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Toxicology**

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**“The reactive pyruvate metabolite dimethylglyoxal in
experimental disease models and the role of *Ilvbl* in its generation
in the brain”**

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Summary

Reactive glucose metabolites are involved in neurological complications of diabetes by the generation of advanced glycated end products (AGEs), which are formed by the interaction between α -dicarbonyls and proteins. AGEs induce oxidative stress, inflammation and tissue damage and have been associated with neuropathy, nephropathy and retinopathy. So far, only the α -dicarbonyls 3-deoxyglucosone, glyoxal and methylglyoxal have been recognized as reactive glucose metabolites and associated with complications in diabetes. Only recently, the α -dicarbonyl dimethylglyoxal (DMG) has been categorized as mammal cellular pyruvate metabolite, and its levels were higher in the plasma of type-1 diabetic mice and in the serum of patients with diabetes. In this thesis, I investigated the α -dicarbonyl DMG in mouse models under pathological conditions and its metabolic pathway in mammals using liquid chromatography coupled to tandem mass spectrometry (LC-MS²).

Here, plasma DMG concentrations were upregulated in mouse experimental models of type-1 and type-2 diabetes. In contrast, high-fat diet did not influence the serum levels of DMG, suggesting that diabetic conditions – but not obesity itself – are associated with plasma DMG upregulation and accumulation. Moreover, DMG levels were enormously augmented in the ipsilateral side of a mouse model of hyperglycemic stroke compared to sham control. Interestingly, DMG levels were also higher in the contralateral hemisphere of the brain of mice with stroke compared to sham controls, showing that the contralateral hemisphere is also affected by ischemic stroke. Furthermore, the current study confirmed that DMG is a post-glycolytic product in mammals and its levels are increased under hypoxic conditions *in vitro*. Then, I investigated the role of the gene *ilvB* acetolactate synthase-like (*Ilvbl*), the mammal orthologue gene of acetolactate synthase that generates DMG from pyruvate in bacteria, yeast and plants. Importantly, *Ilvbl* knockout reduced DMG levels in the brain of mice with type-1 diabetes or hyperglycemic stroke, showing that *Ilvbl* has conserved its role in DMG generation in mammals. Moreover, DMG interacted with lysine, generating the glycated amino acid N ϵ -3-hydroxy-2-butanone lysine (HBL), confirming that DMG is a reactive compound and can glycate proteins generating AGEs. Thus, DMG induced oxidative stress and neuroinflammation in mouse hippocampal neuronal (HT-22) cells, probably based on protein glycation.

In conclusion, this study characterizes the α -dicarbonyl DMG in experimental models under pathological conditions, showing that DMG could play a significant role in diabetic complications and ischemic stroke complications. DMG is the only α -dicarbonyl generated after glycolysis, and the current discovery could explain why cells consuming lactate – such as neurons – are not protected by dicarbonyl stress. Importantly, this study shows that ILVBL plays a significant role in the DMG generation from pyruvate in the brain of acute or chronic hyperglycemic mice. Further investigation

Summary

on DMG and the attenuation of its concentrations may lead to improvement in diabetic and ischemic stroke complications.

Zusammenfassung

Reaktive Glukosemetabolite sind an den neurologischen Komplikationen von Diabetes beteiligt, indem sie sogenannte Advanced Glycation End Products (AGEs) bilden. Diese entstehen durch die Wechselwirkung zwischen α -Dicarbonylen und Proteinen. AGEs induzieren oxidativen Stress, Entzündungen und Gewebeschäden und werden mit Neuropathie, Nephropathie und Retinopathie in Verbindung gebracht. Bislang wurden nur die α -Dicarbonyle 3-Deoxyglucosone, Glyoxal und Methylglyoxal als reaktive Glukosemetabolite identifiziert, die mit Komplikationen bei Diabetes in Verbindung stehen. Kürzlich wurde auch Dimethylglyoxal (DMG) als α -Dicarbonyl und zellulärer Pyruvat-Metabolit von Säugetieren beschrieben. Seine Konzentrationen waren im Plasma von Mäusen mit Typ-1-Diabetes und im Serum von Diabetes-Patienten erhöht. In dieser Arbeit habe ich das α -Dicarbonyl DMG in Mausmodellen unter pathologischen Bedingungen untersucht und seinen Stoffwechselweg in Säugetieren mithilfe der Flüssigchromatographie, gekoppelt an die Tandem-Massenspektrometrie (LC-MS²), analysiert.

In experimentellen Mausmodellen für Typ-1- und Typ-2-Diabetes wurden erhöhte DMG-Konzentrationen im Plasma beobachtet. Im Gegensatz dazu hatte eine fettreiche Ernährung keinen Einfluss auf die DMG-Serumspiegel. Dies deutet darauf hin, dass diabetische Erkrankungen, nicht jedoch Adipositas selbst, mit einer Erhöhung und Akkumulation von DMG im Plasma verbunden sind. Darüber hinaus war der DMG-Spiegel auf der ipsilateralen Seite eines Mausmodells für einen hyperglykämischen Schlaganfall enorm erhöht. Interessanterweise waren die DMG-Spiegel auch in der kontralateralen Hemisphäre des Gehirns von Mäusen mit Schlaganfall erhöht, was zeigt, dass auch diese Hemisphäre von dem ischämischen Schlaganfall betroffen ist. Die aktuelle Studie bestätigte zudem, dass DMG ein postglykolytisches Produkt in Säugetieren ist und seine Konzentrationen unter hypoxischen Bedingungen *in vitro* erhöht sind.

Des Weiteren untersuchte ich die Rolle des Gens *ilvB* acetolactate synthase-like (*ilvbl*). Diese Enzym ist bei Bakterien, Hefen und Pflanzen für die Erzeugung von DMG aus Pyruvat verantwortlich. Wichtig ist, dass der Knockout von *ilvbl* den DMG-Spiegel im Gehirn von Mäusen mit Typ-1-Diabetes oder hyperglykämischem Schlaganfall reduziert. Dies zeigt, dass die Rolle von *ilvbl* bei der DMG-Erzeugung in Säugetieren konserviert wurde. Darüber hinaus konnte gezeigt werden, dass DMG mit Lysin interagiert und die glykierte Aminosäure Nε-3-Hydroxy-2-Butanonelysin (HBL) bildet. Dies bestätigt, dass DMG eine reaktive Verbindung ist, die Proteine unter Bildung von AGEs glykieren kann. Dementsprechend, induzierte DMG oxidativen Stress und Neuroinflammation in neuronalen Zellen des Hippocampus der Maus (HT-22), was wahrscheinlich auf der Glykierung von Proteinen beruht.

Zusammenfassend lässt sich sagen, dass diese Studie das α -Dicarbonyl DMG in experimentellen Modellen unter pathologischen Bedingungen charakterisiert und zeigt, dass DMG eine bedeutende

Zusammenfassung

Rolle bei diabetischen Komplikationen und ischämischen Schlaganfallkomplikationen spielen könnte. DMG ist das einzige α -Dicarbonyl, das nach der Glykolyse entsteht. Die aktuelle Entdeckung könnte erklären, warum Zellen, die Laktat verbrauchen – wie Neuronen – nicht vor Dicarbonylstress geschützt sind. Von Bedeutung ist zudem, dass diese Studie zeigt, dass ILVBL eine bedeutende Rolle bei der DMG-Bildung aus Pyruvat im Gehirn von akut oder chronisch hyperglykämischen Mäusen spielt. Weitere Untersuchungen zu DMG und dessen Konzentration könnten zu einer Verbesserung diabetischer Komplikationen und ischämischer Schlaganfallkomplikationen führen.

Introduction

1. Introduction

1.1. Glucose metabolism

Glucose is the most important metabolic energy source and is essential for life. Chemically, glucose is a monosaccharide characterized by six carbon atoms ($C_6H_{12}O_6$, **Fig. 1.1**) and is a reducing sugar. In plants, glucose is generated from carbon dioxide and water by photosynthesis and stored as cellulose and starch.

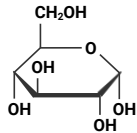


Fig. 1.1 | Glucose

The molecule structure was created with Biorender.com

Generally, humans consume glucose directly or indirectly through diet by sucrose or polysaccharides. Sucrose is a disaccharide composed of glucose and fructose, while polysaccharides (e.g., starch) are long-chained monosaccharide polymers. Some polysaccharides get demolished to glucose and other monosaccharide molecules due to enzymatic actions. For example, sucrose is converted to glucose and fructose by β -fructofuranosidase, and lactose is degraded to glucose and galactose by lactase. Subsequently, glucose is metabolized in cells to produce energy or is stored in liver, fat or muscle cells as glycogen¹.

Glycolysis is an anaerobic metabolic pathway that converts glucose into two pyruvate molecules in the cytosol (**Fig. 1.2**). Glycolysis also produces two molecules of adenosine triphosphate (ATP) and two molecules of reduced nicotinamide adenine dinucleotide (NADH). Glycolysis consists of ten reactions and can be distinguished into two phases: the preparatory phase and the pay-off phase. In the preparatory phase, one glucose molecule is converted to two molecules of glyceraldehyde 3-phosphate (G3P) by consuming two ATP molecules. Therefore, two G3P molecules are metabolized into two pyruvate molecules with the gain of four molecules of ATP and two molecules of NADH. Then, pyruvate is catabolized to L-lactate by lactate dehydrogenase (LDH) or acetyl-CoA by pyruvate dehydrogenase complex (PDC, **Fig. 1.2**). Subsequently, the mitochondrial citrate synthase (CS) catalyzes the condensation of acetyl-CoA with oxaloacetate generating citrate, a Krebs cycle (or citric acid cycle, TCA) and *de novo* lipogenesis substrate (**Fig. 1.2**).

Introduction

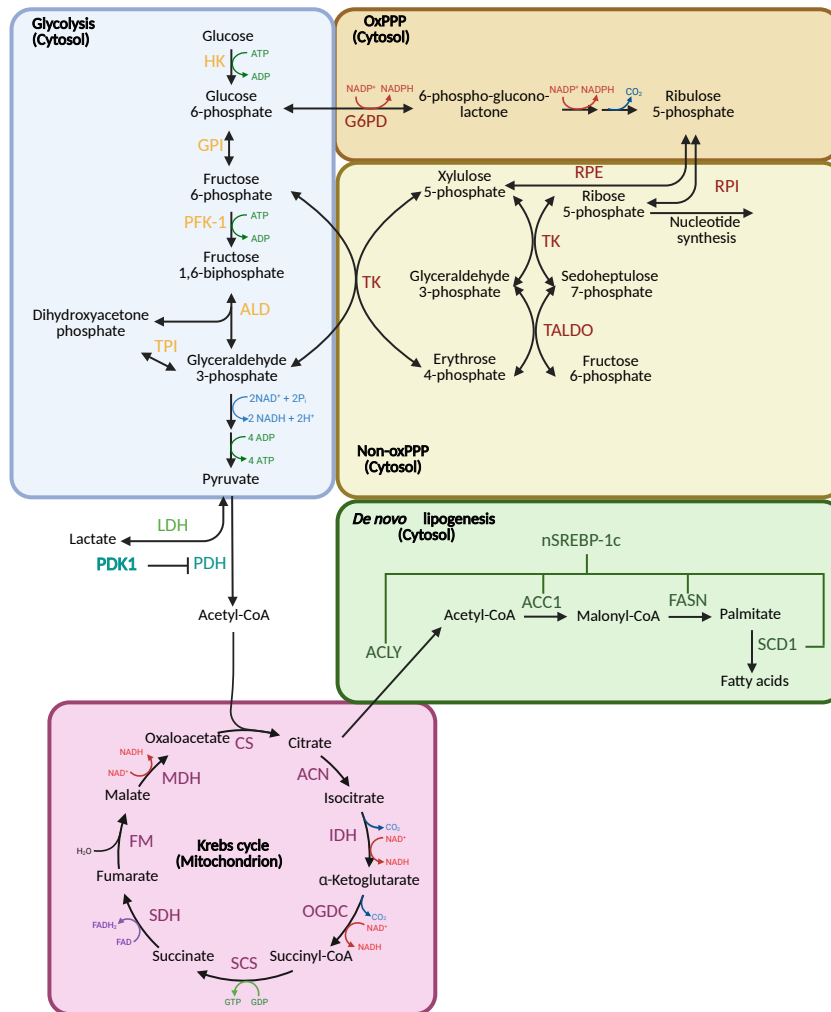


Fig. 1.2 | Schematic illustration of glucose catabolism by glycolysis, oxidative (ox) and non-ox pentose phosphate pathway (PPP), Krebs cycle and de novo lipogenesis.

Detailed abbreviation legend is provided on page 88. The illustration was created with Biorender.com and adapted after TeSlaa, T., Ralser, M., Fan, J., et al., 2023²; and Haddad, A., Mohiuddin, S., S., 2023³.

The Krebs cycle is an aerobic metabolic pathway that generates three molecules of NADH, one equivalent of reduced flavine adenine dinucleotide (FADH₂) and one of guanosine triphosphate (GTP) in the mitochondrion (**Fig. 1.2**). Two acetylic carbons are oxidated during the TCA cycle, generating four electron pairs and two carbon dioxide (CO₂) molecules. Lastly, NADH and FADH₂ molecules interact with oxygen molecules, producing water, whereas the reducing coenzymes are used to generate ATP by oxidative phosphorylation⁴. The phosphate/oxygen (P/O) ratio estimates the generated chemical energy, calculating 2.73 ATP molecules from NADH oxidation and 1.64 ATP molecules from FADH₂ oxidation. Moreover, the TCA metabolite citrate can be converted to fatty acids by *de novo* lipogenesis (**Fig. 1.2**). Glucose is also involved in the generation of nucleotides by the pentose phosphate pathway (PPP, **Fig. 1.2**). Here, the glycolytic product glucose 6-phosphate is converted to ribulose 5-phosphate,

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generating two NADPH molecules². Subsequently, ribulose 5-phosphate is isomerized to ribose 5-phosphate, a precursor of nucleotide synthesis. During the non-oxidative part of the pentose phosphate pathway, ribulose 5-phosphate and ribose 5-phosphate are also catabolized to fructose 6-phosphate and G3P, two glycolytic metabolites².

Apart from the previously described pathways that show the crucial role of glucose in the generation of chemical energy, glucose also generates toxic compounds during its catabolism. Since these metabolites react quickly with other endogenous molecules, they have been recognized as reactive glucose metabolites.

1.2 α -Dicarbonyls

α -Dicarbonyls are organic compounds containing two adjacent carbonyl groups (**Fig. 1.3**). The nomenclature “ α ” refers to the position of the carbon directly attached to the functional group. Chemically, α -dicarbonyls can be distinguished into 1,2-dialdehydes, 1,2-ketoaldehydes and 1,2-diketones. Endogenously, they originate from glucose and are highly reactive. The interaction between α -dicarbonyls and proteins or lipids leads to the formation of advanced glycation end products (AGEs)^{5,6}.

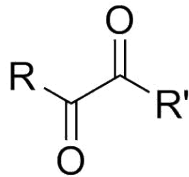


Fig. 1.3 | α -Dicarbonyl

The molecule structure was created by ChemSketch.

1.2.1 3-Deoxyglucosone

3-Deoxyglucosone (3-DG, **Fig. 1.4**) belongs to the group of 1,2-ketoaldehyde, and it is generated from glucose via Maillard reaction⁷ (**Fig. 1.6**). The Maillard reaction is a non-enzymatic reaction that consists of the interaction between the carbonyl group of the reducing sugar, such as glucose, and the amino group of amino acids, followed by the rearrangements of the Amadori products to 3-DG⁷. 3-DG interacts with amino acids, generating AGEs and glycated amino acids like pyrraline, 3-deoxyglucosone lysine dimer (DOLD) and glycated 3-DG in histone H1 (3-DG-H1)⁸⁻¹⁰. On the other hand, 3-DG can be catabolized to 3-deoxyfructose by aldoketo reductases^{11,12}. In addition to its endogenous formation from glucose, 3-DG has been detected in several foods and drinks, such as yoghurt and red wine¹³. Previous studies showed that 3-DG concentrations are upregulated in the serum of patients with diabetes and plasma of type-1 diabetic rats¹⁴⁻¹⁷.

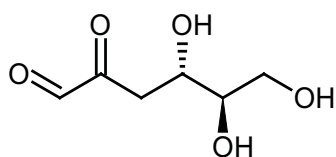


Fig. 1.4 | 3-Deoxyglucosone

The molecule structure was created by ChemSketch.

1.2.2 Glyoxal

Glyoxal (Gx, **Fig. 1.5**) is the smallest dialdehyde and a metabolite generated from glucose degradation, lipid peroxidation and glycated protein degradation. Gx is also a Maillard reaction product (**Fig. 1.6**), during which Gx is generated from both Schiff bases and Amadori products⁶. Moreover, Gx is directly generated from glucose by autooxidation (**Fig. 1.6**) and is also a product of lipid peroxidation of linolenic acid¹⁸. In addition, Gx is taken up with the diet^{13,19,20}. Gx is metabolized to glycolate via the glyoxalase system or to glyoxylate via aldehyde dehydrogenase^{21,22}. Subsequently, glyoxylate is catabolized to oxalate²², and high levels of this metabolite can lead to the formation of calcium oxalate stones in the urinary tract^{22,23}. Gx concentrations were higher in the plasma of patients with diabetes²⁴. Previous studies showed that Gx induced the generation of reactive oxygen species (ROS) in rat hepatocytes and the expression of the proinflammatory gene cyclooxygenase (COX)-2 in human vascular endothelial cells^{25,26}. As 3-DG, Gx can also generate AGEs and glycated amino acids, such as glyoxal-derived lysine dimer (GOLD) and N^ε-carboxymethyl-lysine (CML)²⁷.

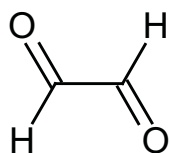


Fig. 1.5 | Glyoxal

The molecule structure was created by ChemSketch.

1.2.3 Methylglyoxal

Methylglyoxal (MG, **Fig. 1.7**) is a 1,2-ketoaldehyde, mainly generated from glucose by glycolysis (**Fig. 1.6**). Specifically, MG is a product of the degradation of the glycolytic isomers G3P and dihydroxyacetone phosphate^{28,29}.

Introduction

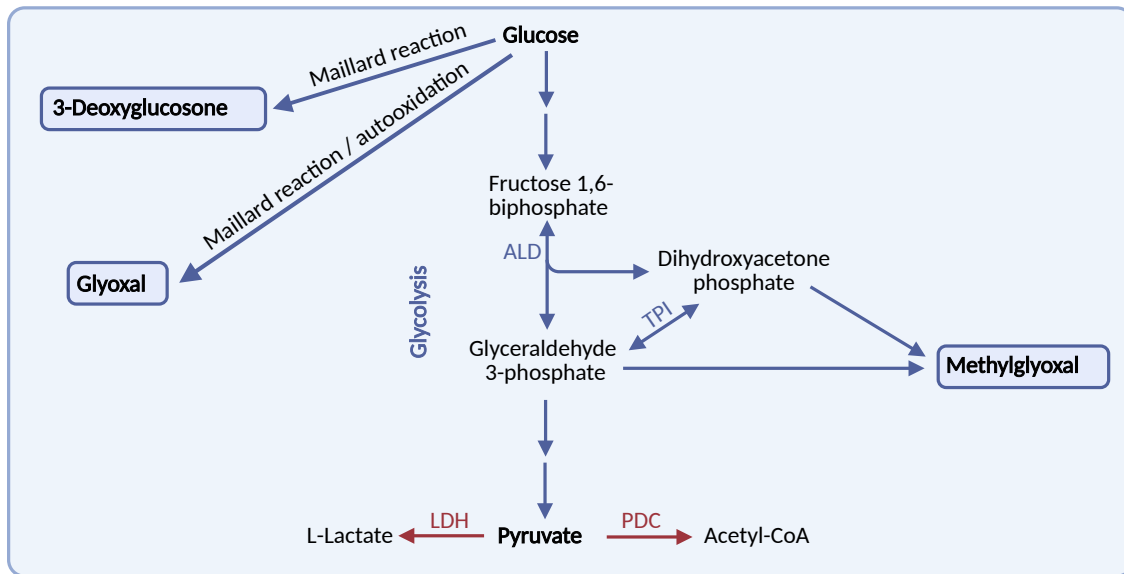


Fig. 1.6 | Schematic illustration of the 3-deoxyglucose, glyoxal and methylglyoxal anabolic pathways.

The illustration was created with Biorender.com. ALD = aldolase, TPI = triose phosphate isomerase, LDH = lactate dehydrogenase, PDC = pyruvate dehydrogenase complex.

Moreover, MG is also generated from fatty acids via the formation of acetone and acetol and from glycine and threonine via aminoacetone³⁰⁻³². In addition, MG is exogenously taken up by the consumption of ordinary food or drinks^{13,20,33}. Interestingly, high levels of MG were found in the Australian *Leptospermum* (Manuka) honey and its concentrations were positively associated with the anti-bacterial proprieties of the honey^{34,35}. MG generates glycated amino acids, such as methylglyoxal-lysine dimer (MOLD), argpyrimidine, and AGEs, by interacting with lysine or arginine^{36,37}. MG induces oxidative stress, inflammation and endothelial dysfunction in type-2 diabetic rats and in control rats treated with MG³⁸. MG is mainly catabolized to D-lactate via the glyoxalase system. More specifically, glyoxalase-1 converts methylglyoxal-reduced glutathione hemithioacetal to S-Lactoylglutathione, while the enzyme glyoxalase-2 converts the previous product to D-lactate^{39,40}.

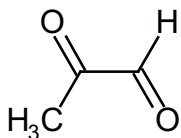


Fig. 1.7 | Methylglyoxal

The molecule structure was created by ChemSketch.

Introduction

1.2.4 Dimethylglyoxal

The polar α -diketone dimethylglyoxal (or diacetyl, DMG, **Fig. 1.9**) is a yellow liquid compound with a strong odor and an intensive buttery and milky taste⁴¹. Due to this peculiar taste, DMG has been used as a flavoring agent in food, such as microwave popcorn or cookie dough. However, the occupational exposition to DMG has been associated with developing the irreversible lung disease bronchiolitis obliterans, known as “popcorn workers’ lung”⁴². Nevertheless, DMG is naturally present in drinks or food such as milk, tea, puddings, cheese, butter and yogurt^{13,20,43-45}. DMG has been reported as a natural product of fermentation and detected in wine and beer^{13,46,47}. In bacteria, plants and yeast, DMG is generated from pyruvate. Pyruvate is converted to α -acetolactate by the enzyme acetolactate synthase (ALS), followed by oxidative decarboxylation to DMG. Lastly, DMG is enzymatically reduced to acetoin and subsequently to 2,3-butanediol (**Fig. 1.8**)⁴⁸. ALS is also involved in the synthesis of the branched-chain amino acids (isoleucine, leucine and valine) in plants and microorganisms⁴⁹⁻⁵¹. However, *ilvB* acetolactate synthase-like (ILVBL, or 2-hydroxyacyl-CoA lyase 2), the mammal orthologue gene of ALS, lost its function to catalyze the branched-chain amino acids, making isoleucine, leucine and valine essential nutrients for mammals.

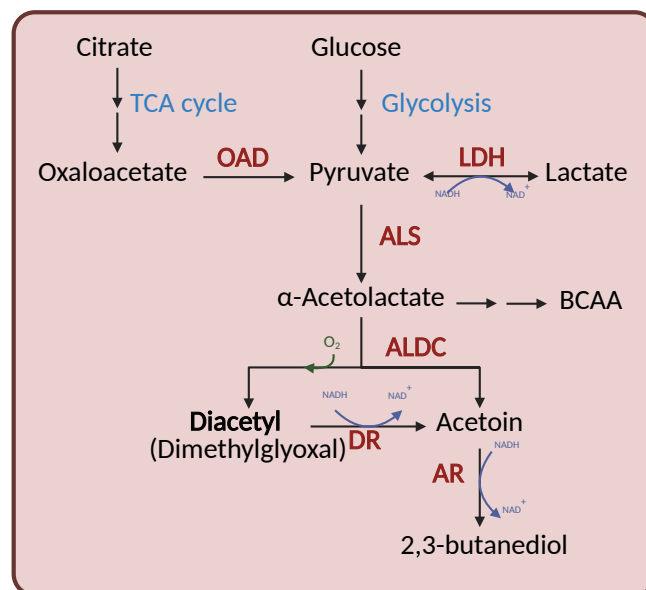


Fig. 1.8 | Schematic illustration of the dimethylglyoxal metabolic pathway in (lactic acid) bacteria.

The Illustration was created with Biorender.com and adapted after Tian, H., *et al.*, 2022⁵²; Lerm, E., *et al.*, 2010⁵³; and Yu, S., Zheng, B., Chen, Z., *et al.*, 2021⁵¹. TCA = tricarboxylic acid, OAD = oxaloacetate decarboxylase, LDH = lactate dehydrogenase, ALS: acetolactate synthase, ALDC = acetolactate decarboxylase, DR = diacetyl reductase, AR = acetoin reductase.

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Recently, DMG has been recognized as an endogenous product of pyruvate metabolism in mice^{54,55}. So far, ILVBL has not been investigated in terms of its role in the formation of DMG in mammals. However, recent studies showed that ILVBL is located in the endoplasmic reticulum and involved in the α -oxidation of 2-hydroxy fatty acids to odd-chain fatty acids in sphingolipids in mammals^{56,57}. So far, DMG has not been associated with diabetes or hyperglycemic conditions. Only recently, Rhein *et al.* found higher plasma and brain DMG concentrations in type-1 diabetic mice^{54,55}.

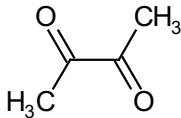


Fig. 1.9 | Dimethylglyoxal

The molecule structure was created by ChemSketch.

1.3 Diabetes mellitus

Diabetes mellitus has been recognized as a disease since antiquity. Based on the high production of urine and the quick passage of water through the body, ancient Greeks coined the term “diabetes” which means “to pass through” to describe this abnormality⁵⁸. Further, the term “mellitus” means “honey”, which refers to the glucose surplus in the urine. In 1889, Minkowski and von Mering, two German physiologists, associated diabetes mellitus with the pancreas because the removal of a dog’s pancreas caused polyuria and higher glucose concentrations in the urine⁵⁹. In 2022, around 830 million people had diabetes and its prevalence has rapidly increased in low- and middle-income countries compared to high-income countries⁶⁰. Diabetes was the 8th leading cause of death in the world in 2021, and the number of deaths almost doubled since 2000⁶¹.

Diabetes mellitus is a chronic disease characterized by high blood glucose levels and is caused by impaired insulin secretion or insulin activity. Insulin is a hormone produced by β -cells of the islets of Langerhans located in the pancreas, and it is generated from proinsulin. After crossing the membrane of the endoplasmic reticulum, proinsulin is converted into insulin, a stable prohormone due to the generation of intramolecular disulfide bridges. Subsequently, the inactive proinsulin is converted to insulin due to the action of prohormone convertases PC2 and PC3 (**Fig. 1.10**)^{62,63}. Insulin is a polypeptide hormone and comprises 51 amino acids with a total molecular weight of 5808 g/mol⁶⁴. In healthy conditions, insulin activates the insulin receptor, a transmembrane receptor tyrosine kinase expressed in adipose tissue, skeletal muscle and other tissues. Insulin receptor activation leads to phosphorylation and activation of the insulin receptor substrate (IRS-1). Then, phosphatidylinositol 3-kinase (PI3K) is activated by phosphorylated IRS-1, inducing the conversion of phosphatidylinositol-4,5-bisphosphate (PIP2) to phosphatidylinositol-3,4,5-bisphosphate (PIP3) and the consequent phosphorylation of protein kinase B (PKB or AKT). The PKB activation leads to the

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release and translocation of glucose transporter type 4 (GLUT4) from intracellular vesicles to the cell membrane (**Fig. 1.11**)^{65,66}. Thus, GLUT4 allows the uptake of glucose in adipose and striated tissue.

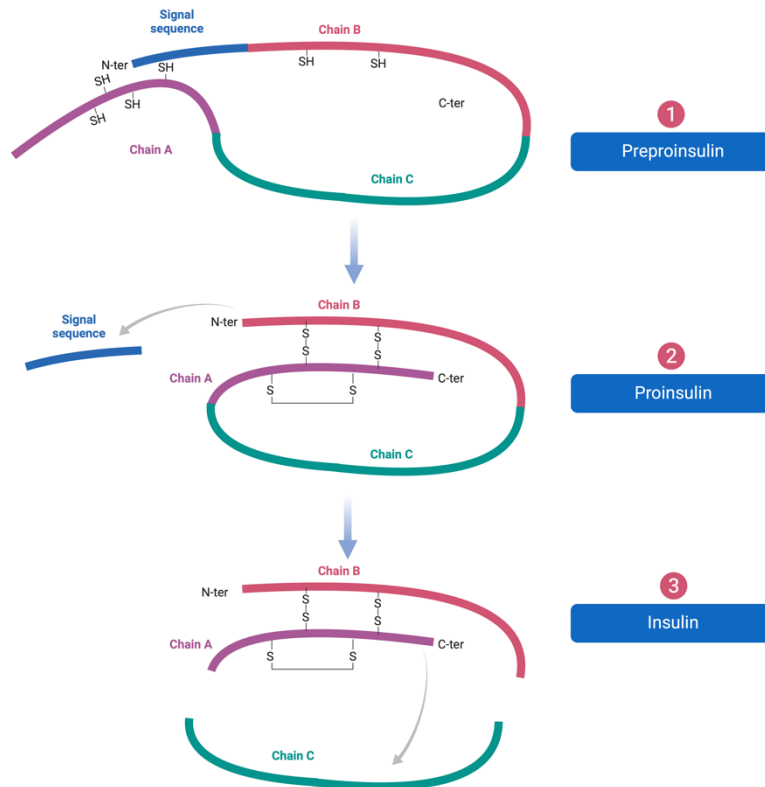


Fig. 1.10 | Schematic illustration of the generation of insulin from preproinsulin.

The illustration was modified after a template with Biorender.com.

The brain, nerve and blood cells take up glucose without insulin mediation⁶⁷. In particular, glucose transporters GLUT1 and GLUT3 are activated independently of insulin concentrations. GLUT 1 is mainly expressed in brain endothelial cells, kidneys, and placenta, and it transports glucose through the blood-brain barrier, whereas GLUT3 is primarily expressed in neurons^{68,69}. Thus, peripheral hyperglycemic conditions increase intracellular glucose concentrations in neurons and brain endothelial cells^{70,71}. Although neurons metabolize glucose by glycolysis, they also take up extracellular lactate generated from glucose in glial cells^{72,73}. In particular, monocarboxylate transporter (MCT)-1 is the carrier of lactate release in the extracellular space, while MCT-2 catalyzes lactate uptake in neurons (**Fig. 1.12**)⁷⁴. According to the World Health Organization (WHO) guidelines, hyperglycemic conditions are characterized by fasting blood glucose concentrations higher than 126 mg/dl (7 mmol/l) on two separate tests⁷⁵. Hyperglycemic conditions can also be diagnosed based on the concentration of glycated hemoglobin (HbA_{1c} > 6.4 %) or by an oral glucose tolerance test (fasting plasma glucose concentrations > 200 mg/dl or 11.1 mM, 2 hours after oral glucose uptake)^{76,77}.

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Diabetes mellitus can be classified into two categories: type-1 and type-2 diabetes. Type-1 diabetes is an autoimmune disease concomitant with the destruction of pancreatic β -cells⁷⁸. The loss of β -cells leads to insulin deficiency and the consequent impediment of GLUT4 release and translocation to the cell membrane (**Fig. 1.11**). Thus, insulin scarcity causes hyperglycemic conditions in the extracellular space. Type-1 diabetes can be diagnosed at any age, with the highest peak of diagnosis during childhood⁷⁹. Patients with type-1 diabetes show a symptomatic picture based on polydipsia, polyuria, higher production of ketone bodies (ketoacidosis) and weight-loss^{78,80,81}. Type-1 diabetes-related symptoms and complications can be attenuated by the treatment with exogenous insulin. In addition, diet management and physical activity could improve the management of type-1 diabetes⁷⁸.

Type-2 diabetes is a chronic disease characterized by insulin resistance (**Fig. 1.11**), partial dysfunction of β -cells and hyperglycemic conditions^{82,83}. Similar to the type-1 diabetic symptoms, type-2 diabetes causes polydipsia, fatigue and polyuria⁸⁴. Type-2 diabetes is related to family history and environmental factors such as a diet rich in sugars and fat, tobacco use and physical inactivity⁸⁵. Thus, obesity is a risk factor for type-2 diabetes, making lifestyle management an important role in the prevention of type-2 diabetes development^{86,87}. Moreover, pharmaceutical intervention can prevent or manage type-2 diabetes. For example, metformin, one of the most common type-2 diabetic drugs, was able to reduce fasting glucose concentrations in plasma and HbA1c values in metformin-treated compared to placebo-treated patients with type-2 diabetes⁸⁸.

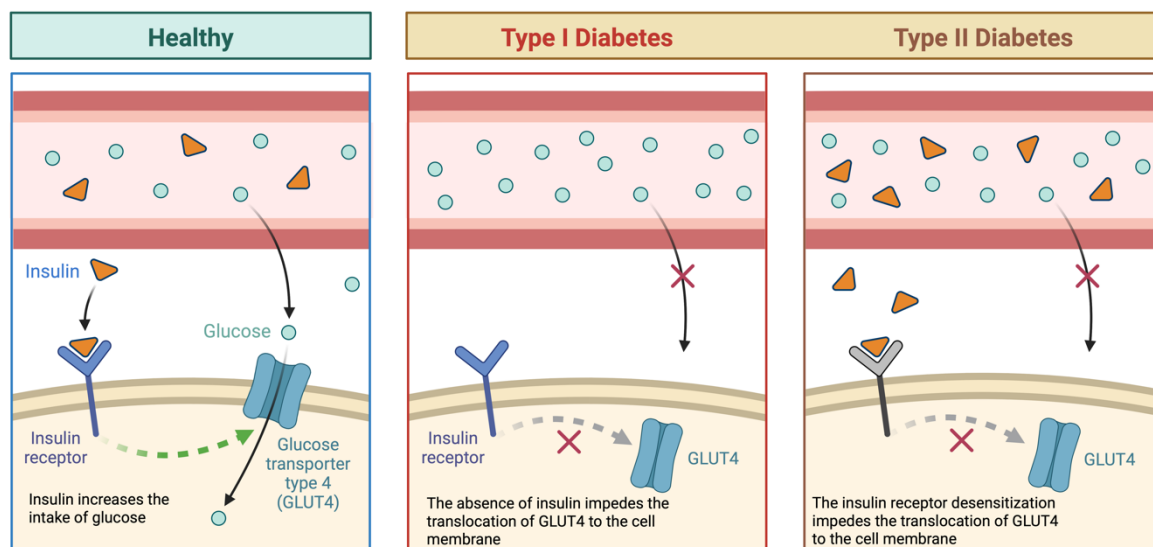


Fig. 1.11 | Schematic illustration of role of insulin in healthy and type-1 and type-2 diabetic organisms.

The illustration was modified after a template with Biorender.com.

Notably, diabetes can lead to macrovascular and microvascular long-term complications^{87,89}. Macrovascular complications of diabetes consist in cerebrovascular diseases (e.g. stroke) and

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peripheral vascular diseases^{87,89}. Diabetic microvascular complications comprise neuropathy, retinopathy and nephropathy^{87,90}. In both macro- and microvasculature, protein glycation and AGE formation by α -dicarbonyls causes alteration of normal protein functions, such as enzymatic activity alteration or glycation of low-density lipoproteins (LDLs) involved in diabetic atherosclerosis^{91,92}. Furthermore, collagen glycation caused by α -dicarbonyls worsened the arterial wall features in type-1 diabetic rats⁹³. Generally, several studies showed that diabetic and hyperglycemic conditions increased levels of glycated amino acids in experimental animal models of type-1 diabetes⁹⁴⁻⁹⁶. In particular, upregulation of glycated amino acids was found in peripheral nerves in diabetic animals and patients, suggesting the important role of these adducts in the development of diabetic neuropathy^{96,97}.

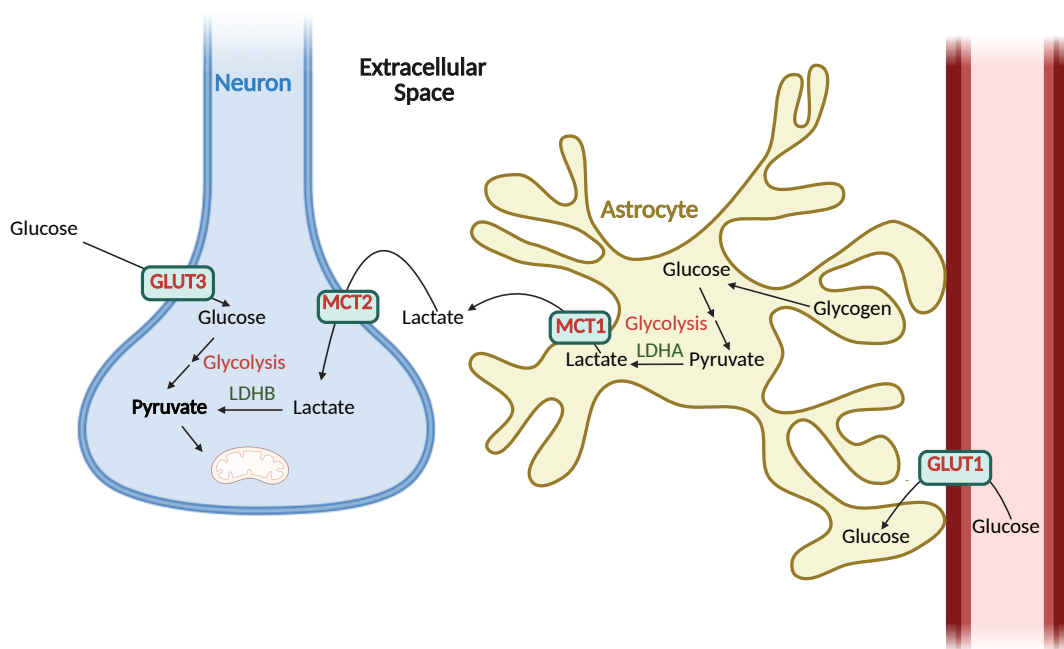


Fig. 1.12 | Schematic illustration of neuron-astrocyte lactate shuttle and lactate consumption in neurons.

The illustration was created with Biorender.com and adapted after Allaman, I., *et al.*, 2015⁹⁸; and Newington, J., T., *et al.*, 2013⁹⁹. GLUT = translocating glucose transporter type, LDH = lactate dehydrogenase, MCT = monocarboxylate transporter.

Previous studies showed that AGEs induced apoptosis in rat neuronal and Schwann cells by interacting with the receptor for AGEs (RAGE), indicating that AGEs could cause diabetic neuropathy through demyelination^{100,101}. RAGE is also expressed in endothelial cells, whose overexpression negatively affects the endothelial membrane repair¹⁰². Moreover, the binding of AGEs with RAGE induces the activation of the nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B) cascade, causing oxidative stress and overexpression of proinflammatory cytokines such as interleukin-1 α and tumor necrosis factor- α (TNF) in endothelial cells and activated (M1) macrophages¹⁰³⁻¹⁰⁶. Furthermore,

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RAGE is expressed in astrocytes and is associated with the neurodegenerative Huntington's disease by NF- κ B translocation in astrocytic nuclei¹⁰⁷.

Therapeutic strategies can decrease glycation and AGE generation, reducing the development of diabetic complications. A British study found that acetylsalicylic acid can prevent cataract in type-1 diabetic mice, suggesting that acetylsalicylic acid can reduce the protein glycation by acetylation of amino groups¹⁰⁸. Moreover, pimagedine (also called aminoguanidine) is a relevant drug in diabetic complications. This molecule can interact with 3-DG and Gx, inhibiting the Maillard reaction and preventing the generation of AGEs^{109,110}. Moreover, MG and DMG also interact with pimagedine *in vitro*^{109,111,112}. However, pimagedine is an investigational drug since the drug approval process was stopped during clinical trials¹⁰⁹.

1.4 Ischemic stroke

Stroke is the second leading cause of death in the world, with the highest incidence in East Asia and East Europe¹¹³. Stroke can be distinguished in hemorrhagic and ischemic stroke. Hemorrhagic stroke is caused by the rupture of a brain blood vessel and consequent bleeding¹¹⁴. However, the majority of strokes globally are classified as ischemic stroke, which consists of an impairment of the blood flow in the brain^{113,115}. While age, sex and family history are unmodifiable risk factors, diabetes mellitus, hypertension, physical activity, depression, tobacco and alcohol consumption, and chronic inflammation are modifiable risk factors which can be controlled by targeted interventions¹¹⁶. Notably, hyperglycemic conditions were also found in patients without diabetes after ischemic stroke^{117,118}. Stress-induced hyperglycemia is caused by increased gluconeogenesis and insulin resistance by the action of several hormones and cytokines. For example, a Danish prospective study showed a positive association between serum cortisol levels and acute stroke injury¹¹⁹. Due to the established correlation between cortisol and blood glucose levels by the upregulation of gluconeogenesis, this study suggested that ischemic stroke induces hypothalamic-pituitary-adrenal axis activation and the consequent hyperglycemia in patients without diabetes¹¹⁹. Moreover, the α -adrenergic agonist epinephrine and other catecholamines augment gluconeogenesis in the liver and consequently blood glucose concentrations¹²⁰. Furthermore, catecholamines increase glucagon secretion by the agonistic interaction with β -adrenergic receptors, inducing the increase of blood glucose levels by glycogenolysis in the liver¹²¹.

Ischemic stroke triggers a cascade, which consists of a series of biochemical reactions potentially leading to neuronal death¹²². Local hypoxic conditions result from the tissue's lack of oxygen due to the low blood supply. Under hypoxia, the hypoxia-inducible factor (HIF)-1 α protein is stabilized based on the inactivation of prolyl hydroxylase¹²³. HIF-1 is a transcription factor comprising HIF-1 α and HIF-

Introduction

1 β subunits¹²⁴. In particular, HIF-1 α increases the expression of the pyruvate dehydrogenase kinase 1 (PDK1), an enzyme that causes the downregulation of pyruvate dehydrogenase (PDH)^{125,126}. PDH is the enzyme that catalyzes the generation of pyruvate to acetyl-CoA. Thus, the inhibition of this gene leads to the downregulation of the TCA cycle. Under these conditions, glycolysis becomes the primary ATP source, generating a significantly lower chemical energy than during physoxia¹²⁷. Moreover, hypoxia and lower energy generation cause the increase of ROS and the consequent damage to cell membranes^{122,128,129}.

Furthermore, the decreased energy production also causes ionic pump damage, leading to the dysregulation of ionic balance with extracellular release of potassium ions (K⁺) and intracellular accumulation of sodium ions (Na⁺)^{122,130}. In addition, ischemia stimulates the synaptic release of glutamate, increasing the activation of α -amino-3-hydroxy-5-methyl-4-isoxazole propionic acid (AMPA) and *N*-methyl-D-aspartate (NMDA) receptors. The activation of AMPA and NMDA receptors leads to membrane depolarization, causing the increase of intracellular calcium ions (Ca²⁺), inducing excitotoxicity^{122,130}. The Ca²⁺ accumulation leads to the stimulation of ROS, phospholipases and proteases¹³¹. Phospholipases catalyze the hydrolysis of phospholipids to fatty acids. Thus, higher activity of phospholipases leads to cell membrane damage since it mainly consists of phospholipids. In particular, phospholipase A2 generates arachidonic acid, which is metabolized to prostaglandins (PG) by COX-1 (or PTGS1) or COX2 (PTGS2) or to leukotrienes in inflammatory cells by the 5-lipoxygenase pathway^{132,133}. Prostaglandins and leukotrienes are eicosanoids involved in inflammation with PGE₂ being one of the most active prostaglandins involved in pain, edema and vasodilatation¹³². On the other hand, Ca²⁺-dependent protease overactivation may also damage the cell membrane by Ca²⁺-dependent matrix metalloproteinases - proteases involved in the degradation of extracellular membranes^{132,134}. Moreover, intracellular Ca²⁺ accumulation stimulates nitric oxide synthases (NOS), an enzyme class that catalyzes the generation of citrulline and nitric oxide (NO) from L-arginine^{135,136}. The interaction of free radicals (\cdot NO) with superoxide (\cdot O₂⁻) generates peroxynitrite (\cdot OONO), a reactive nitrogen species (RNS)¹³⁶. RNS lead to lipid peroxidation, deoxyribonucleic acid (DNA) damage and cell apoptosis^{137,138}. Consequently, ischemic-induced upregulation of ROS and RNS, proinflammatory molecules, and matrix metalloproteinases causes blood-brain barrier (BBB) damage¹³⁴. The BBB is a selective semi-permeable and protective membrane comprising endothelial cells, microglial cells, pericytes and astrocytic end-feet^{139,140}. The BBB plays a critical metabolic and physical role in protecting the central nervous system (CNS) from neurotoxic molecules^{140,141}. In particular, occludin and claudins are tight junction proteins between adjacent endothelial cells and are crucial for the protective role of the BBB¹⁴². Thus, BBB damage leads to neuroinflammation and cerebral edema and worsens the cognitive impairment prognosis^{143,144}.

1.5 Liquid chromatography – tandem mass spectrometry

During this doctoral research, derivatized α -dicarbonyls and glycated amino acids were investigated using liquid chromatography coupled tandem mass spectrometry (LC-MS²). The combination of liquid chromatography with mass spectrometry allows the identification of specific analytes in a complex mixture. Liquid chromatography (LC) and mass spectrometry (MS) are not directly linked due to their incompatibilities, such as the necessity of MS to analyze gas-phase ions and different pressures between LC and MS systems. To solve this problem, liquid chromatography and mass spectrometry are connected by an interface.

1.5.1 Liquid chromatography

Chromatography is a physical technique that separates a mixture into singular components based on their distribution between the stationary and mobile phase¹⁴⁵. The stationary phase may be a solid, liquid or gel. The mobile phase moves in a clear direction and may be a liquid, gas or a supercritical fluid¹⁴⁵. Thus, liquid chromatography is a physical separation technique characterized by a liquid mobile phase. High-performance liquid chromatography (HPLC, previously an acronym for high-pressure liquid chromatography) is characterized by good chromatographic resolution and high pressure (up to 400 bar)¹⁴⁶. These conditions allow a constant flow rate and a reproducible and robust chromatographic process¹⁴⁶. The HPLC system could be illustrated with the following primary apparatus (**Fig. 1.13**):

1. **Mobile phase reservoirs:** An isocratic elution means that the eluent composition stays constant during the chromatographic separation. On the other hand, a gradient elution implies that the mobile phase composition changes gradually or continuously during the elution. Eluents can be distinguished in polar (e.g. water or methanol) or non-polar (e.g. acetonitrile). This is crucial for a proper analyte separation during the elution in this study. Furthermore, eluents can be classified as organic or inorganic. Generally, the inorganic solvent water is mainly used because of its high polarity, safety advantages and costs. In contrast, organic solvents (e.g. methanol) can be preferred to water due to their better efficiency in the electrospray ionization (ESI) system, based on their faster evaporation and lower surface tension¹⁴⁷.
2. **Pump:** This apparatus provides a stable and controlled flow rate to the separation system and the interface^{145,146}.
3. **Injector:** This device introduces the liquid sample into the mobile phase. The injector is a crucial device to ensure precision and accuracy. Air bubbles must not be present in the sample, and an internal standard can reduce inaccuracy problems (e.g., matrix effects)¹⁴⁶. An internal standard is a compound chemically and physically similar to the analytes of interest and added to the

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sample with a known concentration. For MS detection, an isotopically labeled form of the analyte is the ideal internal standard because it does not occur naturally, has a different mass-to-charge ratio (m/z) and shows very similar chemical behavior.

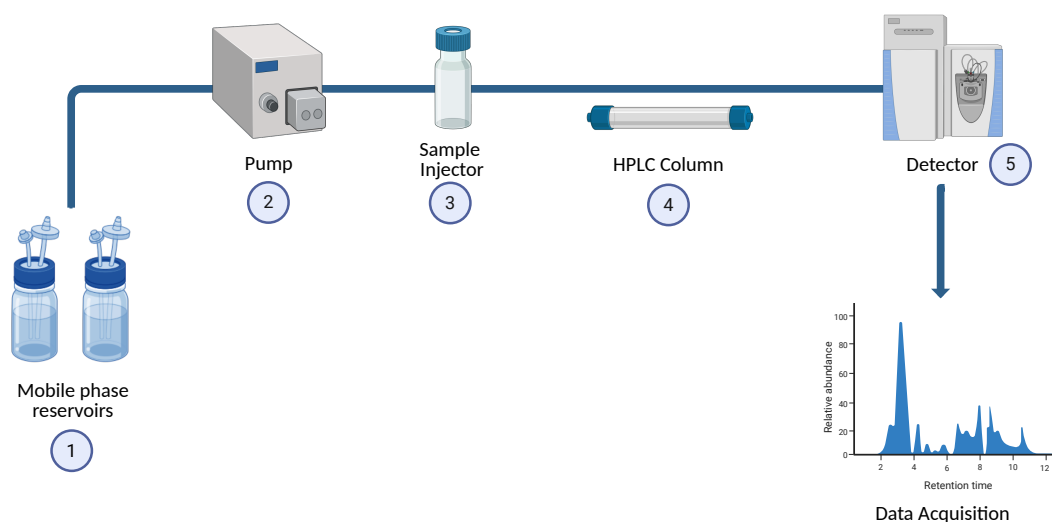


Fig. 1.13 | Schematic illustration of high-performance liquid chromatography (HPLC) system.

The illustration was modified after a template (Eunice Huang) with Biorender.com.

- Stationary phase:** Reverse-phase chromatography is the most used elution procedure in HPLC. Here, the mobile phase is more polar than the stationary phase¹⁴⁵. The most popular stationary phase is the C18 column, characterized by octadecyl alkyl groups bonded to the silica material. In normal-phase chromatography, the stationary phase is more polar than the mobile phase.
- Detector:** This apparatus measures the change in the eluent composition based on the physical (e.g., absorption wavelength of the analyte in an ultraviolet detector) or chemical (e.g., m/z of analyte in an MS detector) characteristics¹⁴⁵.

For LC-MS analysis, LC is used prior to MS detection because this technique allows the separation of molecules based on their polarity, reducing the mixture's complexity (e.g. reducing matrix effect) and contributing to the identification of analytes with the same molecular weight based on different retention times.

1.5.2 Electrospray ionization

As previously mentioned, LC and MS are linked through an interface. ESI is a soft ionization technique that transforms analytes into gas-phase ions to allow their detection with the mass spectrometer¹⁴⁸. In contrast to other interfaces (e.g. electron ionization, EI), ESI can ionize thermally labile molecules, avoiding degradation and fragmentation. This passage occurs at atmospheric pressure^{146,149}.

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Mechanistically, the eluent is introduced in the ionization chamber by a metal capillary with a high voltage (e.g. + 3-4 kV for positive ionization, **Fig. 1.14**). The electric field induces the generation of aerosol composed of highly charged droplets. The positive or negative charges are generated from the oxidation (positive ion mode) or reduction (negative ion mode) of solvent molecules by redox reactions¹⁵⁰. The nebulization is improved by the coaxial sheath nitrogen (N₂) gas¹⁵⁰. Moreover, N₂ supports the decrease of charged droplet size by solvent evaporation¹⁵⁰. Solvent evaporation causes the increase of the charge density of the droplets up to the Rayleigh limit when the Coulomb repulsion is greater than the droplet surface tension. Thus, Coulomb fission (or explosion) occurs, leading to smaller droplets. Solvent evaporation and Coulomb fission occur several times until analytes are ejected from the droplets as gas-phase ions before entering the mass spectrometer¹⁵⁰.

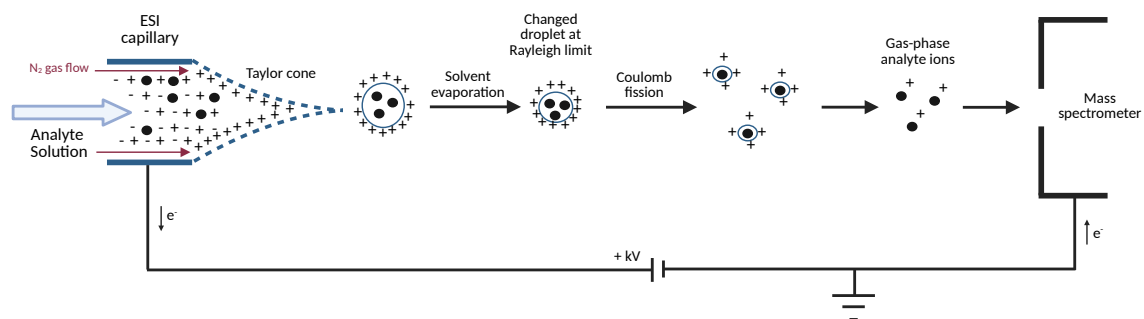


Fig. 1.14 | Schematic illustration of the electrospray ionization (ESI) mechanism in positive mode.

The illustration was modified after a template (Sabitri Lamichhane) with Biorender.com and adapted after Banerjee, S., and Mazumdar, S., 2012¹⁵⁰; and Konermann, L., *et al.*, 2013¹⁴⁸. N₂ = molecular nitrogen.

1.5.3 Mass spectrometry

After ionization, molecules are detected by the mass spectrometer. Analytes are characterized based on their mass to charge ratio (m/z) and physical-chemical properties¹⁵¹. In particular, MS² provides additional identification confidence based on the fragmentation of the analyte of interest.

The resolution (R) is the parameter related to the ability to differentiate between ions with very similar m/z ¹⁴⁶.

$$R = \frac{\text{observed } m/z}{\Delta m/z}$$

In this study, we detected derivatized α -dicarbonyls and glycosylated amino acids with a Thermo Scientific™ TSQ Endura™ triple quadrupole mass spectrometer or Thermo Scientific™ Q-Exactive™ quadrupole-orbitrap™ hybrid high-resolution mass spectrometer. The TSQ Endura ensures high

Introduction

sensitivity and robustness, whereas the high resolution of Q-Exactive allows the identification of ^{13}C -labeled α -dicarbonyls.

- The TSQ Endura triple quadrupole mass spectrometer is a tandem mass spectrometer based on three quadrupoles in series (**Fig. 1.15**). The first (Q1) and third (Q3) quadrupoles are mass analyzers and detect the precursor and product mass, respectively. The second quadrupole (Q2) is used as collision cell, where the precursor ion is fragmented based on the collision with an inert gas (collision-induced dissociation, CID). Multiple reaction monitoring (MRM) is used to detect specific product ions originating from a specific precursor ion. This Q1 to Q3 mass selection is called a mass transition¹⁵¹. Lastly, product ions collide with the detector, generating an electric current detected by a voltmeter¹⁵².

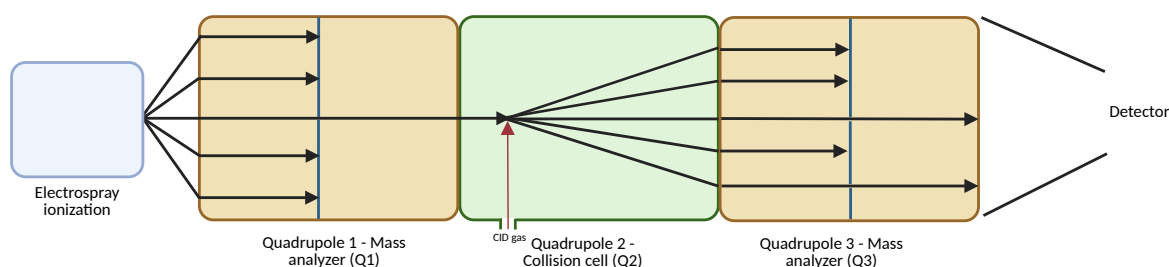


Fig. 1.15 | Schematic illustration of the scan on a triple quadrupole mass spectrometer (MS).

The illustration was modified with Biorender.com after Ardrey, 2003¹⁴⁶; and Yost, 2022¹⁵³. CID = collision-induced dissociation.

- The Q-Exactive™ quadrupole-orbitrap™ hybrid high-resolution mass spectrometer is a tandem mass spectrometer based on combining a quadrupole mass filter and the ion trap Orbitrap mass analyzer (**Fig. 1.16**)¹⁵⁴. Ions are transported from the ESI source into the instrument by a stacked ring ion guide (S-Lens)¹⁵⁵. The S-Lens guarantees high ion current with a low sample amount and low injecting times, due to the reduction of ion losses and larger entrance orifice diameters^{155,156}. Depending on the experimental settings, the quadrupole mass filter allows only the passage of ions of interest prior to their fragmentation in the high-energy collisional dissociation (HCD) collision cell¹⁵⁴. The HCD collision cell and the Orbitrap mass analyzer are separated by the C-trap, which traps the fragments and releases the fragmented ions to Orbitrap mass analyzer, when a certain ion count is achieved¹⁵⁷. Then, a strong electric field attracts the ions to the Orbitrap central electrode. Here, ions are trapped around the central electrode and axially oscillate with a frequency related to their specific m/z . Then, two outer electrodes detect the image current based on the ion axial oscillation¹⁵⁸. The image current

Introduction

from the ions is subsequently processed and converted to frequency and m/z by Fourier Transformation (FT)¹⁵⁴. A full scan with a specific m/z range allows the identification of all molecule ions without fragmentation. Parallel Reaction Monitoring (PRM) is the targeted method used to analyze the product ion spectra from preselected precursor ions with high specificity in a high-resolution mass spectrometer¹⁵⁹.

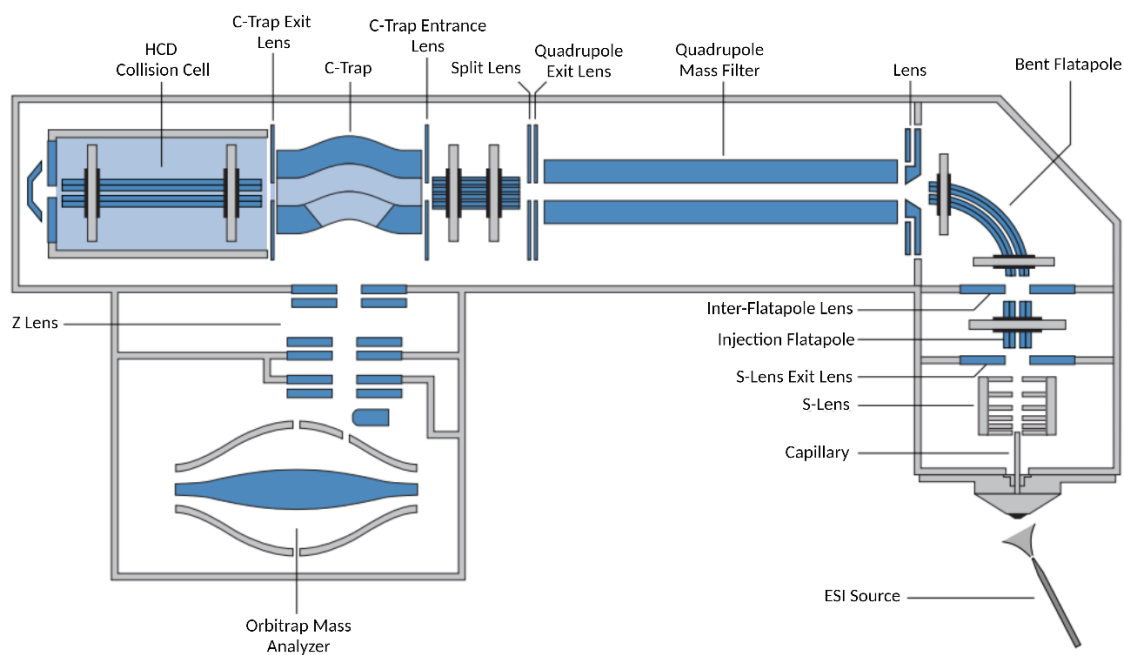


Fig. 1.16 | Schematic and detailed illustration of Q-Exactive mass spectrometer.

The illustration was modified after Michalski, A., *et al.*, 2011¹⁵⁴ with Biorender.com. HCD = high-energy collisional dissociation, S-Lens = stacked ring ion guide, ESI = electrospray ionization.

1.6. Objectives

Diabetes complications are attributed to AGEs, which are generated by the interaction of the α -dicarbonyls with proteins. They induce neuroinflammation, tissue damage and oxidative stress. So far, only 3-DG, Gx and MG have been recognized as reactive glucose metabolites and associated with diabetic complications through protein glycation. Recently, DMG has been classified as a product of cellular pyruvate metabolism and higher concentrations of this compound were found in the serum of patients with diabetes and plasma of type-1 diabetic mice^{54,55}.

The first aim of my doctoral research is a significant characterization of DMG concentrations in several mouse models under pathological conditions. Thus, concentrations of DMG are investigated in plasma, serum, and tissue homogenate of type-1 diabetic, type-2 diabetic, diet-induced obesity and experimental models of hyperglycemic and ischemic stroke.

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In bacteria, yeast and plants, DMG is generated from pyruvate by ALS⁴⁸. Thus, this doctoral thesis aims to improve the knowledge of metabolic pathways involved in the generation of DMG in mammals. In particular, the role of the mammal orthologue gene *Ivbl* is tested in DMG generation using a *Ivbl* knockout mouse model under different pathological conditions. This doctoral thesis also focuses on other characteristics of the reactive glucose metabolite DMG, such as its capacity to glycate amino acids, its ability to cross intestinal and blood-brain barriers and its effect on neuroinflammation and oxidative stress *in vitro*.

In summary, I mainly address the following points in this study:

- Investigation of the α -dicarbonyl DMG in several mouse models (type-1 diabetes, type-2 diabetes, diet-induced obesity and ischemic stroke).
- Evaluation of the role of *Ivbl* in the generation of DMG using *Ivbl* deficient mice.

Materials

2. Materials

2.1 Chemicals, reagents and enzymes

Compound	Manufacturer
[¹² C ₃]-Pyruvate (≥ 99 %)	Sigma Aldrich, St. Louis (USA)
[¹³ C ₃]-Pyruvate (99 %)	Cambridge Isotope Laboratories, Inc., Andover (USA)
[¹³ C ₄]-Dimethylglyoxal	Eptes, Vevey (Switzerland)
2-Methyl-2-butanol	Sigma Aldrich, St. Louis (USA)
2,2,2-Tribromoethanol (Avertin®)	Sigma-Aldrich, St. Louis (USA)
3-Deoxyglucosone (≥ 75 %)	Sigma Aldrich, St. Louis (USA)
Accutase® solution	Sigma Aldrich, St. Louis (USA)
Acetic 5-(chloromethyl)-2-(3,6-diacetoxy-2,7-dichloro-9H-xanthen-9-yl) benzoic anhydride (CM-H ₂ DCFDA)	Thermo Fisher Scientific, Waltham (USA)
Acetonitrile (LC-MS grade, ≥ 99.9 %)	Merck, Darmstadt (Germany)
Argon (99.999 %)	Airliquid, Düsseldorf (Germany)
Bovine serum albumin	Sigma Aldrich, St. Louis (USA)
Bradford reagent	Sigma Aldrich, St. Louis (USA)
D-(+)-Glucose (≥ 99.5 %)	Merck, Darmstadt (Germany)
D-(+)-Saccharose (or Sucrose)	Carl Roth, Karlsruhe (Germany)
D-[¹³ C ₆]-Glucose (≥ 99 %)	Sigma Aldrich, St. Louis (USA)
D4-Methylglyoxal	University Hospital Heidelberg, Heidelberg (Germany)
D8-o-Phenylendiamine (98 %)	CDN Isotopes, Pointe-Claire (Canada)
Deuterated N _ε -(1-carboxyethyl)-L-lysine	PolyPeptide Laboratories, San Diego (USA)
DharmaFECT 4 transfection reagent	Horizon Discovery Group, Cambridge (UK)
Diethylenetriaminepentaacetic acid (DETAPAC)	Sigma Aldrich, St. Louis (USA)
Diethylpyrocarbonate	Sigma-Aldrich, St. Louis (USA)
Dimethyl sulfoxide (DMSO)	Sigma Aldrich, St. Louis (USA)
Dimethylglyoxal (97 %)	Sigma Aldrich, St. Louis (USA)
Formic acid (ULC-MS grade, 99 %)	Biosolve Chimie, Dieuze (France)
Glyoxal (40 % in water)	Sigma Aldrich, St. Louis (USA)
Heparin	Ratiopharm, Ulm (Germany)
Hydrogen chloride (Hydrochloric acid fuming 37 %)	Merck, Darmstadt (Germany)
Hydrogen peroxide solution (30 %)	Merck, Darmstadt (Germany)
Isoflurane	Baxter, Deerfield (USA)
Ketamine 100 mg/ml	Dr. E. Graeb AG, Bern (Switzerland)
M-MLV reverse transcriptase (200 u/μl)	Promega, Madison (USA)
Methanol (LC-MS grade, ≥ 99.9 %, LiChrosolv®)	Merck, Darmstadt (Germany)
Methylglyoxal (40 % in water)	Sigma Aldrich, St. Louis (USA)
Nucleoside triphosphate (dNTP)	Thermo Fisher Scientific, Waltham (USA)
N _ε -(1-Carboxyethyl)-L-lysine	PolyPeptide Laboratories, San Diego (USA)
ON-TARGETplus Mouse <i>I/vbl</i> (216136) siRNA – SMARTpool	Horizon Discovery Group, Cambridge (UK)
ON-TARGETplus Non-targeting pool	Horizon Discovery Group, Cambridge (UK)

Materials

Penicillin-streptomycin	Sigma Aldrich, St. Louis (USA)
Pentobarbital sodium	Boehringer Ingelheim, Ingelheim am Rhein (Germany)
Pierce LTQ ESI negative ion calibration solution	Thermo Fisher Scientific, Waltham (USA)
Pierce LTQ Velos ESI positive ion Calibration solution	Thermo Fisher Scientific, Waltham (USA)
Platinum SYBR Green qPCR SuperMix, Invitrogen	Thermo Fisher Scientific, Waltham (USA)
Poly-D-lysine solution (1.0 mg/ml)	Sigma Aldrich, St. Louis (USA)
Random primers	Promega, Madison (USA)
Ringer's solution	Berlin-Chemie, Berlin (Germany)
RNasin® ribonuclease inhibitor (40 U/μl)	Promega, Madison (USA)
Saline solution	Fresenius Kabi, Bad Homburg vor der Höhe (Germany)
Streptozotocin (≥ 98 %)	Sigma Aldrich, St. Louis (USA)
Tri-sodium citrate dihydrate	Fisher Scientific International, Inc., Pittsburgh (USA)
Trichloroacetic acid (≥ 99 %)	Sigma Aldrich, St. Louis (USA)
Trypsin / EDTA (0.05 % / 0.02 % in DPBS)	PAN-Biotech GmbH, Aidenbach (Germany)
Water (LC-MS grade)	Merck, Darmstadt (Germany)
Xylazine (Rompun®) 2 %	Bayer Vital GmbH, Leverkusen (Germany)

2.2 Buffers and media

Buffer or medium	Manufacturer
Dulbecco's Modified Eagle's Medium (DMEM)	PAN-Biotech GmbH, Aidenbach (Germany)
Dulbecco's Phosphate-buffered saline (DPBS)	Biowest, Nuaille (France)
Fetal Calf Serum (FCS)	Sigma Aldrich, St. Louis (USA)
Gibco™ DMEM, no glucose	Fisher Scientific International, Inc., Pittsburgh (USA)
Gibco™ Opti-MEM™	Fisher Scientific International, Inc., Pittsburgh (USA)
Mouse Moloney murine leukemia virus (M-MLV) buffer	Promega, Madison (USA)
Roswell Park Memorial Institute (RPMI) 1640	Fisher Scientific International, Inc., Pittsburgh (USA)

2.3 Instruments

Instrument	Specification	Manufacturer
Blender	Bullet Blender®, Storm 24	Next Advance, Inc., Troy (USA)
Blood glucose meters	Ascensia Elite XL ACCU-CHECK®, Guide me	Roche Diagnostic, Basel (Switzerland) Roche Diagnostic, Basel (Switzerland)
Cell culture incubators	New Brunswick™ Galaxy® 170 S MIDI 40 10-16679	Eppendorf, Hamburg (Germany) Thermo Fisher Scientific, Waltham (USA) BINDER GmbH, Tuttlingen (Germany)

Materials

Centrifuges	5430 R MIKRO 220R	Eppendorf, Hamburg (Germany) Hettich, Tuttlingen (Germany)
Cryotome	CM3050 S	Leica Biosystems, Wetzlar (Germany)
Electro-coagulator	ICC 50	Erbe Elektromedizin GmbH, Tübingen (Germany)
Freezers	Mediline (- 20 °C) Comfort NoFrost (- 20 °C) HFU T SERIES (- 80 °C)	Liebherr, Bulle (Switzerland) Liebherr, Bulle (Switzerland) Thermo Fisher Scientific, Waltham (USA)
Fridges	Mediline (+ 4 °C) Electronic (+ 4 °C)	Liebherr, Bulle (Switzerland) Bosch, Gerlingen (Germany)
Fume extraction plant	SAFE 2020	Thermo Fisher Scientific, Waltham (USA)
Heat sterilizer	2712	Köttermann®, Ütze (Germany)
High performance liquid chromatography	Dionex Ultimate 3000	Thermo Fisher Scientific, Waltham (USA)
Hot-air sterilizer	Köttermann® 2712	Köttermann GmbH, Uetze (Germany)
Ion source	Heated-electrospray ionization (HESI-II) probe	Thermo Fisher Scientific, Waltham (USA)
Mass spectrometers	TSQ Endura™ Q-Exactive™ Hybrid Quadrupole-Orbitrap™	Thermo Fisher Scientific, Waltham (USA) Thermo Fisher Scientific, Waltham (USA)
Microscope	CK2	Olympus, Tokyo (Japan)
Mini centrifuge	Sprout®	Heathrow Scientific, Vernon Hills (USA)
MS syringe	1750RNR 500 µl	Hamilton Company, Reno (USA)
Multipette®	E3X	Eppendorf, Hamburg (Germany)
Physiological cell culture workstation	InvivoO ₂	Baker HQ, Sanford (USA)
Pipette pump	Pipetus®	Hirschmann® Laborgeräte GmbH & Co. KG, Eberstadt (Germany)
Pipettes	Research® plus (10 µl, 100 µl, 200 µl, 1000 µl, 5 ml)	Eppendorf, Hamburg (Germany)
Plate reader	CLARIOstar	BMG Labtech, Ortenberg (Germany)
qPCR cycler	LightCycler® 96	Roche, Basel (Switzerland)
Rotator	Intelli-Mixer RM-2L	LTF – Labortechnik, Wasserburg am Bodensee (Germany)
Scales	ENTRIS® precision balance (323I-1S) ENTRIS® analytical balance (124I-1S)	Sartorius AG, Göttingen (Germany) Sartorius AG, Göttingen (Germany)
Sonicator	SONOREX DIGIPLUS DL 514 BH	BANDELIN electronic GmbH & Co. KG, Berlin (Germany)
Spectrophotometer	NanoDrop 2000®	Thermo Fisher Scientific, Waltham (USA)
Stereomicroscope	SM33	Helmut Hund GmbH, Wetzlar (Germany)
Temperature control module	TKM-0904	FMI (Föhr Medical Instruments GmbH), Seeheim-Jugenheim (Germany)
Thermomixers	C Compact 5436	Eppendorf, Hamburg (Germany) Eppendorf, Hamburg (Germany) Eppendorf, Hamburg (Germany)
Vortex mixers	REAX 2000	Heidolph, Schwabach (Germany)

Materials

	REAX top Reamix 2789	Heidolph, Schwabach (Germany) Glaswarenfabrik Karl Hecht GmbH & Co. KG, Sondheim vor der Rhön (Germany)
	Vortex-Genie® 2	Scientific Industries, Inc., Bohemia (USA)
Water bath	VWB2	VWR International, Radnor (USA)
Water purification system	Milli-Q® Integral	MilliporeSigma, Burlington (USA)

2.4 Software

Name	Version	Manufacturer
Adobe Acrobat Pro	2024.005.20320	Adobe Inc., San Jose (USA)
Adobe Illustrator	29.2	Adobe Inc., San Jose (USA)
Adobe Photoshop	2024	Adobe Inc., San Jose (USA)
BioRender	-	BioRender, Toronto (Canada)
CLARIOstar data analysis	3.20 R2	BMG Labtech, Ortenberg (Germany)
CLARIOstar software	5.21 R2	BMG Labtech, Ortenberg (Germany)
FreeStyle	1.6	Thermo Fisher Scientific, Waltham (USA)
GraphPad Prism	8.0	GraphPad Software, Boston (USA)
LightCycler® 96	1.1	Roche, Basel (Switzerland)
NanoDrop 2000/2000c	1.5	Thermo Fisher Scientific, Waltham (USA)
Office365	-	Microsoft, Redmond (USA)
Thermo Xcalibur™	4.3	Thermo Fisher Scientific, Waltham (USA)

2.5 Consumables

Name	Specification	Manufacturer
Aluminum foil	LABSOLUTE®	TH. Geyer GmbH & Co. KG, Renningen (Germany)
Butterfly cannula	Safety-Multifly 21 G	Sarstedt, Nümbrecht (Germany)
Cell culture flasks	CELLSTAR® (25 cm ² , 75 cm ²)	Greiner Bio-One GmbH, Kremsmünster (Austria)
Cell culture plates	CELLSTAR® (24-well plate, 96-well plate)	Greiner Bio-One GmbH, Kremsmünster (Austria)
Conical tubes	FALCON® (15 ml, 50 ml)	Corning, Glendale (USA)

Materials

Diets	Teklad Global, 2018, 18 % Protein Rodent Diet, 2918	Inotiv Inc., Lafayette (USA)
	D12492, 60 kcal % Fat 1314	Research Diets Inc., New Brunswick (USA) Altromin Spezialfutter GmbH & Co. KG, Lage (Germany)
EDTA Tubes	Microvette [®] , CB300	Sarstedt, Nümbrecht (Germany)
Glass bottles	Fischerbrand [®]	Fisher Scientific International, Inc., Pittsburgh (USA)
	DURAN [®]	Hirschmann [®] Laborgeräte GmbH & Co. KG, Eberstadt (Germany)
	LABSOLUTE [®]	TH. Geyer GmbH & Co. KG, Renningen (Germany)
Glass vials	MRQ30 [™] 1.2 ml	Sigma Aldrich, St. Louis (USA)
Graduated cylinders	DURAN [®] (500 ml),	Hirschmann [®] Laborgeräte GmbH & Co. KG, Eberstadt (Germany)
Laboratory film	Parafilm [®]	Amcor plc, Zürich (Switzerland)
Liquid chromatography columns	CORTECS [®] T3 (2.7 µm, 100 mm x 2.1 mm)	Waters Corporations, Milford (USA)
	XBridge BEH Amide (2.5 µm, 100 mm x 2.1 mm)	Waters Corporations, Milford (USA)
Needles	Microlance [™] 3, 27G x ½", 0.4 x 13 mm	Becton, Dickinson and Company, Franklin Lakes (USA)
	Reusable Feeding Needle 24	Fine Science Tools, Vancouver (Canada)
Nitrile gloves	Peha-soft [®] Nitrile	Hartmann, Heidenheim an der Brenz (Germany)
Pasteur pipette	LABSOLUTE [®]	TH. Geyer GmbH & Co. KG, Renningen (Germany)
PCR 96-well-plate	LightCycler [®] 480 Multiwell Plate 96, white	Roche, Basel (Switzerland)
Pipette tips	epT.I.P.S. [®] Standard; 2-200 µl, 50-1000 µl; 0.1-5 ml	Eppendorf, Hamburg (Germany)
Reaction tubes	1.5 ml/2 ml Safe-Lock Tubes 1.5 ml/2 ml	Sarstedt, Nümbrecht (Germany) Eppendorf, Hamburg (Germany)
RNA purification kit	NucleoSpin [®] 96 RNA purification kit	Macherey-Nagel GmbH & Co. KG, Düren (Germany)
Scalpels	Feather disposable scalpel (No. 10, 11 and 22)	Feather, Osaka (Japan)
Sealing foil	LightCycler [®] , 480	Roche, Basel (Switzerland)
Serological pipettes	CELLSTAR [®] (5 ml, 10 ml and 25 ml)	Greiner Bio-One GmbH, Kremsmünster (Austria)

Materials

Syringes	1 ml/50 ml	Becton, Dickinson and Company, Franklin Lakes (USA)
Tissue	Precision Wipes™ ABENA®, cosmetic wipes	Kimberly-Clark Corporation, Irving (USA) ABENA A/S, Aabenraa (Denmark)
Vinyl gloves	Vinyl 2000 PF	Meditrade® GmbH, Kiefersfelden (Germany)
Zirconium oxide beads	ZrOB05 (0.5 mm)	Next Advance, Troy (USA)

3. Methods

3.1. Liquid chromatography – tandem mass spectrometry analysis

3.1.1 α -Dicarbonyls

3.1.1.1 α -Dicarbonyl extraction

α -Dicarbonyls were extracted and derivatized as previously described with some modifications^{160,161}. First, the internal standards deuterated MG (d4-MG; 200 nM; 0.2 μ l per μ l plasma or serum and 0.1 μ l per μ l tissue homogenate or cell culture supernatant) and/or [¹³C₃]-pyruvate (200 μ M; 0.2 μ l per μ l plasma and 0.1 μ l per μ l tissue homogenate or cell culture supernatant) were added to 60 μ l plasma, 60 μ l serum, 120 μ l tissue homogenate or 60 μ l cell culture supernatant. Proteins were precipitated by adding ice-cold trichloroacetic acid (TCAA; 25 % w/v, 0.4 μ l per μ l sample). Plasma or serum samples were diluted with 48 μ l LC-MS grade water, whereas tissue homogenate and cell culture supernatant samples were extracted without dilution. Samples were mixed with Vortex-Genie[®] 2 (Scientific Industries, Inc., 10 s) and a thermomixer (4 °C, 10 min, 1,000 rpm), followed by centrifugation (4 °C, 10 min, 14,000 rpm). Afterwards, the supernatant was transferred to a new Eppendorf tube, and the derivatizing agent deuterated o-phenylenediamine (d8-DB; 1 mM, 0.11 μ l per μ l plasma or serum and 0.08 μ l tissue homogenate or cell culture supernatant), freshly dissolved in hydrogen chloride (HCl)/diethylenetriaminepentaacetic acid (DETAPAC; 0.5 mM in 200 mM HCl) was added to the supernatant. Samples were incubated for 4 hours at room temperature in the dark, in order to generate quinoxalines from the interaction between the α -dicarbonyls and derivatizing agent (**Fig. 3.1**).

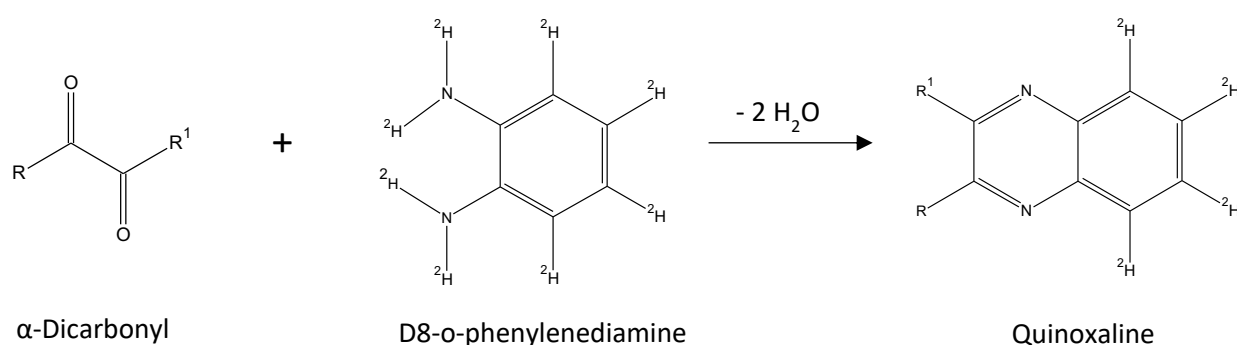


Fig. 3.1 | Illustration of the reaction between α -dicarbonyls and d8-o-phenylenediamine and relative product quinoxaline.

After derivatization, samples were centrifuged (4 °C, 10 min, 14,000 rpm), and the supernatant was transferred to glass vials for LC-MS analysis. Standard solutions were prepared as described below in **Tables 3.1, 3.2** and **3.3** and derivatized as the extracted samples.

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Table 3.1 | Standard solutions for calibration line – Plasma and serum.

DMG = dimethylglyoxal, MG = methylglyoxal, Gx = glyoxal, 3-DG = 3-deoxyglucosone, TCAA = trichloroacetic acid, d8-DB = deuterated o-phenylenediamine.

Calibration point	C0	C1	C2	C3	C4	C5	C6
Stock Solution (µl)	0	3	15	30	60	90	120
Water (LC-MS grade, µl)	120	117	105	90	60	30	0
Internal standard mix (µl)	24	24	24	24	24	24	24
TCAA (µl)	48	48	48	48	48	48	48
Water (LC-MS grade, µl)	96	96	96	96	96	96	96
1 mM d8-DB (µl)	24	24	24	24	24	24	24
Concentrations							
DMG, ¹³ C ₄ -DMG and MG (nM)	0	1.5	7.5	15	30	45	60
Gx and 3-DG (nM)	0	15	75	150	300	450	600
Pyruvate (µM)	0	15	75	150	300	450	600

Table 3.2 | Standard solutions for calibration line – Tissue homogenate.

DMG = dimethylglyoxal, MG = methylglyoxal, Gx = glyoxal, 3-DG = 3-deoxyglucosone, TCAA = trichloroacetic acid, d8-DB = deuterated o-phenylenediamine.

Calibration point	C0	C1	C2	C3	C4	C5
Stock Solution (µl)	0	3	18	45	90	180
Water (LC-MS grade, µl)	180	177	162	135	90	0
Internal standard mix (µl)	18	18	18	18	18	18
TCAA (µl)	72	72	72	72	72	72
1 mM d8-DB (µl)	18	18	18	18	18	18
Concentrations						
DMG, ¹³ C ₄ -DMG and MG (nM)	0	1	6	15	30	60
Gx and 3-DG (nM)	0	10	60	150	300	600
Pyruvate (µM)	0	10	60	150	300	600

Table 3.3 | Standard solutions for calibration line – Cell culture supernatant.

DMG = dimethylglyoxal, MG = methylglyoxal, Gx = glyoxal, 3-DG = 3-deoxyglucosone, TCAA = trichloroacetic acid, d8-DB = deuterated o-phenylenediamine.

Calibration point	C0	C1	C2	C3	C4	C5
Stock Solution (µl)	0	2	9	22.5	45	90
Water (LC-MS grade, µl)	90	88	81	67.5	45	0
Internal standard mix (µl)	9	9	9	9	9	9
TCAA (µl)	36	36	36	36	36	36
1 mM d8-DB (µl)	9	9	9	9	9	9
Concentrations						
DMG and MG (nM)	0	1.33	6	15	30	60
Gx and 3-DG (nM)	0	13.33	60	150	300	600

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3.1.1.2 α -Dicarbonyl detection

The TSQ Endura triple quadrupole mass spectrometer was used to detect the native quinoxalines, while for experiments where ^{13}C -labeled quinoxalines are expected, the Q-Exactive quadrupole-orbitrap hybrid high-resolution mass spectrometer was used. Both mass spectrometers were coupled to a Dionex Ultimate 3000 HPLC system by heated-electrospray ionization (HESI-II). Derivatized α -dicarbonyls were separated using the reverse phase C18 column Cortecs[®] T3 (100 mm x 2.1 mm x 2.7 μm) at 35 °C. For gradient elution, 0.1 % formic acid in LC-MS grade water as mobile phase A and 0.1 % formic acid in LC-MS grade acetonitrile as mobile phase B were used. An isocratic step of 5 % B with a flow rate of 0.2 ml/min was applied for 2 min. Subsequently, B was increased to 50 % in 5 min and raised to 100 % between 7 and 11 min. The column was washed in these conditions for 1 min, followed by an augmentation of the flow rate to 0.3 ml/min for 3 min. Then, B was reduced to 50 % between 15 and 17.5 min. Lastly, the re-equilibration occurred between 17.5 and 21 min back with 5 % B and 0.2 ml/min flow rate. Ion source settings are listed in **Tables 3.4, 3.5** and **3.6**. Detailed information for detecting quinoxalines is provided in **Tables 3.7** and **3.8**. MRM (TSQ-Endura) or full MS data-dependent MS² acquisition (Top 10) in combination with PRM (Q-Exactive) was applied to detect and identify the molecules in the positive ionization mode. Absolute quantification was performed with an external calibration line based on the ratio of the areas under the peaks to the internal standard. Relative quantification was based only on the ratio to the internal standard.

Table 3.4 | Ion source parameters for derivatized α -dicarbonyl method.

Ion source	
Spray voltage (kV)	4.6 (Positive mode)
Sheath gas (Arb)	30
Auxiliary gas (Arb)	10
Capillary temperature (°C)	300
Vaporized temperature (°C)	100

Table 3.5 | Further instrument setting – TSQ Endura.

Q1 = First quadrupole, Q3 = third quadrupole, CID = collision-induced dissociation.

MRM properties	
Q1 resolution (FWHM)	0.7
Q3 resolution (FWHM)	0.4
CID gas (mTorr)	2.5
Chromatographic peak width (s)	20

Table 3.6 | Further instrument setting – Q-Exactive.

IT = injection time, AGC = Automatic gain control, NCE = Normalized collision energy.

Full MS	
Resolution	70,000

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AGC target	3e ⁶
Maximum IT (ms)	200
Scan range	50 – 750 <i>m/z</i>
dd-MS²	
Resolution	17,500
AGC target	1e ⁵
Maximum IT (ms)	100
Loop count	10 (= Top 10)
Isolation window	0.4 <i>m/z</i>
Stepped NCE (eV)	10, 50, 100
dd-Settings	
Minimum IT (ms)	5e ³
Exclude isotopes	-
Dynamic exclusion (s)	20
PRM – MS²	
Resolution	17,500
AGC target	5e ⁵
Maximum IT (ms)	100
Isolation window	0.6 <i>m/z</i>
Stepped NCE (eV)	10, 50, 100

Table 3.7 | α -Dicarbonyls specifications (TSQ Endura; *m/z* of α -dicarbonyls refers to the respective d4-quinoxaline derivate).

MG = methylglyoxal, 3-DG = 3-deoxyglucosone, Gx = glyoxal, DMG = dimethylglyoxal.

Compound	Retention time (min)	Precursor ion (<i>m/z</i>)	Product ion (<i>m/z</i>)	Collision energy (V)
d4-MG	7.35	153.13	83.05	35
			99.07	35
			125.1	35
[¹³ C ₃]-Pyruvate	6.58	168.11	96.07	35
			139.11	35
3-DG	5.84	239.13	149.10	35
			161.10	35
			175.12	35
			203.11	35
Gx	6.84	135.09	81.06	35
			99.07	35
			108.07	35
MG	7.38	149.10	81.06	35
			99.07	35
			122.09	35
DMG	7.76	163.12	81.06	35
			99.07	35
			122.09	35
Pyruvate	6.58	165.09	96.07	35
			137.10	35

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Table 3.8 | α -Dicarbonyls specifications (Q-Exactive; m/z of α -dicarbonyls refers to the respective d4-quinoxaline derivate).

3-DG = 3-deoxyglucosone, Gx = glyoxal, MG = methylglyoxal, DMG = dimethylglyoxal.

Compound	^{12}C - or ^{13}C -labeled Ion (m/z)
3-DG	239.13283
3-DG (M+6)	245.15295
Gx	135.08548
Gx (M+2)	137.09220
MG	149.10113
MG (M+2)	151.10784
MG (M+3)	152.11120
DMG	163.11678
DMG (M+2)	165.12349
DMG (M+4)	167.13020
Pyruvate	165.09615
Pyruvate (M+3)	168.10616

3.1.2 Glycated amino acids

3.1.2.1 Glycated amino acid extraction

Glycated amino acids were extracted by adding 5 μl the internal standard deuterated N_ϵ -(1-carboxyethyl)-L-lysine (d4-CEL, 800 nM) to 50 μl brain homogenate sample. Then, 180 μl 0.1 % formic acid in LC-MS grade acetonitrile was added to the sample for protein precipitation. The sample was mixed with Vortex-Genie[®] 2 (Scientific Industries, Inc., 10 s), followed by incubation for 60 min at -20 °C and centrifugation (4 °C, 30 min, 14,000 rpm). 120 μl supernatant was removed and placed into a new Eppendorf tube prior to a second centrifugation (4 °C, 30 min, 14,000 rpm). Lastly, the supernatant was transferred into a glass vial for LC-MS measurements. The CEL standard solutions were prepared as described below in **Table 3.9**.

Table 3.9 | CEL standard solutions for calibration line.

CEL = N_ϵ -(1-carboxyethyl)-L-lysine

Calibration point	C0	C1	C2	C3	C4	C5	C6
800 μM CEL solution (μl)	0	7.5	22.5	30	37.5	52.5	60
Water (LC-MS grade, μl)	60	52.5	37.5	30	22.5	7.5	0
Internal standard (μl)	6	6	6	6	6	6	6
0.1 % formic acid in acetonitrile (LC-MS grade, μl)	216	216	216	216	216	216	216

3.1.2.2 Glycated amino acid detection

Glycated amino acids were detected using the Q-Exactive quadrupole-orbitrap hybrid mass spectrometer coupled to a Dionex Ultimate 3000 HPLC system by HESI-II. Glycated amino acids were

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separated using the XBridge BEH Amide column (100 mm x 2.1 cm x 2.5 μ m) at 40 °C. For gradient elution, 0.1 % formic acid in LC-MS grade water as mobile phase A and 0.1 % formic acid in LC-MS grade acetonitrile as mobile phase B were used. Initially, an isocratic step of 95 % B was applied for 3 min with a flow rate of 0.4 ml/min. Then, B was decreased to 60 % in 3 min, followed by a further decrease of B to 30 % in 6 min. During a subsequent washing step, the mobile phase was kept stable for 5 min. Lastly, B was increased to starting conditions in 2 min and held constant for 6 min. Ion source settings are listed in **Table 3.10**. Detailed information for detecting glycated amino acids is provided in **Table 3.11**. Full MS data-dependent MS² acquisition (Top 10) was applied to detect and identify the molecules in the positive ionization mode. Relative quantification of *N*_ε-3-hydroxy-2-butanone lysine (HBL) was based only on the ratio of the absolute area to the internal standard.

Table 3.10 | Ion source parameter for glycated amino acid method.

Ion source	
Spray voltage (kV)	3.5 (Positive mode)
Sheath gas (Arb)	35
Auxiliary gas (Arb)	10
Capillary temperature (°C)	300
Vaporized temperature (°C)	200
Full MS	
Resolution	70,000
AGC target	3e ⁶
Maximum IT (ms)	200
Scan range	200 – 600 <i>m/z</i>
dd-MS²	
Resolution	17,500
AGC target	1e ⁶
Maximum IT (ms)	50
Loop count	10 (= Top 10)
Isolation window	0.4 <i>m/z</i>
Stepped NCE (eV)	30
dd-Settings	
Minimum IT (ms)	5e ³
Exclude isotopes	-
Dynamic exclusion (s)	10

Table 3.11 | Glycated amino acid specifications (Q-Exactive).

CEL = *N*_ε-(1-carboxyethyl)-L-lysine, HBL = *N*_ε-3-hydroxy-2-butanone lysine.

Compound	¹²C- or ¹³C-labeled Ion (m/z)
d4-CEL	223.15959
CEL	219.13448
HBL	233.14958

Methods

3.1.3 Tissue sample preparation and protein determination

Frozen brain tissue (prefrontal cortex: 20-80 mg; hemispheres: 40-130 mg) and frozen liver tissue (50-150 mg) were dissected in the cryotome (-20 °C). The tissue piece was immediately transferred to an Eppendorf tube containing a similar volume of zirconium oxide beads and cold LC-MS grade water (300 µl, 750 µl, or 500 µl, respectively). The tissue was homogenized in a blender (Bullet Blender, 4 °C, 3 min, speed 8) and centrifuged (4 °C, 5 min, 2,000 g). The supernatant was collected in a new Eppendorf tube and diluted with LC-MS grade water to reach a protein concentration between 0.20 and 1.25 mg/ml. Protein concentration of diluted homogenate samples was determined using the Bradford assay. 5 µl standard solutions (from 10 mg/ml bovine serum album, BSA, **Table 3.12**) and samples were added to separated wells of a 96-well plate.

Table 3.12 | Standard solution for Bradford assay calibration line.

BSA = bovine serum album.

Protein content (mg/ml)	10 mg/ml BSA (µl)	LC-MS water (µl)
1.25	50	350
1	50	450

Protein content (mg/ml)	1 mg/ml BSA (µl)	LC-MS water (µl)
0.8	80	20
0.6	60	40
0.4	40	60
0.2	20	80

Then, 250 µl Bradford reagent was added to each well and incubated in the dark for 10 min. The absorbance was measured at 595 nm with a plate reader (CLARIOstar), and the protein concentration was obtained using the external calibration line.

3.2 Animal experiments

Animals were housed in groups of three to five in cages under a 12-h light/dark cycle at 23 °C. They had *ad libitum* access to food (#1314, Altromin, except high-fat diet, HFD) and water. C57BL/6 N wild-type mice were ordered from Charles River Europe. *Ilvl*^{-/-} mice (*Ilvl*^{em1(IMPC)Bay} null allele (C57BL/6 N), MGI:1351911) were kindly provided by the Knockout Mouse Phenotyping Project (KOMP2), while *Ilvl*^{+/+} mice were obtained by heterozygous breeding. Male leptin receptor-deficient (*db/db*) mice were used as model of type 2 diabetes. *db/+* or *db/db* (BKS(D)-*Lep*^{db}/JOrlRj) mice were ordered from Janvier Labs (France). Ines Stölting, Dr. Zaib Ali Shaheryar, Teresa Christina Faupel, and Ümit Özorhan, all members of the Institute of Experimental and Clinical Pharmacology and Toxicology at the University of Lübeck, conducted the following animal experiments.

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3.2.1 Type-1 diabetes mouse model

Under anesthetic conditions induced by isoflurane, male C57BL/6J, *Ilvbl^{+/+}* or *Ilvbl^{-/-}* mice were treated with 50 mg/kg streptozotocin (STZ, 12 mg/ml in 50 mM tri-sodium citrate dihydrate buffer, pH = 4.5) via intraperitoneal (i.p.) injection for 5 consecutive days. During these days, sucrose water (10 % w/v) was provided to the animals to prevent hypoglycemia. Glucose levels were evaluated on tail blood (10 μ l) using glucose test stripes (Ascensia Elite XL, Roche Diagnostics). Glucose levels were measured 2, 12 or 15 weeks after STZ injections. Mice were excluded from further analysis if blood glucose did not rise to >11.1 mM 6 weeks after STZ administration. Twelve or 15 weeks after STZ injections, mice were deeply anesthetized with Xylazine/Ketamine (24 mg/kg in 0.9 % saline solution; 200 mg/kg) or Avertin[®] (2,2,2—tribromoethanol) dissolved in 2-methyl-2-butanol (15-20 μ l/g body weight; 2.5 % v/v in saline solution), followed by an intracardial collection of whole blood in ethylenediaminetetraacetic acid (EDTA) containing tubes. After centrifugation (4 °C, 5 min, 14,000 rpm), plasma was collected and snap frozen in liquid nitrogen. Perfusion using 15-20 ml Ringer's solution containing heparin (10 IU/ml) was performed by entering a butterfly cannula into the left ventricle, while the right atrium was incised using scissors. All organ samples, including the brain, were snap frozen in liquid nitrogen and stored at -80 °C.

3.2.2 High-fat diet (HFD)

Male C57BL/6J mice were fed with a standard diet (Teklad Global, 2018, 18 % Protein Rodent Diet, irradiated, 2918, Inotiv) or HFD (D12492, 60 kcal % Fat, Research Diets, Inc.) for 12 weeks. Under fasting conditions, glucose levels were measured using glucose test stripes (ACCU-CHECK[®], Guide me, Roche Diagnostics). Mice were euthanized by decapitation, followed by a collection of whole blood from the mouse trunk in Eppendorf tubes. After centrifugation (4 °C, 15 min, 6,000 rpm), serum was collected and stored at -80 °C. Serum samples were shipped from the Department of Physiology of the University of Santiago de Compostela-Instituto de Investigación Sanitaria in Santiago de Compostela (Spain).

3.2.3 Germ-free mice

Female specific-pathogen-free (SPF) and germ-free mice were housed in gnotocages and shipped from the Zentrale Tierhaltung of the Universitätsklinikum Schleswig-Holstein in Kiel (Germany). All mouse sterility tests were negative and measured by 16S Polymerase Chain Reaction (PCR) and microbial cultures. Twelve-15-week-old mice were euthanized by cervical dislocation under anesthesia with isoflurane. Whole blood was intracardially collected in EDTA containing tubes and EDTA plasma was obtained as described before.

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3.2.4 Permanent middle cerebral artery occlusion (pMCAO)

Hyperglycemic ischemic stroke was induced by [$^{13}\text{C}_6$] glucose injection and permanent occlusion of the distal middle cerebral artery (MCAO) in female and male *Ilvbl^{+/+}* and *Ilvbl^{-/-}* mice at the age of 8-16 weeks. The mice were deeply anesthetized with an i.p. injection of pentobarbital (10 $\mu\text{l/g}$ body weight). Subsequently, saline solution (NaCl, 0.9 % w/v, 0.2 ml per mouse) or [$^{13}\text{C}_6$]-glucose solution (50 mg dissolved in 0.2 ml saline solution per mouse) was injected i.p. before sham or pMCAO surgery. Under anesthetic conditions, the mice were placed under the microscope (Helmut Hund) in right lateral recumbency. To maintain the temperature at 37 °C, the mice were placed on a heating pad. The temperature was continuously monitored using a rectal thermometer. Then, a skin incision of 2 cm was performed between the left ear and the left eye. Drops of saline solution were added to the tissue in order to keep it moist. After removing the temporal muscle and drilling a burr hole, the middle cerebral artery was occluded with a microbipolar electro-coagulator (Model ICC 50, Erbe Elektromedizin GmbH). Then, the mice were kept in the cage under the infrared lamp. For sham surgery, mice were anesthetized, and a skin incision was made, followed by skin closure with a suture. The mice were re-anesthetized 25 min after pMCAO or 50 min after sham or pMCAO using Avertin[®] (2,2,2—tribromoethanol) dissolved in 2-methyl-2-butanol (15-20 $\mu\text{l/g}$ body weight; 2.5 % v/v in saline solution), followed by an intracardial collection of whole blood. EDTA plasma was obtained as described before. Then, the mice were transcardially perfused with Ringer's solution containing heparin (10 IU/ml). Afterwards, the ipsilateral and contralateral sides of the brain were snap-frozen in liquid nitrogen, and samples were stored at -80 °C. Glucose levels were measured before the surgery, 25 min after glucose administration, and before the perfusion using glucose test stripes (Ascensia Elite XL, Roche Diagnostics). The mice were excluded from further analysis if blood glucose levels did not rise to >11.1 mM.

3.2.5 Acute and chronic dimethylglyoxal treatment of mice

To assess the intestinal absorption of DMG, a dose of 5 mg/kg [$^{13}\text{C}_4$] DMG was administered to three male C57BL/6J mice via oral gavage (250 μl), whereas control mice were treated with saline solution. Mice were sacrificed 20 min after the treatment under deeply anesthetic conditions using Xylazine/Ketamine (24 mg/kg in 0.9 % saline solution; 200 mg/kg), by an intracardial collection of blood. EDTA plasma was obtained as described before. The brain and liver were frozen in liquid nitrogen after the perfusion using 15-20 ml Ringer's solution containing heparin (10 IU/ml). Samples were stored at -80 °C. For chronic experiments, the drinking water of mice was supplemented with 500 mg/l native DMG, resulting in a dosage of approximately 100 mg/kg/day. The water was changed every two days, and the water consumption was tracked. After 15 weeks, mice were deeply anesthetized with Xylazine/Ketamine (24 mg/kg in 0.9 % saline solution; 200 mg/kg), followed by an intracardial

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collection of blood. EDTA plasma was obtained as described before. The brain was frozen in liquid nitrogen after the perfusion using 15-20 ml Ringer's solution containing heparin (10 IU/ml). Samples were stored at -80 °C.

3.3. *In vitro* experiments

In vitro experiments were performed on bEnd.3 mouse brain endothelial cells, HT-22 mouse hippocampal neuronal cells, and Hep G2 human liver cancer cells. bEnd.3 cells (ATCC, CRL-2299) are derived from BALB/c mice and immortalized via polyoma middle T antigen, whereas HT-22 cells are derived from the HT-4 cell line. Hep G2 cells are immortalized cells from an Argentinian 15-year-old Caucasian male¹⁶². The composition of used media is listed in **Table 3.13**.

Table 3.13 | Medium composition for each cell line.

Cell line	Medium composition
bEnd.3 Mouse brain endothelial cells	Dulbecco's Modified Eagle's Medium (DMEM) + 10 % Fetal Calf Serum (FCS) + 1 % penicillin-streptomycin (100 U/ml; 0.1 mg/ml)
Hep G2 Human liver cancer cells	Roswell Park Memorial Institute (RPMI) 1640 + 10 % Fetal Calf Serum (FCS) + 1 % penicillin-streptomycin (100 U/ml; 0.1 mg/ml)
HT-22 Mouse hippocampal neuronal cells	Dulbecco's Modified Eagle's Medium (DMEM) + 10 % Fetal Calf Serum (FCS) + 1 % penicillin-streptomycin (100 U/ml; 0.1 mg/ml)

The cells were split when they reached a confluence of approximately 90 %. After washing cells with 10 ml Dulbecco's phosphate buffered saline (DPBS), cells were treated with 3 ml accutase (bEnd.3 and HT-22 cells) or 2 ml trypsin (Hep G2 cells) to facilitate the cell detachment at 37 °C for 5-10 min. Then, 8 ml medium was added to the old 75 cm² flask and the subculture was transferred to a new 75 cm² flask with a dilution of 1:20, 1:10 or 1:5. During the experiments, cells were seeded with a concentration of 1 x 10⁵ cells/ml or 2 x 10⁵ cells/ml and incubated for two days to reach the proper confluence.

3.3.1 Generation of ¹³C-labeled α -dicarbonyls

bEnd.3 cells were treated with 25 mM [¹²C₆] glucose, [¹³C₆] glucose or 4 mM [¹³C₃] pyruvate in the cell culture medium for 6 hours under normoxic or hypoxic (0.1-0.6 % O₂) conditions at 37 °C. For that, native glucose, labeled glucose or labeled pyruvate were freshly dissolved in glucose-free Dulbecco's Modified Eagle's Medium (DMEM) with 10 % fetal calf serum (FCS) and penicillin-streptomycin (100 U/ml; 0.1 mg/ml). After 6 hours, medium (300 μ l) was frozen in liquid nitrogen. Cells were washed with DPBS, and collected by adding TCAA (7.14 % w/v, 300 μ l) and detaching the cells with a cell scraper, or lysed by adding buffer RA1 as described in chapter 3.3.5. Medium and cells were stored at -80 °C.

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3.3.2 Detection of reactive oxygen species (ROS) after dimethylglyoxal treatment

Oxidative stress in bEnd.3, HT-22 and Hep G2 cells was determined using the ROS-sensitive fluorescent dye CM-H₂DCFDA. Fifty μ l dye was dissolved in 21.6 μ l sterile dimethyl sulfoxide (DMSO, 4 mM), followed by dilution of the 4 mM dye solution (20 μ l) in 20 ml DPBS (dilution 1:1000). Cells were washed with DPBS before the treatment with 4 μ M dye solution (200 μ l per well) for 30-40 min in the dark at 37 °C and 5 % CO₂. Subsequently, the dye solution was discarded, and the cells were washed with DPBS and treated with different concentrations of DMG (in DPBS containing 5 mM glucose, **Table 3.14**) for 10 min in the dark at 37 °C and 5 % CO₂.

Table 3.14 | Dilutions of DMG in 5 mM glucose in DPBS.

DMG = dimethylglyoxal, DPBS = Dulbecco's phosphate buffered saline.

<i>DMG concentration (μM)</i>	<i>500 mM DMG solution (μl)</i>	<i>5 mM glucose in DPBS (μl)</i>
500	4	3996

<i>DMG concentration (μM)</i>	<i>500 μM DMG solution (μl)</i>	<i>5 mM glucose in DPBS (μl)</i>
200	1200	1800
50	200	1800

<i>DMG concentration (μM)</i>	<i>200 μM DMG solution (μl)</i>	<i>5 mM glucose in DPBS (μl)</i>
100	500	500
20	100	900

<i>DMG concentration (μM)</i>	<i>50 μM DMG solution (μl)</i>	<i>5 mM glucose in DPBS (μl)</i>
5	100	900

The fluorescent signal was detected at 492-495 nm excitation with a 517-527 nm emission wavelength. As positive control, 10 μ M hydrogen peroxide was added simultaneously. Cell-free wells served as negative controls. HT-22 and Hep G2 cells were seeded on poly-D-lysine-coated wells for these experiments. A stock solution of poly-D-lysine (1 mg/ml) was diluted with sterile DPBS to 0.1 mg/ml (1:10). The wells were coated with 200 μ l of the diluted poly-D-lysine solution overnight at room temperature. Subsequently, the wells were washed twice with sterile DPBS and seeded with HT-22 or Hep G2 cells.

Methods

3.3.3 *Ilvbl* knockdown in bEnd.3 cells

To reduce the expression of *Ilvbl*, bEnd.3 cells were transfected with ON-TARGETplus Mouse SMARTpool of four small interfering ribonucleic acids (siRNAs, **Table 3.15**) against *Ilvbl* or with relative control (ON-TARGETplus Non-Targeting pool). The siRNA pellet (5 nmol) was resuspended in RNase-free water (diethylpyrocarbonate in milli-Q water, 1 g/l) reaching a solution concentration of 20 μ M. The solution was placed on a rotator for 30 min at room temperature, followed by a further dilution with RNase-free water to 5 μ M. To increase the efficiency of the transfection, an antibiotic-free medium (DMEM + 10 % FCS, 400 μ l) was added to the well at least 4 hours before the transfection. siRNA (5 μ M, 2.5 μ l per well) was diluted in a reduced-serum medium (Opti-MEM®; 47.5 μ l per well). The DharmaFECT 4 transfection reagent (2.5 μ l per well) was diluted in a reduced-serum medium (47.5 μ l per well). Both solutions were incubated for 5 min at room temperature. Then, the solutions were mixed, followed by 20 min of incubation at room temperature. Finally, 100 μ l transfection solution was added to each well containing 400 μ l of the antibiotic-free medium. Cells were incubated for 40 hours at 37 °C (5 % CO₂). After the transfection, cells were treated with 25 mM [¹³C₆] glucose or 4 mM [¹³C₃] pyruvate as described above. The supernatant was frozen in liquid nitrogen and stored at -80 °C.

Table 3.15 | *Ilvbl* siRNA sequences.

Ilvbl = IlvB acetolactate synthase like; siRNA = small interfering ribonucleic acid.

siRNA number	Sequence
1	GCUUAGAGCUGCCGUGGAG
2	GGUCAAGGUACUUCGUGAA
3	GGGCUGAGGAGCUUCGGAA
4	GGACCCAGAUUUCUCGAGA

3.3.4 Dimethylglyoxal treatment of HT-22 cells

Confluent HT-22 cells were treated with 0 μ M, 20 μ M, 100 μ M, 200 μ M or 500 μ M DMG (**Table 3.16**) in DMEM containing 25 mM glucose, 10 % FCS, and 1 % penicillin-streptomycin for 24 hours at 37 °C and 5 % CO₂. To avoid DMG contaminations due to its high volatility, cells were seeded in three different 24-well plates based on the DMG concentrations (First 24-well plate: 0 μ M; Second 24-well plate: 20 μ M and 100 μ M; Third 24-well plate: 200 μ M and 500 μ M) and the three 24-well plates were placed in three individual conventional incubators.

Methods

Table 3.16| Concentrations of DMG in medium.

DMG = dimethylglyoxal.

<i>DMG concentration (μM)</i>	<i>500 mM DMG solution (μl)</i>	<i>Medium (μl)</i>
500	10	9990

<i>DMG concentration (μM)</i>	<i>500 μM DMG solution (μl)</i>	<i>Medium (μl)</i>
200	2000	3000
100	1000	4000

<i>DMG concentration (μM)</i>	<i>200 μM DMG solution (μl)</i>	<i>Medium (μl)</i>
20	300	2700

3.3.5 Real-time PCR after *I/vb1* knockdown or dimethylglyoxal treatment

RNA from bEnd.3 or HT-22 cells was extracted by NucleoSpin® 96 RNA purification kit (Macherey-Nagel) at room temperature according to manufacturer's instructions. Initially, cells were washed with DPBS and lysed by adding 350 μl buffer RA1. Afterwards, the lysate was filtrated through the NucleoSpin® Filter to reduce viscosity and centrifuged for 1 min at 11,000 x *g*. After adding 350 μl ethanol (70 %) to the lysate, the cell homogenate was loaded to the NucleoSpin® Column and centrifuged for 30 s at 11,000 x *g*. Then, the salt was removed from the membrane by adding 350 μl membrane desalting buffer for a more efficient DNase digestion (15 min, room temperature). Later, the membrane was washed with 200 μl Buffer RA2 to stop the previous reaction and twice with Buffer RA3. The membrane was centrifuged for 2 min at 11,000 x *g* to let it dry, followed by the elution of RNA in 40 μl RNase-free water through centrifuging for 1 min at 11,000 x *g*. To evaluate the RNA concentration, 2 μl sample was measured by UV-VIS spectrophotometer at 260 nm. Based on the RNA concentration, samples were diluted with RNase-free water to reach a concentration of 20 ng/μl. Subsequently, RNA was converted to complementary DNA (cDNA) by reverse transcription. Master mix solution (15 μl, **Table 3.17**) containing reverse transcriptase was added to 35 μl RNA solution (700 ng), and the solution was incubated for 10 min at room temperature, followed by consecutive incubation for 90 min at 37 °C.

Table 3.17| Composition of the reverse transcription master mix solution.

Compound	Volume per 35 μl sample (μl)
Mouse Moloney murine leukemia virus (M-MLV) buffer	10
Nucleoside triphosphate (dNTP, 25 mM)	2
Random primers	1
RNasin (40 U/μl)	1
M-MLV-transcriptase	1

Methods

Then, 23 μ l SuperMix solution was added to a PCR-96-well plate. Detailed information on the composition of the SuperMix solution is provided in **Table 3.18**.

Table 3.18 | Composition of SuperMix solution.

Compound	Volume (μ l)
Platinum SYBR Green qPCR SuperMix	12.5
RNase-free water	9
Forward primer (10 pmol/ μ l)	0.75
Reverse primer (10 pmol/ μ l)	0.75

Lastly, 2 μ l cDNA sample was mixed with 23 μ l SuperMix, while 2 μ l RNase-free water was added to a well as negative control. The PCR-96-well plate was sealed with an adhesive PCR sealing foil, and after centrifugation, the PCR-96-well plate was placed in the Light Cycler. After the preincubation cycle for 10 min at 95 °C, the target cDNAs were amplified with 38 cycles (30 s at 95 °C, 30 s at 60 °C and 30 s at 72 °C), followed by a melting cycle (10 s at 95 °C, 60 s at 65 °C and 1 s at 97°C). Primers for real-time PCR are listed in **Table 3.19**. β -actin or Cyclophilin A (*Ppia*) were used as housekeeping genes for data normalization according to the $\Delta\Delta$ threshold cycle ($\Delta\Delta Ct$) method.

$$\Delta Ct = Ct(\text{gene}) - Ct(\text{Housekeeping gene})$$

$$\Delta\Delta Ct = \Delta Ct - \text{Average } \Delta Ct(\text{Control})$$

$$\text{Relative Gene mRNA Expression} = \frac{2^{-\Delta\Delta Ct}}{\text{Average } 2^{-\Delta\Delta Ct}(\text{Control})}$$

Table 3.19 | Primers for real-time PCR.

Ppia = Cyclophilin A, *Ilvbl* = IlvB acetolactate synthase like, *Pla2g4a* = Phospholipase A2 Group IVA, *Ptges* = prostaglandin E synthase, *Ptgs2* = prostaglandin-endoperoxide synthase 2, *Bim* = BCL2 Like 11.

Gene	Species	Direction	Sequence
<i>Ppia</i>	Mouse	forward	5'-AGGTCCTGGCATCTTGTCCAT-3'
		reverse	5'-GAACCGTTTGTGTTTGGTCCA-3'
β -Actin	Mouse	forward	5'-ATGGAATCCTGTGGCATCCAT-3'
		reverse	5'-TTCTGCATCCTGTCAGCAATG-3'
<i>Ilvbl</i>	Mouse	forward	5'-CCCAGGTCCAGTGTTTGTGG-3'
		reverse	5'-ACGGCAGCTCTAAGCTTGTT-3'
<i>Pla2g4a</i>	Mouse	forward	5'-GAAGGCACAGAGAAGCCTGAG-3'

Methods

<i>Ptges</i>	Mouse	reverse	5'-ATGCTGAACCGTAGGTCTGG-3'
		forward	5'-CTTGCGGACTTGGTGTCTCT-3'
<i>Ptgs2</i>	Mouse	reverse	5'-GCACTCAAAGGACGGTGGTA-3'
		forward	5'-CATCCCCTTCTGCGAAGTT-3'
<i>Bim</i>	Mouse	reverse	5'-CATGGGAGTTGGGCAGTCAT-3'
		forward	5'-ACAGAACCGCAAGCTTCCAT-3'
		reverse	5'-CAGATCTCAGGTTCTCCTGAGA-3'

3.4. Statistical analysis

Data were analyzed using GraphPad Prism 8 (GraphPad Software) with the suggestion of Dr. Sonja Binder (Rhein, S., Costalunga, R., Inderhees, J. *et al.*, 2024⁵⁵). Significance was considered if p value < 0.05. Detailed statistical information is provided in the statistical table on page 78. Parametric statistics (e.g., t-test, ANOVA) were only applied if variances were homogeneous between groups (tested by Brown-Forsythe, Levene's or F -test, depending on the statistical method used) and if data respected the Gaussian distribution of the residuals by D'Agostino-Pearson test. If the previous assumptions were not met or the sample size was small, non-parametric methods were used as described in the statistical table on page 78. Two-tailed tests were applied if not indicated otherwise. Greenhouse-Geisser correction was used in ANOVA statistics if the sphericity assumption was violated (Mauchly test). Outliers were identified by the ROUT method ($Q = 1\%$). No data points were excluded if not stated otherwise in the statistical table on page 78.

4. Results

Parts of the following results have already been published in the manuscript “The reactive pyruvate metabolite dimethylglyoxal mediates neurological consequences of diabetes” by Rhein, S., Costalunga, R., Inderhees, J. *et al.* in 2024⁵⁵.

4.1 Concentrations of the α -dicarbonyl dimethylglyoxal are elevated in diabetic mice

To measure α -dicarbonyls in plasma, serum, tissue homogenate, and cell culture supernatant and lysate, quinoxalines were generated by taking advantage of the reaction between the α -dicarbonyls and the derivatizing reagent d8-DB. As previously described in the method part, quinoxalines were detected using LC-MS². First, I measured α -dicarbonyl and pyruvate levels in the plasma of mice treated with STZ (**Fig. 4.1a**). STZ is an alkylating antineoplastic drug that induces the destruction of beta cells of the mammalian pancreas, preventing the generation and the subsequent release of insulin in the bloodstream^{163,164}. Consequently, STZ injections induced type-1 diabetes in the treated mice^{163,164,165}. For this reason, STZ treatment elevated concentrations of glucose in the blood (**Fig. 4.1b**). As expected, type-1 diabetic mice significantly drank more water compared to the control mice (**Fig. 4.1c**). As already shown in other studies, concentrations of 3-DG (2.30-fold) and MG (1.49-fold) were increased in the mouse plasma 15 weeks after the STZ injections^{166,167} (**Fig. 4.1d**). At the same time, concentrations of Gx were not significantly changed, even though there was a trend towards an increase in the STZ-treated mice (1.44-fold, **Fig. 4.1d**). Interestingly, DMG concentrations were also significantly elevated 1.36-fold in the plasma of type-1 diabetic mice compared to the control (**Fig. 4.1d**). Moreover, pyruvate concentrations were decreased 15 weeks after the STZ injections (**Fig. 4.1f**). To investigate the potential association between periphery and central nervous system, α -dicarbonyls were measured in homogenates of the prefrontal cortex. Here, only DMG was significantly elevated in the type-1 diabetic mice (1.52-fold), whereas no differences were observed in the concentrations of Gx or MG between treatments (**Fig. 4.1e**). 3-DG was not detected in the brain, probably due to the low concentrations of this metabolite in the prefrontal cortex homogenate (**Fig. 4.1e**). Further, pyruvate concentrations were unchanged between the two treatments in the brain (**Fig. 4.1g**). Based on these findings, we wanted to measure the levels of α -dicarbonyls and pyruvate in the plasma and tissue homogenates of leptin receptor-deficient *db/db* mice, an established model of type-2 diabetes¹⁶⁸. First, *db/db* mice significantly gained more weight than the heterozygous littermates *db/+* mice (**Fig. 4.2a, b**). Moreover, *db/db* mice developed hyperglycemia (**Fig. 4.2c**).

Results

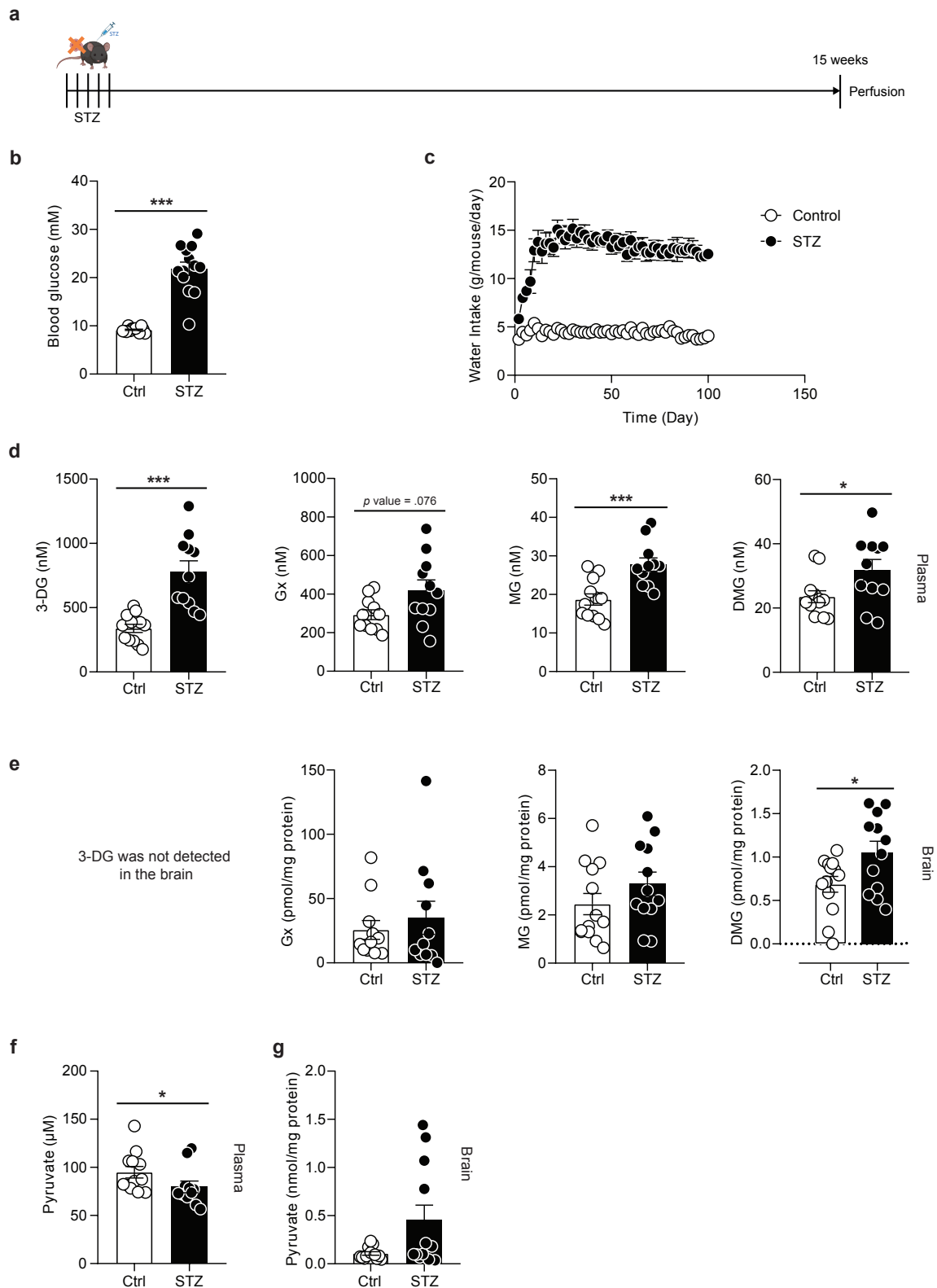


Fig. 4.1| Type-1 diabetes increases dimethylglyoxal concentrations in plasma and brain.

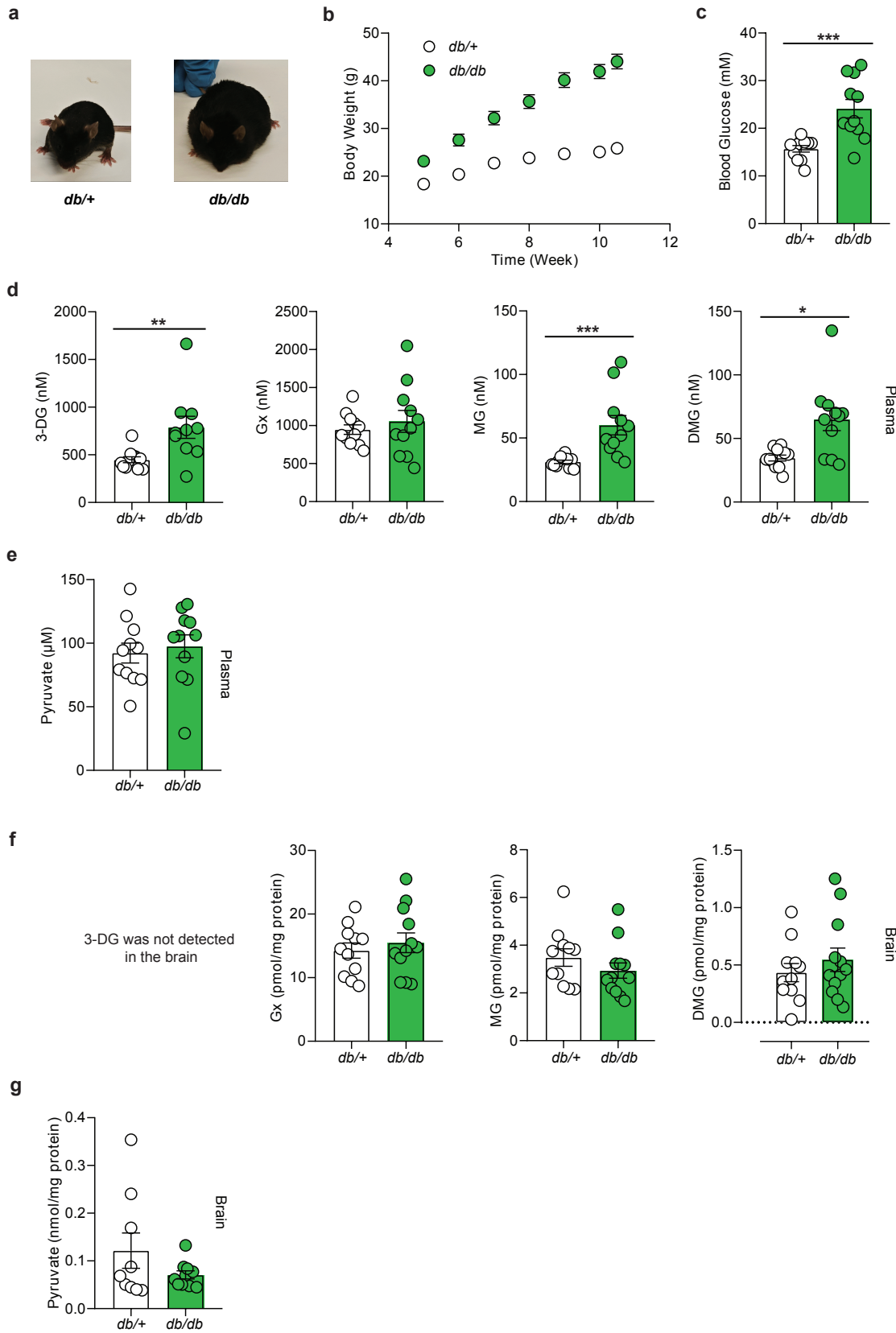
a Timeline of streptozotocin (STZ)-induced diabetes and sample collection in mice. Part of the image was created with BioRender.com. **b** Blood glucose concentrations 15 weeks after vehicle or STZ injections ($n=13$ per group). **c** Tap water intake of control and STZ-treated mice (50 time points per group, 4-6 cages per group). **d** Plasma concentrations of 3-deoxyglucosone (3-DG), glyoxal (Gx), methylglyoxal (MG) and dimethylglyoxal (DMG) in mice

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15 weeks after vehicle ($n=11-12$) or STZ ($n=11$) injections. **e** Concentrations of Gx, MG and DMG in mouse brain homogenate 15 weeks after vehicle ($n=11-13$) or STZ ($n=11-12$) injections. **f** Concentrations of pyruvate in mouse plasma 15 weeks after vehicle ($n=12$) or STZ ($n=11$) injections. **g** Concentrations of pyruvate in mouse brain homogenate 15 weeks after vehicle or STZ injections ($n=12$ per group). For normalization, deuterated methylglyoxal (d4-MG) and [$^{13}\text{C}_3$] sodium pyruvate were used as internal standards (**d-g**). Values are means \pm SEM. Statistical comparisons by two-tailed Mann-Whitney U test (**b**; **d**, 3-DG and Gx; **e**, Gx; **f**; **g**) or two-tailed unpaired t test (**d**, MG and DMG; **e**, MG and DMG). * $p < 0.05$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

Importantly, DMG concentrations were significantly increased 1.88-fold in the plasma of *db/db* mice, similar to 3-DG (1.76-fold) and MG (1.92-fold, **Fig. 4.2d**). In contrast, Gx and pyruvate levels were not changed between the two genotypes (**Fig. 4.2d, e**). In addition, Gx, MG, DMG and pyruvate concentrations were unaltered in the prefrontal cortex homogenate between the genotypes (**Fig. 4.2f, g**). Following the results in the type-1 diabetic mouse model, 3-DG was not detected in the brain of *db/+* or *db/db* mice (**Fig. 4.2f**). Furthermore, concentrations of MG and pyruvate were significantly elevated in the liver homogenate of type-2 diabetic mice, while 3-DG and DMG levels were not changed between the groups (**Fig. 4.2h, i**). In contrast, Gx levels were downregulated in the liver of *db/db* mice compared to the *db/+* mice (**Fig. 4.2h**). The obese phenotype of the *db/db* mice suggests that obesity could be involved in the upregulation of the levels of DMG and the other α -dicarbonyls. Therefore, levels of α -dicarbonyls were measured in the serum of mice fed with HFD for 12 weeks, an established model of diet-induced obesity¹⁶⁹. As expected, the body weight of HFD-fed mice was significantly higher than the body weight of mice fed with standard diet (**Fig. 4.3a**). Even though the HFD led to hyperglycemic conditions (**Fig. 4.3b**), concentrations of 3-DG, MG or DMG were not influenced by the diet (**Fig. 4.3c**). Interestingly, Gx concentrations were significantly higher in mice fed with HFD than in controls (**Fig. 4.3c**). These results suggest that diabetes, but not obesity itself, elevates the levels of DMG.

Results



Results

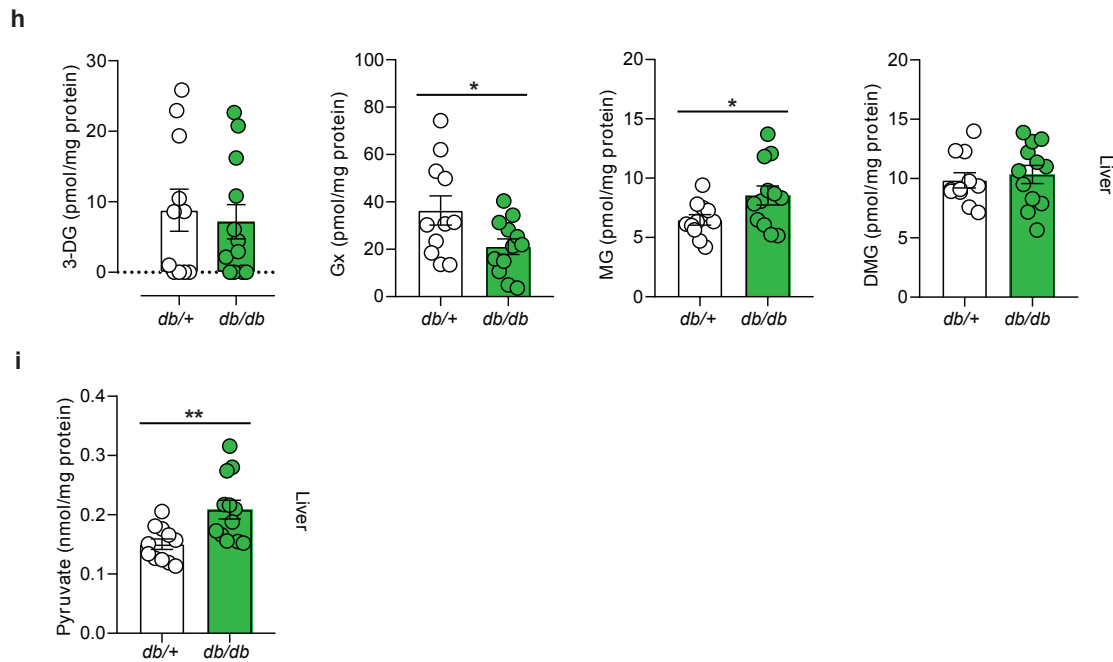


Fig. 4.2 | Type-2 diabetes increases dimethylglyoxal concentrations in plasma.

a Pictures of leptin receptor-deficient *db/db* mouse and heterozygous *db/+* littermate. **b** Body weight over time ($n=12$ per group) in 10-11-week-old *db/+* and *db/db* mice. **c** Blood glucose concentrations ($n=11$ per group) in 10-11-week-old *db/+* and *db/db* mice. **d** Plasma concentrations of 3-deoxyglucosone (3-DG), glyoxal (Gx), methylglyoxal (MG) and dimethylglyoxal (DMG) in *db/+* ($n=11$) and *db/db* ($n=10-11$) mice. **e** Concentrations of pyruvate in plasma of *db/+* and *db/db* mice ($n=11$ per group). **f** Concentrations of Gx, MG and DMG in brain homogenate of *db/+* ($n=11$) and *db/db* ($n=12$) mice. **g** Brain homogenate concentrations of pyruvate in *db/+* ($n=9$) and *db/db* ($n=10$) mice. **h** Liver homogenate concentrations of 3-DG, Gx, MG and DMG in *db/+* ($n=11$) and *db/db* ($n=12$) mice. **i** Pyruvate concentrations in liver homogenate of *db/+* ($n=11$) and *db/db* ($n=12$) mice. For normalization, deuterated methylglyoxal (d4-MG) and [$^{13}\text{C}_3$] sodium pyruvate were used as internal standards (**d-i**). Values are means \pm SEM. Statistical comparisons by 2-way RM ANOVA (**b**), two-tailed Mann-Whitney U test (**c; d; g**) or two-tailed unpaired *t* test (**e; f; h; i**). * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

Results

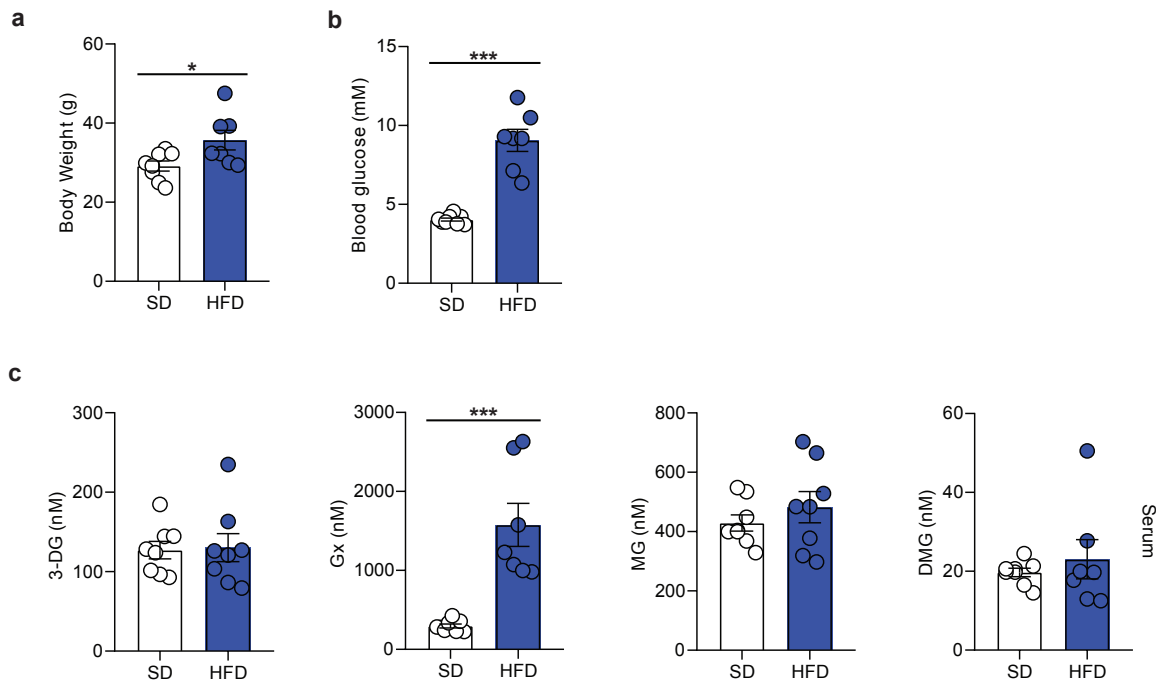


Fig. 4.3 | High-fat diet does not increase serum dimethylglyoxal.

a Body weight of mice fed with standard diet (SD, $n=8$) or high-fat diet (HFD, $n=7$) for 12 weeks. **b** Blood glucose concentrations of mice fed with SD ($n=8$) or HFD ($n=7$) for 12 weeks. **c** Serum concentrations of 3-deoxyglucosone (3-DG), glyoxal (Gx), methylglyoxal (MG) and dimethylglyoxal (DMG) in mice fed with SD ($n=8$) or HFD ($n=7-8$) for 12 weeks. For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (c). Values are means \pm SEM. Statistical comparisons by two-tailed unpaired t test (**a**; **c**, 3-DG and MG) or two-tailed Mann-Whitney U test (**b**; **c**, Gx and DMG). * $p < 0.05$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

4.2 Hypoxia stimulates the dimethylglyoxal generation from glucose or pyruvate

The previous results show that DMG is raised under diabetic conditions. Former studies of our group showed that DMG is endogenously generated from glucose^{54,55}. Moreover, DMG contained two or four glucose-derived carbons, suggesting that DMG is generated from two C-C blocks of glucose^{54,55}. Indeed, DMG is generated from two molecules of pyruvate^{54,55}. Interestingly, hypoxic conditions promote glycolysis due to the stabilization of HIF-1 α ^{170,171}. Thus, I wanted to evaluate the effect of hypoxia on the generation of DMG and other α -dicarbonyls. Furthermore, in plants, fungi and prokaryotes, ALS is an enzyme involved in the synthesis of DMG from pyruvate¹⁷². The mammal orthologue gene *Ilvbl* could have maintained the function of a DMG catalyst by α -acetolactate as intermediate compound in mammals.

Results

First, to evaluate if cells hold α -dicarbonyls in the intracellular space, bEnd.3 cells were treated with 25 mM native or [$^{13}\text{C}_6$] glucose for 6 hours under hypoxic conditions (0.3 % O_2 , **Fig. 4.4a**). Here, α -dicarbonyls were measured in both supernatant and cell lysate. [$^{13}\text{C}_6$] 3-DG, [$^{13}\text{C}_2$] Gx, [$^{13}\text{C}_3$] pyruvate, [$^{13}\text{C}_2$] DMG and [$^{13}\text{C}_4$] DMG were only detected in the supernatant, suggesting the tendency of the cells to secrete these reactive glucose metabolites to the medium (**Fig. 4.4b, c, e, f**). In contrast, [$^{13}\text{C}_2$] MG and [$^{13}\text{C}_3$] MG were detected in the cells, probably due to the higher levels of this metabolite compared the other α -dicarbonyls (**Fig. 4.4d**). However, [$^{13}\text{C}_2$] MG and [$^{13}\text{C}_3$] MG were higher in the medium compared to the cell lysate (**Fig. 4.4d**). Moreover, the treatment with [$^{13}\text{C}_6$] glucose elevated the generation of [$^{13}\text{C}_2$] DMG, even though this metabolite is also generated from native glucose (**Fig. 4.4f**). Since α -dicarbonyls are mainly secreted in the supernatant, medium was the proper target for the evaluation of α -dicarbonyl levels in the next experiments *in vitro*.

To test the role of HIF-1 α and ILVBL in generating DMG, mouse brain endothelial bEnd.3 cells, transfected with *Ilvbl* siRNA for 40 hours, were treated with 25 mM [$^{13}\text{C}_6$] glucose for 6 hours under normoxic or hypoxic (0.1-0.5 %) conditions (**Fig. 4.5a**). First, the *Ilvbl* siRNA transfection significantly lowered the expression of *Ilvbl* mRNA to 28 % compared to mRNA expression in the control cells transfected with the scramble siRNA (**Fig. 4.5b**). The expression of *Ilvbl* mRNA was not changed based on oxygen concentration (**Fig. 4.5b**). Interestingly, levels of [$^{13}\text{C}_6$] 3-DG and [$^{13}\text{C}_2$] Gx in the medium were not influenced by the concentration of oxygen (**Fig. 4.5c, d**). In contrast, [$^{13}\text{C}_3$] MG and [$^{13}\text{C}_3$] pyruvate levels were increased under hypoxic conditions (**Fig. 4.5e, f**). Importantly, half-labeled and fully-labeled DMG levels were also upregulated under hypoxia (**Fig. 4.5g**), indicating that hypoxia promotes the generation of DMG, similar to pyruvate and MG. Further, *Ilvbl* knockdown did not influence the generation of DMG or the other α -dicarbonyls, neither under atmospheric nor hypoxic conditions (**Fig. 4.5c, d, e, g**). In contrast, *Ilvbl* knockdown significantly reduced fully-labeled pyruvate levels under hypoxic conditions (**Fig. 4.5f**). Lastly, we treated bEnd.3 cells with 4 mM [$^{13}\text{C}_3$] pyruvate for 6 hours under atmospheric or hypoxic (0.6 % O_2) conditions, 40 hours after transfection with *Ilvbl* siRNA (**Fig. 4.6a**). Even though no changes were observed in the levels of [$^{13}\text{C}_3$] pyruvate (**Fig. 4.6b**), [$^{13}\text{C}_2$] DMG and [$^{13}\text{C}_4$] DMG levels were significantly increased under hypoxic conditions (**Fig. 4.6c**). Similar to the previous experiment, the generation of labeled DMG from [$^{13}\text{C}_3$] pyruvate was not influenced by *Ilvbl* knockdown (**Fig. 4.6c**). On the other hand, the overexpression of *Ilvbl* after transfection of bEnd.3 cells with a plasmid stimulated the formation of [$^{13}\text{C}_4$] DMG from [$^{13}\text{C}_6$] glucose under hypoxic conditions⁵⁵. Labeled forms of other α -dicarbonyls were not detected (data not shown) after the treatment with [$^{13}\text{C}_3$] pyruvate.

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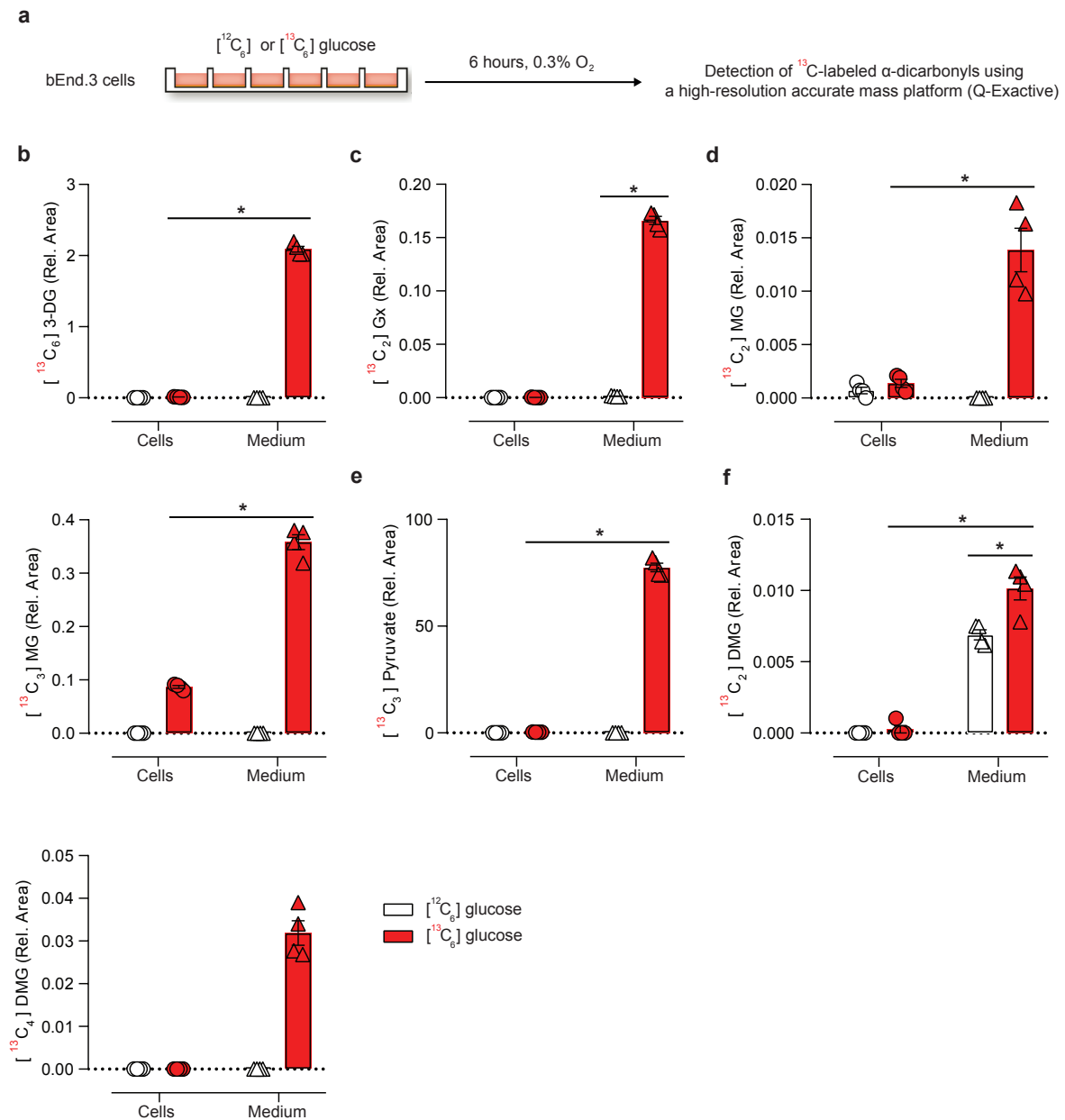


Fig. 4.4 | α -Dicarbonyls are excreted from cells to the medium.

a Treatment of mouse brain endothelial bEnd.3 cells with native or $[^{13}\text{C}_6]$ glucose for 6 hours under hypoxic (0.3 % O_2) conditions. **b** $[^{13}\text{C}_6]$ 3-deoxyglucosone ($[^{13}\text{C}_6]$ 3-DG) in the medium or cell lysate ($n=4$ per group). **c** $[^{13}\text{C}_2]$ glyoxal ($[^{13}\text{C}_2]$ Gx) in the medium or cell lysate ($n=4$ per group). **d** $[^{13}\text{C}_2]$ methylglyoxal ($[^{13}\text{C}_2]$ MG) and $[^{13}\text{C}_3]$ MG in the medium or cell lysate ($n=4$ per group). **e** $[^{13}\text{C}_3]$ pyruvate in the medium or cell lysate ($n=4$ per group). **f** $[^{13}\text{C}_2]$ dimethylglyoxal ($[^{13}\text{C}_2]$ DMG) and $[^{13}\text{C}_4]$ DMG in the medium or cell lysate ($n=4$ per group). For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**b-f**). Values are means \pm SEM. Statistical comparisons by two-tailed Mann-Whitney U test (**b**; **c**; **d**; **e**) or two-tailed Mann-Whitney U test followed by Bonferroni–Holm correction (**f**). * $p < 0.05$. Detailed information on the test statistics is provided in the Statistical table.

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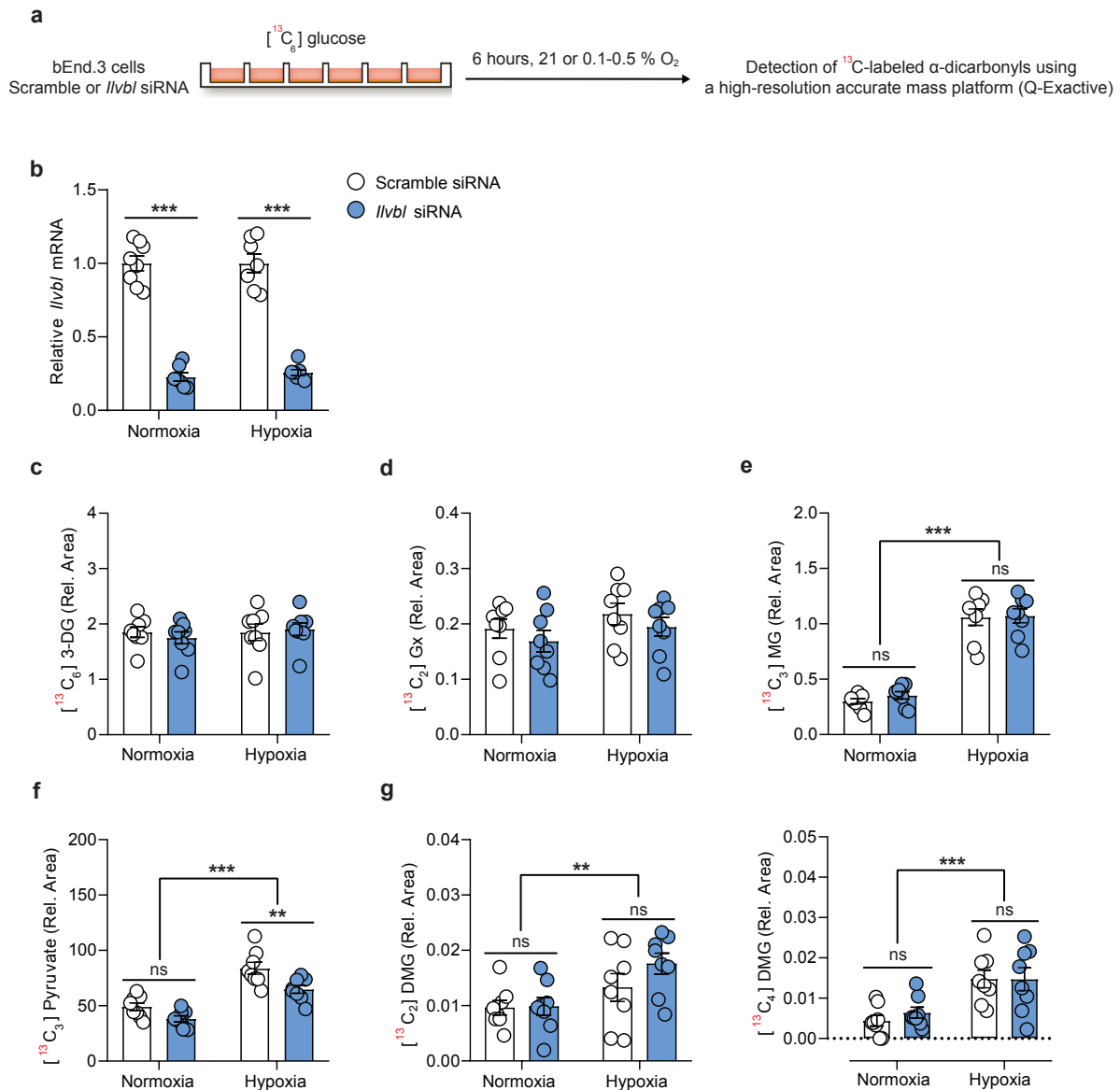


Fig. 4.5 | Hypoxic conditions increase levels of dimethylglyoxal, but *Ilvbl* is not involved in the generation of dimethylglyoxal from glucose *in vitro*.

a Treatment of mouse brain endothelial bEnd.3 cells with $[^{13}\text{C}_6]$ glucose for 6 hours under normoxic or hypoxic (0.1-0.5 % O_2) conditions. Before the treatment, cells were transfected with scramble or *Ilvbl* siRNA for 40 hours. **b** Relative *Ilvbl* mRNA expression in bEnd.3 cells treated with scramble ($n=7-8$ per group) or *Ilvbl* ($n=8$ per group) siRNA for 40 hours. **c** $[^{13}\text{C}_6]$ 3-deoxyglucosone ($[^{13}\text{C}_6]$ 3-DG) in the medium of control or *Ilvbl* knockdown cells ($n=8$ per group). **d** $[^{13}\text{C}_2]$ glyoxal ($[^{13}\text{C}_2]$ Gx) in the medium of control or *Ilvbl* knockdown cells ($n=8$ per group). **e** $[^{13}\text{C}_3]$ methylglyoxal ($[^{13}\text{C}_3]$ MG) in the medium of control or *Ilvbl* knockdown cells ($n=8$ per group). **f** $[^{13}\text{C}_3]$ pyruvate in the medium of control or *Ilvbl* knockdown cells ($n=8$ per group). **g** $[^{13}\text{C}_2]$ dimethylglyoxal ($[^{13}\text{C}_2]$ DMG) and $[^{13}\text{C}_4]$ DMG in the medium of control or *Ilvbl* knockdown cells ($n=8$ per group). For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**c-g**). Values are means \pm SEM. Statistical comparisons by Scheirer-Ray-Hare test followed by two-tailed Mann-Whitney U post hoc tests and Bonferroni-Holm correction (**b**), Scheirer-Ray-Hare test (**c; e; g, $[^{13}\text{C}_4]$ DMG**), 2-way ANOVA (**d; g, $[^{13}\text{C}_2]$ DMG**) or 2-way ANOVA followed by

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Sidak's post hoc tests (f). $**p < 0.01$; $***p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

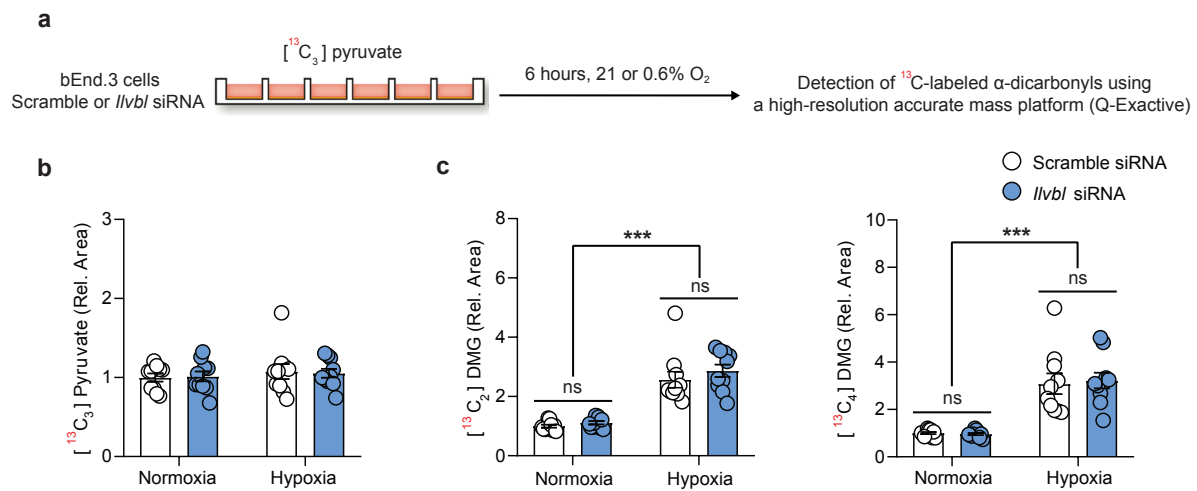


Fig. 4.6 *Ilvbl* does not influence the generation of dimethylglyoxal from pyruvate *in vitro*.

a Treatment of mouse brain endothelial bEnd.3 cells with [¹³C₃] pyruvate for 6 hours under normoxic or hypoxic (0.6 % O₂) conditions. Before the treatment, cells were transfected with scramble or *Ilvbl* siRNA for 40 hours. **b** [¹³C₃] pyruvate in the medium of control or *Ilvbl* knockdown cells ($n=10$ per group). **c** [¹³C₂] dimethylglyoxal ([¹³C₂] DMG) and [¹³C₄] DMG in the medium of control or *Ilvbl* knockdown cells ($n=10$ per group). For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**b**; **c**). Values are means \pm SEM. Statistical comparisons by Scheirer-Ray-Hare test. $***p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

4.3 ILVBL is involved in the generation of dimethylglyoxal in the brain of hyperglycemic and ischemic mice

Previous studies showed that *Ilvbl* overexpression augmented the DMG levels *in vitro*⁵⁵. Thus, I wanted to evaluate the role of ILVBL in the generation of DMG *in vivo*. *Ilvbl*^{-/-} mice (**Fig. 4.7a**) did not show any particular phenotype and were fertile. Under basal conditions, levels of DMG were not changed in plasma, brain and peripheral organs between *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice (**Fig. 4.7b-f**). Since hypoxic conditions increased the generation of DMG *in vitro*, we wanted to evaluate ischemic conditions and DMG formation *in vivo*. First, to confirm that DMG is generated from glucose in our model and to evaluate whether *Ilvbl* influences the DMG generation, *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice received an intraperitoneal injection of saline solution or 50 mg/0.2 ml [¹³C₆] glucose prior to inducing ischemic stroke by pMCAO (**Fig. 4.8a**). Here, half-labeled and fully-labeled DMG were detected in the plasma and whole-brain homogenate of mice treated with [¹³C₆] glucose 25 min after pMCAO (**Fig. 4.8b, d**), whereas labeled forms of DMG were not generated in mice treated with saline solution (**Fig. 4.8b** and data not shown). This analysis showed that DMG is a product of glucose metabolism *in vivo*.

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Moreover, levels of native DMG were higher in the plasma of mice treated with [$^{13}\text{C}_6$] glucose compared to the control (**Fig. 4.8b**). In contrast, native DMG levels were lower in the whole-brain homogenate of [$^{13}\text{C}_6$] glucose-treated mice compared to the control (**Fig. 4.8c**). Moreover, no differences were observed in the generation of labeled forms of DMG between the ischemic ipsilateral and the contralateral hemispheres of the brain (**Fig. 4.8d**). Lastly, the presence of *Ilvbl* did not influence the concentration of DMG either in the plasma or in both sides of the brain, 25 min after pMCAO (**Fig. 4.8b – d**).

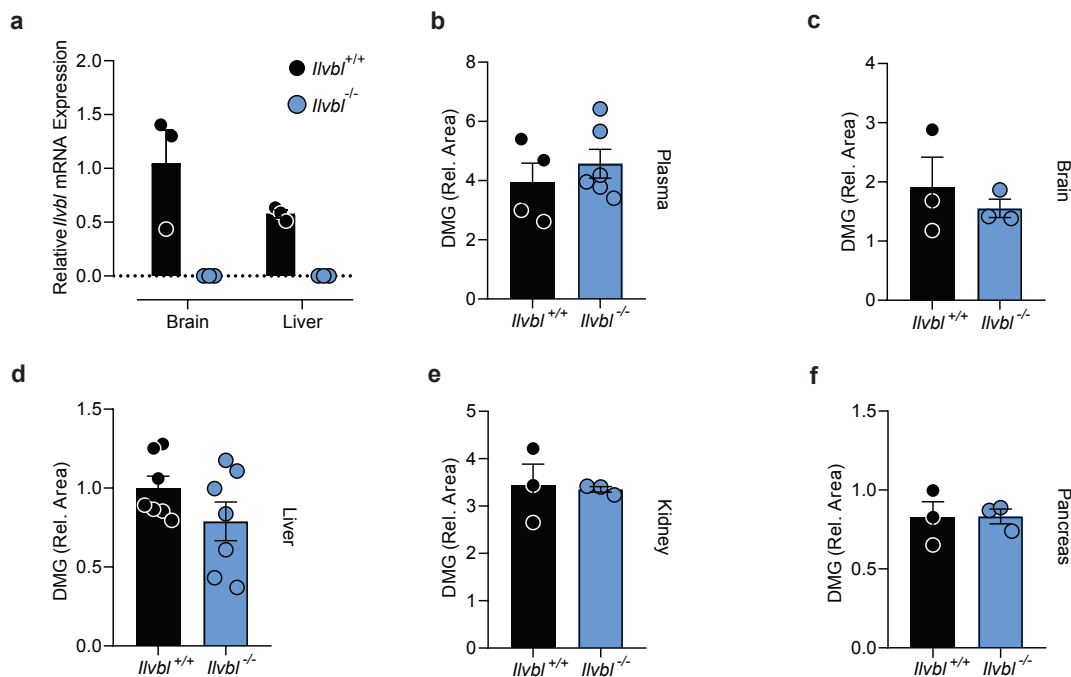


Fig. 4.7 | *Ilvbl* deficiency does not influence the levels of dimethylglyoxal under basal conditions.

a Relative *Ilvbl* mRNA expression in brain and liver of *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice ($n=3$ per group). **b** Dimethylglyoxal (DMG) levels in plasma of *Ilvbl*^{+/+} ($n=4$) and *Ilvbl*^{-/-} ($n=6$) mice under basal conditions. **c** DMG levels in brain homogenate of *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice ($n=3$ per group) under basal conditions. **d** DMG levels in liver homogenate of *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice ($n=7$ per group) under basal conditions. **e** DMG levels in kidney homogenate of *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice ($n=3$ per group) under basal conditions. **f** DMG levels in pancreas homogenate of *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice ($n=3$ per group) under basal conditions. For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**b-f**). Values are means \pm SEM. Statistical comparisons by two-tailed unpaired *t* test (**b**; **c**; **d**; **f**) or two-tailed Mann-Whitney U test (**e**). Detailed information on the test statistics is provided in the Statistical table.

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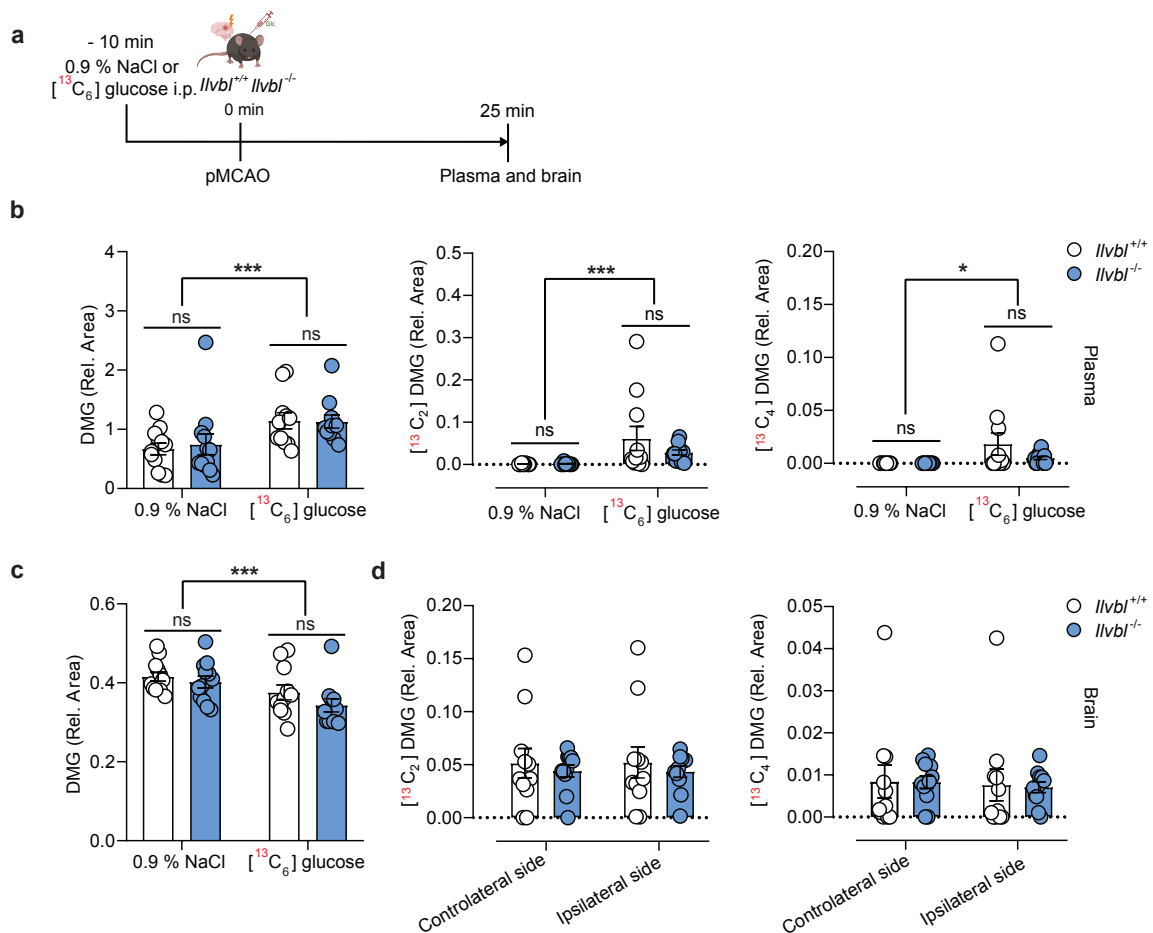


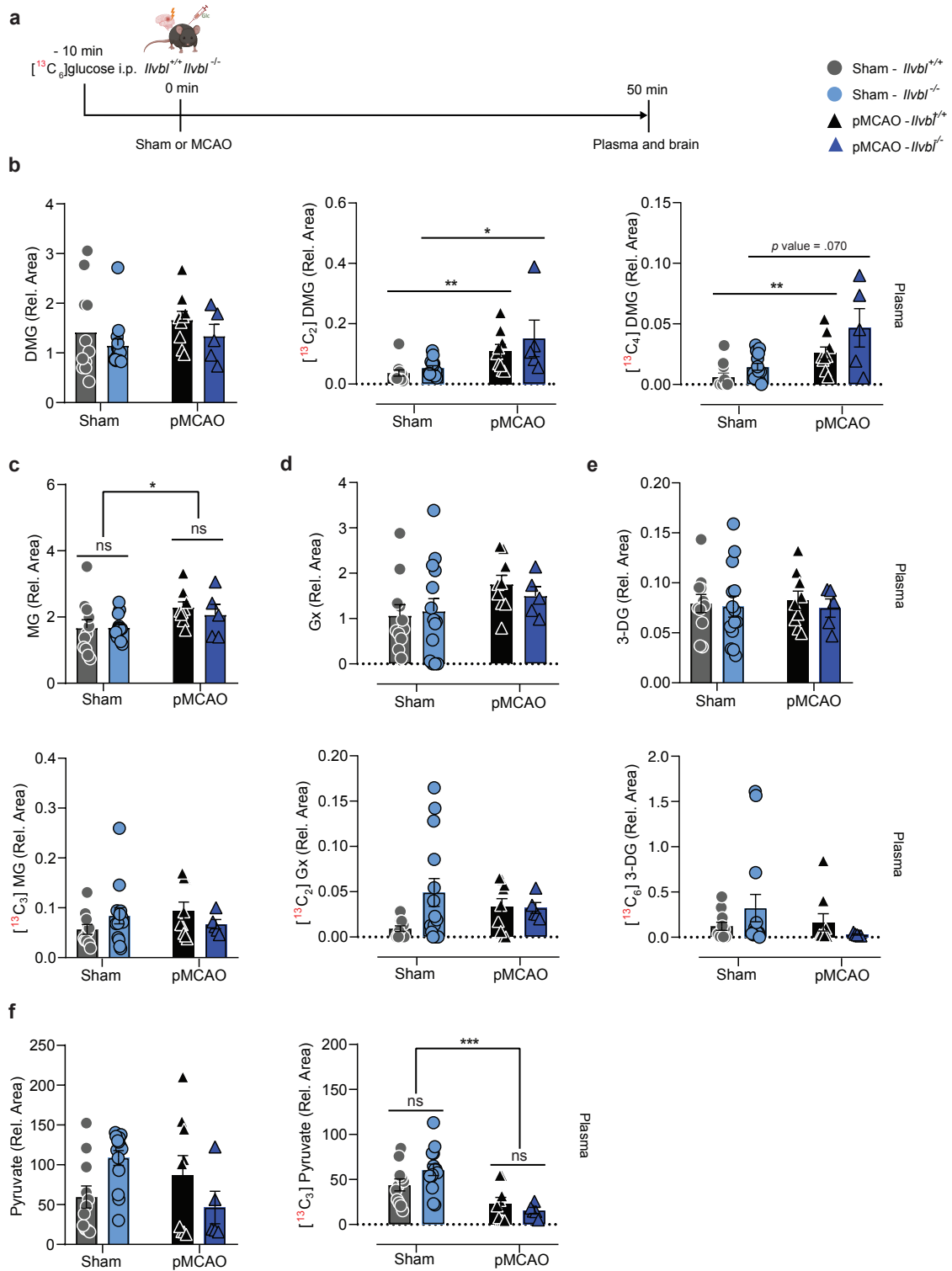
Fig. 4.8 | Dimethylglyoxal is a product of glucose metabolism *in vivo*.

a Timeline of saline or [$^{13}\text{C}_6$] glucose injection, occlusion of the distal middle cerebral artery (MCAO), and sample collection. Part of the image was created with BioRender.com. **b** Dimethylglyoxal (DMG), [$^{13}\text{C}_2$] DMG and [$^{13}\text{C}_4$] DMG in plasma of *Ilvbl* $^{+/+}$ or *Ilvbl* $^{-/-}$ mice treated with saline ($n=12$ per group) or [$^{13}\text{C}_6$] glucose ($n=11$ per group) solutions prior to MCAO. **c** DMG in brain homogenate (average of ipsi- and contralateral sides) of *Ilvbl* $^{+/+}$ or *Ilvbl* $^{-/-}$ mice treated with saline ($n=12$ per group) or [$^{13}\text{C}_6$] glucose ($n=11$ per group) solutions prior to MCAO. **d** [$^{13}\text{C}_2$] DMG and [$^{13}\text{C}_4$] DMG in the contralateral and ipsilateral sides of acute hyperglycemic *Ilvbl* $^{+/+}$ or *Ilvbl* $^{-/-}$ MCAO-treated mice treated with [$^{13}\text{C}_6$] glucose. For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**b-f**). Values are means \pm SEM. Statistical comparisons by Scheirer-Ray-Hare test (**b; c**) or 2-way RM ANOVA (**d**). * $p < 0.05$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

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Further, to evaluate if hypoxia/ischemia indeed stimulate the generation of DMG from glucose *in vivo*, we performed sham or pMCAO treatment in acute hyperglycemic mice by injecting 50 mg/0.2 ml [$^{13}\text{C}_6$] glucose. In this experiment, *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice were sacrificed 50 min after the sham or pMCAO treatment (**Fig. 4.9a**). First, levels of labeled forms of DMG, but not native DMG, were significantly higher in the plasma of ischemic mice compared to the sham control (**Fig. 4.9b**), suggesting the ischemic conditions stimulate the production of DMG from glucose. However, DMG levels were not influenced by the presence of *Ilvbl* in the plasma (**Fig. 4.9b**). Furthermore, native MG levels were significantly higher in the plasma of ischemic mice compared to the sham (**Fig. 4.9c**), whereas levels of native 3-DG, Gx and pyruvate and fully-labeled 3-DG, Gx and MG were not changed depending on surgeries (**Fig. 4.9c – f**). Interestingly, fully-labeled pyruvate levels were lower in the plasma of hyperglycemic and ischemic mice compared to the control (**Fig. 4.9f**). Lastly, as expected, *Ilvbl* knockout did not influence the levels of the other α -dicarbonyls or pyruvate (**Fig. 4.9c – f**). Subsequently, we measured levels of α -dicarbonyls and pyruvate in the homogenates of the whole contralateral or ipsilateral side of the brain. Interestingly, ischemic stroke significantly augmented levels of native and labeled forms of DMG in both contralateral and ipsilateral sides of the brain compared to the sham treatment (**Fig. 4.9g**), indicating that hypoxia/ischemia enhances the generation of DMG in the brain *in vivo*. Moreover, native, half-labeled and fully-labeled DMG levels were significantly higher in the ipsilateral compared to the contralateral hemisphere of the brain of the acute hyperglycemic and ischemic mice, while levels of native and labeled forms of DMG were not changed between the brain sides of sham-treated mice (**Fig. 4.9g**). Importantly, *Ilvbl* knockout lowered levels of native and half-labeled DMG in the ischemic side of the brain (**Fig. 4.9g**). Native DMG levels were reduced even in the contralateral side of MCAO-treated *Ilvbl* knockout mice (**Fig. 4.9g**). In contrast, levels of DMG were not influenced by *Ilvbl* deficiency in the sham-treated mice (**Fig. 4.9g**). Levels of native Gx, Mg, pyruvate and fully-labeled MG and pyruvate were not affected by *Ilvbl* deficiency in the brain (**Fig. 4.9h – j**). However, ischemic stroke induced the generation of native MG, Gx and pyruvate in the ipsilateral side of the brain (**Fig. 4.9h – j**). In contrast, pMCAO reduced the levels of fully-labeled MG, even though the reduction was attenuated in the ipsilateral hemisphere (**Fig. 4.9h**). Lastly, native 3-DG and fully-labeled forms of 3-DG and Gx were not detected in the brain homogenate (data not shown). Taken together, these findings suggest that DMG is generated at least partially by *Ilvbl* in the brain of acute hyperglycemic and ischemic mice, 50 min after pMCAO. In contrast, *Ilvbl* does not influence the plasma or brain DMG levels in mice 25 min after pMCAO, probably due to a shorter latency time for glucose to be metabolized to dimethylglyoxal.

Results



Results

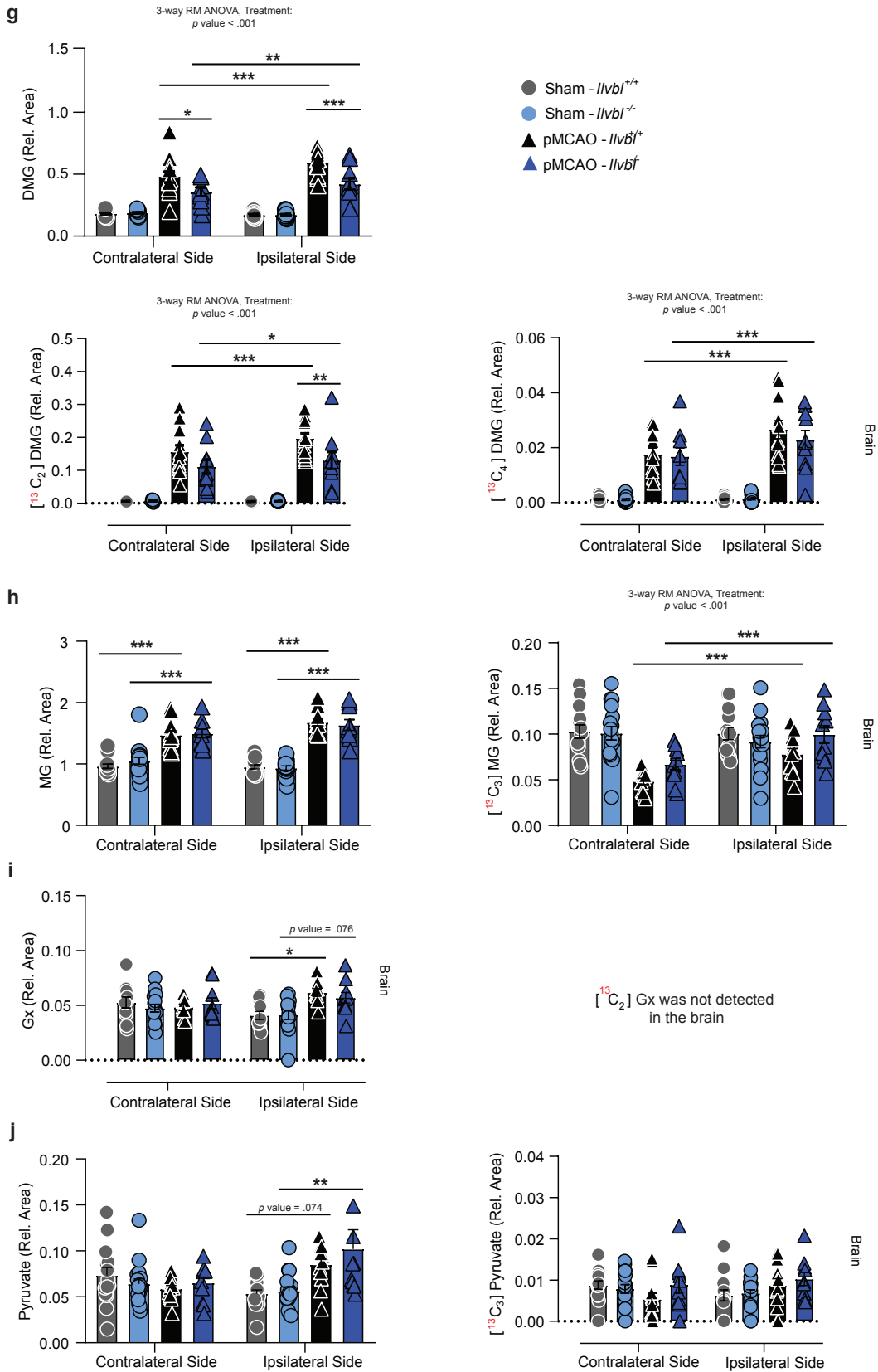


Fig. 4.9 | *Ilvbl* is involved in the generation of dimethylglyoxal in the brain of acute hyperglycemic and ischemic mice.

Results

a Timeline of [$^{13}\text{C}_6$] glucose injection, sham surgery or occlusion of the distal middle cerebral artery (MCAO), and sample collection. Part of the image was created with BioRender.com. **b** Dimethylglyoxal (DMG), [$^{13}\text{C}_2$] DMG and [$^{13}\text{C}_4$] DMG in plasma of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=11$, *Ilvbl*^{+/+}; $n=14$, *Ilvbl*^{-/-}) or pMCAO ($n=9$, *Ilvbl*^{+/+}; $n=5$, *Ilvbl*^{-/-}). **c** Methylglyoxal (MG) and [$^{13}\text{C}_3$] MG in plasma of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=11$, *Ilvbl*^{+/+}; $n=14$, *Ilvbl*^{-/-}) or pMCAO ($n=9$, *Ilvbl*^{+/+}; $n=5$, *Ilvbl*^{-/-}). **d** Glyoxal (Gx) and [$^{13}\text{C}_2$] Gx in plasma of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=11$, *Ilvbl*^{+/+}; $n=14$, *Ilvbl*^{-/-}) or pMCAO ($n=9$, *Ilvbl*^{+/+}; $n=5$, *Ilvbl*^{-/-}). **e** 3-Deoxyglucosone (3-DG) and [$^{13}\text{C}_6$] 3-DG in plasma of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=11$, *Ilvbl*^{+/+}; $n=14$, *Ilvbl*^{-/-}) or pMCAO ($n=9$, *Ilvbl*^{+/+}; $n=5$, *Ilvbl*^{-/-}). **f** Pyruvate and [$^{13}\text{C}_3$] pyruvate in plasma of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=11$, *Ilvbl*^{+/+}; $n=14$, *Ilvbl*^{-/-}) or pMCAO ($n=9$, *Ilvbl*^{+/+}; $n=5$, *Ilvbl*^{-/-}). **g** DMG, [$^{13}\text{C}_2$] DMG and [$^{13}\text{C}_4$] DMG in the contralateral and ipsilateral sides of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=14$, *Ilvbl*^{+/+}; $n=17$, *Ilvbl*^{-/-}) or pMCAO ($n=12$, *Ilvbl*^{+/+}; $n=10$, *Ilvbl*^{-/-}). **h** MG and [$^{13}\text{C}_3$] MG in the contralateral and ipsilateral sides of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=14$, *Ilvbl*^{+/+}; $n=17$, *Ilvbl*^{-/-}) or pMCAO ($n=12$, *Ilvbl*^{+/+}; $n=10$, *Ilvbl*^{-/-}). **i** Gx in the contralateral and ipsilateral sides of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=11$, *Ilvbl*^{+/+}; $n=15$, *Ilvbl*^{-/-}) or pMCAO ($n=9$, *Ilvbl*^{+/+}; $n=10$, *Ilvbl*^{-/-}). **j** Pyruvate and [$^{13}\text{C}_3$] pyruvate in the contralateral and ipsilateral sides of *Ilvbl*^{+/+} or *Ilvbl*^{-/-} mice after sham surgery ($n=14$, *Ilvbl*^{+/+}; $n=17$, *Ilvbl*^{-/-}) or pMCAO ($n=12$, *Ilvbl*^{+/+}; $n=10$, *Ilvbl*^{-/-}). For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**b-j**). Values are means \pm SEM. Statistical comparisons by Scheirer-Ray-Hare test followed by two-tailed Mann–Whitney U post hoc tests and Bonferroni–Holm correction (**b**), Scheirer-Ray-Hare test (**c**; **d**, [$^{13}\text{C}_2$] Gx; **e**, [$^{13}\text{C}_6$] 3-DG), 2-way ANOVA (**d**, Gx; **e**, 3-DG; **f**), 3-way RM ANOVA followed by Sidak’s post hoc tests (**g**; **h**; **i**; **j**) * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

4.4 ILVBL is involved in the generation of dimethylglyoxal in the brain of type-1 diabetic mice

Thereafter, I wanted to explore the role of ILVBL in generating DMG in a type-1 diabetic mouse model. Here, plasma was collected before and 12 weeks after the STZ injections (**Fig. 4.10a**). As expected, blood glucose concentrations were significantly higher 12 weeks after STZ injections compared to the same mice before the STZ injections (**Fig. 4.10b**). Notably, *Ilvbl*^{-/-} mice developed hyperglycemia like their *Ilvbl*^{+/+} littermates (**Fig. 4.10b**). Levels of 3-DG and Gx were higher in plasma of *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice 12 weeks after the STZ injections (**Fig. 4.10c**). In contrast, MG levels were unchanged after the latency time (**Fig. 4.10c**). At the same time, levels of DMG were upregulated in plasma compared to the baseline (**Fig. 4.10c**). Neither the generation of DMG nor of the other α -dicarbonyls in plasma were influenced by *Ilvbl* (**Fig. 4.10c**). Likewise, *Ilvbl* did not influence levels of α -dicarbonyls in the liver homogenate (**Fig. 4.10d**). Then, we measured the levels of α -dicarbonyls in the prefrontal cortex homogenate of the STZ-treated mice. Importantly, DMG levels were reduced in the brain of *Ilvbl*^{-/-} compared to *Ilvbl*^{+/+} mice (**Fig. 4.10e**), indicating that *Ilvbl* stimulates the local generation of DMG in the brain of type-1 diabetic mice. In contrast, as negative control, levels of brain Gx and MG were similar between the genotypes (**Fig. 4.10e**). Like in the previous analyses, 3-DG was not detected in

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the brain homogenate (Fig. 4.10e). Therefore, ILVBL increases the production of DMG in the brain of type-1 diabetic mice.

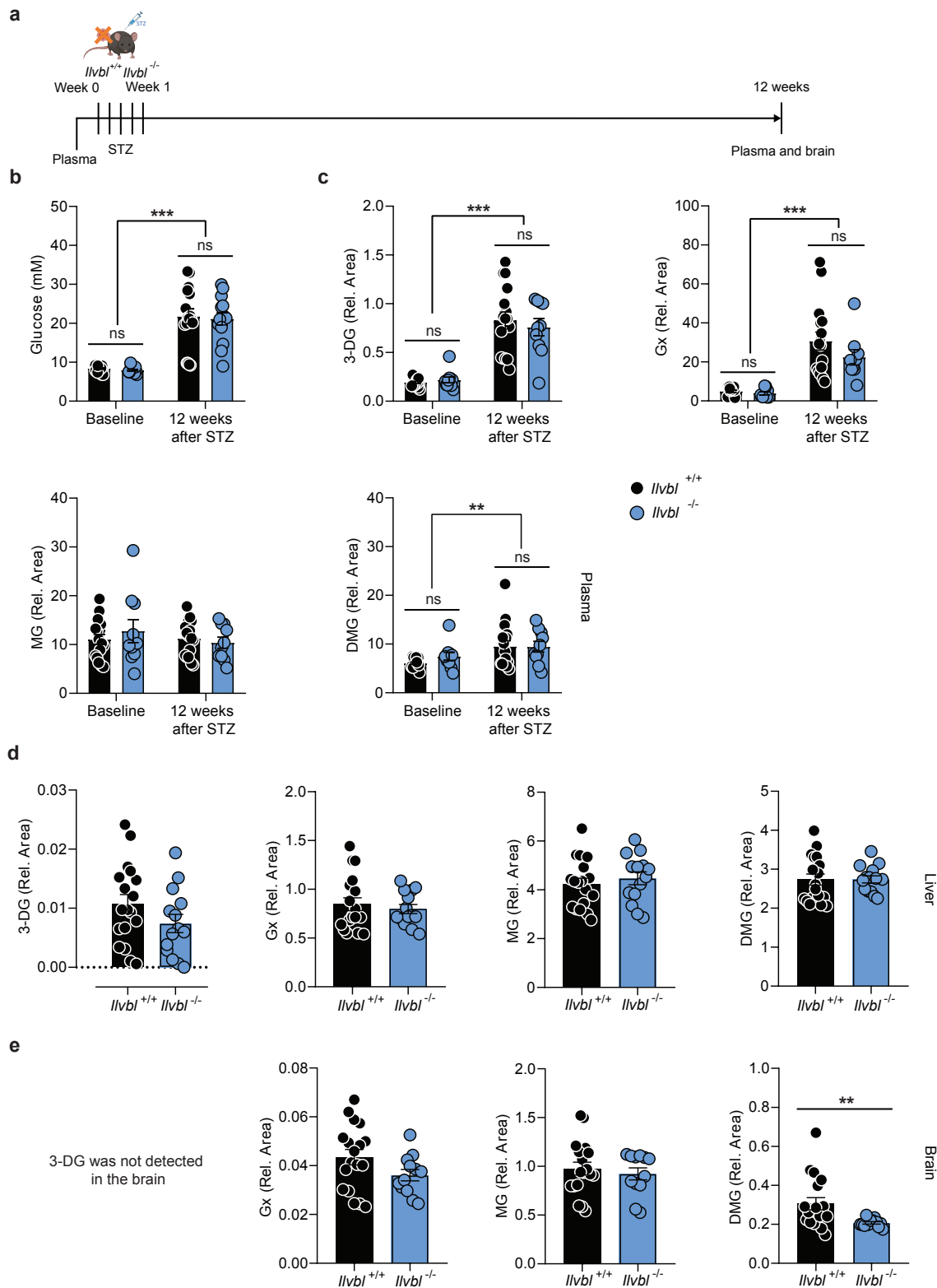


Fig. 4.10 | *Ilvbl* is involved in the generation of dimethylglyoxal in the brain of mice with type-1 diabetes.

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a Timeline of plasma collection before the treatment, streptozotocin (STZ)-induced diabetes, and sample collection 12 weeks after STZ injections. **b** Blood glucose concentrations of *Ilvbl^{+/+}* ($n=18$) and *Ilvbl^{-/-}* ($n=14$) mice at baseline and 12 weeks after STZ treatment. **c** 3-deoxyglucosone (3-DG), glyoxal (Gx), methylglyoxal (MG) and dimethylglyoxal (DMG) in plasma of *Ilvbl^{+/+}* ($n=16$) and *Ilvbl^{-/-}* ($n=9-10$) mice at baseline and 12 weeks after STZ treatment. **d** 3-DG, Gx, MG and DMG in the liver homogenate of *Ilvbl^{+/+}* ($n=18$) and *Ilvbl^{-/-}* ($n=14$) mice 12 weeks after STZ treatment. **e** Gx, MG and DMG in the brain homogenate of *Ilvbl^{+/+}* ($n=18$) and *Ilvbl^{-/-}* ($n=12$) mice 12 weeks after STZ treatment. For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard (**c-e**). Values are means \pm SEM. Statistical comparisons by 2-way RM ANOVA (**b**; **c**), two-tailed unpaired *t* test (**d**, 3-DG, Gx and MG; **e**, Gx and MG) or two-tailed Mann-Whitney U test (**d**, DMG; **e**, DMG). ** $p < 0.01$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

4.5 The gut microbiota does not influence plasma dimethylglyoxal concentrations

As previously mentioned, DMG is generated from glucose in the mammal metabolism and is a product of pyruvate metabolism via ALS in bacteria, yeast and prokaryotes. Bacteria and yeasts are microorganisms that are part of the mammal gut microbiota.

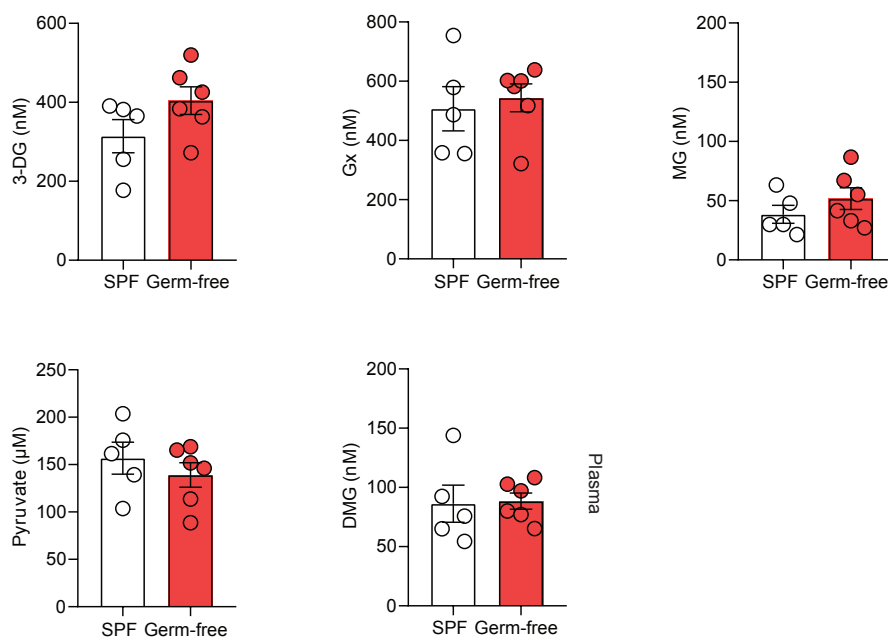


Fig. 4.11 | The gut microbiota does not influence plasma dimethylglyoxal concentrations.

3-Deoxyglucosone, glyoxal, methylglyoxal, pyruvate and dimethylglyoxal in plasma of specific-pathogen-free (SPF, $n=5$) or germ-free mice ($n=6$). For normalization, deuterated methylglyoxal (d4-MG) and [$^{13}\text{C}_3$] sodium pyruvate were used as internal standards. Values are means \pm SEM. Statistical comparisons by two-tailed unpaired *t* test. Detailed information on the test statistics is provided in the Statistical table.

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To evaluate the influence of gut microbiota on plasma levels of DMG in mammals, LC-MS² analysis was performed to detect α -dicarbonyls in the plasma of SPF and germ-free mice. SPF mice are a suitable control model for germ-free mice since they have gut microbiota but are pathogen-free. Interestingly, we did not find any differences in the levels of 3-DG, Gx, MG, pyruvate and DMG between the two groups (**Fig. 4.11**). These results show that the microbiome of SPF mice does not significantly contribute to the DMG levels in the mouse bloodstream.

4.6 Dimethylglyoxal is the precursor of *N*_ε-3-hydroxy-2-butanonelysine (HBL) in hyperglycemic mice

Reactive glucose metabolites are involved in the pathophysiology of diabetes by the formation of AGEs. AGEs are non-enzymatically generated by the interaction between α -dicarbonyls and proteins¹⁷³.

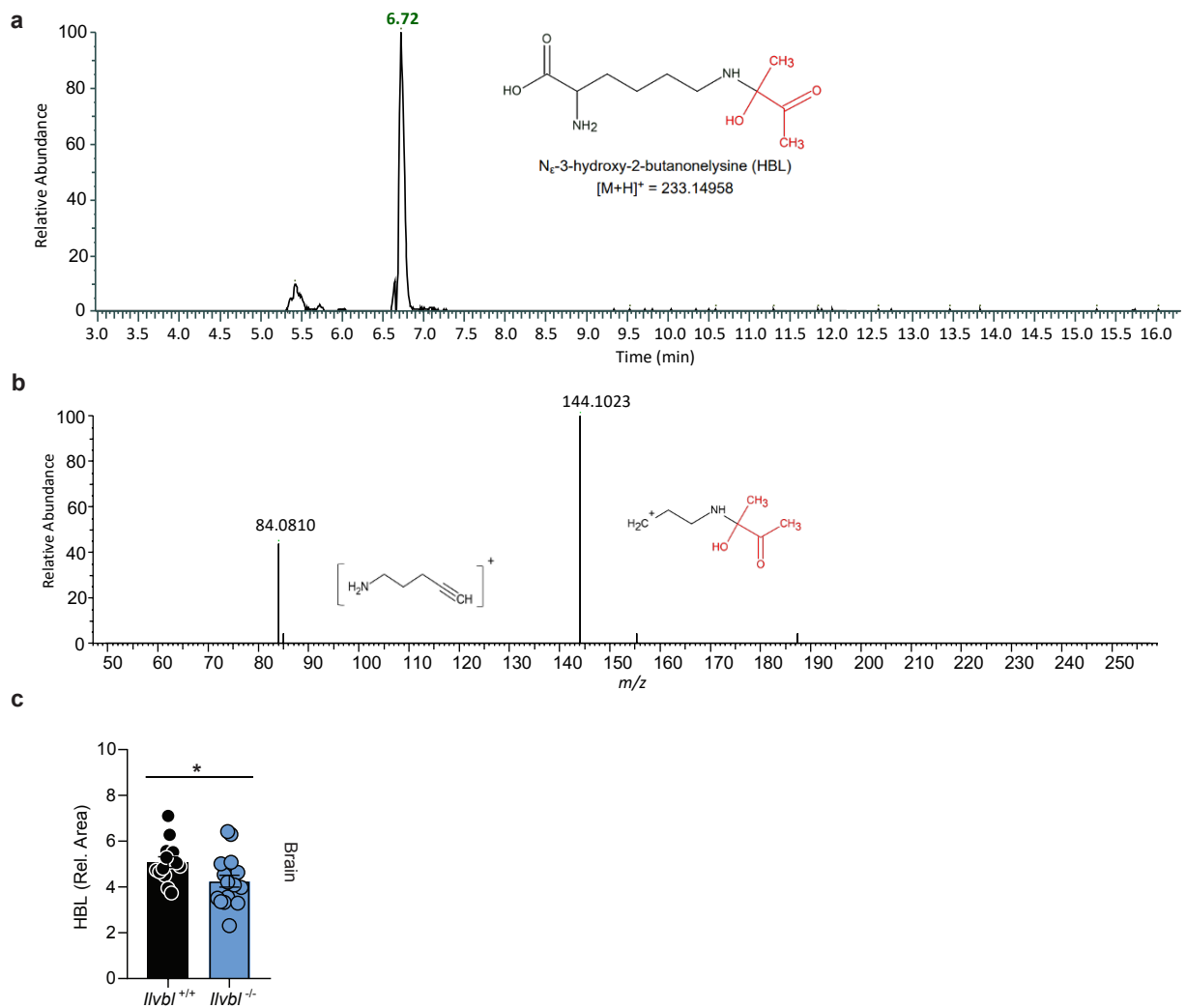


Fig. 4.12 | Dimethylglyoxal reacts with lysine to the glycated amino acid *N*_ε-3-hydroxy-2-butanonelysine *in vivo*.

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a Representative chromatogram of Nε-3-hydroxy-2-butanonelysine (HBL, retention time = 6.72 min; m/z = 233.14958) in an acute hyperglycemic mouse brain. **b** Representative fragmentation spectrum of HBL (fragment m/z = 84.0810, and 144.1023) in an acute hyperglycemic mouse brain. **c** Levels of HBL in the brain homogenate of *Ilvbl*^{+/+} ($n=14$) or *Ilvbl*^{-/-} ($n=17$) mice with acute hyperglycemia. For normalization, labeled standard d4-Nε-carboxyethyllysine (d4-CEL) was used as internal standard. The molecules were created by ChemSketch and published in Rhein, S., Costalunga, R., Inderhees, J., *et al.*, 2024⁵⁵. Values are means \pm SEM. Statistical comparisons by two-tailed unpaired *t* test (**c**). * $p < 0.05$. Detailed information on the test statistics is provided in the Statistical table.

As well established in the literature, α -dicarbonyls react mainly with basic amino acids^{173,174}. Therefore, we wanted to evaluate the presence of dimethylglyoxal-glycated amino acids in the brain of acute hyperglycemic mice. Notably, HBL - a compound generated by the interaction between dimethylglyoxal and lysine - was identified based on the precursor mass (m/z = 233.14958), retention time and fragmentation spectrum. The retention time of HBL was 6.72 min (**Fig. 4.12a**), passing the stationary phase just slightly faster than the internal standard d4-CEL (6.88 min), a structurally similar compound. Moreover, two fragments were of a respective m/z of 84.0810 and 144.1023, fitting the predicted structure of HBL (**Fig. 4.12b**). Interestingly, HBL levels were lowered in the brain of *Ilvbl*^{-/-} mice compared to the *Ilvbl*^{+/+} littermates (**Fig. 4.12c**). These results confirm the role of *Ilvbl* in the generation of DMG and the ability of DMG to interact with amino acids *in vivo*, as described for other α -dicarbonyls.

4.7 Dimethylglyoxal crosses the intestinal and blood-brain barriers

Once established that DMG is a product of glucose metabolism in mammals and could generate glycated amino acids, I wondered if ingested DMG can pass the intestine and be distributed from the bloodstream to the organs. To evaluate the intestinal absorption of dimethylglyoxal, [¹³C₄] DMG (5 mg/kg) was administrated to three mice via oral gavage (**Fig. 4.13a**). This way, I was able to track the route of [¹³C₄] DMG due to the ability of high-resolution mass spectrometry to distinguish native or labeled compounds based on the exact mass.

Notably, [¹³C₄] DMG was detected in the plasma of mice treated with [¹³C₄] DMG 20 min after the gavage (**Fig. 4.13b**), demonstrating that DMG can cross the intestinal barrier. Interestingly, [¹³C₄] DMG was also detected in the brain homogenate, suggesting that DMG is able to cross the BBB (**Fig. 4.13c**). Moreover, we detected [¹³C₄] DMG in the liver homogenate (**Fig. 4.13d**), proving that DMG can also be distributed to peripheral organs. Lastly, labeled forms of 3-DG, Gx, MG or pyruvate were not detected in the plasma or tissue homogenates (data not shown), suggesting that DMG is not catabolized to pyruvate or the other α -dicarbonyls.

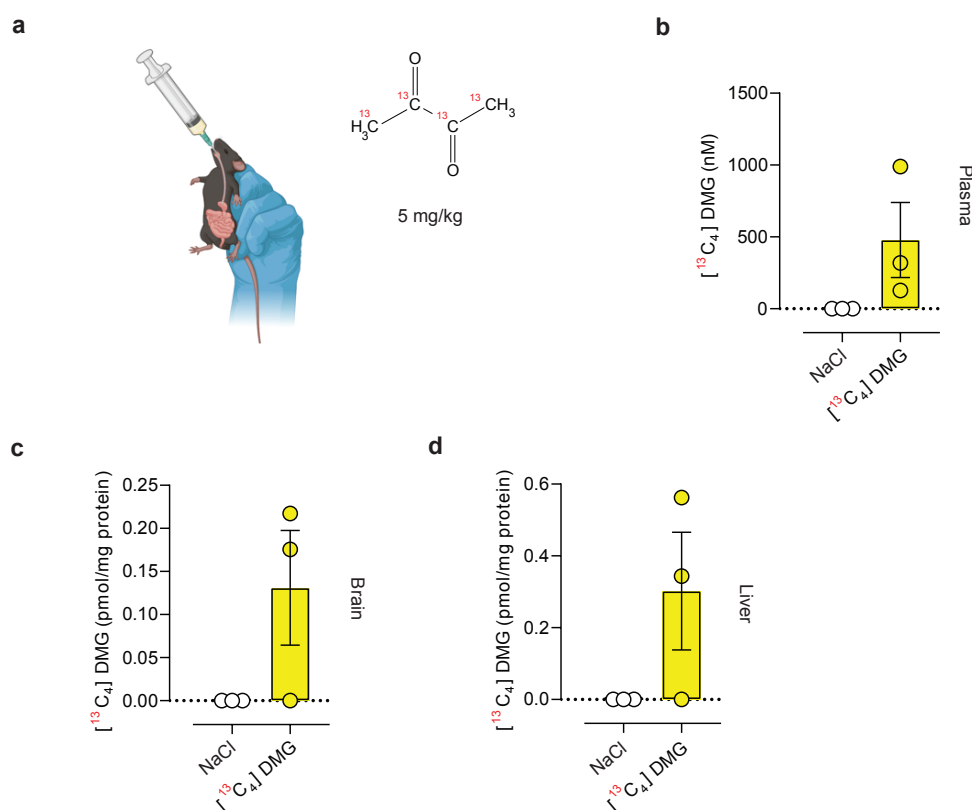


Fig. 4.13 | Dimethylglyoxal crosses the intestinal and blood-brain barriers.

a Treatment of wild-type mice with saline solution or 5 mg/kg $[^{13}\text{C}_4]$ dimethylglyoxal ($[^{13}\text{C}_4]$ DMG) solution via oral gavage. The molecule was created using ChemSketch. **b** $[^{13}\text{C}_4]$ DMG concentrations in plasma 20 min after gavage of mice with NaCl or $[^{13}\text{C}_4]$ DMG ($n = 3$ per group). **c** Concentrations of $[^{13}\text{C}_4]$ DMG in brain homogenate 20 min after gavage of mice with NaCl or $[^{13}\text{C}_4]$ DMG ($n = 3$ per group). **d** Concentrations of $[^{13}\text{C}_4]$ DMG in liver homogenate 20 min after gavage of mice with NaCl or $[^{13}\text{C}_4]$ DMG ($n = 3$ per group). For normalization, deuterated methylglyoxal (d4-MG) was used as internal standard. Values are means \pm SEM. Detailed information on the test statistics is provided in the Statistical table.

4.8 Long-term dimethylglyoxal treatment increases plasma dimethylglyoxal concentrations

Based on the ability of DMG to cross the intestinal barrier, investigating the long-term consequences of DMG exposure in mice was possible by administering the compound via water. Wild-type mice were treated with native DMG (100 mg/kg/day) dissolved in drinking water for 15 weeks (**Fig. 4.14a**). Mice treated with DMG were normoglycemic like control mice (**Fig. 4.14b**).

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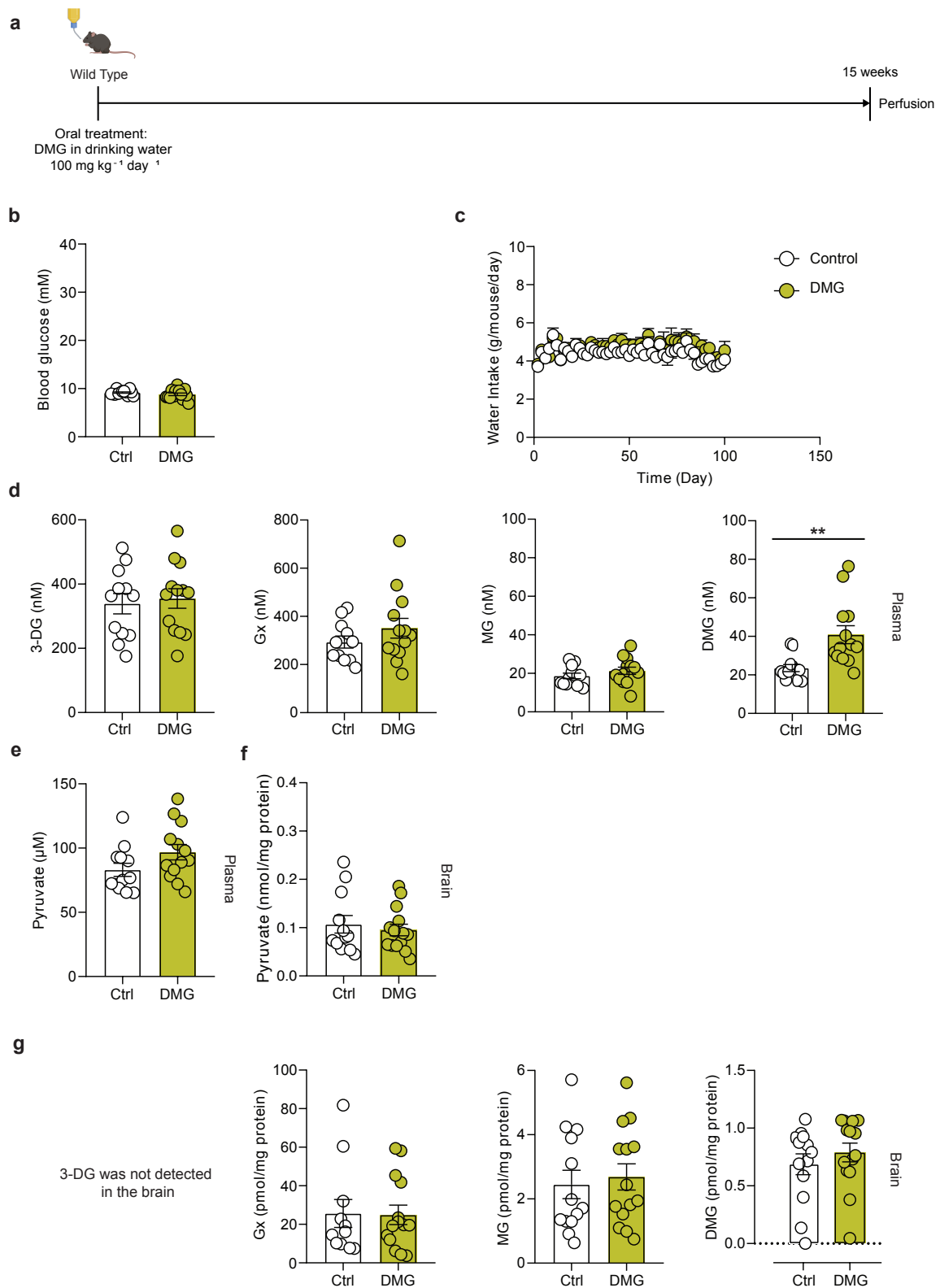


Fig. 4.14 | Long-term treatment with dimethylglyoxal increases concentrations of dimethylglyoxal in the plasma.

a Timeline of treatment with dimethylglyoxal (DMG) in drinking water and sample collection after 15 weeks. Part of the image was created with BioRender.com. **b** Blood glucose concentrations after 15 weeks of DMG oral treatment (Control, $n=13$; DMG, $n=14$). **c** Water intake of control and STZ-treated mice with tap water and water

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intake of mice with DMG in tap water (50 time points per group, 4-6 cages per group). **d** 3-Deoxyglucosone (3-DG), glyoxal (Gx), methylglyoxal (MG) and DMG concentrations in plasma after 15 weeks of DMG oral treatment (Control, $n=11-12$; DMG, $n=13$). **e** Plasma pyruvate concentrations after 15 weeks of DMG oral treatment (Control, $n=12$; DMG, $n=13$). **f** Pyruvate concentrations in brain homogenate after 15 weeks of DMG oral treatment (Control, $n=12$; DMG, $n=14$). **g** Gx, MG and DMG concentrations in brain homogenate after 15 weeks of DMG oral treatment (Control, $n=11-13$; DMG, $n=14$). For normalization, deuterated methylglyoxal (d4-MG) and [$^{13}\text{C}_3$] sodium pyruvate were used as internal standards (**d-g**). Values are means \pm SEM. Statistical comparisons by two-tailed Mann-Whitney U test (**b**; **d**, Gx and DMG; **g**, Gx and DMG), Kruskal-Wallis followed by Dunn's post hoc tests (**c**), two-tailed unpaired t test (**d**, 3-DG and MG; **e**; **f**; **g**, MG). * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

Even though this drug has a very intense smell and taste, DMG presence did not influence the water intake between control and DMG-treated mice (**Fig. 4.14c**)^{175,176}. As expected, the long-term treatment with DMG increased the plasma concentrations of DMG compared to the control group (**Fig. 4.14d**), to a similar level than in the STZ-treated mice (**Fig. 4.1d**). Moreover, 3-DG, Gx, MG or pyruvate levels were not changed between the two treatments, confirming that DMG is not a precursor of other α -dicarbonyls (**Fig. 4.14d, e**). The same results were observed regarding Gx, MG and pyruvate concentrations in the brain homogenate (**Fig. 4.14f, g**). As in previous analyses, 3-DG was not detected in the brain (**Fig. 4.14g**). Importantly, even though we proved that DMG can cross the BBB (**Fig. 4.13c**), the concentration of DMG was not changed in the brain by the chronic treatment with oral DMG (**Fig. 4.14g**), in contrast to the DMG upregulation in the type-1 diabetic mouse model (**Fig. 4.1e**).

4.9 Dimethylglyoxal induces oxidative stress and neuroinflammation *in vitro*

Previous studies showed that MG augments oxidative stress^{38,177}, thus I wondered if DMG has similar effects *in vitro*. I detected ROS production with the fluorescent dye CM-H₂DCFDA in bEnd.3 cells, Hep G2 cells and HT-22 cells. In bEnd.3 cells and in Hep G2 cells, oxidative stress is proportionally augmented by DMG in a concentration-dependent manner (**Fig. 4.15a, b**). In accordance, the highest concentration (500 μM) of DMG also increased the generation of ROS in the HT-22 cells (**Fig. 4.15c**). These findings show that DMG induces oxidative stress in cells. Lastly, to evaluate the neuroinflammatory effects of DMG, I treated HT-22 cells with DMG for 24 hours in a conventional incubator (37 °C, 5 % CO₂). Interestingly, DMG induced the expression of the pro-inflammatory genes phospholipase A2 Group IVA (*Pla2g4a*), prostaglandin E synthase (*Ptges*) and prostaglandin-endoperoxide synthase 2 (*Ptgs2*) and the expression of the pro-apoptotic gene BCL2 Like 11 (*Bim*) (**Fig. 4.15d**).

Results

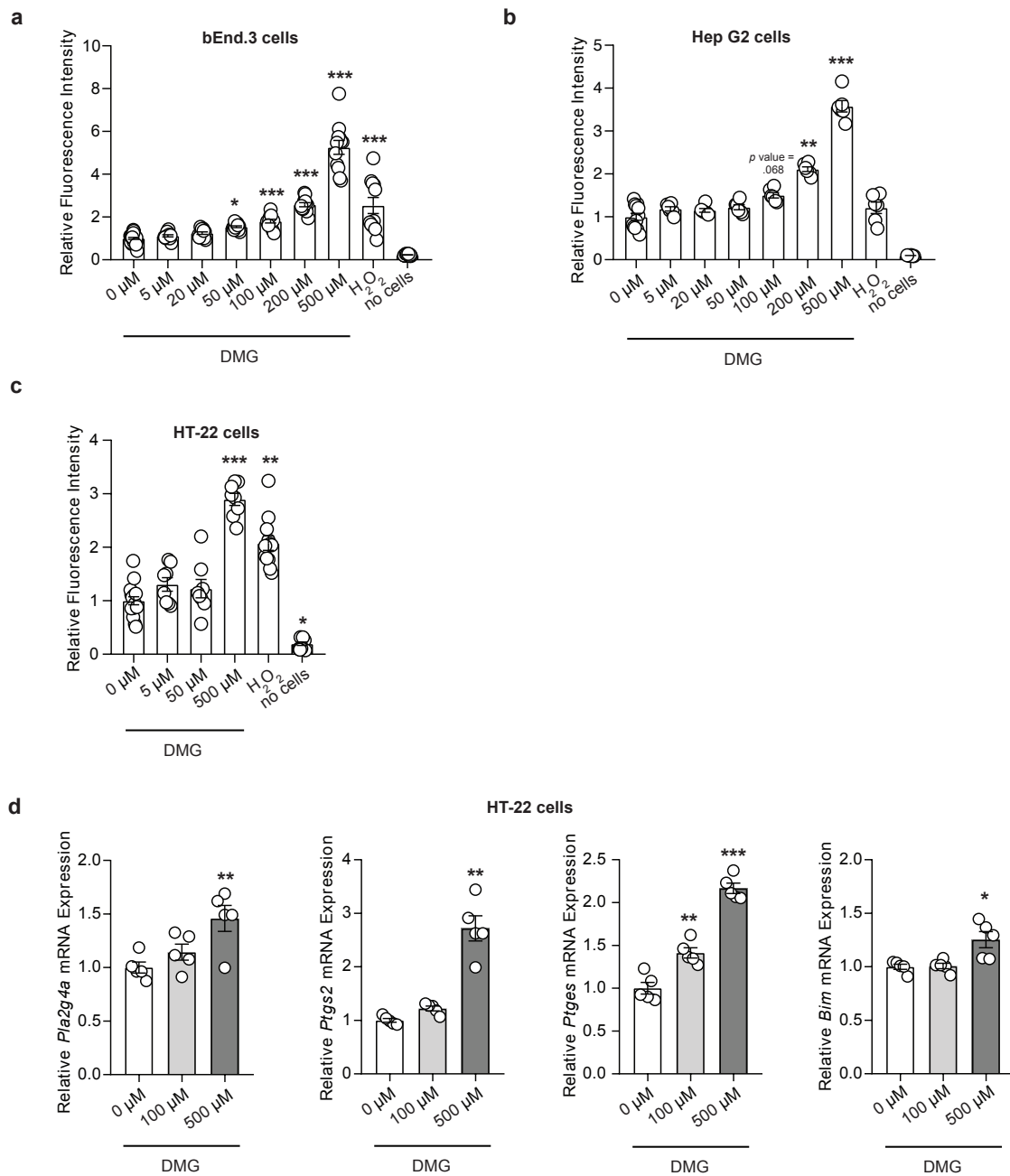


Fig. 4.15 | Dimethylglyoxal induces oxidative stress and neuroinflammation *in vitro*.

a Induction of reactive oxygen species (ROS) in mouse brain endothelial bEnd.3 cells ($n=11-12$ per group, $n=24$ for $0 \mu\text{M}$ DMG). **b** Induction of ROS in human liver cancer Hep G2 cells ($n=6$ per group, $n=12$ for $0 \mu\text{M}$ DMG). **c** Induction of ROS in mouse hippocampal neuronal HT-22 cells ($n=8$ per group, $n=16$ for $0 \mu\text{M}$ DMG). **d** mRNA expression of pro-inflammatory or pro-apoptotic genes in HT-22 cells ($n=5$ per group) treated with DMG for 24 hours. Values are means \pm SEM. Statistical comparisons by Kruskal-Wallis followed by Dunn's post hoc tests (**a**; **b**; **c**; **d**, *Ptgs2* and *Bim*) or one-way ANOVA followed by Dunnett's post hoc tests (**d**, *Pla2g4a* and *Ptges*). * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. Detailed information on the test statistics is provided in the Statistical table.

5. Discussion

5.1 Dimethylglyoxal upregulation under diabetic conditions

Reactive glucose metabolites are involved in diabetic complications through the generation of AGEs¹⁷⁸. So far, only α -dicarbonyls 3-DG, Gx and MG have been in-depth investigated and associated with diabetic complications^{9,27,36}. 3-DG and Gx are non-enzymatically generated from glucose by Maillard reaction, whereas MG is also a glycolytic metabolite^{6,7,29}. As described in the introduction, diabetic and hyperglycemic conditions increase concentrations of 3-DG, Gx and MG, leading to higher concentrations of AGEs^{14,16,24,96}. Thus, AGEs upregulation and their interaction with RAGE have been associated with diabetic neuropathy, retinopathy and nephropathy^{101,179}.

First, the current study shows that type-1 diabetic conditions increase 3-DG concentrations in mouse plasma, suggesting that the STZ-treated mouse model may be suitable for studying the dicarbonyl stress in diabetes^{16,166}. Since 3-DG is a non-enzymatic glucose metabolite and the Maillard reaction occurs *in vivo*, its plasma concentrations are positively and directly associated with blood glucose concentration in the bloodstream. Moreover, to the best of my knowledge, the current study shows the first measurements of 3-DG concentration in a mouse model of type-2 diabetes. As expected, hyperglycemic conditions increased 3-DG concentrations in *db/db* mice. In line with the experimental diabetes models, 3-DG upregulation was also observed in the serum of patients with type-1 and type-2 diabetes^{14,55}. To my knowledge, Rhein *et al.* and I first reported Gx analyses in type-1 diabetic mice, while this current study shows the first Gx concentration measurements in a mouse model of type-2 diabetes⁵⁴. Gx levels were not upregulated in type-1 or type-2 diabetes mice, whereas Gx concentrations were higher in patients with type-2 diabetes⁵⁵. Thus, Gx is not a suitable α -dicarbonyl for evaluating dicarbonyl stress in experimental diabetes models. On the other hand, previous studies and the current research have shown that plasma or serum MG concentrations are upregulated in both type-1 and type-2 diabetic animals^{167,180}. In contrast, another previous study showed that type-1 diabetic conditions do not change MG concentrations⁵⁴. Even though lack of insulin prevents glucose uptake if it depends on insulin, hyperglycemic conditions lead to higher glucose uptake in non-insulin-dependent cells⁷¹. Moreover, glycogenesis is reduced by insulin deficiency, leading to higher glucose concentration in the extracellular space and probably to a higher generation of MG by non-insulin-dependent cells¹⁸¹. Thus, glycolytic metabolites are also generated and released in the bloodstream independently of insulin sensitivity. Furthermore, since hyperglycemic conditions reduce glyoxalase I activity, MG degradation is inhibited and levels are probably higher under diabetic conditions¹⁸². The upregulation of MG has also been observed in patients with type-2 diabetes, showing that the *db/db* mouse model is also a proper experimental model for investigating the role of MG in diabetic complications^{55,183}. Pyruvate was also investigated during the current study, as it is the endpoint of the

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glycolytic pathway. Generally, researchers measure lactate levels rather than pyruvate because lactate can easily be detected and is associated with metabolic dysfunction^{184,185}. However, the current results showed that plasma pyruvate concentrations are lowered in the type-1 diabetic mice probably because it is metabolized to lactate. This research also shows that MG and pyruvate are upregulated in the liver of *db/db* mice. Since they are both glycolytic products, their upregulation could be caused by the overexpression of glycolytic genes in *db/db* mouse liver¹⁸⁶.

Only recently, α -dicarbonyl DMG has been recognized as a reactive glucose metabolite, since it is a product of glucose and pyruvate metabolism in mammal cells⁵⁴. As mentioned in the introductory part of this thesis, DMG was previously not associated with hyperglycemia or glucose metabolism in mammals. In 2013, a research reported that DMG was detected in the breath of patients with diabetes only after oral glucose administration, but researchers associated this finding with glucose metabolism in mouth bacteria¹⁸⁷. Recently, Rhein *et al.* found that plasma and brain DMG concentrations are higher in type-1 diabetic mice⁵⁴. In my thesis, the upregulation of DMG in the plasma and brain of type-1 diabetic mice was evident, confirming the previous results. Thus, our studies reported that type-1 diabetes causes DMG increase in mouse plasma, like 3-DG and MG. Furthermore, DMG was the only α -dicarbonyl upregulated in the brain of STZ-injected animals. Then, this thesis shows the measurement of DMG concentrations for the first time in type-2 diabetic mouse plasma, brain and liver. As found in type-1 diabetic mice, plasma DMG concentrations were upregulated in *db/db* mice, coherently with the higher levels of other α -dicarbonyls in this mouse model. Similar to MG, hyperglycemic conditions may increase DMG by the higher metabolism rate of glucose after non-insulin-dependent uptake. As a confirmation of the upregulation of DMG under diabetic conditions, a clinical study showed that serum DMG concentrations are augmented in patients with type-1 and type-2 diabetes⁵⁵. Even though DMG concentrations are slightly lower in humans, mouse experimental models of type-1 and type-2 diabetes used during the current thesis are suitable for the evaluation of DMG-mediated dicarbonyl stress in diabetes. Since obesity is an established phenotype and risk factor of type-2 diabetes, α -dicarbonyls were analyzed in diet-induced obese mice. My analyses showed that serum DMG levels are not increased in mice fed with HFD, like 3-DG and MG. In contrast, HFD increased the concentration of Gx. Even though HFD caused an increase in blood glucose concentration, not even the close glucose metabolite 3-DG was affected. Recently, a Dutch study showed that fasting levels of 3-DG, Gx and MG are not changed between non-diabetic lean and obese men, whereas only postprandial levels of 3-DG and MG are upregulated in obese men¹⁸⁸. Importantly, they fed men using a mixed meal containing 44 % of energy from carbohydrates and 46.6 % of energy from fat¹⁸⁸. Since the HFD mouse model has been considered a model of early type-2 diabetes, glucose introduced by diet is not properly converted to glycogen in the liver, probably leading to higher glucose conversion to reactive glucose metabolites in non-insulin-dependent cells¹⁸⁹. In the current study, obese mice

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were fed with an HFD containing 60 % kcal from fat and only 20 % kcal from carbohydrates, whereas control mice were fed with a standard diet containing 18 % kcal from fat and 58 % kcal from carbohydrates. Thus, the low carbohydrate consumption could explain why 3-DG, MG and DMG were not changed in diet-induced obese mice. For further investigation of DMG with a diet-induced obesity model, I recommend developing the diet-induced obesity model using HFD and subsequently feeding the mice with a higher content of carbohydrates, identical to control mice. This way, DMG concentrations will be investigated in obese and control mice on the same high-carbohydrate diet. Moreover, almost one-third of HFD consists of lard (31.66 % w/w), which comprises 9.5 % w/w linoleic acid and 0.8 % w/w linolenic acid¹⁹⁰. My analyses showed that Gx concentrations are dramatically increased in mice fed with HFD compared to the control group. Likely, lipid peroxidation of linoleic and linolenic acids causes the upregulation of Gx due to the significant presence of lard in the HFD formula^{18,191}. As mentioned in the introduction, high Gx concentrations can cause calcium oxalate stone accumulation in the urinary tract by its metabolism to glyoxylate and then oxalate^{22,23}. Nephrolithiasis can be prevented by diuretic treatment or diet modifications such as reduction of sodium intake, enhancement of fluid intake and reduction of oxalate intake¹⁹². Thus, the current research suggests that lard could play a potential role in generating oxalate stones. Further research could investigate the association between lard intake and nephrolithiasis in experimental models and/or clinical studies.

In summary, diabetic conditions elevate plasma DMG concentration, theoretically leading to DMG-mediated dicarbonyl stress. Dicarbonyl stress is a metabolic condition that comprises upregulation and accumulation of α -dicarbonyls. As mentioned at the beginning of this chapter, dicarbonyl stress and diabetic complications have been attributed only to 3-DG, Gx and MG so far. Rhein *et al.* and my findings suggest that DMG could be a meaningful α -dicarbonyl involved in developing diabetic complications⁵⁴.

5.2 Generation of the pyruvate metabolite dimethylglyoxal by ILVBL in mammals under pathological conditions

In plants, bacteria and yeast, DMG is generated from pyruvate, a metabolite produced from glucose via glycolysis, or from the TCA metabolite citrate by malolactic fermentation^{53,193}. Indeed, malolactic fermentation increases the DMG concentration in wine, increasing the buttery aroma¹⁹⁴. Rhein *et al.* found that bEnd.3 cells generate DMG from glucose by pyruvate as an intermediate product⁵⁵. After the C-1 decarboxylation of pyruvate, the C-2 and C-3 of two pyruvate molecules interact, generating a DMG molecule⁵⁵. In prokaryotes and yeasts, DMG is produced from pyruvate by α -acetolactate formation. Here, the enzyme ALS is involved in the formation of α -acetolactate from pyruvate¹⁹⁵. Subsequently, DMG is generated from α -acetolactate by oxidative decarboxylation. The current study

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has investigated the role of *Ilvbl*, the mammal orthologue of ALS, in the generation of DMG in mammals. To investigate the role of *Ilvbl in vitro*, bEnd.3 cells were transfected with *Ilvbl* siRNA. Beforehand, this research shows that DMG is secreted from the cells to the media, like all other α -dicarbonyls. For this reason, all following *in vitro* experiment outcomes were obtained by measuring α -dicarbonyls in the media. bEnd.3 cells were chosen because they are vulnerable to MG-mediated dicarbonyl stress, and they metabolize both glucose and lactate¹⁹⁶⁻¹⁹⁸. In the first experiment using *Ilvbl* siRNA, transfected bEnd.3 cells were treated with [¹³C₆] glucose under normoxic or hypoxic conditions. The use of the labeled form of glucose allows the isotopic tracking of the catabolism of glucose and the generation of labeled forms of α -dicarbonyls, avoiding the ambiguity caused by the inevitable presence of native α -dicarbonyls. First, my experiment confirmed that glucose is a precursor of DMG in mammal cells. Here, hypoxia increased MG, pyruvate and DMG levels, whereas 3-DG and Gx levels were not influenced by oxygen concentration. As already quoted in the introduction, hypoxic conditions increase the stability of the protein HIF-1 α , and its activation inhibits the enzyme PDH through its inhibitor PDK1¹²⁵. Since PDH is downregulated, the metabolism shifts the ATP generation from the mitochondrial TCA cycle to the cytosolic glycolysis. Thus, HIF-1 α increases the expression of glycolytic genes and glucose transporters, besides the upregulation of LDH and the consequent lactate increase¹²⁵. The upregulation of glycolysis induces the glycolytic products MG and pyruvate and the post-glycolytic product DMG. In these experiments, [¹³C₂] DMG was increased under hypoxic conditions, suggesting that it is a product of the interaction between a [¹³C₃] pyruvate and a native [¹²C₃] pyruvate. However, [¹³C₂] DMG was also detected in cells treated with native glucose, indicating that this isotopic metabolite could be naturally generated from native [¹³C₁] pyruvates with a carbon-13 in position 2 or 3. Here, the relative area of [¹³C₂] DMG was about one hundredth of the relative area of native DMG, consistent with the ratio of 1/100 for ¹³C/¹²C (data not shown). Since [¹³C₂] DMG levels were higher in cell media after treatment with [¹³C₆] glucose compared with native glucose, [¹³C₂] DMG seems to be generated both from the condensation of a [¹³C₃] pyruvate and a native [¹²C₃] pyruvate and the interaction between two native [¹³C₁] pyruvates. Lastly, 3-DG and Gx are non-enzymatic products of glucose, thus HIF-1 α stabilization does not influence the levels of these reactive glucose metabolites. [¹³C₄] DMG was also generated in bEnd.3 cells treated with [¹³C₃] pyruvate, and its levels were higher under hypoxic conditions. These results confirm that DMG is a post-glycolytic metabolite in mammals, and its generation is enhanced by the downregulation of PDH activity and the consequent shift of pyruvate catabolism. [¹³C₄] DMG was the only α -dicarbonyl generated from [¹³C₃] pyruvate, confirming that 3-DG, Gx and MG are only generated during the first part of glucose metabolism. In her doctoral thesis, Rhein showed that [¹³C₄] DMG is downregulated in the media of bEnd.3 cells transfected with *Ilvbl* siRNA, under hypoxic conditions⁵⁴. In contrast, my results show that *Ilvbl* knockdown does not influence the formation of [¹³C₄] DMG from [¹³C₆] glucose or [¹³C₃] pyruvate

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in vitro, neither in normoxia nor hypoxia. However, overexpression of *Ilvbl* leads to increased DMG levels in bEnd.3 cell media under hypoxic conditions⁵⁵. Thus, the role of *Ilvbl* in the DMG generation *in vivo* is investigated and discussed in the current thesis. First, *Ilvbl* knockout mice were fertile and showed no particular phenotype. Moreover, *Ilvbl* deficiency did not influence the generation of DMG in plasma, brain or peripheral organs of healthy mice. As mentioned above, hypoxia induces the generation of DMG, as well as the glycolytic products MG and pyruvate. To stimulate DMG formation, hyperglycemic ischemic stroke was induced by the administration of [¹³C₆] glucose prior to pMCAO. Hypoxic conditions occur during ischemic stroke due to the lower blood supply and the lack of oxygen distribution in the brain. Thus, ischemic conditions can stimulate the upregulation of glycolysis, and the lower chemical energy generation caused by the downregulation of the TCA cycle contributes to cell membrane damage by enhancing oxidative stress¹²⁸. Acute hyperglycemic conditions were induced, representing the fact that ischemic stroke can induce hyperglycemia even in patients without diabetes^{117,118}. Moreover, a previous study showed that plasma DMG levels are increased in acute hyperglycemic and ischemic mice⁵⁵. Therefore, the current experimental model of ischemic and hyperglycemic stroke is a suitable model for the evaluation of DMG-mediated dicarbonyl stress.

In the first model, normoglycemic and hyperglycemic *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice were sacrificed 25 min after pMCAO. The current study confirms that hyperglycemic conditions increase plasma DMG levels in ischemic mice. As partially mentioned above, Rhein *et al.* previously found a significant plasma upregulation of DMG in stroke-induced mice 50 min after pMCAO, whereas an insignificant positive trend was observed in mice sacrificed 30 min after pMCAO⁵⁵. In contrast, my data showed lower DMG levels in the brain of hyperglycemic mice, whereas Rhein's study showed no differences between the two groups⁵⁵. Thus, future studies should be performed to investigate DMG catabolism in the brain. It would be interesting to evaluate if DMG downregulation is caused by its interaction with amino acids or its catabolism to hydrophilic metabolites. This experiment also showed that plasma and brain [¹³C₂] and [¹³C₄] DMG are generated from [¹³C₆] glucose, confirming that DMG is a glucose metabolite *in vivo*. Lastly, *Ilvbl* deficiency did not influence the plasma or brain DMG levels in normoglycemic or hyperglycemic ischemic mice 25 min after pMCAO. In the following experiment, hyperglycemic mice were sacrificed 50 min after pMCAO. Here, normoglycemic mice were not studied since I confirmed that plasma DMG levels are higher in hyperglycemic mice, and labeled forms of DMG are generated from [¹³C₆] glucose *in vivo*. Instead, mice with sham surgery were included in this study to evaluate the effect of ischemia – and not only hyperglycemia – in the DMG generation. First, plasma [¹³C₂] and [¹³C₄] DMG concentrations were upregulated in ischemic mice, probably due to the higher glycolytic gene expression caused by hypoxia. In support of this hypothesis, native MG levels were also upregulated in hyperglycemic and stroke-induced ischemic mice, whereas ischemic stroke did not influence the non-glycolytic glucose metabolites 3-DG and Gx levels. In contrast, plasma [¹³C₃] pyruvate levels were

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downregulated in ischemic mice, probably because hypoxia also enhances the conversion of pyruvate to lactate^{125,199}. Lactate upregulation in stroke play have a positive role in protecting against neuronal damage²⁰⁰. As mentioned in the introduction, ischemic stroke induces the upregulation of glutamate, causing excitotoxicity due to increased Ca^{2+} concentration in cells^{122,130}. A Swiss group found that lactate plays a neuroprotective role against excitotoxicity through increased and released chemical energy²⁰¹. On the contrary, ischemic stroke increased native pyruvate in the ipsilateral side of the brain, probably by glycolytic upregulation under hypoxic/ischemic conditions. However, this result cannot exclude the enhanced shift from pyruvate to lactate in the brain. In support of this hypothesis, two Chinese studies showed that lactate is upregulated in the ipsilateral side of the brain of ischemic rats compared to the sham group, 60 min after surgeries^{202,203}. Moreover, native MG and Gx levels were also higher in the ipsilateral hemisphere of the ischemic mice. In addition, ischemic stroke increases MG levels in the contralateral side of the brain. Several studies showed that the contralateral side – and not only the ipsilateral side – of the brain is metabolically affected by ischemic stroke in animal models^{202,203}.

In the current study, brain DMG levels were markedly increased in stroke-induced ischemic mice. Interestingly, [¹³C₂] and [¹³C₄] DMG generation occurred from [¹³C₆] glucose in both ipsilateral and contralateral hemispheres of the brain after ischemic stroke, whereas they were absent in the brain of sham-treated mice. Therefore, the current thesis proposes that hyperglycemic and ischemic stroke may cause DMG-mediated dicarbonyl stress, suggesting that DMG may play an important role in ischemic stroke complications. Recently, Rhein, Inderhees *et al.* found that Gx, MG and their glycated amino acids are positively correlated with poor outcomes in patients with acute ischemic stroke¹¹⁸. Furthermore, during the current study, DMG levels were higher in the ipsilateral compared to the contralateral hemisphere of the brain of ischemic mice. Since the ischemic hemisphere is affected by higher anaerobic glycolysis and lower ATP generation, the brain's contralateral hemisphere could compensate for the lack of chemical energy caused by ischemic stroke, increasing glucose uptake and metabolism. Therefore, DMG upregulation could be explained by higher glucose uptake in cells of the contralateral hemisphere. Future experimental and clinical studies may focus on the role of the contralateral side in glucose metabolism under hyperglycemic and ischemic stroke. Importantly, my research shows that *Ilvbl* knockout decreased DMG levels in the ipsilateral and contralateral hemispheres of the brain after hyperglycemic and ischemic stroke. Specifically, *Ilvbl* deficiency was more efficient in DMG reduction in the ipsilateral than the contralateral side of the brain. Since type-1 diabetic conditions increase DMG concentrations, STZ-injected *Ilvbl*^{+/+} and *Ilvbl*^{-/-} mice were also investigated in DMG generation. Here, *Ilvbl* deficiency also lowered DMG levels in the brain but did not influence plasma DMG levels. Thus, the current research found that *Ilvbl* plays a significant role in DMG generation in mammals, as well as in procaryotes and yeast. However, the role of *Ilvbl* was only

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observed in the brain of diabetic and acute hyperglycemic stroke-induced ischemic mice, whereas *Ilvbl* deficiency did not affect DMG levels in healthy mice.

In summary, my studies have shown that DMG is a glucose metabolite generated by the condensation of two pyruvate molecules in mammals. Under pathological conditions, ILVBL catalyzes the catabolism of two pyruvates to α -acetolactate, an unstable metabolite converted to DMG by oxidative decarboxylation (Fig. 5.1)²⁰⁴.

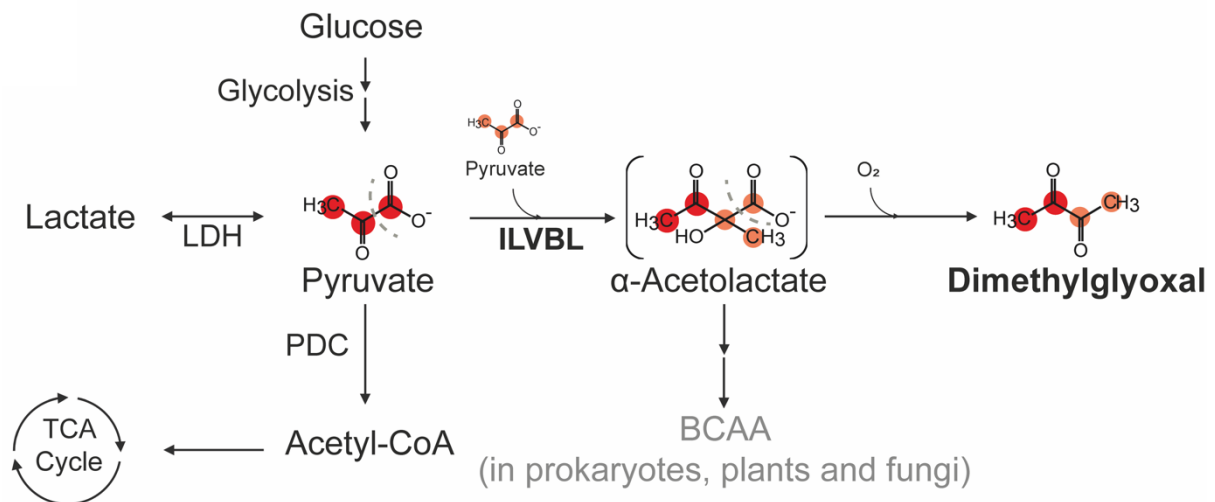


Fig. 5.1| Proposed schematic anabolic pathway to dimethylglyoxal in mammals.

The illustration was created by Biorender.com and published in Rhein, S., Costalunga, R., Inderhees, J., *et al.*, 2024⁵⁵. LDH = lactate dehydrogenase, TCA = tricarboxylic acid, PDC = pyruvate dehydrogenase, BCAA = branched-chain amino acids.

5.3 Gut microbiota does not contribute to plasma dimethylglyoxal concentrations

Once it was established that cellular glucose metabolism generates DMG and ILVBL is only partly involved in its formation in mammals, I wondered if other sources of DMG contribute to its plasma concentrations. Since bacteria and yeasts inhabit the intestine and form the gut microbiota, their contribution in the plasma DMG concentration has been investigated in this thesis. Intestinal microbiota plays a significant role in metabolic disorders and disease development²⁰⁵. For example, alteration of the gut microbiota composition can lead to dysbiosis, a condition caused by several risk factors such as a diet rich in animal fat and proteins, a sedentary life, alcohol intake and smoking²⁰⁵. Dysbiosis can reduce insulin secretion, causing hyperglycemic conditions, and is associated with type-2 diabetes²⁰⁵. Future research may evaluate the consequence of dysbiosis in generating DMG since these conditions increase blood glucose concentration. Dysbiosis conditions can be developed in germ-free mice by human fecal microbiota transplantation, even though the human-microbiota-associated

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(HMA) mouse model has significant limitations²⁰⁶. However, this current study did not focus on microbiota alterations affecting the mammal cellular DMG generation but on intestinal bacteria and yeasts contribution to DMG concentration in the bloodstream. Specifically, gut microbiota comprises lactobacilli, enterobacteria, and streptococcus, and their ability to generate DMG has been reported in the literature²⁰⁷⁻²¹⁰. To investigate whether a potential DMG generation in the intestine contributes to plasma DMG concentration in mammals, DMG and other α -dicarbonyl concentrations were measured in the plasma of SPF and germ-free mice. Germ-free mice are animals completely deprived of microorganisms, and they are characterized by memory impairment, increased BBB permeability and dysregulation in metabolism and brain gene expression^{211,212}. SPF mice possess microbiota but are free of pathogens and were used as control. The current study showed that plasma DMG concentrations were not influenced by microbiota. These findings do not exclude that DMG is a potential metabolite of microbiota but show that microbiota does not significantly influence the concentration of DMG in mammal plasma. Thus, further studies must be conducted to verify if DMG is a gut microbiota metabolite. For example, mice could be treated with [¹³C₆] glucose via oral gavage or dissolved in drinking water, and [¹³C₄] DMG presence could be investigated in the intestine. Importantly, the current research does not support the idea that any potential intervention in the microbiota would reduce DMG-mediated dicarbonyl stress. Moreover, microbiota did not influence the bacterial product MG and pyruvate concentrations in plasma²¹³. Lastly, as expected, 3-DG and Gx levels were not altered by microbiota since they are not cellular metabolites.

In summary, DMG is generated from pyruvate via ILVBL in mammals, whereas gut microbiota does not contribute to its levels in plasma. Therefore, other sources of DMG have to be investigated in further experiments. In bacteria, DMG is a product of alanine and aspartate catabolism by pyruvate as an intermediate²¹⁴. Since the amino acid catabolism cannot explain the partial role of ILVBL in DMG formation, other enzymes can be involved in its generation. An unpublished genome-wide association study recently showed a statistically significant association between the hepatic gene *Orosomuroid 2* (*ORM2*, or α -1-acid glycoprotein) and DMG in humans. Moreover, *ORM2* can play an anti-inflammatory role in the brain and bind small molecules^{215,216}. *ORM2* is highly and mainly expressed in the liver, and it is released in the bloodstream²¹⁷. Therefore, α -dicarbonyl measurements in the plasma of *Orm2* knockout mice can elucidate its role in the metabolism of dimethylglyoxal.

5.4. The role of dimethylglyoxal in diabetic complications

At this stage, we know that DMG is upregulated under diabetic or ischemic conditions and is generated from glucose in mammalian cells. Dicarbonyl stress is caused by a substantial accumulation of α -dicarbonyls in blood and tissues, causing diabetic complications²¹⁸. So far, dicarbonyl stress has been mainly associated with MG, in addition to 3-DG and Gx. Consequently, dicarbonyl stress is

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characterized by the upregulation of glycated amino acids and AGEs, generated by the interaction of α -dicarbonyls with amino acids or proteins. Rhein and I found that DMG interacts with lysine, generating HBL⁵⁴. Rhein detected HBL in the plasma of acutely dimethylglyoxal-treated mice, whereas I identified HBL in the brain of acute hyperglycemic mice⁵⁴. HBL was identified based on its retention time, precursor ion m/z and fragmentation spectrum. HBL retention time was 6.72 min, passing the column faster than the internal standard d4-CEL. Since glycated amino acids were separated using a hydrophilic column, nonpolar molecules were eluted faster than polar compounds. Since HBL contains an extra methyl group compared to d4-CEL, it is less polar than the internal standard, which explains why HBL is less retained by the stationary phase and elutes faster than d4-CEL. The precursor ion was detected with m/z of 233.14956, suggesting a molecule structure generated by a nucleophilic reaction between the lysine amino group and a carbonyl group of DMG (**Fig. 5.2**). Moreover, the fragmentation spectrum elucidated the structure of HBL by detecting two fragments. The first fragment is characterized by m/z of 84.0810, associated with only lysine structure, while the second fragment includes DMG and partial lysine structures (**Fig. 4.12b**). Importantly, *Ilvbl* deficiency lowered levels of HBL in the brain of acute hyperglycemic mice, confirming the importance of ILVBL in DMG formation *in vivo*.

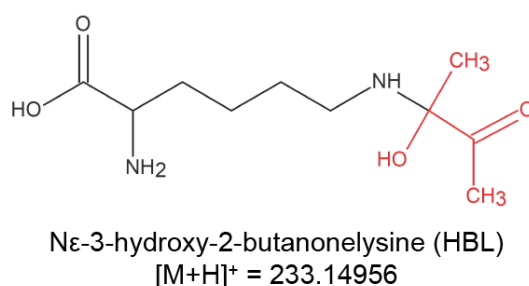


Fig. 5.2| Proposed molecular structure of HBL.

The molecule was created by ChemSketch and published in Rhein, S., Costalunga, R., Inderhees, J., *et al.*, 2024⁵⁵.

Rhein detected further dimethylglyoxal-based glycated amino acids in the plasma of DMG-injected mice, based on the interaction between DMG with lysine or arginine⁵⁴. However, my measurements did not detect other glycated amino acids. An explanation is that DMG injection markedly increased plasma DMG levels, increasing the possibility of DMG interacting with amino acids and increasing the amount of these adducts above the limit of detection⁵⁵.

In summary, our findings showed that DMG can interact with amino acids like 3-DG, Gx and MG. Thus, DMG is a reactive glucose metabolite, and its role in dicarbonyl stress has to be investigated. Notably, the reactivity of α -dicarbonyls occurs in non-hydrated form because water molecules can interact with the carbonyl groups, generating two hydrophilic groups per carbonyl group and preventing a

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nucleophilic addition. Since this organic reaction occurs under acid or basic conditions, further studies could verify the impact of the hydration of dicarbonyls *in vivo*. However, DMG has the highest non-hydrated fraction compared to MG and Gx (27 % versus 1 % and 0.005 %, respectively) in aqueous solutions due to the highest number of methyl groups^{219,220}. This fact suggests that DMG could be crucial in diabetic complications, theoretically contributing more to dicarbonyl stress than other α -dicarbonyls. In this thesis, I confirmed that DMG generates oxidative stress in brain endothelial cells⁵⁴. Endothelial cells are characterized by RAGE expression, and its binding with AGEs causes oxidative stress^{102,103}. Thus, the current data suggest that DMG can react with proteins, causing oxidative stress in endothelial cells. Rhein *et al.* found that DMG causes higher oxidative stress than MG in bEnd.3 cells and in macrophages⁵⁵. Moreover, the current thesis shows that DMG also induced ROS generation in hippocampal neuronal cells and liver cells, suggesting that DMG can cause dicarbonyl stress in neurons and peripheral organs. As discussed in the introduction, neurons can generate chemical energy from glucose via glycolysis or lactate generated in glial cells and released in the intracellular space^{72,73}. In a review published in 2013, Felipe Barros reported that neurons are protected from dicarbonyl stress since glycolysis occurs in astrocytes and neurons consume lactate without generating MG²²¹. Our latest findings show that DMG is a reactive glucose metabolite that can be generated in neurons from extracellular lactate, and it is responsible for inducing oxidative stress, probably through the interaction of its adducts with neuronal RAGEs²²². Thus, the binding of DMG-based AGEs to RAGEs may activate the enzyme NADPH oxidase²²³. Indeed, both AGE-RAGE engagement and NADPH oxidase cause cytokine and chemokine overexpression and activate the NF- κ B cascade, besides ROS enhancement^{103,105,222,224}. Moreover, this study shows that DMG induced the expression of neuronal pro-inflammatory genes *Pla2g4a*, *Ptgs2*, and *Ptges*, encoding enzymes involved in the anabolism of prostaglandins. *Pla2g4a* expression increases arachidonic acid formation, which is subsequently converted to PGH₂ by COXs. In particular, *Ptgs2* is an inducible COX isoform under inflammatory conditions, even though constitutive *Ptgs2* is present in the brain²²⁵. Subsequently, PGH₂ is converted to PGE₂ by *Ptges*. Interestingly, PGE₂ levels are higher in patients with diabetes and positively correlated with hyperglycemic conditions²²⁶. In particular, upregulation of PGE₂ has been observed in patients with diabetic retinopathy, which may be caused and worsened by accumulation of AGEs^{227,228}. Moreover, neuroinflammatory effects of DMG have been confirmed *in vivo*^{54,55}. DMG also induced the expression of the pro-apoptotic gene *Bim* in hippocampal neuronal cells. Neuronal *Bim* has been associated with neuron death in Alzheimer's Disease (AD), and AGEs have been linked to neuronal dysfunction and pathogenesis of neurological diseases^{229,230}. Thus, glycation of protein with DMG may play a role in cognitive impairment and the development of neurological diseases.

Since diabetic and hyperglycemic conditions increase the risk of vascular dementia, a mouse model of chronic DMG upregulation had to be developed to investigate its role in developing neuronal diabetic

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complications²³¹⁻²³³. Chronic DMG concentration can be potentially increased by the long-term consumption of drinking water containing DMG. First, to evaluate whether DMG can cross the intestinal barrier is crucial, mice were treated with [¹³C₄] DMG via oral gavage and sacrificed 20 min after the treatment. The current study showed that [¹³C₄] DMG was detected in the plasma of treated mice, proving that DMG can cross the intestine. Moreover, this experiment shows that DMG can cross the BBB and be distributed to peripheral organs since [¹³C₄] DMG was detected in the brain and liver. Based on these findings, mice were treated with 100 mg kg⁻¹ day⁻¹ native DMG in drinking water for 15 weeks. Plasma DMG concentrations were upregulated in a mouse model of long-term treatment with DMG, similar to the plasma concentrations of DMG in type-1 diabetic mice. However, brain DMG concentrations did not differ between DMG-treated mice and controls, suggesting that the dose of DMG in drinking water should be increased in future experiments in order to replicate brain DMG concentration of type-1 mice. Anyhow, long-term treatment with DMG caused cognitive impairment and BBB damage, similar to neurological complications in type-1 diabetic mice⁵⁵. Since diabetic conditions increase DMG concentrations and long-term DMG treatment induces cognitive deficits, DMG may play an important role in the development of dementia in diabetes. Thus, future studies must be implemented to develop strategies focused on DMG reduction or the hindrance of protein glycation caused by DMG. Besides lifestyle improvement and dietary correction, pharmacological strategies may be investigated for DMG-mediated dicarbonyl stress reduction. For example, combining insulin and metformin lowered DMG levels in patients with diabetes⁵⁵. Metformin mainly affects the liver, reducing gluconeogenic flux and blood glucose concentrations²³⁴. Thus, this drug increases the conversion of pyruvate to lactate, possibly causing the reduction of DMG levels. On the other hand, its mechanism of action causes lactate accumulation, which can rarely lead to lactic acidosis²³⁵. Even though metformin is considered safe, it can develop further side effects such as nausea, vomiting, headache and metallic taste²³⁵. Nevertheless, the role of metformin in reducing DMG generation and mitigating the consequence of dicarbonyl stress should be further investigated in experimental and clinical diabetes. As mentioned in the introduction, acetylsalicylic acid may compete with DMG and other α -dicarbonyls in post-translational protein modification, reducing the glycation of proteins²³⁶. Indeed, acetylsalicylic acid and paracetamol prevent cataract development in type-1 diabetic rats¹⁰⁸. Therefore, acetylsalicylic acid effects could be investigated in preventing diabetic complications in experimental models of diabetes and/or long-term DMG intake. Moreover, the reverse strategy consists of reducing α -dicarbonyl availability to decrease protein glycation. So far, the investigational drug pimagedine has been studied in the reduction of protein glycation through its interaction with α -dicarbonyls¹¹⁰. However, pimagedine has not been approved for therapeutical use¹⁰⁹. Then, pharmacological strategies can be investigated to reduce DMG production and/or stimulate DMG degradation. Previously, this thesis has shown that DMG is generated from pyruvate via ILVBL.

Discussion

ILVBL is a druggable enzyme since its orthologue ALS is inhibited in other species. Since the 1980s, several classes of herbicides have been used as antagonists of ALS to suppress weed growth²³⁷. This pesticide class inhibits the BCAA synthesis, causing a reduction of cell division and cell death²³⁷. However, preliminary data showed that ALS-inhibitor treatment does not affect the generation of labeled DMG in bEnd.3 cells treated with [¹³C₆] glucose²³⁸. Therefore, further research has to be conducted to discover proper ILVBL antagonists. However, *Ilvbl* deficiency did not reduce the infarct volume or BBB damage compared to *Ilvbl*^{+/+} 2 days after pMCAO⁵⁵. Moreover, DMG reduction in *Ilvbl*^{-/-} mice did not influence BBB properties or neuroinflammatory states in type-1 diabetic mice (data not shown). Thus, these findings suggest addressing resources to other strategies in lowering dicarbonyl stress mediated by DMG.

Detoxification of Gx and MG is regulated by the glyoxalase system, based on their aldehyde structure^{21,40}. On the other hand, DMG is an α -diketone and, therefore, is not metabolized by the glyoxalase system. Actually, brain glyoxalase I activity is inhibited by DMG²³⁹. Thus, the downregulation of glyoxalase I under hyperglycemic conditions may also be explained by the upregulation of DMG, worsening dicarbonyl stress states¹⁸². In bacteria, DMG is catabolized to acetoin by diacetyl reductase (dicarbonyl/L-xylulose reductase, DR or DCXR), followed by acetoin reduction to 2,3-butanediol by acetoin reductase (AR)⁴⁸. A previous study found that mammal diacetyl reductase could metabolize DMG to acetoin, and that this enzyme can catalyze the oxidoreduction reaction between L-xylulose and xylitol²⁴⁰. DR deficiency has been observed in 1 in 3,300 people with Ashkenazi Jewish ancestry due to genetic mutations, causing pentosuria due to accumulation of L-xylulose in the urine²⁴¹⁻²⁴³. Regarding the role of AR, a research group found that 2,3-butanediol is a metabolite of acetoin in mammalian liver homogenates in 1971²⁴⁴. Therefore, the role of DR and AR in DMG elimination should be investigated by downregulation and/or overexpression. Future research can further explore the formation of [¹³C₄] acetoin and [¹³C₄] 2,3-butanediol from [¹³C₄] DMG in mammal cell lines.

Moreover, my unpublished preliminary data suggest that Hep G2 cells are able to lower DMG concentrations in the media. Since the liver plays a crucial role in the detoxification and metabolism of drugs, the Hep G2 cell line is suitable for the evaluation of DMG degradation. If these assumptions are confirmed, one could try to stimulate DMG elimination by upregulation of DR and AR activities in liver cells.

5.5 Conclusions

This research has investigated the α -dicarbonyl DMG in several mouse models under pathological conditions. Importantly, the current thesis has demonstrated that DMG concentrations are upregulated in mouse models of type-1 and type-2 diabetes (**Fig. 5.3**). Moreover, the current study has shown that acute hyperglycemia and ischemic stroke markedly increased DMG levels in the ischemic

Discussion

hemisphere of the brain, whereas plasma DMG levels were only slightly increased in this experimental model (**Fig. 5.3**). The current work has confirmed that DMG is a post-glycolytic metabolite in mammals, and its production is higher under hypoxic conditions (**Fig. 5.3**). Therefore, the post-glycolytic DMG generation explains why cells consuming lactate – such as neurons and brain endothelial cells – are subjected to dicarbonyl stress, even though the pyruvate generation is not exclusively based on glycolysis. Importantly, this research has demonstrated that *Ilvbl* is involved in the generation of DMG in the brain of mice under chronic or ischemic hyperglycemia. Notably, the current study has identified HBL, a glycated amino acid generated by nucleophilic addition between the lysine amino group and the carbonyl group of DMG. Thus, this finding suggests the ability of DMG to interact with proteins, generating AGEs. The engagement of DMG-based AGEs with RAGE causes oxidative stress, neuroinflammation, BBB damage and development of cognitive impairment, mimicking neurological complications of diabetes (**Fig. 5.3**)⁵⁵.

In summary, DMG is crucial in developing dicarbonyl stress under diabetic or ischemic conditions. The discovery of DMG as a reactive pyruvate metabolite significantly contributes to a better understanding of dicarbonyl stress in neurological diabetic complications and the development of potential therapeutic strategies to reduce dicarbonyl effects.

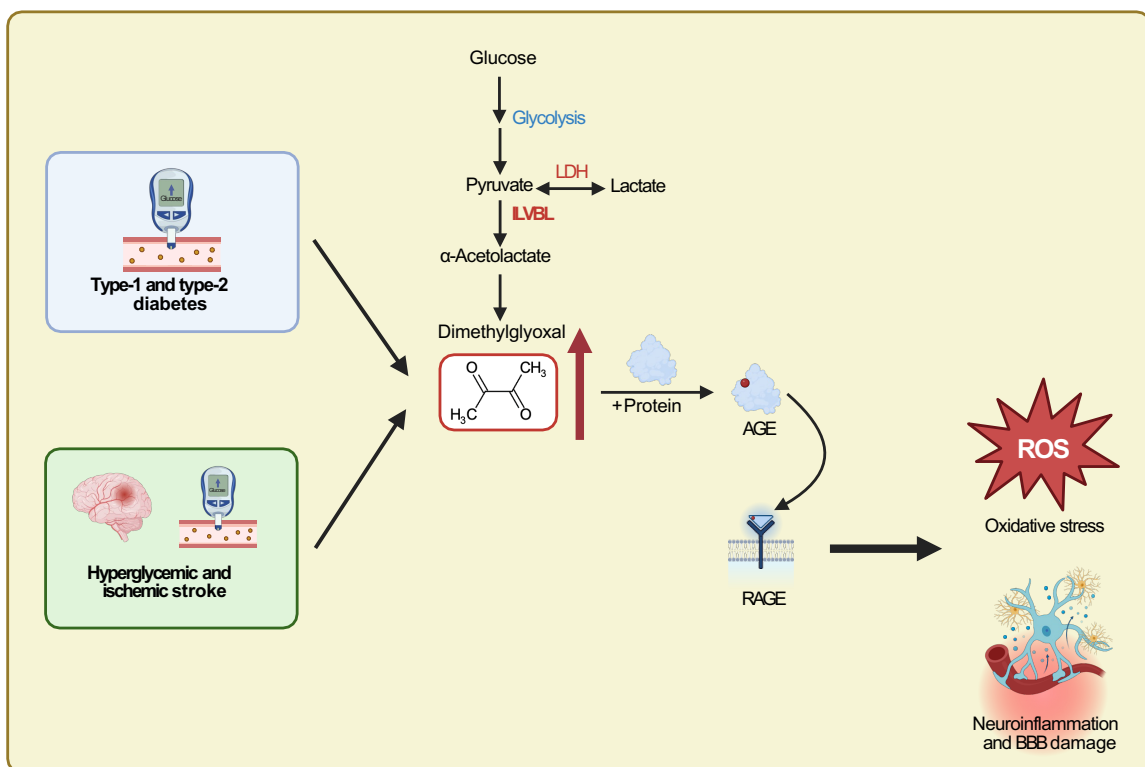


Fig. 5.3| Schematic illustration of dimethylglyoxal generation in mammal cells and its role in diabetic or ischemic complications.

Discussion

This illustration was created with Biorender.com and Adobe Photoshop 2024 and modified after Inderhees, J., *et al.*, submitted²⁴⁵. LDH = lactate dehydrogenase, ILVBL = ilvB acetolactate synthase-like, AGE = advanced glycation end product, RAGE = receptor for advanced glycation end product, ROS = reactive oxygen species, BBB = blood-brain barrier.

Statistical table

Statistical table

Table 6.1 | Statistical Table

Figure	Sample size (n)	Statistical test	Values	Comments
1b	13 mice/group	Two-tailed Mann-Whitney U test	$p < .001$	
1c	50 time points/group, 4-6 cages/group	Mixed-effects model (REML)	Time: $F(4.5, 44.2) = 13.0, p < .001$ Treatment: $F(1, 10) = 147.7, p < .001$	
1d	3-DG, MG and DMG: Control: 12 mice STZ: 11 mice Gx: 11 mice/group	3-DG and Gx: Two-tailed Mann-Whitney U test MG and DMG: Two-tailed unpaired t test	3-DG: $p < .001$ Gx: $p = .076$ MG: $T(21) = 4.0, p < .001$ DMG: $T(21) = 2.3, p = .030$	Value excluded: Gx: 1 outlier (Control)
1e	Gx: 11 mice/group MG and DMG: Control: 13 mice STZ: 12 mice	Gx: Two-tailed Mann-Whitney U test MG and DMG: Two-tailed unpaired t test	Gx: $p = .797$ MG: $T(23) = 1.3, p = .219$ DMG: $T(23) = 2.3, p = .028$	Values excluded: Gx: 2 outliers (Control) and 1 outlier (STZ)
1f	Control: 12 mice STZ: 11 mice	Two-tailed Mann-Whitney U test	$p = .023$	
1g	12 mice/group	Two-tailed Mann-Whitney U test	$p = .160$	Value excluded: 1 outlier (Control)
2b	12 mice/group	2-way RM ANOVA	Time: $F(2.2, 47.5) = 457.6, p < .001$ Genotype: $F(1, 22) = 75.8, p < .001$ Interaction: $F(6, 132) = 109.0, p < .001$	
2c	11 mice/group	Two-tailed Mann-Whitney U test	$p < .001$	
2d	3-DG: <i>db/+</i> : 11 mice <i>db/db</i> : 10 mice Gx, MG and DMG: 11 mice/group	Two-tailed Mann-Whitney U test	3-DG: $p = .003$ Gx: $p = .078$ MG: $p < .001$ DMG: $p = .010$	
2e	11 mice/group	Two-tailed unpaired t test	$T(20) = 0.4, p = .664$	
2f	<i>db/+</i> : 11 mice <i>db/db</i> : 12 mice	Two-tailed unpaired t test	Gx: $T(21) = 0.6, p = .543$ MG: $T(21) = 1.1, p = .273$ DMG: $T(21) = 0.9, p = .403$	
2g	<i>db/+</i> : 9 mice <i>db/db</i> : 10 mice	Two-tailed Mann-Whitney U test	$p = .905$	Values excluded: 1 outlier (<i>db/+</i>) and 2 outliers (<i>db/db</i>)
2h	<i>db/+</i> : 11 mice <i>db/db</i> : 12 mice	Two-tailed unpaired t test	3-DG: $T(21) = 0.4, p = .673$ Gx: $T(21) = 2.2, p = .036$ MG: $T(21) = 2.2, p = .040$ DMG: $T(21) = 0.5, p = .634$	
2i	<i>db/+</i> : 11 mice <i>db/db</i> : 12 mice	Two-tailed unpaired t test	$T(21) = 3.1, p = .005$	
3a	Standard Diet: 8 mice High-Fat Diet: 7 mice	Two-tailed unpaired t test	$T(13) = 2.5, p = .029$	
3b	Standard Diet: 8 mice High-Fat Diet: 7 mice	Two-tailed Mann-Whitney U test	$p < .001$	
3c	3-DG and MG: 8 mice/group Gx and DMG: Standard Diet: 8 mice High-Fat Diet: 7 mice	3-DG and MG: Two-tailed unpaired t test Gx and DMG: Two-tailed Mann-Whitney U test	3-DG: $T(14) = 0.1, p = .883$ Gx: $p < .001$ MG: $T(14) = 0.9, p = .383$ DMG: $p = .694$	Values excluded: Gx: 1 outlier (HFD) DMG: 1 outlier (HFD)
4b	4 wells/group	Native glucose: Descriptive only Labeled glucose: Two-tailed Mann-Whitney U test	$p = .029$	
4c	4 wells/group	Cells: Descriptive only Supernatant: Two-tailed Mann-Whitney U test	$p = .029$	
4d	4 wells/group	Native glucose: Descriptive only Labeled glucose: Two-tailed Mann-Whitney U test	MG (M+2): $p = .029$ MG (M+3): $p = .029$	

Statistical table

4e	4 wells/group	Native glucose: Descriptive only Labeled glucose: Two-tailed Mann-Whitney U test	$p = .029$	
4f	4 wells/group	DMG (M+2): Native glucose: Descriptive only Labeled glucose: Two-tailed Mann-Whitney U test, Bonferroni-Holm correction Supernatant: Two-tailed Mann-Whitney U test, Bonferroni-Holm correction Cells: Descriptive only DMG (M+4): Descriptive only	DMG (M+2): Labeled glucose: $p = .029$ Supernatant: $p = .020$	
5b	Scramble siRNA: 8 wells (Normoxia) and 7 wells (Hypoxia) <i>Ilvbl</i> siRNA: 8 wells/group	Scheirer-Ray-Hare test with Mann-Whitney post hoc tests, Bonferroni-Holm correction	Oxygen: $\chi^2 (1) = 5.1, p = .577$ siRNA: $\chi^2 (1) = 21.0, p < .001$ Interaction: $\chi^2 (1) = 0.2, p = .697$ Normoxia: Scramble siRNA vs <i>Ilvbl</i> siRNA: $p < .001$ Hypoxia: Scramble siRNA vs <i>Ilvbl</i> siRNA: $p < .001$	
5c	8 wells/group	Scheirer-Ray-Hare test	Oxygen: $\chi^2 (1) = 0.7, p = .407$ siRNA: $\chi^2 (1) = 0.02, p = .880$ Interaction: $\chi^2 (1) = 0.5, p = .498$	
5d	8 wells/group	2-way ANOVA	Oxygen: $F (1,28) = 2.0, p = .165$ siRNA: $F (1,28) = 1.5, p = .224$ Interaction: $F (1,28) = 0.01, p = .982$	
5e	8 wells/group	Scheirer-Ray-Hare test	Oxygen: $\chi^2 (1) = 23.3, p < .001$ siRNA: $\chi^2 (1) = 0.3, p = .598$ Interaction: $\chi^2 (1) = 0.3, p = .598$	
5f	8 wells/group	2-way ANOVA followed by Sidak's post-hoc tests (p -values adjusted for multiple comparisons)	Oxygen: $F (1,28) = 60.6, p < .001$ siRNA: $F (1,28) = 14.4, p < .001$ Interaction: $F (1,28) = 1.1, p = .312$ Normoxia: Scramble siRNA vs <i>Ilvbl</i> siRNA: $p = .117$ Hypoxia: Scramble siRNA vs <i>Ilvbl</i> siRNA: $p = .004$	
5g	8 wells/group	DMG (M+2): 2-way ANOVA DMG (M+4): Scheirer-Ray-Hare test	DMG (M+2): Oxygen: $F (1,28) = 9.2, p = .005$ siRNA: $F (1,28) = 1.5, p = .236$ Interaction: $F (1,28) = 1.2, p = .291$ DMG (M+4): Oxygen: $\chi^2 (1) = 13.4, p < .001$ siRNA: $\chi^2 (1) = 0.2, p = .678$ Interaction: $\chi^2 (1) = 0.7, p = .407$	
6b	10 wells/group	Scheirer-Ray-Hare test	Oxygen: $\chi^2 (1) = 0.4, p = .512$ siRNA: $\chi^2 (1) = 0.1, p = .725$ Interaction: $\chi^2 (1) = 0.001, p = .978$	
6c	10 wells/group	Scheirer-Ray-Hare test	DMG (M+2): Oxygen: $\chi^2 (1) = 29.3, p < .001$ siRNA: $\chi^2 (1) = 1.1, p = .304$ Interaction: $\chi^2 (1) = 0.0, p > .999$ DMG (M+4): Oxygen: $\chi^2 (1) = 29.3, p < .001$ siRNA: $\chi^2 (1) = 0.0, p > .999$ Interaction: $\chi^2 (1) = 0.2, p = .626$	
7a	3 mice/group	Descriptive only		
7b	<i>Ilvbl</i> ^{+/+} : 4 mice <i>Ilvbl</i> ^{-/-} : 6 mice	Two-tailed unpaired t test	$T (8) = 0.8, p = .448$	

Statistical table

7c	3 mice/group	Two-tailed unpaired t test	$T(4) = 0.7, p = .533$	
7d	7 mice/group	Two-tailed unpaired t test	$T(12) = 1.5, p = .170$	
7e	3 mice/group	Two-tailed Mann-Whitney U test	$p = .700$	
7f	3 mice/group	Two-tailed unpaired t test	$T(4) = 0.1, p = .954$	
8b	Saline Injection: 12 mice/group Glucose injection: 11 mice/group	Scheirer-Ray-Hare test	DMG (M): Genotype: $\chi^2(1) = 0.03, p = .866$ Injection: $\chi^2(1) = 13.5, p < .001$ Interaction: $\chi^2(1) = 0.01, p = .916$ DMG (M+2): Genotype: $\chi^2(1) = 0.5, p = .501$ Injection: $\chi^2(1) = 29.3, p < .001$ Interaction: $\chi^2(1) = 0.003, p = .954$ DMG (M+4): Genotype: $\chi^2(1) = 0.4, p = .468$ Injection: $\chi^2(1) = 29.5, p < .001$ Interaction: $\chi^2(1) = 0.01, p = .917$	
8c	Saline Injection: 12 mice/group Glucose injection: 11 mice/group	Scheirer-Ray-Hare test	Genotype: $\chi^2(1) = 2.1, p = .150$ Injection: $\chi^2(1) = 11.2, p < .001$ Interaction: $\chi^2(1) = 0.3, p = .578$	
8d	11 mice/group	2-way RM ANOVA	DMG (M+2): Genotype: $F(1,20) = 0.3, p = .608$ Side: $F(1,20) = 0.003, p = .959$ Interaction: $F(1,20) = 0.1, p = .727$ DMG (M+4): Genotype: $F(1,20) = 0.01, p = .935$ Side: $F(1,20) = 2.3, p = .143$ Interaction: $F(1,20) = 0.1, p = .753$	
9b	Sham – <i>Ilvb1^{+/+}</i> : 11 mice Sham – <i>Ilvb1^{-/-}</i> : 14 mice pMCAO – <i>Ilvb1^{+/+}</i> : 9 mice pMCAO – <i>Ilvb1^{-/-}</i> : 5 mice	Scheirer-Ray-Hare test followed by two-tailed Mann-Whitney U post hoc tests, Bonferroni-Holm correction	DMG (M): Treatment: $\chi^2(1) = 2.7, p = .100$ Genotype: $\chi^2(1) = 1.0, p = .310$ Interaction: $\chi^2(1) = 0.3, p = .580$ DMG (M+2): Treatment: $\chi^2(1) = 14.8, p < .001$ Genotype: $\chi^2(1) = 1.6, p = .201$ Interaction: $\chi^2(1) = 0.5, p = .480$ <i>Ilvb1^{+/+}</i> : Sham vs MCAO: $p = .002$ <i>Ilvb1^{-/-}</i> : Sham vs MCAO: $p = .014$ DMG (M+4): Treatment: $\chi^2(1) = 11.7, p < .001$ Genotype: $\chi^2(1) = 2.3, p = .131$ Interaction: $\chi^2(1) = 0.6, p = .445$ <i>Ilvb1^{+/+}</i> : Sham vs MCAO: $p = .004$ <i>Ilvb1^{-/-}</i> : Sham vs MCAO: $p = .070$	
9c	Sham – <i>Ilvb1^{+/+}</i> : 11 mice Sham – <i>Ilvb1^{-/-}</i> : 14 mice pMCAO – <i>Ilvb1^{+/+}</i> : 9 mice pMCAO – <i>Ilvb1^{-/-}</i> : 5 mice	Scheirer-Ray-Hare test	MG: Treatment: $\chi^2(1) = 5.5, p = .020$ Genotype: $\chi^2(1) = 0.3, p = .560$ Interaction: $\chi^2(1) = 0.8, p = .365$ MG (M+3): Treatment: $\chi^2(1) = 0.9, p = .331$ Genotype: $\chi^2(1) = 0.3, p = .593$ Interaction: $\chi^2(1) = 1.8, p = .178$	
9d	Sham – <i>Ilvb1^{+/+}</i> : 11 mice Sham – <i>Ilvb1^{-/-}</i> : 14 mice pMCAO – <i>Ilvb1^{+/+}</i> : 9 mice	Gx (M): 2-way ANOVA Gx (M+2): Scheirer-Ray-Hare test	Gx (M): Treatment: $F(1,35) = 3.2, p = .081$	

Statistical table

	pMCAO – <i>Ilvb1^{+/+}</i> : 5 mice		Genotype: $F(1,35) = 0.1, p = .779$ Interaction: $F(1,35) = 0.4, p = .542$ Gx (M+2): Treatment: $\chi^2(1) = 2.9, p = .090$ Genotype: $\chi^2(1) = 2.9, p = .089$ Interaction: $\chi^2(1) = 0.6, p = .438$	
9e	Sham – <i>Ilvb1^{+/+}</i> : 11 mice Sham – <i>Ilvb1^{-/-}</i> : 14 mice pMCAO – <i>Ilvb1^{+/+}</i> : 9 mice pMCAO – <i>Ilvb1^{-/-}</i> : 5 mice	3-DG (M): 2-way ANOVA 3-DG (M+6): Scheirer-Ray-Hare test	3-DG (M): Treatment: $F(1,35) = 0.01, p = .942$ Genotype: $F(1,35) = 0.2, p = .628$ Interaction: $F(1,35) = 0.04, p = .836$ 3-DG (M+6): Treatment: $\chi^2(1) = 1.7, p = .194$ Genotype: $\chi^2(1) = 0.01, p = .929$ Interaction: $\chi^2(1) = 1.0, p = .326$	
9f	Sham – <i>Ilvb1^{+/+}</i> : 11 mice Sham – <i>Ilvb1^{-/-}</i> : 14 mice pMCAO – <i>Ilvb1^{+/+}</i> : 9 mice pMCAO – <i>Ilvb1^{-/-}</i> : 5 mice	2-way ANOVA	Pyruvate (M): Treatment: $F(1,35) = 1.0, p = .323$ Genotype: $F(1,35) = 0.1, p = .323$ Interaction: $F(1,35) = 6.7, p = .014$ Sham: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i> : $p = .120$ MCAO: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i> : $p = .637$ <i>Ilvb1^{+/+}</i> : Sham vs MCAO: $p = .794$ <i>Ilvb1^{-/-}</i> : Sham vs MCAO: $p = .132$ Pyruvate (M+3): Treatment: $F(1,35) = 19.9, p < .001$ Genotype: $F(1,35) = 0.4, p = .539$ Interaction: $F(1,35) = 2.7, p = .106$	
9g	Sham – <i>Ilvb1^{+/+}</i> : 14 mice Sham – <i>Ilvb1^{-/-}</i> : 17 mice pMCAO – <i>Ilvb1^{+/+}</i> : 12 mice pMCAO – <i>Ilvb1^{-/-}</i> : 10 mice	3-way RM ANOVA followed by Sidak's post hoc tests (p -values adjusted for multiple comparisons)	DMG (M): Side: $F(1,49) = 25.1, p < .001$ Treatment: $F(1,49) = 157.8, p < .001$ Genotype: $F(1,49) = 10.0, p = .003$ Contralateral side – <i>Ilvb1^{+/+}</i> : Sham vs MCAO: $p < .001$ Contralateral side – <i>Ilvb1^{-/-}</i> : Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{+/+}</i> : Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{-/-}</i> : Sham vs MCAO: $p < .001$ Contralateral side – Sham: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i> : $p > .999$ Contralateral side – MCAO: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i> : $p = .017$ Ipsilateral side – Sham: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i> : $p > .999$ Ipsilateral side – MCAO: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i> : $p < .001$ Sham – <i>Ilvb1^{+/+}</i> : Contralateral side vs ipsilateral side: $p > .999$ Sham – <i>Ilvb1^{-/-}</i> : Contralateral side vs ipsilateral side: $p = .978$ pMCAO – <i>Ilvb1^{+/+}</i> : Contralateral side vs ipsilateral side: $p < .001$ pMCAO – <i>Ilvb1^{-/-}</i> : Contralateral side vs ipsilateral side: $p = .007$	

Statistical table

			<p>DMG (M+2): Side: $F(1,49) = 29.8, p < .001$ Treatment: $F(1,49) = 144.2, p < .001$ Genotype: $F(1,49) = 5.3, p = .025$</p> <p>Contralateral side – <i>Ilvb1^{+/+}</i>: Sham vs MCAO: $p < .001$ Contralateral side – <i>Ilvb1^{-/-}</i>: Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{+/+}</i>: Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{-/-}</i>: Sham vs MCAO: $p < .001$ Contralateral side – Sham: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i>: $p > .999$ Contralateral side – MCAO: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i>: $p = .184$ Ipsilateral side – Sham: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i>: $p > .999$ Ipsilateral side – MCAO: <i>Ilvb1^{+/+}</i> vs <i>Ilvb1^{-/-}</i>: $p = .007$ Sham – <i>Ilvb1^{+/+}</i>: Contralateral side vs ipsilateral side: $p > .999$ Sham – <i>Ilvb1^{-/-}</i>: Contralateral side vs ipsilateral side: $p > .999$ pMCAO – <i>Ilvb1^{+/+}</i>: Contralateral side vs ipsilateral side: $p < .001$ pMCAO – <i>Ilvb1^{-/-}</i>: Contralateral side vs ipsilateral side: $p = .030$</p> <p>DMG (M+4): Side: $F(1,49) = 54.6, p < .001$ Treatment: $F(1,49) = 126.4, p < .001$ Genotype: $F(1,49) = 0.4, p = .524$</p> <p>Contralateral side – <i>Ilvb1^{+/+}</i>: Sham vs MCAO: $p < .001$ Contralateral side – <i>Ilvb1^{-/-}</i>: Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{+/+}</i>: Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{-/-}</i>: Sham vs MCAO: $p < .001$ Sham – <i>Ilvb1^{+/+}</i>: Contralateral side vs ipsilateral side: $p > .999$ Sham – <i>Ilvb1^{-/-}</i>: Contralateral side vs ipsilateral side: $p > .999$ pMCAO – <i>Ilvb1^{+/+}</i>: Contralateral side vs ipsilateral side: $p < .001$ pMCAO – <i>Ilvb1^{-/-}</i>: Contralateral side vs ipsilateral side: $p < .001$</p>	
9h	Sham- <i>Ilvb1^{+/+}</i> : 14 mice Sham- <i>Ilvb1^{-/-}</i> : 17 mice pMCAO- <i>Ilvb1^{+/+}</i> : 12 mice pMCAO- <i>Ilvb1^{-/-}</i> : 10 mice	3-way RM ANOVA followed by Sidak's post hoc tests (p -values adjusted for multiple comparisons)	<p>MG (M): Side: $F(1,49) = 3.9, p = .055$ Treatment: $F(1,49) = 150.3, p < .001$ Genotype: $F(1,49) = 0.1, p = .776$</p> <p>Contralateral side – <i>Ilvb1^{+/+}</i>: Sham vs MCAO: $p < .001$ Contralateral side – <i>Ilvb1^{-/-}</i>: Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{+/+}</i>: Sham vs MCAO: $p < .001$ Ipsilateral side – <i>Ilvb1^{-/-}</i>: Sham vs MCAO: $p < .001$</p>	

Statistical table

			<p>MG (M+3): Side: $F(1,49) = 40.4, p < .001$ Treatment: $F(1,49) = 14.1, p < .001$ Genotype: $F(1,49) = 1.2, p = .287$</p> <p>Contralateral side – $Ilvb1^{+/+}$: Sham vs MCAO: $p < .001$ Contralateral side – $Ilvb1^{-/-}$: Sham vs MCAO: $p = .016$ Ipsilateral side – $Ilvb1^{+/+}$: Sham vs MCAO: $p = .278$ Ipsilateral side – $Ilvb1^{-/-}$: Sham vs MCAO: $p > .999$ Sham – $Ilvb1^{+/+}$: Contralateral side vs ipsilateral side: $p > .999$ Sham – $Ilvb1^{-/-}$: Contralateral side vs ipsilateral side: $p > .999$ pMCAO – $Ilvb1^{+/+}$: Contralateral side vs ipsilateral side: $p < .001$ pMCAO – $Ilvb1^{-/-}$: Contralateral side vs ipsilateral side: $p < .001$</p>	
9i	Sham- $Ilvb1^{+/+}$: 11 mice Sham- $Ilvb1^{-/-}$: 15 mice MCAO- $Ilvb1^{+/+}$: 9 mice MCAO- $Ilvb1^{-/-}$: 10 mice	3-way RM ANOVA followed by Sidak's post hoc tests (p -values adjusted for multiple comparisons)	<p>Side: $F(1,41) = 0.002, p = .969$ Treatment: $F(1,41) = 8.0, p = .007$ Genotype: $F(1,41) = 0.2, p = .639$</p> <p>Contralateral side – $Ilvb1^{+/+}$: Sham vs MCAO: $p > .999$ Contralateral side – $Ilvb1^{-/-}$: Sham vs MCAO: $p > .999$ Ipsilateral side – $Ilvb1^{+/+}$: Sham vs MCAO: $p = .013$ Ipsilateral side – $Ilvb1^{-/-}$: Sham vs MCAO: $p = .076$</p>	Values excluded: Sham- $Ilvb1^{+/+}$: 3 mice (outliers) Sham- $Ilvb1^{-/-}$: 2 mice (outliers) MCAO- $Ilvb1^{+/+}$: 3 mice (outliers)
9j	Sham- $Ilvb1^{+/+}$: 14 mice Sham- $Ilvb1^{-/-}$: 17 mice MCAO- $Ilvb1^{+/+}$: 12 mice MCAO- $Ilvb1^{-/-}$: 10 mice	3-way RM ANOVA followed by Sidak's post hoc tests (p -values adjusted for multiple comparisons)	<p>Pyruvate (M): Side: $F(1,49) = 2.9, p = .095$ Treatment: $F(1,49) = 6.9, p = .012$ Genotype: $F(1,49) = 0.5, p = .481$</p> <p>Contralateral side – $Ilvb1^{+/+}$: Sham vs MCAO: $p = .939$ Contralateral side – $Ilvb1^{-/-}$: Sham vs MCAO: $p > .999$ Ipsilateral side – $Ilvb1^{+/+}$: Sham vs MCAO: $p = .074$ Ipsilateral side – $Ilvb1^{-/-}$: Sham vs MCAO: $p = .002$</p> <p>Pyruvate (M+3): Side: $F(1,49) = 0.1, p = .711$ Treatment: $F(1,49) = 0.6, p = .429$ Genotype: $F(1,49) = 1.2, p = .274$</p>	
10b	$Ilvb1^{+/+}$: 18 mice $Ilvb1^{-/-}$: 14 mice	2-way RM ANOVA	<p>Time: $F(1,30) = 97.3, p < .001$ Genotype: $F(1,30) = 0.2, p = .688$ Interaction: $F(1,30) < 0.01, p = .933$</p>	
10c	3-DG, MG and DMG: $Ilvb1^{+/+}$: 16 mice $Ilvb1^{-/-}$: 10 mice Gx: $Ilvb1^{+/+}$: 16 mice $Ilvb1^{-/-}$: 9 mice	2-way RM ANOVA	<p>3-DG: Time: $F(1,24) = 89.7, p < .001$ Genotype: $F(1,24) = 0.1, p = .759$ Interaction: $F(1,24) = 0.6, p = .455$ Gx:</p>	Value excluded: Gx: 1 outlier at 12 weeks (value was also excluded at baseline)

Statistical table

			Time: $F(1,23) = 48.4, p < .001$ Genotype: $F(1,23) = 1.6, p = .223$ Interaction: $F(1,23) = 1.3, p = .265$ MG: Time: $F(1,24) = 1.1, p = .302$ Genotype: $F(1,24) = 0.1, p = .779$ Interaction: $F(1,24) = 1.5, p = .240$ DMG: Time: $F(1,24) = 9.4, p = .005$ Genotype: $F(1,24) = 0.5, p = .494$ Interaction: $F(1,24) = 0.7, p = .406$	
10d	<i>Ilvbl</i> ^{+/+} : 18 mice <i>Ilvbl</i> ^{-/-} : 14 mice	3-DG, Gx and MG: Two-tailed unpaired t test DMG: Two-tailed Mann-Whitney U test	3-DG: $T(30) = 1.5, p = .155$ Gx: $T(30) = 0.6, p = .568$ MG: $T(30) = 0.7, p = .519$ DMG: $p = .640$	
10e	<i>Ilvbl</i> ^{+/+} : 18 mice <i>Ilvbl</i> ^{-/-} : 12 mice	Gx and MG: Two-tailed unpaired t test DMG: Two-tailed Mann-Whitney U test	Gx: $T(28) = 1.7, p = .100$ MG: $T(28) = 0.569, p = .574$ DMG: $p = .003$	
11	SPF: 5 mice Germ-free: 6 mice	Two-tailed unpaired t test	3-DG: $T(9) = 1.7, p = .130$ Gx: $T(9) = 0.4, p = .675$ MG: $T(9) = 1.1, p = .305$ Pyruvate: $T(9) = 0.8, p = .418$ DMG: $T(9) = 0.1, p = .897$	
12c	<i>Ilvbl</i> ^{+/+} : 14 mice <i>Ilvbl</i> ^{-/-} : 17 mice	Two-tailed unpaired t test	$T(29) = 2.4, p = .025$	
13b	3 mice/group	Descriptive only		
13c	3 mice/group	Descriptive only		
13d	3 mice/group	Descriptive only		
14b	Control: 13 mice DMG: 14 mice	Two-tailed Mann-Whitney U test	$p = .243$	
14c	50 time points/group, 4-6 cages/group	Mixed-effects model (REML)	Time: $F(49,482) = 6.5, p < .001$ Treatment: $F(1,10) = 0.8, p = .381$	
14d	3-DG, MG and DMG: Control: 12 mice DMG: 13 mice Gx: Control: 11 mice DMG: 13 mice	3-DG and MG: Two-tailed unpaired t test Gx and DMG: Two-tailed Mann-Whitney U test	3-DG: $T(23) = 0.4, p = .718$ Gx: $p = .392$ MG: $T(23) = 0.4, p = .718$ DMG: $p = .001$	Value excluded: Gx: 1 outlier (Control)
14e	Control: 12 mice DMG: 13 mice	Two-tailed unpaired t test	$T(23) = 1.7, p = .096$	
14f	Control: 12 mice DMG: 14 mice	Two-tailed unpaired t test	$T(24) = 0.6, p = .581$	Value excluded: 1 outlier (Control)
14g	Gx: Control: 11 mice DMG: 14 mice MG and DMG: Control: 13 mice DMG: 14 mice	Gx and DMG: Two-tailed Mann-Whitney U test MG: Two-tailed unpaired t test	Gx: $p = .893$ MG: $T(25) = 0.4, p = .696$ DMG: $p = .350$	Values excluded: Gx: 2 outliers (Control)
15a	24 wells (0 μ M DMG), 11 wells (5 μ M DMG and 10 μ M H ₂ O ₂) and 12 wells (20 μ M DMG, 50 μ M DMG, 100 μ M DMG, 200 μ M DMG, 500 μ M DMG and no cells)	Kruskal-Wallis followed by Dunn's post hoc tests (<i>p</i> -values adjusted for multiple comparisons)	$\chi^2(9) = 101.0, p < .001$ 0 μ M DMG vs 5 μ M DMG: $p > .999$ 0 μ M DMG vs 20 μ M DMG: $p > .999$ 0 μ M DMG vs 50 μ M DMG: $p = .021$ 0 μ M DMG vs 100 μ M DMG: $p < .001$ 0 μ M DMG vs 200 μ M DMG: $p < .001$ 0 μ M DMG vs 500 μ M DMG: $p < .001$	

Statistical table

			<p>0 μM DMG vs 10 μM H₂O₂: $p < .001$ 0 μM DMG vs no cells: $p = .287$</p>	
15b	12 wells (0 μM DMG) and 6 wells (5 μM DMG, 20 μM DMG, 50 μM DMG, 100 μM DMG, 200 μM DMG, 500 μM DMG, 10 μM H ₂ O ₂ and no cells)	Kruskal-Wallis followed by Dunn's post hoc tests (p -values adjusted for multiple comparisons)	<p>$\chi^2 (9) = 45.9, p < .001$</p> <p>0 μM DMG vs 5 μM DMG: $p > .999$ 0 μM DMG vs 20 μM DMG: $p > .999$ 0 μM DMG vs 50 μM DMG: $p > .999$ 0 μM DMG vs 100 μM DMG: $p = .068$ 0 μM DMG vs 200 μM DMG: $p = .003$ 0 μM DMG vs 500 μM DMG: $p < .001$ 0 μM DMG vs 10 μM H₂O₂: $p > .999$ 0 μM DMG vs no cells: $p = .431$</p>	
15c	16 wells (0 μM DMG), 8 wells (5 μM DMG, 50 μM DMG and 500 μM), and 12 wells (10 μM H ₂ O ₂ and no cells)	Kruskal-Wallis followed by Dunn's post hoc tests (p -values adjusted for multiple comparisons)	<p>$\chi^2 (6) = 53.1, p < .001$</p> <p>0 μM DMG vs 5 μM DMG: $p > .999$ 0 μM DMG vs 50 μM DMG: $p > .999$ 0 μM DMG vs 500 μM DMG: $p < .001$ 0 μM DMG vs 10 μM H₂O₂: $p = .003$ 0 μM DMG vs no cells: $p = .043$</p>	
15d	5 wells/group	<p><i>Pla2g4a</i> and <i>Ptges</i>: One-way ANOVA followed by Dunnett's post-hoc tests (p-values adjusted for multiple comparisons)</p> <p><i>Ptgs2</i> and <i>Bim</i>: Kruskal-Wallis followed by Dunn's post hoc tests (p-values adjusted for multiple comparisons)</p>	<p><i>Pla2g4a</i>: $F (2,12) = 7.15, p = .009$</p> <p>0 μM vs 100 μM DMG: $p = .429$ 0 μM vs 500 μM DMG: $p = .006$</p> <p><i>Ptgs2</i>: $\chi^2 (2) = 12.0, p < .001$</p> <p>0 μM vs 100 μM DMG: $p = .207$ 0 μM vs 500 μM DMG: $p = .001$</p> <p><i>Ptges</i>: $F (2,12) = 87.44, p < .001$</p> <p>0 μM vs 100 μM DMG: $p = .001$ 0 μM vs 500 μM DMG: $p < .001$</p> <p><i>Bim</i>: $\chi^2 (2) = 8.4, p = .007$</p> <p>0 μM vs 100 μM DMG: $p > .999$ 0 μM vs 500 μM DMG: $p = .017$</p>	

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Abbreviations

Abbreviations

(d4-)CEL	(Deuterated) N ϵ -(1-carboxyethyl)-L-lysine
3-DG	3-Deoxyglucosone
3-DG-H1	Glycated 3-deoxyglucosone in histone 1
ACC1	Acetyl-CoA carboxylases 1
ACLY	Adenosine triphosphate-citrate lyase
ACN	Aconitase
AD	Alzheimer's Disease
ADP	Adenosine diphosphate
AGC	Automatic gain control
AGE	Advanced glycation end product
ALD	Fructose-biphosphate aldolase
ALDC	Acetolactate decarboxylase
ALS	Acetolactate synthase
AMPA	α -Amino-3-hydroxy-5-methyl-4-isoxazole propionic acid
AR	Acetoin reductase
ATP	Adenosine triphosphate
BBB	Blood-brain barrier
bEnd.3 cells	Mouse brain endothelial cells
Bim	BCL2 Like 11
BSA	Bovine serum albumin
cDNA	Complementary Deoxyribonucleic acid
CID	Collision-induced dissociation
CML	N- ϵ -carboxymethyllysine
CNS	Central nervous system
COX, or PTGS	Cyclooxygenase, or prostaglandin-endoperoxide synthase
CS	Citrate synthase
Ct	Threshold cycle
d8-DB	Deuterated o-phenylenediamine
Db/db	Leptin receptor-deficient
DETAPAC	Diethylenetriaminepentaacetic acid
DMEM	Dulbecco's Modified Eagle's Medium
DMG	Dimethylglyoxal
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
dNTP	Nucleoside triphosphate
DOLD	3-deoxyglucosone lysine dimer
DPBS	Dulbecco's phosphate buffered saline
DR, or DCXR	Diacetyl reductase, or dicarbonyl/L-xylulose reductase
e⁻	Electron
EDTA	Ethylenediaminetetraacetic acid
EI	Electron ionization
ESI	Electrospray ionization
FAD(H₂)	(Reduced) flavine adenine dinucleotide
FASN	Fatty acid synthase

Abbreviations

FCS	Fetal Calf Serum
FM	Fumarase
FT	Fourier Transformation
G3P	Glyceraldehyde 3-phosphate
G6PD	Glucose 6-phosphate dehydrogenase
GDP	Guanosine diphosphate
GLUT	Glucose transporter type
GOLD	Glyoxal-derived lysine dimer
GPI	Glucose 6-phosphate isomerase
GTP	Guanosine triphosphate
Gx	Glyoxal
HbA_{1c}	Glycated hemoglobin
HBL	<i>N</i> _ε -3-hydroxy-2-butanonelysine
HCD	High-energy collisional dissociation
Hep G2 cells	Human liver cancer cells
HESI-II	Heated-electrospray ionization
HFD	High-fat diet
HIF-1	Hypoxia-inducible factor 1
HK	Hexokinase
HPLC	High-performance mass spectrometry, or high-pressure mass spectrometry
HT-22 cells	Mouse hippocampal neuronal cells
I.p.	Intraperitoneal injection
IDH	Isocitrate dehydrogenase
ILVBL	IlvB acetolactate synthase like, or 2-hydroxyacyl-CoA lyase 2
IRS-1	Insulin receptor substrate
IT	Injection time
LC	Liquid chromatography
LDH	Lactate dehydrogenase
LDL	Low density lipoprotein
M-MLV	Mouse Moloney murine leukemia virus
<i>m/z</i>	Mass-to-charge ratio
MCT	Monocarboxylate transporter
MDH	Malate dehydrogenase
MG	Methylglyoxal
MOLD	Methylglyoxal-lysine dimer
MRM	Multiple reaction monitoring
MS	Mass spectrometry
MS²	Tandem mass spectrometry
NaCl 0.9 %	Saline solution
NAD(H)	(Reduced) nicotinamide adenine dinucleotide
NCE	Normalized collision energy
NF-κB	Nuclear factor kappa-light-chain-enhancer of activated B cells
NMDA	<i>N</i> -methyl-D-aspartate
NOS	Nitric oxide synthases
nSREBP-1c	Sterol regulatory element-binding protein-1c
OAD	Oxaloacetate decarboxylase
OGDC	α-Ketoglutarate dehydrogenase
ORM2	Orosomucoid 2

Abbreviations

PBK, or AKT	Protein kinase B
PC	Prohormone convertase
PCR	Polymerase Chain Reaction
PDC	Pyruvate dehydrogenase complex
PDH	Pyruvate dehydrogenase
PDK1	Pyruvate dehydrogenase kinase 1
PFK-1	Phosphofructokinase-1
PG	Prostaglandin
PI3K	Phosphatidylinositol 3-kinase
PIP	Phosphatidylinositol 4,5-biphosphate
Pla2g4a	Phospholipase A2 Group IVA
pMCAO	Permanent middle cerebral artery occlusion
Ppia	Cyclophilin A
PPP	Pentose Phosphate Pathway
PRM	Parallel Reaction Monitoring
Ptges	Prostaglandin E synthase
Q1	First quadrupole
Q2	Second quadrupole
Q3	Third quadrupole
R	Resolution
RAGE	Receptor for advanced glycation end product
RNA	Ribonucleic acid
RNS	Reactive nitrogen species
ROS	Reactive oxygen species
RPE	Ribulose 5-phosphate 3-epimerase
RPI	Ribose 5-phosphate isomerase
S-Lens	Stacked ring ion guide
SCD1	Stearoyl-CoA desaturase-1
SCS	Succinyl-CoA dehydrogenase
SDH	Succinyl dehydrogenase
siRNA	Small interfering ribonucleic acid
SPF	Specific-pathogen-free
STZ	Streptozotocin
TALDO	Ribose 5-phosphate isomerase, transaldolase
TCA	Tricarboxylic acid cycle, citric acid cycle, or Krebs cycle
TCAA	Trichloroacetic acid
TK	Thiamine-dependent enzyme transketolase
TNF	Tumor necrosis factor- α
TPI	Triose phosphate isomerase
WHO	World Health Organization

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Eidesstattliche Erklärung

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Hiermit versichere ich an Eides statt, dass ich die vorliegende Dissertation ohne fremde Hilfe und ohne Benutzung anderer als der angegebenen Quellen und Hilfsmittel angefertigt und die den benutzten Quellen wörtlich oder inhaltlich entnommenen Stellen als solche kenntlich gemacht habe. Diese Arbeit wurde in gleicher oder ähnlicher Form.



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