass ihr immer an mich geglaubt habt und mir das alles ermöglicht habt!

Und dir Steve gilt der größte Dank, deswegen kommst du zum Schluss.. Du warst und bist mein „Fels in der Brandung“, du hast mich zurück auf den Boden geholt und es immer verstanden mich aufzuheitern. Ohne dich hätte ich die Herausforderung niemals angenommen und gemeistert, weit weg von zu Hause eine Dr. Arbeit zu machen. In allem was ich tue gibst du mir den nötigen Halt und ich freue mich wahnsinnig auf die kommende kleine (oder große ;-)) Herausforderung, die wir uns geschenkt haben. ;-)
Am Ende wird immer alles gut.. Danke, dass es dich gibt und dass du bei mir bist.

EIDESSTAATLICHE ERKLÄRUNG

Die vorliegende Dissertation habe ich eigenständig und ohne unerlaubte Hilfe angefertigt unter Beachtung der „Grundsätze zur Sicherung guter wissenschaftlicher Praxis“, die mir von der Heinrich-Heine-Universität Düsseldorf nahegelegt worden.. Die Dissertation wurde in der vorgelegten oder in ähnlicher Form noch bei keiner anderen Institution eingereicht. Ich habe bisher keine erfolglosen Promotionsversuche unternommen.

(Diana Röhrborn)

Düsseldorf, den