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Untersuchungen zum Einfluss von Glykierung und Glykosylierung auf Meningeomzellen

Dissertation zur Erlangung des akademischen Grades Doktor der Medizinischen Wissenschaften (Dr. rer. medic.) in der Fachrichtung Molekulare Medizin

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Posttranslationale Modifikationen wie Glykierung und Glykosylierung von Oberflächenproteinen oder Zelladhäsionsmolekülen sind sowohl an der Entstehung als auch an der Metastasierung von Tumoren beteiligt.

Meningeome sind die am häufigsten diagnostizierten nicht-malignen intrakranialen Tumore und auch die Inzidenz von nicht –malignen Meningeomen steigt mit dem Alter. Wie die meisten Tumore, erzeugen auch Meningeome bevorzugt durch anaerobe Glykolyse Energie (Warburg Effekt) und synthetisieren so vermehrt den Metaboliten Methylglyoxal (MGO). MGO ist dafür bekannt mit Aminogruppen zu reagieren und dabei *Advanced Glycation Endproducts* (AGEs) zu bilden. Diese Reaktion wird auch als Glykierung bezeichnet. AGEs sind dafür bekannt im Alter vermehrt zu akkumulieren.

Zur Untersuchung der Effekte von Glykierung anhand von Meningeomzellen wurden zum einen die benigne Zelllinie BEN-MEN-1 und zum anderen die maligne Zelllinie IOMM-Lee genutzt. Wie alle menschlichen Zellen, sind auch Meningeomzellen sialyliert. Im Golgi werden die Sialinsäuren beispielsweise an Glykanstrukturen, Ganglioside oder auch Glykoproteine mit Hilfe von Sialyltransferasen gesetzt. Während dieser Arbeit konnte gezeigt werden, dass posttranslationale Modifikationen wie Glykierung und Sialylierungen einen elementaren Einfluss auf die Malignität in Meningeomen haben.

Die Glykierung erhöht das invasive Verhalten der benignen Meningeome, wohingegen in malignen Meningeomen gegenteilige Effekte in der *real time cell analysis* (RTCA) beobachtet werden konnten. Als nächstes konnte im Immunoblot gezeigt werden, dass die Glykierung der benignen Zelllinie zu einer Erhöhung der E-Cadherin - und einer Verminderung der N-Cadherin – Expression führt. Zusätzlich konnte in der *quantitative real time polymerase chain reaction* (qPCR) beobachtet werden, dass die Glykierung zu einer Veränderung der Expression von Sialyltransferasen wie ST3GAL1/2/3/5/6, ST6GAL1/2, ST6GALNAC2/6 und ST8SIA1/2 führt, welche vor allem für einen direkten oder indirekten Einfluss auf die Tumorentwicklung bekannt sind. Die verminderte Expression von ST3GAL5 führte zu sinkenden GM3-Gangliosid- Expression in der glykierten benignen Zelllinie, welches mit Hilfe der *Porous Graphitized Carbon* (PGC) *nano-Liquid Chromatography* (LC)- *Electro Spray Ionization* (ESI)-*Mass Spectrometry* (MS)/MS /MS *analysis* nachgewiesen werden konnte.

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1. Einleitung

1.1 Meningeome

Meningeome entspringen den Meningealzellen der Arachnoidea und gehören zu den am häufigsten vorkommenden nicht-malignen Tumoren. Die WHO (World Health Organization) teilt die Meningeome nach Unterschieden in Histologie und klinischem Verhalten in Grad 1, 2 und 3 ein [1–3].

Das WHO Grad 1 Meningeom ist das am häufigsten vorkommende (benignen, 80 - 90 % aller diagnostizierten Meningeome) und ist dabei das am langsamsten wachsende Meningeom und hinzukommend haben diese eine niedrige Rezidiv-Rate [1,4]. Meningeome des WHO Grades 2 (atypisch, 10-20 % aller diagnostizierter Meningeome) werden aufgrund der erhöhten Rezidiv-Rate in WHO Grad 2 eingeteilt. Die Inzidenz für nicht maligne Meningeome steigt mit dem Alter und steigt dramatisch bei Personen über 65 Jahren [3,5]. Die 10- Jahres- Überlebensrate für nicht- maligne Meningeome liegt bei ca 87 %. Das Alter hat einen starken Einfluss auf das Überleben des Patienten nach der Diagnose (10- Jahres- Überlebensrate bei Jugendlichen und jungen Erwachsenen: 94,5 % vs. Erwachsene > 40 Jahre: 81,2 %). Auch das Areal der Meningeome hat einen Einfluss auf das Überleben des Patienten nach der Diagnose. Die relative 10- Jahres- Überlebensrate für Meningeome in zerebralen Bereichen liegt bei ca. 83,5 %, wohingegen die 10- Jahres- Überlebensrate bei Patienten mit Meningeomen in spinalen Regionen eine deutliche höhere Überlebensrate (95,5 %) haben. Des Weiteren erkranken Frauen 2,3-mal häufiger an nicht-maligne Meningeome als Männer [3,5].

Das Meningeom Grad 3 (maligne, 1 - 3 % aller diagnostizierten Meningeome) sind für ein aggressives Wachstumsverhalten und Invasivität bekannt [1,4]. Die durchschnittliche Überlebensrate für maligne Meningeome liegt bei 53 (95% KI: 48-58) Monaten. Die relative 10- Jahres-Überlebensrate von malignen Meningeomen liegt bei unter 60 %. Für das Überleben nach der Diagnose eines malignen Meningeoms spielt auch hier das Alter eine elementare Rolle [3,5].

1.2 Entstehung von Methylglyoxal/ Glyoxal im Stoffwechsel

Carbonyl-Spezies wie Methylglyoxal (MGO) oder Glyoxal (GO) werden hauptsächlich als Beiprodukt während der Glykolyse aber auch durch Autooxidation von Glukose gebildet. Durch Degradation von Glukose mittels Retro-Aldol-Kondensation entsteht MGO. Aber auch durch Deprotonierung von Glukose werden 1,2-Enol oder 2,3-Enol und dabei auch 1-Deoxyglucoson (1-DG) oder 3-Deoxyglucoson (3-DG) gebildet. Die Fragmentierung von 3-DG kann zur Generierung von MGO führen [6]. Die Glykolyse wird als Signalweg des Zytoplasmas beschrieben und wird von allen Zellen im menschlichen Körper zur Energieerzeugung genutzt. Glukose wird mit Hilfe des Enzyms Hexokinase unter Nutzung eines Adenosintriphosphates (ATP) zu Glukose-6-Phosphat (G- 6- P). Diese irreversible Reaktion führt zu einer Hemmung der Hexokinase-Aktivität. Als nächstes wird Fruktose-6-Phosphat (F-6-P) aus G-6-P mittels G-6-P-Isomerase erzeugt und anschließend durch eine weitere Phosphorylierung durch die Phosphofruktokinase zu Fruktose-1,6-bisphosphat (F-1,6-bisP). Diese Reaktion ist nicht nur irreversibel, sondern auch der wichtigste regulatorische Schritt innerhalb der Glykolyse. Im Folgenden teilt eine Aldolase F-1,6-bisP in Glyceraldehyd-3-P (GAH-3-P) und Dihydroxyacetonphosphat (DHA-P). Letztere wird mit Hilfe der Triosephosphat-Isomerase (TIM) in GAH-3-P umgewandelt [7–9]. Durch nicht enzymatische Eliminierung der Phosphorylierungsstellen von GAH-3-P und DHA-P wird letztendlich Methylglyoxal gebildet [10].



Abbildung 1: Schematische Darstellung der Sialinsäure-Biosynthese von Glucose zur Sialinsäure, Dicarbonyl-Verbindungen und der Sialylierung von Glykoproteinen (zum Beispiel N-Glykane, O-Glykane und Ganglioside) im endoplasmatischen Retikulum und Golgi. GAH-3-P = Glyceraldehyd-3-Phosphat; DHA-P = Dihydroxyaceton-Phosphat; MGO = Methylglyoxal; GO = Glyoxal; GlcNAc = N-Acetyl-Glucosamin; Man =Mannose; Gal = Galaktose; Neu5Ac = N-Acetyl-Neuraminsäure; GNE = UDP-N-Acetyl-Glukosamin-2-epimerase/N-Acetyl-Mannosamin-Kinase; ER = Endoplasmatisches Retikulum. Darstellung nach Selke et al 2021 [11].

1.3 Posttranslationale Modifikationen

Posttranslationale Modifikationen (PTMs) sind Veränderungen an Proteinen, die nach der Translation stattfinden. Häufig vorkommende PTMs sind zum Beispiel Phosphorylierung, Methylierung, Acetylierung, Glykosylierung oder auch Ubiquitinierung, aber auch Glykierung gehören dazu [12]. In dieser Arbeit wird vor allem auf die Glykierung und Sialylierung, welche eine Form der Glykosylierung darstellt, eingegangen.

1.3.1 Glykierung

Die Glykierung beschreibt eine nicht-enzymatische Reaktion bei der sich Carbonyl-Gruppen von Dicarbonylen (zum Beispiel MGO oder GO) oder von Monosacchariden (zum Beispiel Glukose oder Fruktose) mit Aminogruppen von Proteinen oder Peptiden verbinden [13]. Die Glykierung wird auch als Maillard Reaktion bezeichnet und wird in 3 Hauptstadien eingeteilt. In der frühen Phase, wobei vor allem Monosaccharide mit freien Aminogruppen von Proteinen, Nukleinsäuren und Lipiden reagieren, wird eine instabile Schiff'sche Base und durch Neuordnung ein stabiles Ketoamin (Amadori-Produkt) gebildet [13,14]. In der fortgeschrittenen Phase werden durch Oxidation und Dehydrierung Dicarbonyle aus dem Amadori-Produkt gebildet. Diese sind stärker reaktiv als die Monosaccharide und reagieren erneut mit freien Aminogruppen. In der späten Phase reagieren diese Glykierungsagenten erneut mit Aminogruppen durch Oxidation, Dehydrierung und zyklische Reaktionen, formen schlussendlich AGEs [15].

1.3.2 Glykosylierung

Die Glykosylierung ist definiert als ein enzymatischer Prozess bei dem glykosidische Bindungen zwischen einfachen Zuckern oder Glykanen mit anderen Zuckern, Lipiden oder Proteinen gebildet werden [16]. Glykoproteine enthalten Glykan oder Glykanketten, welche in N- und O-Glykane eingeteilt werden. Die N-Glykosylierung setzt Glykane an Aminogruppen von Asparagin (Asn, N) an Glykosylierungsmuster Asn-X-Serin (Ser)/Threonin (Thr) (X steht für alle Aminosäuren außer für Prolin (Pro)). Die O-Glykosylierung setzt Glykane an Sauerstoff Atome von Hydroxylgruppen von Ser (S)- oder Thr (T)- Resten. Die N-Glykane werden in Mannose-reiche, Hybride und komplexe Glykane eingeteilt [17].

In dieser Arbeit wird speziell auf die Sialylierung eingegangen, welche eine Form der Glykosylierung darstellt. Vor allem die veränderte α 2,3- und α 2,6- verbundene Sialylierung ist mit der Tumorentwicklung assoziiert [18].

1.3.2.1 Sialylierung

Bei der Sialylierung werden Sialinsäuren auf andere Zucker, Lipide oder Proteine mit Hilfe von Sialyltransferasen (STs) transferiert. STs gehören zu den Typ II Transmembranproteinen und sind im Golgi lokalisiert. Wie viele andere Glykosyltransferasen bestehen die STs aus einer Nterminale Domäne, welche im Zytoplasma liegt, einer einzelnen Transmembran-Domäne mit 16-20 Aminosäure-Resten, einer Stammregion und einer konservierten C-terminalen katalytischen Domäne (300 ± 20 Aminosäure-Reste) im Golgi-Lumen [19]. Im Menschen sind aktuell 20 STs bekannt. Diese nutzen die CMP-aktivierte N-acetyl-5-Neuraminsäure (Neu-5-Ac; Sia) als Substrat und transferieren diese auf zum Beispiel Ganglioside, N- oder O-Glykane sowie auf Glykoproteine. Die STs werden in 4 Familien entsprechend ihrer Verbindung, die sie eingehen, aufgeteilt. Die Familie der β -Galaktosid α 2,3- Sialyltransferase (ST3Gal) besteht aus 6 Mitgliedern und transferieren über eine α 2,3 Verbindung Sialinsäuren (Sia) auf Galaktose (Gal). Die β -Galaktosid α 2,6- Sialyltransferase (ST6Gal) hat hingegen nur 2 bekannte Mitglieder. Die, dieser Gruppe angehörigen STs vermitteln den Transfer von Sia auf Galaktose in einer α 2,6 Verbindung. Die STs, die Sia auf N-acetyl galactosamin (GalNAc) übertragen werden GalNAc α 2,6- Sialyltransferase (St6GalNAc) genannt (6 Mitglieder). Der Transfer von Sia auf eine andere Sia in einer a 2,8 Verbindung wird durch die a 2,8 Sialyltransferase (ST8Sia) durchgeführt und hat auch 6 Mitglieder [20].



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Abbildung 2: Übersicht zur Funktion der Sialyltransferase-Familien.
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Es sind die 4 verschiedenen Familien der STs dargestellt. ST3Gal = β -Galaktosid α 2,3- Sialyltransferase; ST6Gal = β -Galaktosid α 2,6- Sialyltransferase; ST6GalNAc = N-Acetyl-Galaktosamin (GalNAc) α 2,6- Sialyltransferase;ST8Sia = α 2,8 Sialyltransferase; CMP-Neu-5-Ac = CMP-aktivierte Sialinsäure; Neu-5-Ac = Sialinsäure. Die Strukturen wurden nach dem Consortium of Functional Glycomics (CFG) dargestellt: gelbes Quadrat = N- Acetyl-Galaktosamin; gelber Kreis = Galaktose; pinker Diamant = N-Acetyl-Neuraminsäure. Verändert nach Rosenstock et al 2020 [21]

1.4 Zelladhäsionsmoleküle

Zelladhäsionsmoleküle (*cell adhesion molecules*; CAMs) sind Oberflächenproteine, die an Zell-Zell-Interaktion und an Zell-Matrix-Interaktion beteiligt sind. Die Adhäsionsmoleküle lassen sich in 4 Familien einteilen: Integrin- Rezeptor Familie, die Immunglobulin (Ig) Superfamilie, Selektine und Cadherine [22]. Wobei in dieser Arbeit vor allem auf die Cadherine eingegangen wird.

1.4.1 Cadherine

Cadherine sind homophile Ca²⁺ abhängige Zell-Zell-Adhäsionsmoleküle, die eine Zell-Zell-Interaktion über ihre fünf extrazellulären Domänen (*adherens junction*) vermitteln. Die klassischen Cadherine sind das epitheliale, plazentale und neurale Cadherin (E-, P- and N- Cadherin). Sie spielen im Zell-Zell-Kontakt, Gewebestrukturierung und Tumorentwicklung eine wichtige Rolle [23]. Die intrazellulär vorliegende Catenin- Bindungsdomäne (CBD) ist entscheidend für die Cadherin-Funktion und spielt eine wichtige Rolle im Erhalt der epithelialen Integrität. Sie bindet direkt an β -Catenin und p120. Diese wiederrum binden an α - Catenin und bilden somit die Verbindung zwischen Cadherin und dem Zytoskelett [24–26]. Mit Hilfe dieser Verbindung können physikalische und biochemische Signale weitergeleitet werden. β -Catenin kann aber auch die Aktivierung verschiedener Gene wie c-Myc und Cyclin-D1 unterstützen und so zu Veränderungen in der Zellmorphologie, Proliferation und Beweglichkeit führen [27].

1.5 Gangliosid Biosynthese

Ganglioside sind Glykosphingolipide welche Sia enthalten. Die Biosynthese der Ganglioside beginnt mit Ceramid (Cer) im endoplasmatischen Retikulum (ER) und wird im Golgi-Apparat fortgesetzt. Im Cis-Golgi wird Cer mittels Glucosylceramid Synthase glucosyliert und Glucosylceramid (GlcCer) gebildet [28]. Die meisten Ganglioside werden aus Laktosylceramid (LacCer) erzeugt (Gangliosid GM4 als Ausnahme wird aus Galaktosylceramid (GalCer) erzeugt), welches im trans-Golgi aus GlcCer generiert wird. Das erste Gangliosid GM3 entsteht durch den Transfer von Sia auf LacCer durch die ST3Gal5 (GM3- Synthase) [29]. Durch sequentielles Hinzufügen von Sia auf GM3 wird zuerst GD3 und durch erneute Addition GT3 gebildet. Dies wird durch die Sialyltransferase ST8Sia1 vermittelt. Die Ganglioside GM3, GD3 und GT3 dienen als Ausgangspunkt für weitere wesentlich komplexere Ganglioside, welche in a-, b- und c- Serien eingeteilt werden [30].



Abbildung 3: Schematische Darstellung der Gangliosid-Biosynthese.

Ceramid = Cer; Galaktosylceramid = GalCer; Monosialogangliosid 4= GM4; Glukosylceramid = GlcCer; Laktosylceramid = LacCer; β -Galaktosid α 2,3- Sialyltransferase 5= ST3Gal5; Monosialogangliosid 3 = GM3; α 2,8 Sialyltransferase 1 = ST8Sia1; Disialogangliosid 3 = GD3; Trisialogangliosid 3 = GT3. Die Strukturen wurden nach dem Consortium of Functional Glycomics (CFG) dargestellt: gelber Kreis = Galaktose; blauer Kreis = Glukose; pinker Diamant = N-Acetyl-Neuraminsäure. Verändert nach Selke et al 2021 [11].

2. Zielstellung

Ziel dieser Arbeit war es die Rolle der altersabhängigen Glykierung und Glykosylierung speziell der Sialylierung bei der Malignität von Meningeomen zu untersuchen. Diese am häufigsten vorkommende gutartige intrakraniale Tumorart umfasst drei Grade. Zum Einfluss von Glykierung auf die unterschiedlichen Grade der Meningeome ist derzeit nichts bekannt.

Dazu sollten benigne und maligne Zelllinien kultiviert und mittels verschiedener Carbonylhaltiger Medien manipuliert und verändert werden. Hierfür sollte der Nachweis der Glykierung mittels Immunoblot erbracht, der Einfluss hinsichtlich der Zellviabilität mittels 3-(4,5-Dimethylthiazol-2-yl) -2,5-diphenyltetrazoliumbromid (MTT)- Test, sowie die Rolle in Adhäsion, Migration und im invasiven Verhalten mit Hilfe des *Real-Time Cell Analyzers* (RTCA) untersucht werden. Anschließend sollte der Einfluss von Glykierung auf die Expression von Oberflächenproteinen in beiden Tumorgraden im Immunoblot analysiert werden.

Als nächstes sollte der Einfluss der altersabhängigen Glykierung auf die Sialylierung ermittelt werden. Dazu sollten zuvor Unterschiede in der Expression aller Sialyltransferasen zwischen benigner und maligner Zelllinie mit Hilfe der *Polymerase Chain Reaction* (PCR) untersucht werden. Darüber hinaus sollte der Einfluss von Glykierung auf die Sialylierung in der *quantitative real time* PCR (qPCR) auf die benigne bzw. maligne Zelllinie analysiert werden. Ziel hierbei war es herauszufinden, welche posttranslationale Modifikationen (am Beispiel der Meningeome) einen verstärkten oder verminderten Einfluss auf die Malignität haben und somit zur Tumorentwicklung beitragen.

3. Diskussion

Posttranslationale Modifikationen haben einen großen Einfluss auf die Funktionalität und Eigenschaften von Zellen. In dieser Arbeit sind nicht nur die Einflüsse von Glykierung auf verschiedene Meningeomzellen und dessen Sialylierung, sondern auch die Expression des Gangliosids GM3 dargestellt.

Zur Rolle des Glykierungsagenten MGO in Meningeomen ist vor dieser Arbeit nichts bekannt gewesen. Während dieser Arbeit konnte gezeigt werden, dass die altersabhängige Glykierung mit Hilfe von MGO verschiedener Meningeomgrade unterschiedliche Auswirkungen hat. Zum einen wird die glykierte benigne Zelllinie (BEN-MEN-1) in ihrem invasiven Verhalten verstärkt und essentielle Zelladhäsionsmoleküle wie E- und N-Cadherine in ihrer Expression verändert und zum anderen die maligne Zelllinie (IOMM-Lee) im invasiven Verhalten inhibiert. Beide Meningeomzelllinien sind unterschiedlich in der Expression ihrer Sialyltransferasen beeinflusst.

3.1 MGO nimmt als Glykierungsagens Einfluss auf die Funktionalität von Meningeomzellen

In vorrangegangen Studien konnte gezeigt werden, dass in Personen mit Diabetes und oder in Personen höheren Alters die MGO Konzentration erhöht ist [31]. Auch einen Zusammenhang zwischen Diabetes und einem erhöhten Risiko an Krebs zu erkranken konnte in Studien beobachtet werden [32,33]. Andererseits gibt es gegensätzliche Daten, die zum einen eine positive [34,35] oder auch einen gegenläufigen Zusammenhang zwischen Diabetes, Serum-Glukose-Konzentration und einem erhöhten Risiko für Meningeome aufzeigen [36].

Der Einfluss von MGO auf die Meningeomzellen hinsichtlich der Zytotoxizität zeigte, dass ≤ 0,3 mM MGO als physiologische Konzentrationen keinen Einfluss auf die Zellviabilität hat. Eine Studie von Chaplen und Kollegen hat gezeigt, dass MGO eine zelluläre Konzentration von 0,3 mM erreichen kann [37] und dass 90 - 99 % des zellulären MGO *in vivo* an Makromolekülen gebunden vorliegt [38,39]. Bei höheren nicht-physiologischen MGO-Konzentrationen konnte eine Verminderung der Zellviabilität beobachtet werden. Dies konnte auch in der mikroskopischen Inaugenscheinnahme nachgewiesen werden. Mit steigender MGO Konzentration haben sich die Zellen weniger ausgebreitet und waren apoptotisch. Zum Nachweis des programmierten Zelltodes (Apoptose) wurde im Immunoblot die Caspase 3 Aktivität nachgewiesen (keine publizierten Daten). Die gespaltene und aktivierte Caspase 3 ist einer der Schlüsselenzyme für den programmierten Zelltod. Auch andere Arbeitsgruppen konnten gleiches in humanen Glioblastom-Multiformen T98G und U87MG Zellen sowie in SH- SY5Y Neuroblastomzellen beobachten [40,41]. Des Weiteren hat sich die Arbeitsgruppe um Lee mit einem entscheidenden Signalweg für das Zellüberleben (gp130/STAT3 Signalweg) in Schwannom RT4 Zellen der Ratte, PC12- sowie U87 Gliom-Zellen auseinandergesetzt. Sie konnten auch eine sinkende Zellviabilität, vermittelt durch den gp130/STAT3 Signalweg und damit einhergehend eine erhöhte Zytotoxizität nachweisen [42]. Das steigende Signal mit steigender MGO Konzentration im Immunoblot, zeigt einen Zuwachs glykierter Proteine und tritt daher als Schmier auf allen Banden auf. Dies wurde auch in anderen Studien beobachtet [43,44].

In vielen Studien konnte gezeigt werden, dass die Glykierung mit Hilfe von MGO einen Einfluss auf Proliferation, Adhäsion, Migration, Invasion und somit auf die Malignität haben kann [45–48].

Die altersabhängige Glykierung mit 0,3 mM MGO von Meningeomzellen konnte keinen Unterschied hinsichtlich der Adhäsion auf verschiedenen Substraten (Kollagen IV, Fibronektin) im Vergleich zur jeweiligen Kontrolle zeigen. Die Meningeome bevorzugen die Adhäsion auf Fibronektin, was auch mit vorläufigen, aber nicht publizierten Daten zur Integrin- Expression (α 4, 5, 6 and β 1, 3, 4) übereinstimmt. Diese Integrine sind auch dafür bekannt eine Rolle in einer Vielzahl von Funktionen wie Adhäsion, Invasion und Proliferation in Meningeomen zu spielen [49–51].

Die Behandlung mit MGO scheint gewebespezifisch unterschiedliche Auswirkungen zu erzeugen. Zum einen konnte in Neoplasien des Kolons und der Hepar eine reduzierte und zum anderen im Neuroblastom eine erhöhte Migration nach MGO-Behandlung nachgewiesen werden [45,46,48]. Für die Meningeomzellen konnte kein Einfluss auf die Chemotaxis durch die altersabhängige Glykierung mittels 0,3 mM MGO beobachtet werden.

Die benignen Meningeomzellen zeigten ein stärker invasives Verhalten nach der Behandlung mit 0,3 mM MGO, wohingegen in den malignen Meningeomzellen ein reduziertes invasives Verhalten nach der MGO-Behandlung zu beobachten war. In *anaplastic thyroid cancer* (ATC) Zellen wurde nach der Behandlung mit MGO eine Erhöhung der Invasivität erfasst [47]. Dies konnte auch in Neuroblastomzellen bestätigt werden [48]. In einer Studie mit hepatozellulären Karzinomen führte die MGO-Behandlung zu einer Verminderung der Invasivität [45]. Aber auch hier scheint die Behandlung mit MGO nicht nur gewebespezifische Auswirkungen, sondern auch die Menge, die diese erzeugt, scheint gewebespezifisch zu sein. Eine geringe Konzentration von 5 μ M MGO führt in ATC Zellen zu einer erhöhten und in hepatozellulären Karzinomen zu einer Verminderung der Invasivität [45,47]. In Neuroblastomzellen führte eine Behandlung mit 0,1 mM MGO zu einem erhöhten Invasionsverhalten [48].

Utsuki und Kollegen sprechen invasiven Meningeomen eine niedrige E-Cadherin Expression zu [52]. Im Modell dieser Arbeit konnte eine niedrige Expression in den BEN-MEN-1- und eine hohe Expression von E-Cadherin in IOMM-Lee-Zellen im Immunoblot nachgewiesen werden. Nach der Glykierung mit MGO stieg die Expression in den benignen und sank in den malignen Meningeomzellen. In einzelnen Studien des Ovarialkarzinoms und des inflammatorischen Mammakarzinoms, konnte E-Cadherin gefunden werden [53,54]. Dies bedeutet, dass nicht in jeder Tumorentität der Verlust der E-Cadherin Expression für eine erhöhte Malignität steht. Zusätzlich wurde in mehreren Studien beschrieben, dass E-Cadherin zu einer erhöhten Formation zu Kolonien aber zu einer verminderten Invasivität, Apoptose-Rate und Dissemination führt und somit von den Zellen für die Metastasierung benötigt wird [55]. Andererseits ist die N-Cadherin- Expression in der glykierten benignen Zelllinie BEN-MEN-1 vermindert gegenüber den unglykierten Zellen. Eine Studie um Camand und Kollegen von 2012 ergab, dass eine reduzierte N-Cadherin- Expression in einer schnelleren und weniger gerichteten Migration von Glioblastomen mündet [56] und auch eine in vitro sowie in vivo Studie mit der C6 Gliomzelllinie stellte fest, dass eine erhöhte N-Cadherin-Expression zu einer Erniedrigung der Invasivität führt [57]. Viele Studien sehen einen Zusammenhang zwischen der N-Cadherin- und der Matrix-Metalloproteinase-9 (MMP-9) - Expression [58,59]. Vorläufige nicht publizierte Ergebnisse zur MMP-9 Expression haben eine Erhöhung nach der Behandlung mit 0,3 mM MGO in BEN-MEN-1 gezeigt. Dies müsste in Zukunft genauer untersucht werden. Man könnte vermuten, dass dies nur ein Grund für das steigende invasive Verhalten in der benignen Zelllinie ist.

3.2 MGO nimmt als Glykierungsagens Einfluss auf die Sialylierung von Meningeomzellen

Viele Arbeitsgruppen konnten einen Einfluss von Sialylierung auf die Tumorgenese beobachten [60–62]. Veränderte Expressionsmuster verschiedener Glykosyltransferasen wurden in vielen verschiedenen humanen Tumorentitäten beschrieben [63,64]. Jedoch ist bisher wenig bekannt über den Einfluss von Glykierung auf die Glykosylierung. Die Glykierung wird in verschiedenen Tumoren, aufgrund des Warburg Effekts, als erhöht beschrieben [65,66].

In Tumoren der Ovarien konnte gezeigt werden, dass eine Überexpression der Sialyltransferase ST3GAL1 zu einer *Transforming Growth Factor* (TGF)- β1- induzierten epithelialen-mesenchymalen-Transition, Migration und Invasion führt. In einem Knockdown konnte das Gegenteil beobachtet werden [67]. Die ST3GAL1-Expression in der benignen glykierten Zelllinie war auch erhöht. In der Arbeitsgruppe um Mehta et al. konnte gezeigt werden, dass in Tumoren mit einem positiven perineuralen Invasionsstatus eine erhöhte

ST3GAL2-Expression aufweisen [68]. Auch in der benignen Zelllinie konnte eine erhöhte ST3GAL2-Expression nachgewiesen werden. Die Expression von ST3GAL3, welche wichtig für die Biosynthese von Disialogangliosid (GD)1a und Trisialogangliosid (GT)1b im Gehirn ist [62], war in der glykierten BEN-MEN-1 Zelllinie erhöht und in der glykierten IOMM-Lee Zelllinie vermindert. In diesem Modell wurde in beiden glykierten Meningeom-Zelllinien eine verminderte ST3GAL5- Expression gefunden. ST3GAL5 transferiert an Lactosylceramid Sialinsäuren und bildet somit Monosialogangliosid (GM)3 und wird daher auch GM3- Synthase genannt [69]. Eine andere Studie schreibt der GM3-Synthase eine Hemmung der Phosphorylierung des epidermal Growth Factor Receptor (EGFR) zu, was wiederum zu einer Verminderung der Zellproliferation führt [70]. Als nächstes wird die Widerstandsfähigkeit gegenüber oxidativen Stress und Strahlentherapie, aufgrund der Hochregulierung des Extracellular Signal-regulated Kinases (ERK) vermittelt über die veränderte GM3-Synthase-Expression modifiziert [29]. Die Absolutmenge von GM3 in der glykierten benignen Meningeomzelllinie war reduziert. Dies ist kohärent mit der Expression von ST3GAL5 in den glykierten BEN-MEN-1-Zellen. In einer Studie von Yamashita und Kollegen konnte in einer GM3-Synthase-Knockout-Maus nicht nur eine Liganden-induzierte Insulinrezeptor-Phosphorylierung, sondern auch eine erhöhte Glukose-Sensitivität und Insulintoleranz, gezeigt werden [71]. Eine verminderte GM3-Expression führt zu einer gehemmten Zellbeweglichkeit und Adhäsion vermittelt durch eine ERK-Phosphorylierung, einer erhöhten Ras-Expression, was wiederum die Migration durch *Mitogen-Activated Protein Kinase* (MAPK) reguliert [29,72–74]. Ein anderes Glykierungsagens (Glyoxal, GO) hat in der benignen Meningeomzelllinie BEN-MEN-1 ebenfalls eine Herunterregulierung von ST3GAL5 zur Folge. In der malignen Meningeomzelllinie IOMM-Lee konnte keine Veränderung der ST3GAL5 Expression beobachtet werden. Dies könnte eine, für viele verschiedene Tumorentitäten im Zusammenhang mit Glykierung beschriebene, erhöhte Glyoxalase 1 Aktivität, welche Dicarbonyle degradiert, erklären [75–77]. Auch die ST3GAL6-Expression, welche eine elementare Rolle in der Synthese von funktionellen Sialyl-Lewis X haben [78], war in beiden glykierten Meningeom-Zelllinien reduziert. In mehreren Studien konnte durch eine reduzierte ST3GAL6-Expression eine reduzierte Migration und Invasion in Zelllinien des Harnblasenkarzinoms (5637 und J82 Urinary Bladder Carcinom (UBC) Zellen) [79] und auch zu einer verminderten Adhäsion und Migration in Multiplen Myelomzellen dargestellt werden [80].

In der Gruppe der Sialyltransferasen, die Sialinsäuren in einer α 2,6 Verbindung auf Galaktose transferieren, konnte eine erhöhte ST6GAL1-Expression in den glykierten BEN-MEN-1 Zellen nachgewiesen werden. Dies konnte auch in anderen Tumorentitäten wie Prostata, Glioblastom, Pulmo oder in Geweben der Mamma nachgewiesen werden [81–84]. In einer anderen Studie in A549 und H1299 Zellen (Zelllinien der Bronchialkarzinome) führte eine

verminderte ST6GAL1-Expression zu verminderten MMP-Expressionen und einem gehemmten invasiven Verhalten [82]. Andererseits hatte ST6GAL1 eine Tumor-suppressive Wirkung im Urothelkarzinom [85]. In vielen Tumorentitäten konnte eine erhöhte ST6GAL2 Expression nachgewiesen werden und vor allem in Mammakarzinomen war dies mit einer erhöhten Expression von *intracellular adhesion molecule* (ICAM)-1, *vascular adhesion molecule* (VCAM)-1, MMP2 oder auch MMP9 verbunden [86,87].

In der glykierten benignen Meningeomzelllinie BEN-MEN-1 wurde eine sinkende ST6GALNAC2-Expression beobachtet. Die verminderte Expression von ST6GALNAC2 ist mit einer schlechteren Prognose für den Patienten mit Mammakarzinom aber auch im Kolorektalen Karzinom assoziiert [88,89]. Im Mammakarzinom konnte die Metastasensupprimierende Wirkung der ST6GALNAC2-Expression nachgewiesen werden [90]. Andererseits konnte eine andere Arbeitsgruppe um Schneider et al 2001 zeigen, dass eine hohe ST6GALNAC2 Expression mit Metastasierungen ins Lymphsystem korrelieren [91]. In der glykierten BEN-MEN-1 Zelllinie war die ST6GALNAC4 Expression erhöht. Eine erhöhte Expression dieser Sialyltransferase führte zu einer verminderten O-Glykan-Kettenverlängerung [92]. In Folikulären Thyroid Karzinom (Follicular Thyroid Carcinoma, FTC) -238 Zellen konnte in vitro und in vivo eine Inhibition des invasiven Verhalten durch eine verminderte Expression des ST6GALNAC4- Gens erzeugt werden [93]. In diesem Modell könnte eine geringere ST6GALNAC5 Expression in beiden glykierten Meningeomzelllinien ein Zeichen für eine Transformation sein, denn die Expression dieser Sialyltransferase ist auf das Hirngewebe beschränkt und synthetisiert GD1a [94]. Die glykierten BEN-MEN-1 Zellen zeigten eine erhöhte Expression von ST6GALNAC6. In mehreren Studien konnte eine erhöhte ST6GALNAC6-Expression, welche für die Synthese von Sialyl-Lewis (a) bekannt ist, im Tumor des Kolons beobachtet werden. Die erhöhte Expression steht im Zusammenhang mit Mechanismen, die die Tumorentwicklung vorantreiben [95,96].

In zerebralen Metastasen des malignen Melanoms ist eine erhöhte ST8SIA1 Expression (GD3-Synthase) auch für eine erhöhte GD3-Synthese verantwortlich. Dies führt zu einer schlechteren Prognose für den Patienten [97]. Auch im Glioblastom konnte eine erhöhte Malignität durch eine erhöhte Expression von GD3 sowie GD2 beobachtet werden und ST8SIA1 wird im Glioblastom sogar als elementarer Treiber für die Malignität beschrieben [98,99]. In diesem Modell hat die Glykierung zu einer erhöhten Expression in der benignen Zelllinie und zu einer Erniedrigung der ST8SIA1 Expression in der malignen Zelllinie geführt. In einer Studie zu Meningeomen und GD3 und GD2 Expression, konnte die Arbeitsgruppe um Mennel et al zeigen, dass die Expressionsmuster abhängig vom Ursprung des Tumors sind [100]. Im nicht kleinzelligen Bronchialkarzinom wurde eine erhöhte ST8SIA2 Expression mit einem erhöhten Rezidiv-Risiko in Verbindung gebracht [101]. Dies könnte auch eine Rolle in

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glykierten BEN-MEN-1 Zellen im Zusammenhang mit dem erhöhten invasiven Verhalten spielen. ST8SIA5 ist bekannt für die Synthese von GD1c/GT1a Tetrasialogangliotetraosyl-Ceramid (GQ)1b aus GM1b/GD1a/GT1b. In der glykierten benignen Zelllinie ist diese Sialyltransferase erhöht [102]. Zusammenfassend kann gesagt werden, dass die Behandlung der Meningeomzellen mit einem hochreaktiven Dicarbonyl wie MGO, direkt bzw. indirekt über Veränderungen der E- und N-Cadherin Expression und über die vorwiegende Steigerung der Expression der Sialyltransferasen in benignen Meningeomzellen zu einer verstärkten Invasivität und somit zu einer erhöhte Malignität führt. Die maligne Zelllinie zeigte eine vorwiegende Verminderung der Expression der Sialyltransferasen mit der altersabhängigen Glykierung und eine Senkung des invasiven Verhaltens.

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5. Thesen

- 1. Methylglyoxal als Glykierungsagens wirkt konzentrationsabhängig zytotoxisch auf die Meningeomzellen.
- 2. Methylglyoxal glykiert die Meningeomzellen konzentrationsabhängig.
- 3. Die Adhäsion ist durch die altersabhängige Glykierung in Meningeomzellen nicht beeinflusst.
- 4. Die Chemotaxis in Meningeomzellen ist durch die altersabhängige Glykierung nicht verändert.
- 5. Ein Zusammenhang zwischen altersabhängiger Glykierung und einem erhöhten invasiven Verhalten ist in benignen Meningeomzellen ersichtlich.
- Die altersabhängige Glykierung verändert die Expressionsmuster der Sialyltransferasen in benignen Meningeomzellen, sodass sie indirekt oder direkt eine Rolle in der Tumorentwicklung spielen könnten.

6. Publikationsteil

6.1 Glycation of benign meningioma cells leads to increased invasion Philipp Selke ¹, Philip Rosenstock ¹, Kaya Bork ¹, Christian Strauss ², Rüdiger Horstkorte ^{1, *} and Maximilian Scheer ^{1,2}

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Abstract: Meningiomas are the most common non-malignant intracranial tumors. Like most tumors, meningiomas prefer anaerobic glycolysis for energy production (Warburg effect). This leads to an increased synthesis of the metabolite methylglyoxal (MGO). This metabolite is known to react with amino groups of proteins. This reaction is called glycation, thereby building advanced glycation endproducts (AGEs). In this study, we investigated the influence of glycation on two meningioma cell lines, representing the WHO grade I (BEN-MEN-1) and the WHO grade III (IOMM-Lee). Increasing MGO concentrations led to the formation of AGEs and decreased growth in both cell lines. When analyzing the influence of glycation on adhesion, chemotaxis and invasion, we could show that the glycation of meningioma cells resulted in increased invasive potential of the benign meningioma cell line, whereas the invasive potential of the malignant cell line was reduced. In addition, glycation increased the E-cadherin- and decreased the N-cadherin-expression in BEN-MEN-1 cells, but did not affected the cadherin-expression in IOMM-Lee cells.

Keywords: Meningioma; intracranial tumor; glycation; methylglyoxal; MGO; AGE; advanced glycation endproducts; invasion; chemotaxis; adhesion

Introduction

Meningioma represents the most common non-malignant intracranial tumor (Goldbrunner et al., 2016; Ostrom et al., 2018; Holleczek et al., 2019; Ostrom et al., 2019).

Like many tumors, meningiomas need large amounts of glucose as primary energy source, because they mainly metabolize glucose to lactate during anaerobic glycolysis (Warburg effect) (Bharadwaj et al., 2015), which generates only low amounts of adenosine triphosphate (ATP). This changed (anaerobic) energy metabolism is one of the "hallmarks of cancer" (Gill et al., 2016). In line with this, there is a correlation between serum glucose levels and meningioma risk (Michaud et al., 2011; Edlinger et al., 2012; Wiedmann et al., 2013; Niedermaier et al., 2015). However, there are many inconsistent data suggesting a positive (Schneider et al., 2005; Schwartzbaum et al., 2005) or inverse (Bernardo et al., 2016) relationship between diabetes and serum glucose levels and the risk of meningioma. Patients with type 2 diabetes have a decreased survival after surgical resection of a WHO grade I meningioma (Nayeri et al., 2016).

Methylglyoxal (MGO) has been discussed as a possible linker between diabetes and serum glucose levels and cancer (Bellier et al., 2019), since diabetic patients and aged individuals have elevated MGO concentrations (Rabbani and Thornalley, 2015). Some authors even propose MGO as a tumor promoting agent (Bellahcène et al., 2018; Antognelli et al., 2019). Approximately 0.1 - 0.4 % of the glucose is transformed to MGO during glycolysis as a regular side product from dihydroxyacetone phosphate or glyceraldehyde-3-phosphate (Allaman et al., 2015). Importantly, MGO is 20,000 times more reactive than glucose and reacts mainly with proteins (through arginine, lysine, and cysteine residues) or to a lower degree also with DNA or lipids, thereby forming advanced glycation endproducts (AGEs) (Kalapos, 2008; Falone et al., 2012; Schalkwijk, 2015). This non-enzymatic reaction between the carbonyl groups of dicarbonyls (like MGO or glyoxal) or sugars (like glucose or fructose) and the amino groups of proteins is called glycation (Ahmed, 2005; Rabbani and Thornalley, 2008). Electrophilic carbonyl groups of glucose or other reactive sugars react with free amino groups of amino acids and forming a non-stable Schiff base. This reaction is called classical Maillard reaction. Further rearrangement leads to formation of a more stable ketosamine (Amadori product). The formation of Schiff bases and Amadori products are reversible reactions. In later reactions, they form irreversible adducts or protein crosslinks (Paul and Bailey, 1996; Ahmed, 2005). The process of producing AGEs affects all proteins including cell adhesion molecules or receptors and proteins of the extracellular matrix (Pedchenko et al., 2005; Rabbani and Thornalley, 2012).

It was previously suggested that application of MGO lead to altered adhesion and migration (Loarca et al., 2013; Antognelli et al., 2019; Nokin et al., 2019).

Cadherins represent cell adhesion molecules that mediate Ca²⁺-dependent homophilic interaction with cadherin molecules on the surface of neighboring cells. The cytoplasmic domain binds downstream to members of the catenin protein family and regulates functions like cell-cell interactions (Harrison et al., 2011; Mège and Ishiyama, 2017). Cadherins also play an important role in the epithelial – mesenchymal-transition (EMT). The EMT describes the change of epithelial markers like E-cadherin to mesenchymal markers like N-cadherin or Vimentin and can promote migration of transformed cells (Gloushankova et al., 2017; Mendonsa et al., 2018). Decreasing E-cadherin expression is mostly associated with weakening of cell-cell adhesion in tumor progression (Rodriguez et al., 2012). Expression of N-cadherin is closely related to tumor invasion and metastasis (Cao et al., 2019).

In the present study, we analyzed differences between benign and malignant meningioma cell lines before and after glycation using MGO. We could show that physiological MGO concentrations had no effect on cell morphology, metabolic activity, chemotaxis and adhesion. However, the invasiveness of the benign meningioma cells was increased whereas the invasiveness of the malignant meningioma cells was reduced in the presence of MGO, which means that glycation resulted in a switch of benign tumor to a more aggressive tumor cell. Furthermore, glycation led to increased E-cadherin and reduced N-cadherin-expression in the benign meningioma cells.

Results

MGO-treatment of meningioma cells interferes with their morphology

First of all, we analyzed whether treatment with MGO affects meningioma cells by comparing their morphology. Therefore, we cultured both cell lines in absence or presence of MGO for 24 h. Representative micrographs for the benign BEN-MEN-1 cells are shown in figure 1 A and for the malignant IOMM-Lee cells in figure 1 B. When cells were cultured in the presence of 0.1 or 0.3 mM MGO, we could not observe any changes in the morphology compared with untreated control cells. BEN-MEN-1 cells had a typical meningothelial shape and grew in monolayers. IOMM-Lee cells were more epithelial-like and grew as multilayers. After treatment with 0.6 mM MGO, we observed less cells and morphological differences compared with the controls. When culturing cells in presence of 1.0 mM MGO, cells became round and we observed less cells and less spreading in both cultures.

Control 0.1 mM MGO 0.3 mM MGO 0.6 mM MGO 1.0 mM MGO Control 0.1 mM MGO 0.3 mM MGO

0.6 mM MGO



1.0 mM MGO



Figure 1. Micrographs of meningioma cells after 24 h MGO-treatment. Cells (A = BEN-MEN-1 and **B** = IOMM-Lee) were cultured in the absence (control) or presence of different concentrations (0.1 mM, 0.3 mM, 0.6 mM and 1.0 mM) of MGO. Scale bar in white: 50 µm.

В



Α

High concentrations of MGO interfere with the cell viability of meningioma cells

Since morphology was changed in presence of 0.6 mM MGO or more, we examined the cell viability of both meningioma cell lines, after culturing in absence or presence of different concentrations of MGO (figure 2). We measured decreased cell viability after incubation with high concentrations of MGO. For the benign cell line, we could not show significant differences at MGO concentrations up to 0.6 mM. Only at 1.0 mM MGO, cell viability was significantly reduced compared with untreated controls (BEN-MEN-1; figure 2 A). For the malignant cell line (IOMM-Lee; figure 2 B), we observed similar effects. Only at 1.0 mM MGO, there was a significant difference compared with control, which confirmed our microscopic observations presented in figure 1 A and B. Furthermore, we analyzed caspase 3 expression by Western blot analysis. Caspase 3 was only expressed in cultures treated with 1.0 mM MGO and not in cultures treated with 0.1, 0.3 or 0.6 mM MGO (data not shown), indicating that only very high concentrations of MGO induce apoptosis in our experiments.



Figure 2. Cell viability of meningioma cell lines after 24 h MGO-treatment. Cell viability was analyzed using an MTT-assay for BEN-MEN-1 (**A**) and IOMM–Lee cells (**B**). Cells were seeded in absence (Ctrl) or presence of MGO (0.1 mM, 0.3 mM, 0.6 mM and 1.0 mM). Both cell lines showed a decreasing metabolic activity with increasing concentration of MGO. Statistical analysis was performed using t-test and error bars represent SD (n= 7; p < 0.005 = ***; (BEN-MEN-1: p = 0.0027; IOMM-Lee: p = 0.00045)).

Increased glycation with increasing concentrations of MGO

Next, we wanted to examine whether treatment of meningioma cells with MGO led to glycation. For this, we cultured both meningioma cell lines in the presence (0.1 mM, 0.3 mM, 0.6 mM and 1.0 mM) or absence of MGO for 24 h. To verify the effect of the treatment, we performed immunoblotting using anti-AGE antibodies. We could show that increasing MGO concentrations led to increasing AGE-signals, which is shown in figure 3 A and C for BEN-MEN-1 and in figure 3 B and D for IOMM-Lee cells. Glycation is quantified in figure 3 B and D. We found significant increase of glycation already at concentrations of 0.3 mM MGO (figure 3 E).



Figure 3. Glycation of meningioma cells. **A** Ponceau S staining of the total proteins (left side) and immunoblot (right side) of BEN-MEN-1 with different MGO concentrations. Controls (Ctrl) were cells without MGO treatment. We used an anti-AGE antibody to verify cellular glycation. **B**: Ponceau S staining of the total proteins (left side) and immunoblot (right side) of IOMM-Lee cells with different MGO concentrations. Controls (Ctrl) were cells without MGO treatment. We used an anti-AGE antibody to verify cellular glycation **C**: Representative quantification of the blot of BEN-MEN-1 cells shown in A. **D**: Representative quantification of the blot of IOMM-Lee cells shown in B. **E**. Quantification of glycation of BEN-MEN-1 and IOMM-Lee after treatment with 0.3 mM MGO. Non-glycated cells were used as controls (Ctrl). Statistical analysis was performed using t-test and error bars represent SD (n= 4; (BEN-MEN-1: p = 0.0452; IOMM-Lee: p = 0.0143)).

MGO has no effect on the adhesion of meningioma cells to ECM components

We then analyzed the effect of glycation on adhesion of the two meningioma cell lines. Since 0.3 mM MGO had no effect on the cell viability of both meningioma cell lines and led to significant formation of AGEs, we decided to use 0.3 mM MGO for all further experiments. To quantify adhesion, we cultured both meningioma cell lines in E-plates. Cells were seeded in absence or presence of MGO on two different matrices (collagen IV or fibronectin) which were in addition preincubated with or without MGO. **Fehler! Verweisquelle konnte nicht gefunden werden.** Figure 4 A and B show the adhesion of both meningioma cell lines on the two different matrices. No significant difference in adhesion could be detected in both cell lines after MGO treatment. Please note, that we observed that BEN-MEN-1 cells adhere much better on both substrates compared to IOMM-Lee cells and that both cancer cells prefer fibronectin to collagen IV as substrate.



Figure 4. Adhesion of meningioma cells with MGO-treatment. BEN-MEN-1 (BM1) (**A**) and IOMM-Lee (IOMM) (**B**) cells were seeded in absence (Ctrl) or presence of 0.3 mM MGO on collagen IV (left) or fibronectin (right). Graphs display adhesion on collagen IV and fibronectin with or without treatment with untreated or treated cells after 2 h. Grey and black bars in **A** and **B** represent the untreated matrix with untreated cells as control. Untreated matrix and treated BEN-MEN-1 cells (BM1 Gly; light green bar) or treated IOMM cells (IOMM Gly; yellow bar). The green (BM1 + Mtx Gly) and orange (IOMM + Mtx Gly) bars show cell adhesion of treated matrix with untreated BEN-MEN-1 and IOMM-Lee cells. Dark green (BM1 Gly + Mtx Gly) and red (IOMM Gly + Mtx Gly) bars represent treated matrix with treated BEN-MEN-1 and IOMM-Lee cells. Dark green (BM1 Gly + Mtx Gly) and red (IOMM Gly + Mtx Gly) bars represent treated matrix with treated BEN-MEN-1 and IOMM-Lee cells. Dark green (BM1 Gly + Mtx Gly) bars represent treated matrix with treated BEN-MEN-1 and IOMM-Lee cells. Dark green (BM1 Gly + Mtx Gly) and red (IOMM Gly + Mtx Gly) bars represent treated matrix with treated BEN-MEN-1 and IOMM-Lee cells. Dark green (BM1 Gly + Mtx Gly) and red (IOMM Gly + Mtx Gly) bars represent treated matrix with treated BEN-MEN-1 and IOMM-Lee cells. Dark green (BM1 Gly + Mtx Gly) and red (IOMM Gly + Mtx Gly) bars represent treated matrix with treated BEN-MEN-1 and IOMM-Lee cells Error bars represent SD (n = 4), (Mtx = Matrix; Gly = MGO treatment).

MGO has no effect on chemotaxis of meningioma cells

Since MGO leads to glycation of almost all cellular proteins, we next wanted to analyze whether cell surface receptors are in general inactivated after glycation. We therefore investigated the impact of glycation on the chemotaxis, which is mediated by cell surface receptors. We cultured both meningioma cell lines in CIM-plates for 24 h. Cells were cultured again in the absence or presence of 0.3 mM MGO. Figure 5 A and B show the chemotactic cell migration after 12 h or 24 h. Treatment with MGO had no effect, neither on BEN-MEN-1 (Figure 5 A) nor on IOMM-Lee cells (Figure 5 B). Please note that chemotaxis of malignant IOMM-Lee cells is higher in contrast to benign BEN-MEN-1 cells.



Figure 5. Chemotaxis of meningioma cells. BEN-MEN-1 (**A**) and IOMM-Lee (**B**) were cultured for 24 h in the absence (Ctrl) or presence of 0.3 mM MGO. Graphs display relative chemotaxis (presented as cell indices) with treatment (MGO) or without treatment (Ctrl) for 12 h and 24 h. Error bars represent SD (n = 4).

<u>Glycation increases invasiveness of the benign cell line and decreases the invasiveness of</u> <u>malignant cell line</u>

Since invasiveness is the most important parameter in most tumors, we finally wanted to examine whether there are changes in invasiveness due to glycation. From our chemotaxis experiments, we knew already that glycation does not interfere with the function of cellular receptors in general. We therefore cultured meningioma cell lines in CIM-plates for 48 h on matrigel in absence or presence of 0.3 mM MGO. Figure 6 A displays the invasion over 48 h for both cell lines. Untreated IOMM-Lee cells are more invasive compared with BEN-MEN-1

cells. BEN-MEN-1 (figure 6 B) cells had a significantly increased invasion after MGO-treatment after 24 h, 36 h and 48 h compared with the untreated controls. This effect could be also observed in another benign meningioma cell line (HBL-52) (data not shown). Interestingly, the malignant cell line (IOMM-Lee, figure 6 C) showed a significant reduction in their invasiveness over 48 h.



Figure 6. Invasion of meningioma cells. BEN-MEN-1 (**A**, **B**) and IOMM-Lee (**A**, **C**) were cultivated for 48 h in absence (Ctrl) or presence of 0.3 mM MGO. Graphs display invasion (presented as cell indices) with treatment (MGO) or without treatment (Ctrl) for 12 h, 24 h (BEN-MEN-1: p = 0.012; IOMM-Lee: p = 0.0347), 36 h (BEN-MEN-1: p = 0.0112; IOMM-Lee: p = 0.0324; IOMM-Lee: p = 0.0374). In the graphs **B** and **C** normalized cell indices were shown for both cell lines relative to the controls. Statistical analysis was performed using t-test. Error bars represent SD (n= 4; p<0.05= *).

Glycation influences the expression of E- and N-Cadherin in benign meningioma cells
Finally, we wanted to investigate whether MGO treatment influences the expression of members of the cadherin family, which are involved in epithelial-mesenchymal or mesenchymal-epithelial-transition. Therefore, we cultured meningioma cells in absence or presence of 0.3 mM MGO for 24 h and performed immunoblotting using anti-E- and N-cadherin antibodies (figure 7). The expression of E- and N-cadherin in IOMM-Lee was not changed after glycation (figure 7 A-D). However, glycation of BEN-MEN-1 cell line resulted in increasing expression of E-cadherin (figure 7 A and B) and decreasing expression of N-cadherin (figure 7 C and D).



Figure 7. Cadherin expression of meningioma cells with and without MGO-treatment. **A.** BEN-MEN-1 and IOMM-Lee were cultured in the absence or presence of 0.3 mM MGO and E-Cadherin was analyzed by Westernblot. **B.** Quantification of E-Cadherin expression in BEN-MEN-1 (p = 0.0406) and IOMM-Lee cells before (Ctrl) and after treatment with 0.3 mM MGO (n=3). **C.** BEN-MEN-1 and IOMM-Lee were cultured in the absence or presence of 0.3 mM MGO and MGO and N-Cadherin was analyzed by Westernblot. **D.** Quantification of N-Cadherin expression in BEN-MEN-1 (p = 0.0276) and IOMM-Lee cells before (Ctrl) and after treatment with 0.3 mM mGO and N-Cadherin was analyzed by Westernblot. **D.** Quantification of N-Cadherin expression in BEN-MEN-1 (p = 0.0276) and IOMM-Lee cells before (Ctrl) and after treatment with 0.3 mM mGO (n=7). All statistical analysis (B;D) were performed using t-test. Error bars represent SD (p<0.05= *).

Discussion

Little is known about the role of MGO and glycation on meningioma cells. In this study, we analyzed the effect of MGO-treatment and glycation on two meningioma cell lines, representing the WHO grade I (BEN-MEN1) and the WHO grade III (IOMM-Lee). We could show that treatment with MGO led to glycation and modulated the invasiveness of both meningioma cell lines. However, glycation did not affect cell adhesion and chemotaxis of these cell lines.

Up to 90 – 99 % of cellular MGO is bound in vivo to macromolecules; however, cellular concentrations up to 0.3 mM have been reported (Thornalley, 1996; Chaplen, 1998; Chaplen et al., 1998). Our data on cell viability using the MTT assay showed that meningioma cells have no significantly reduced metabolism at physiological concentration of 0.3 mM MGO, but are influenced by MGO at high non-physiological concentrations. This could be confirmed via microscopy, where fewer cells and less cell spreading were observed and in immunoblotting in high concentrations, we could detect the cleaved- caspase-3 activity, which is one of the key player of programmed cell death (i. e. apoptosis) (data not shown). Similar observations have been shown in human glioblastoma multiforme T98G, U87MG cells and SH-SY5Y neuroblastoma cells, where MGO interfered with proliferation (Yin et al., 2012; Paul-Samojedny et al., 2016). Another study showed that MGO affects rat schwannoma RT4 cells, PC12 cells and U87 glioma cells in cell viability by decreasing of the key signaling pathway for cell survival (gp130/STAT3 signaling) and as a consequence promotes cytotoxicity (Lee et al., 2009)

MGO led in our hands to detectable glycation of meningioma cell proteins. The influence of glycation on adhesion, migration, invasion and apoptosis of cancer cells could be demonstrated in several recent studies (Loarca et al., 2013; He et al., 2016; Scheer et al., 2020) . Our data show that cell adhesion of meningioma cells is not altered at physiological relevant MGO concentrations. Meningioma cells prefer fibronectin as substrate, what is in line with their integrin expression (α 4, 5, 6 and β 1, 3, 4) (preliminary data not shown), which are also known to be involved in proliferation, adhesion, migration and invasion in meningiomas (Bello et al., 2000; Chen et al., 2009; Gogineni et al., 2011; Nigim et al., 2019).

Our data on chemotaxis indicate that glycation of meningioma cells does not lead to a general loss of function. MGO-treatment seems to have cell-specific effects on behavior, since migration was reduced in liver and colon cancer cells and increased in neuroblastoma cells (Loarca et al., 2013; He et al., 2016; Scheer et al., 2020).

However, our results from the invasion of the meningioma cells indicate that MGO-treatment leads to a higher degree of invasiveness in benign meningioma cells, consequently to increased aggressiveness of meningioma cells. Antognelli et al. have shown that MGO treatment increases the invasion in anaplastic thyroid cancer (ATC) cells (Antognelli et al., 2019). This observation was also confirmed in neuroblastoma cells (Scheer et al., 2020). In liver cancer, it has been shown that invasion was inhibited by MGO treatment (Loarca et al., 2013). However, one has to keep in mind that the concentrations of MGO treatments were different in most studies. Low concentration of 5 μ M MGO resulted in an increased invasion in ATC cells and a decreased invasion in liver cancer cells (Loarca et al., 2013; Antognelli et al., 2019). In neuroblastoma cells, increased invasiveness occurred after treatment with 0.1 mM MGO (Scheer et al., 2020).

Carnel et al. proposed an E-cadherin-integrin crosstalk during cancer invasion and metastasis (Canel et al., 2013). Although Utsuki and colleagues have shown that low expression of Ecadherin is associated with invasive meningioma (Utsuki et al., 2005), we found high expression of E-cadherin in the malignant grade III IOMM-Lee cells and low expression in the benign grade I BEN-MEN-1 cells (see blots in figure 7). Glycation led to increased expression of E-cadherin in BEN-MEN-1 cells, which fits nicely to the increased invasiveness after glycation. On the other hand, we found decreased expression of N-cadherin in BEN-MEN-1 cells. Asano and colleagues reported for gliomas, that an increased expression of N-cadherin correlated with a decreased invasiveness (Asano et al., 2004). Another study has shown that a decreased expression of N-cadherin resulted in a faster and less-directed migration of tumor cells (Camand et al., 2012). In our model, it appears that increased expression of E-cadherin and a decreased expression of N-cadherin are associated with a more invasive behaviour. Many studies suggest a correlation between N-cadherin expression and matrix metalloproteinase-9 (MMP-9) (Suyama et al., 2002; Walker et al., 2014; Hsu et al., 2016). Preliminary data suggest an up-regulation of MMP-9 in BEN-MEN-1 cells after treatment with 0.3 mM MGO (data not shown). Although this has to be validated, one could speculate this as one reason for the increased invasion of this cell line.

Further studies should include expression analysis of the receptor of advanced glycation endproducts (RAGE), since Dai and colleagues showed that the AGE-induced RAGE-signalling pathways promotes development and progression of meningiomas (Dai et al., 2018) and several other studies suggested also an involvement of RAGE in tumor progression (Abe and Yamagishi, 2008; Takino et al., 2010; Ahmad et al., 2018). In our hands, RAGE expression was increased in both cell lines after glycation (data not shown).

In summary, we propose that glycation has a specific effect on different cancer cells. Glycation promotes invasiveness of a WHO grade I meningioma cell line in vitro, but decreases invasive

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behavior in a WHO grade III meningioma cell line. Further studies are necessary, which could include strategies for "de-glycation", which may be important for future cancer treatment.

Materials and Methods

Cell culture

The human benign meningioma cell line BEN-MEN-1 was obtained from Leibniz-Institute DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany) and the human malignant meningioma cell line IOMM-Lee (ATCC® CRL-3370TM) was obtained from American Type Culture Collection (ATCC, Manassas, USA). Both cell lines were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 100 µg/mL of streptomycin, 100 U/mL of penicillin, 4 mM glutamine and 10 % fetal bovine serum (FBS, Sigma Aldrich, St. Louis, MO, USA) at 37 °C in a 5 % CO2 incubator. The cell lines were split every 2 - 3 days with 0.1 % Trypsin-EDTA (Ethylenediaminetetraacetic acid) solution for 2 min.

Cell viability and cell morphology assays

The cell viability of glycated BEN-MEN-1 and IOMM-Lee cells was measured using an MTT (Methylthiazolyldiphenyl-tetrazolium bromide, Sigma Aldrich) assay. Both cell lines were seeded into 96-well plates at a density of 7.8 x 10^4 / cm² cells per well in DMEM with 1 % FBS. After 2 h of attachment, cells were treated with different concentrations of MGO (Sigma Aldrich, 40% aqueous solution; diluted in 1xPBS; 0.1 mM, 0.3 mM, 0.6 mM and 1.0 mM). Controls (Ctrl) were cells (BEN-MEN-1, IOMM-Lee) without MGO treatment. Cell lines were cultivated for 24 h. Morphology of the cells was acquired with bright field microscopy (Axiovert 100, Carl Zeiss AG, Oberkochen, Germany). MTT was diluted to a final concentration of 0.5 mg/mL in normal growth medium and cells were incubated for 2 h with 100 µL MTT solution per well. After elimination of MTT-containing medium, residual formazan crystals were dissolved in 150 µL Dimethylsulfoxid (DMSO). The absorption values were measured (Plate-Reader, Clariostar, BMG Labtech GmbH, Ortenberg, Germany) at a wavelength of 570 nm (background 630 nm). The untreated control cells were set to 1 of cell viability. The changes in cell viability of the treated cells were calculated in relation to the untreated control.

Glycation and Immunoblotting

Cells were seeded in 12-well plates at a density of 3.95×10^4 / cm² in DMEM with 1 % FBS. After 2 h of attachment, the cells were treated with different concentrations of MGO (0.1 mM, 0.3 mM, 0.6 mM and 1.0 mM). Controls (Ctrl) were cells (BEN-MEN-1, IOMM-Lee) without

MGO treatment. The cell lines were cultivated for 24 h. Cells were directly lysed in hot SDSsample buffer (2.5 % sodium dodecyl sulfate, 0.06 M TRIS (tris(hydroxymethyl)aminomethane) pH 6.8, 10 % glycerin, 0.01 % brome phenol blue, 10 mM dithiothreitol in TBS-T (TRIS buffered saline- 0.1 % tween)) to isolate the total protein. Proteins were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE, 10 %) and transferred to a nitrocellulose membrane using western blot techniques. The monoclonal anti-AGE antibody Carboxymethyllysine (CML)-26 (0.05 µg/mL, Abcam, Cambridge, UK) together with the secondary peroxidase-coupled antibody (ImmunoResearch Inc., Eagan, USA) was used to detect the glycation. Detection of E- and N-cadherin expression were done with monoclonal anti-E-cadherin antibody (0.05 µg/mL, Abcam, Cambridge, UK) and with monoclonal anti-Ncadherin antibody (0.0483 µg/mL, Abcam, Cambridge, UK) and a secondary peroxidasecoupled antibody (ImmunoResearch Inc., Eagan, USA). Images were taken using Chemidoc MP imaging system (Bio-Rad Laboratories, Hercules, USA). Ponceau S staining (0.1 % Ponceau S, 3 % trichloroacetic acid and 3 % sulfosalicylic acid) of total loaded protein and GAPDH (Glyceraldehyde 3-phosphate dehydrogenase) (0.04 µg/ml, Santa Cruz Biotechnology Inc., Dallas, USA) were used as loading controls. Band intensity of proteins of interest were transformed into numeric values using Image lab software (Bio-Rad Laboratories, Hercules) and normalized to the corresponding ponceau S staining to quantify the results.

Examination of adhesion with Real Time Cell Analysis

Fibronectin and collagen IV at a concentration of 10 µg/mL were used for each experiment and were added to the wells of the 96X E-plates® (ACEA Biosciences, San Diego, USA) and incubated for 1 h at 37 °C. E-plates® have gold microelectrode biosensors in each well of ACEA's electronic microtiter plates. After a washing step with PBS, the wells were incubated with 0.5 % BSA solution in PBS for 20 min. Before the cells and media were added, the wells were washed with PBS. The cells were trypsinized and detached. The reaction was stopped and the cells were resuspended in media with 1 % FBS. 50 µl serum-free media was added to every well in order to measure the background signal. Cells were added in density of 1.5625×10^4 / cm². The adhesion of cell lines was measured as changes in impedance with the Real Time cell electronic sensing (RT-CES®) system (ACEA Biosciences) and monitored every 15 min for a period of 4 h. The measurement was done with the Real Time Cell Analyzer dual purpose (RTCA DP) Analyzer (ACEA Biosciences,) as Cell Index (CI). The index is calculated as follows: CI = (impedance at time point n – impedance in the absence of cells) / nominal impedance value.

Examination of chemotaxis with Real Time Cell Analysis

Chemotaxis was analyzed in 96X Cellular invasion and migration (CIM)-plates (ACEA Biosciences). The CIM-plates are composed of an upper and a lower chamber. The bottom surface of the upper chamber consists of a microporous membrane where cells can migrate through. Underneath the membrane, a gold electrode detects the presence of adherent cells. 160 μ I DMEM with 20 % FBS were added in the lower chamber. 50 μ I DMEM with 1 % FBS were added in the upper chamber. CIM-plates were incubated for 1 h at 37 °C, followed by background measurement. Cells were trypsinized, detached, the reaction was stopped and the cells were resuspended in media with 1 % FBS. Cells were added to the upper chamber in density of 7.8 x 10⁴/ cm². The chemotaxis on every label was measured as changes in impedance with the RT-CES® system and monitored every 15 min for a period of 24 h. The measurement was conducted with the RTCA DP Analyzer (ACEA Biosciences) and displayed with the RTCA program 2.0 (ACEA Biosciences).

Examination of invasion with Real Time Cell Analysis

Invasion was analyzed in 96X CIM-plates (ACEA Biosciences). The CIM-plates are composed of an upper and a lower chamber. The bottom surface of the upper chamber consists of a microporous membrane where cells can migrate through. On the underside of this membrane a gold electrode detects the presence of adherent cells. To investigate the invasion, 800 μ g/ml Basement Membrane Matrix, lactose dehydrogenase-elevating virus (LDEV)-free Matrigel® (Corning, Minneapolis, MN, USA) were added in the upper chamber. After an incubation for 4 h at 37 °C, 160 μ l DMEM with 20 % FBS were added in the lower chamber and 50 μ l DMEM with 1 % FBS were added in the upper chamber. The CIM-plates were incubated for 1 h at 37 °C. Afterwards, the background signal was measured. Cells were trypsinized and detached. The reaction was stopped by adding media with 1 % FBS and the cells were resuspended. Cells were added to the upper chamber in density of 1.1 x 10⁵/ cm². Invasion was measured as changes in impedance with the RT-CES® system and monitored every 15 min for a period of 48 h. The measurement was carried out with the RTCA DP Analyzer (ACEA Biosciences) and displayed with the RTCA program 2.0 (ACEA Biosciences).

Statistical analysis

All analyses and visualizations were performed using OriginPro 2019 software (OriginLab Corporation, Northampton, USA). Paired student t-test against the control group, both cell lines or a theoretical value of 1 (due to data normalization) were executed. Figures show the average mean with standard deviation (SD) and levels of significance are represented within the figures.

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Conflicts of Interest

The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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6.2 Glycation interferes with the expression of sialyltransferases in meningiomas

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Abstract: Meningiomas are the most common non-malignant intracranial tumors and prefer, like most tumors, anaerobic glycolysis for energy production (Warburg effect). This anaerobic glycolysis leads to an increased synthesis of the metabolite methylglyoxal (MGO) or glyoxal (GO), which is known to react with amino groups of proteins. This reaction is called glycation, thereby building advanced glycation endproducts (AGEs). In this study, we investigated the influence of glycation on sialylation in two meningioma cell lines, representing the WHO grade I (BEN-MEN-1) and the WHO grade III (IOMM-Lee). In the benign meningioma cell line, glycation led to differences in expression of sialyltransferases (ST3GAL1/2/3/5/6; ST6GAL1/2; ST6GALNAC2/6, and ST8SIA1/2), which are known to play a role in tumor progression. We could show that glycation of BEN-MEN-1 cells led to decreased expression of ST3Gal5. This resulted in decreased synthesis of the ganglioside GM3, the product of ST3Gal5. In the malignant meningioma cell line, we observed changes in expression of sialyltransferases (ST3GAL1/2/3; ST6GALNAC5 and ST8SIA1) after glycation which correlates with less aggressive behavior.

Keywords: intracranial tumor; methylglyoxal; MGO; Sialylation, tumorigenesis, posttranslational modification

Introduction

Meningiomas arise from the arachnoid and are the most common non-malignant intracranial tumor [1-5]. They are classified according to WHO (World Health Organization) in grades I, II, and III. The benign grade I represents the most frequent subtype (>80%), has a low risk of recurrence and slow growth [5,6]. As opposed to benign meningioma, grade III meningiomas (anaplastic, rhabdoid, and papillary subtype) are rare (1-3%) and little is known about factors that influence their survival and malignity. The present surgical, medicinal, and radiotherapeutic treatments are not adequate to manage the morbidity and mortality in this subtype [7–10].

Like many other tumors, meningiomas use glucose as a primary energy source (Warburg effect), which is considered as one of the "hallmarks of cancer" [11–13].

During glycolysis, up to 0.4 % of the glucose is converted into methylglyoxal (MGO). MGO is a typical side product of glyceraldehyde-3-phosphate, which is generated by the aldolase reaction from fructose-1,6-bisphosphate. Please note that MGO is more than 20,000 times more reactive than glucose [11]. Previous studies showed that MGO concentrations are elevated in diabetic and or aged individuals [14]. Many studies suggest that diabetes is linked to an increased risk of cancer [15,16]. In line with this, there is a correlation between serum glucose levels and meningioma risk [17,18]. However, there are contrary data suggesting a positive [19,20] or inverse [21] correlation between diabetes and serum glucose levels and the risk of meningioma. For example, patients with type 2 diabetes have a decreased survival after surgical resection of a WHO grade I meningioma [22].

The dicarbonyl MGO reacts primarily with proteins (through arginine, lysine, and cysteine residues) or to a small extent also with DNA and lipids. This non-enzymatic reaction between the carbonyl groups of dicarbonyls (i.e. MGO) or monosaccharides (i.e. glucose) and the amino groups of proteins is called glycation [23,24]. Another important glycating agent is glyoxal (GO), which is formed by degradation of glucose or autoxidation of glycoaldehyde to glyoxal [25]. Glycation is much stronger with dicarbonyls than with monosaccharides [26]. The endproducts of this reaction are called advanced glycation endproducts (AGEs) [27–29]. Recently, we demonstrated that glycation through MGO led to an increased invasive behavior in benign meningioma cells [30]. Several other studies propose MGO as a tumor-promoting agent [31,32].

Another common posttranslational modification is glycosylation. In contrast to glycation, glycosylation is an enzymatic addition of carbohydrates, glycans to a non-carbohydrate-structure, commonly a lipid or protein in the endoplasmatic reticulum (ER)/Golgi. Sialylation is

of deep interest and describes the addition of sialic acids (Sia) to lipids (i.e. gangliosides) or proteins (i.e. neural cell adhesion molecule (NCAM)) through sialyltransferases (ST) [33].



Figure 1: Schematic representation of the Sia biosynthesis from glucose to Sia and glycation agents (MGO/GO) and sialylation of glycoproteins (i.e. N-glycans, O-glycans or gangliosides) in the endoplasmatic reticulum and Golgi. G-3-P = glyceraldehyde-3-phosphate; DHA-P = Dihydroxyaceton phosphate; MGO = methylglyoxal; GO = glyoxal; GlcNAc = N-acetyl-glucosamine; Man =Mannose; Gal = Galactose; Neu5Ac = N-acetyl-neuraminic acid; GNE = UDP-N-acetyl glucosamine 2-epimerase/N-acetyl mannosamine kinase; ER = Endoplasmatic reticulum

N-acetyl neuraminic acid (Neu5Ac) represents the major Sia of mammals. It is synthesized from UDP-N-acetyl glucosamine (UDP-GlcNAc) in the cytosol [34]. The key enzyme of the Sia biosynthesis is the bifunctional UDP-N-acetyl glucosamine 2-epimerase/N-acetyl mannosamine kinase (GNE) [35]. Sialylation is taking place in the Golgi and is catalyzed by STs. They are 20 known STs in humans, which use CMP-activated Sia as substrate (figure 1). These STs are subdivided into 4 families dedicated to the carbohydrate linkages they synthesize: beta-galactoside alpha 2,3- sialyltransferases (ST3Gal1-6), beta-galactoside alpha 2,6- sialyltransferases (ST6Gal1-2), N-acetyl galactosamine (GalNAc) alpha 2,6- sialyltransferases (ST6GalNAc1-6) and alpha 2,8-sialyltransferases (ST8Sia1-6) [36,37]. The members of the ST3Gal family transfer Sia from CMP-Sia to terminal galactose residues

through 2,3 linkages, whereas the two known members of the ST6Gal family do this through 2,6 linkages. The six members of the ST6GalNAc family transfer Sia from CMP-Sia to GalNAc residues via 2,6 linkages. In addition, the ST8Sia-family transfer Sia from CMP-Sia to other terminal Sia residues by 2,8-linkages [36,37]. High blood glucose concentrations in individuals with diabetes result in a UDP-GlcNAc dependent change to more complex N-glycans [38]. Especially glycoproteins with only few N-glycosylation sites such as transforming growth factor β (TGF β) or glucose transporter 4 (GLUT4) show rapid response to increasing GlcNAc concentrations causing complex glycan formation and branching [39]. Gangliosides are glycosphingolipids that contain Sias. The synthesis of gangliosides begins with ceramide (Cer) in the ER. During GM3-synthesis Cer will be glucosylated by the glucosylceramid synthase. After this step in the cis-golgi, glucosylceramide is converted in the trans-golgi to lactosylceramide [40]. This is the substrate for GM3-synthase (ST3Gal5). It is known that GM3 plays a role during several diseases (chronic inflammation, insulin resistance or cancer) [41–43].

In this study, we compared the expression of STs in benign and malignant meningioma cells and found significant differences between these two. Furthermore, we investigated the role of the glycating metabolite MGO on the expression of STs in both benign and malignant meningioma cells. Thereby we could show that glycation has a dramatic effect on the expression of STs and consequently on the GM3 expression. As a result, this could change sialylation-dependent tumor progression in meningioma.

Materials and Methods

Cell culture

The human benign meningioma cell line BEN-MEN-1 was obtained from Leibniz-Institute DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany) and the human malignant meningioma cell line IOMM-Lee (ATCC® CRL-3370TM) was obtained from American Type Culture Collection (ATCC, Manassas, USA). Both cell lines were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 100 µg/mL of streptomycin, 100 U/mL of penicillin, 4 mM glutamine, and 10 % fetal bovine serum (FBS, Sigma Aldrich, St. Louis, MO, USA) at 37 °C in a 5 % CO₂ incubator. The cell lines were split every 2 - 3 days with 0.1 % Trypsin-EDTA (Ethylenediaminetetraacetic acid) solution for 2 min.

Glycation and Real-Time PCR analysis

Cells were seeded in 12-well plates at a density of 3.95×10^4 / cm² in DMEM with 1 % FBS. After 2 h of attachment, the cells were treated with 0.3 mM MGO or GO. Controls (Ctrl) were cells (BEN-MEN-1, IOMM-Lee) without MGO or GO treatment. The cell lines were cultivated for 24 h. RNA was isolated using the Quick-RNATM MiniPrep Kit (Zymo Research, Irvine, CA, USA) according to the manufacturer's instructions. The quality and concentration of the RNA were analyzed using the NanoDrop 1000 Spectrophotometer (Thermo Fisher Scientific). RNA (2 µg) was transcribed into cDNA using SuperScriptTM II Reverse Transcriptase according to the manufacturer's instructions were performed using DreamTaq DNA polymerase (Thermo Fisher Scientific), and products were separated on a 1.5 % agarose gel. The following conditions were used: initial denaturation for 2 min at 95 °C, 35 cycles (30 s at 95 °C, 30 s at 55 °C, 30 s at 72 °C), final elongation for 5 min at 72 °C. We use for all sialyltransferases the same primer pairs which were used in a previous study [44].

The sialyltransferase expression of untreated meningioma cell lines (BEN-MEN-1; IOMM- Lee) and after 24 h of glycation with 0.3 mM MGO were measured via quantitative real-time PCR (qPCR) using the iQTM 5 Multicolor Real-Time PCR Detection System (Biorad, Hercules, CA, USA) and qPCR GreenMaster (Jena Bioscience, Jena, Germany) with the same primer pairs used for normal PCR. The following conditions were used for qPCR: initial denaturation for 1:30 min at 95 °C, 40 cycles (10 s at 95 °C, 10 s at 62 °C, 25 s at 72 °C), final elongation for 1 min at 72 °C followed by a melting curve analysis. The expression level of sialyltransferases in control and glycated cell lines was determined relatively to GAPDH (165 bp; fw: GGAGCGAGATCCCTCCAAA; rv: ATGACGAACATGGGGGCATC), calculated as Δ CT. The control was relatively computed to glycated cell line (2 - $\Delta\Delta$ CT). All reactions were performed in triplicates.

Cultivation of BEN-MEN-1 cells and Preparation of GSL-glycan alditols released from BEN-MEN-1 cells

Extraction of GSLs and preparation of GSL-glycan alditols from cells were performed in triplicate as previously described [45]. The cells were cultivated until 80 % of confluence and followed by 24 h treatment with and without 0.3 mM MGO. Shortly, $2x 10^6$ cells were harvested, washed and resuspended with 200 µL of water. The cell samples were lysed by vortexing and sonication for 30 min. In this step, 2.5 µL of 0.5 µM ganglioside GT1b in ethanol was added as a spiked internal standard to monitor sample preparation and to normalize roughly absolute quantification. Chloroform (550 µL) was added to the samples followed by 15 min sonication. Methanol (350 µL) was added to the cell pellets and incubated for 4 h with shaking at room

temperature. The upper phase containing GSLs was collected after centrifugation at 2700 × g for 20 min. Then, 400 μ L of chloroform/methanol (2:1, v/v) was added, followed by adding 400 μ L of methanol/water (1:1, v/v). After sonication and centrifugation, the upper phase was collected and pooled to the previous sample. The process of adding methanol/water (1:1, v/v), sonication, centrifugation and removing upper phase was repeated another two times. In each replicate, the upper phase was collected and replaced by the same volume of methanol/water (1:1, v/v). The combined upper phases were dried under vacuum in an Eppendorf Concentrator 5301 (Eppendorf, Hamburg, Germany) at 30°C.

Before the purification of the GSLs using reverse- phase (RP) SPE, the samples were dissolved in 100 μ L methanol followed by the addition of 100 μ L water. TC18-RP- cartridges were prewashed with 2 mL of chloroform/methanol (2:1, v/v), 2 mL of methanol followed by equilibration with 2 mL methanol/water (1:1, v/v). The extracted GSLs were loaded to the cartridge and washed with 2 mL methanol/water (1:1, v/v). The GSLs were eluted from the column with 2 mL methanol and 2 mL chloroform/methanol (2:1, v/v). The samples were dried under vacuum in an Eppendorf Concentrator at 30°C.

To release the glycans from the GSLs, a mixture of EGCase I (12 mU, 2 μ L), EGCase I buffer (4 μ L) and water (34 μ L) (pH 5.2) was added to each sample and incubated for 36 h at 37°C. The released glycans were collected and loaded on TC18-RP-cartridges, which had been preconditioned with 2 mL of methanol and 2 mL of water. The samples were washed with 200 ul of water and residual glycans were loaded to the cartridge. Then, 500 μ L of water was added to the cartridge to wash the glycans from the column. The flow-through and wash fractions were pooled and dried in an Eppendorf Concentrator at 30°C.

The reduction was carried out with slight modifications following the same procedure as described in previous work [45,46]. In brief, GSL-glycans were reduced to alditols in 20 μ L of sodium borohydride (500 mM) in potassium hydroxide (50 mM) for 2 h at 50°C. Subsequently, 2 μ L of glacial acetic acid was added to acidify the solution and quench the reaction. The desalting of GSL-glycans was performed as previously described. Glycan alditols were eluted with 50 μ L of water twice. The combined flow-through and eluate were pooled and dried under vacuum in an Eppendorf Concentrator at 30°C. The carbon SPE clean-up was performed and the purified glycan alditols were re-suspended in 20 μ L of water prior to *Porous Graphitized Carbon (PGC) nano-Liquid Chromatography (LC)- Electro Spray Ionization (ESI)-Mass Spectrometry (MS)/MS /MS analysis.*

Analysis of GSL-glycan alditols using PGC nano-LC-ESI-MS/MS

The analysis of glycan alditols was performed using PGC nano-LC-ESI-MS/MS following a method described previously [45,46]. Measurements were performed on an Ultimate 3000 Ultra High Performance Liquid Chromatography (UHPLC) system (Thermo) equipped with a home-packed PGC trap column (5 μ m Hypercarb, 320 μ m x 30 mm) and a home-packed PGC nano-column (3 μ m Hypercarb 100 μ m x 150 mm) coupled to an amaZon ETD speed ion trap (Bruker, Bremen, Germany). Mobile phase A consisted of 10 mM ABC, while mobile phase B was 60% (v/v) acetonitrile/10 mM ABC. The trap column was packed with 5 μ m particle size PGC stationary phase from Hypercarb PGC analytical column (size 100 × 4.6 mm, 5 μ m particle size, Thermo) while the PGC nano-column (size 30 × 4.6 mm, 3 μ m particle size, Thermo).

To analyze glycans, 2 μ L injections were performed and trapping was achieved on the trap column using a 6 μ L/min loading flow in 1% solvent B for 5 min. Separation was achieved with a linear gradient from 1% to 50% solvent B over 73 min was applied followed by a 10 min wash step using 95% of B at a 0.6 μ L/min flow rate. The column was held at a constant temperature of 35°C.

Ionization was achieved using the nanoBooster source (Bruker) with a capillary voltage of 1000 V applied and a dry gas temperature of 280°C at 3 L/min and isopropanol enriched nitrogen at 3 psi. MS spectra were acquired within an m/z range of 340-1850 in enhanced mode using negative ion mode, smart parameter setting was set to m/z 900. MS/MS spectra were recorded using the top 3 highest intensity peaks.

Structures of detected glycans were studied by MS/MS in negative mode. Glycan structures were assigned based on the known MS/MS fragmentation patterns in negative-ion mode [47,48], elution order, and general glycobiological knowledge, with help of Glycoworkbench [49] and Glycomod [50] software. To get an estimate of the glycan amount per cell, glycan intensity was normalized to the intensity of the internal standard GT1b. Then, assuming complete release of glycans and similar response factors between released glycan and GT1b standard, the number of glycans per cell was estimated.

Structures are depicted according to the Consortium of Functional Glycomics (CFG). Blue square is *N*-acetylglucosamine; yellow square is *N*-acetylgalactosamine; blue circle is glucose; yellow circle is galactose; red triangle is fucose; purple diamond is *N*-acetylneuraminic acid, grey diamond is *N*-glycolylneuraminic acid.

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Statistical analysis

All analyses and visualizations were performed using OriginPro 2019 software (OriginLab Corporation, Northampton, USA). Paired student t-test against the control group, both cell lines of a theoretical value of 1 (due to data normalization) were executed. Figures show the average mean with standard deviation (SD) and levels of significance are represented within the figures.

Results

Expression of sialyltransferases in meningioma cell lines

Since there is evidence that sialyltransferases have an impact on tumorigenesis, we analyzed benign (BEN-MEN-1) and malignant (IOMM-Lee) meningioma cell lines regarding differences in expression of sialyltransferases (figure 2, table 1). Figure 2A shows the expression of ST3GAL1-6 in BEN-MEN-1 and IOMM-Lee. ST3GAL1-ST3GAL3 and ST3GAL5-ST3GAL6 were detected in both cell lines. The band intensity of ST3GAL2 was higher in the malignant cell line compared with the benign cell line whereas the ST3GAL3, ST3GAL5-6 band intensities were higher in BEN-MEN-1 compared to the malignant cell line. Agarose gel of ST6GAL1-2 is shown in figure 2B for both cell lines. ST6GAL2 was only expressed in the benign cell line. In contrast, no differences could be found in terms of band intensity of ST6GAL1 in both cell lines. The expression of ST6GALNAC1-6 for both cell lines is shown in figure 2C. In contrast to IOMM-Lee, a weak band in ST6GALNAC2 was detectable in BEN-MEN-1. Expression of ST6GALNAC4-6 was detectable in both cell lines. The band intensities of ST6GALNAC5 and ST6GALNAC6 were higher in IOMM-Lee compared to BEN-MEN-1. The expression of ST8SIA1-6 in both cell lines is shown in figure 2D. For ST8SIA1-2 and ST8SIA5-6, the expression has been detected in both meningioma cell lines. In BEN-MEN-1 we observed a higher expression of ST8SIA2 and ST8SIA6 compared to the malignant cell line. Again, the band intensity of ST8SIA5 was stronger in IOMM-Lee compared to the benign cell line.



Figure 2: Expression of 20 Sialyltransferases (agarose gel) in BEN-MEN-1 and IOMM-Lee. Figure 2**A**: Expression of ST3GAL1-6. Figure 2**B**: Expression of ST6GAL1-2, Figure 2**C**: Expression of ST6GALNAC1-6, Figure 2**D**: Expression of ST8SIA1-6.

Table 1: Overview of sialyltransferase expressions in both meningioma cell lines

GENE	BEN-MEN-1	IOMM-Lee
ST3GAL1	+++	+++
ST3GAL2	+	++
ST3GAL3	+++	+++
ST3GaAL4	-	-
ST3GAL5	+++	+++
ST3GAL6	+++	+++
ST6GAL1	+++	+++
ST6GAL2	++	-
ST6GALNAC1	-	-
ST6GALNAC2	+	-

ST60	GALNAC3	-	-
ST60	GALNAC4	+++	+++
ST60	GALNAC5	++	+++
ST60	GALNAC6	++	++
ST	F8SIA1	+++	+++
ST	F8SIA2	+++	+
ST	T8SIA3	-	-
ST	F8SIA4	-	-
ST	T8SIA5	+	+
ST	F8SIA6	+++	+

Sialyltransferases are more affected by MGO in benign cell line

Since the expression of sialyltransferases is different in the benign and malignant meningioma cell lines, we quantified the sialyltransferase mRNA expression level after 24 h of glycation of the cells to verify the influence of glycation on sialylation. Figure 3 displays the different mRNA expressions of ST3GAL1-6 in BEN-MEN-1 (figure 3A) and IOMM-Lee (figure 3B). Glycation led to changes in ST expression. In the benign cell line, we observed an increased overall expression, whereas we noticed a decreased overall expression of STs in the malignant cell line. ST3GAL1 (1.4812 \pm 0.115 fold change), ST3GAL2 (3.143 \pm 0.476 fold change), and ST3GAL3 (1.28 \pm 0.189 fold change) expression were increased in contrast to non-glycated cells in BEN-MEN-1. Furthermore, the relative expression of ST3GAL5 (0.7863 \pm 0.0933 fold change) and ST3GAL6 (0.572 \pm 0.126 fold change) were decreased in contrast to non-glycated cells. The relative expression of ST3GAL1 (0.601 \pm 0.223 fold change), ST3GAL2 (0.288 \pm 0.0535.fold change), ST3GAL3 (0.6175 \pm 0.217 fold change), ST3GAL5 (0.4561 \pm 0.1271 fold change), ST3GAL6 (0.502 \pm 0.1325 fold change) were decreased in contrast to non-glycated cells in the malignant cell line.



Figure 3: Relative mRNA expression of ST3GAL1-6 in BEN-MEN-1 (**A**) and IOMM- Lee (**B**). Figure 3**A**: Normalized control (**grey**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**green**). Figure 3**B**: Normalized control (**black**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**red**). Statistical analysis was performed using t-test and error bars represent SD (n= 4; (ST3GAL1: p = 0.0054 (**A**), p = 0.0267 (**B**); ST3GAL2: p = 0.0022 (**A**), p = 0.0002 (**B**); ST3GAL3: p = 0.0414 (**A**), p = 0.0276 (**B**); ST3GAL5: p = 0.0286 (**A**), p = 0.0051 (**B**); ST3GAL6: p = 0.0097 (**A**), p = 0.0073 (**B**)).

Figure 4 shows the expression of ST6GAL-family in BEN-MEN-1 (figure 4A) and IOMM-Lee (figure 4B). Glycation led to opposing changes in the expression of this sialyltransferase. We observed a higher expression in the benign cell line after treatment with MGO (3.2402 ± 0.962 fold change) whereas no changes could be measured in the glycated malignant cell line (1.018 \pm 0.164 fold change). The expression of ST6GAL2 was only detected in BEN-MEN-1 and increased after treatment with MGO (1.624 ± 0.188 fold change).



Figure 4: Relative mRNA expression of ST6GAL1-2 in BEN-MEN-1 (**A**) and IOMM- Lee (**B**). Figure 4**A**: Normalized control (**grey**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**green**). Figure 4**B**: Normalized control (**black**) and the mRNA expression after 24 h treatment with 0.3 mM MGO (**red**). Statistical analysis was performed using t-test and error bars represent SD (n= 4; (ST6GAL1: p = 0.0274 (**A**), p = 0.863 (**B**); ST6GAL2: p = 0.0213 (**A**)).

Moreover, the mRNA expression of ST6GALNAC1-6 in BEN-MEN-1 (figure 5A) and IOMM-Lee (figure 5B) is also differently altered after glycation. ST6GALNAC2 expression decreased after glycation in contrast to the untreated benign cell line (0.6807 ± 0.1106 fold change). ST6GALNAC4 expression is not affected in BEN-MEN-1 (2.556 ± 1.232 fold change) and IOMM-Lee (1.005 ± 0.2552 fold change), but glycation decreased the mRNA expression of ST6GALNAC5 in both cell lines (0.5575 ± 0.283 ; 0.5991 ± 0.2174). Glycation led to a higher expression of ST6GALNAC6 in the benign cell line (1.5141 ± 0.1999). ST6GALNAC6 expression is not influenced by glycation in the malignant cell line (0.839 ± 0.203).



Figure 5: Relative mRNA expression of ST6GALNAC1-6 in BEN-MEN-1 (**A**) and IOMM- Lee (**B**). Figure 5**A**: Normalized control (**grey**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**green**). Figure 5**B**: Normalized control (**black**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**red**). Statistical analysis was performed using t-test and error bars represent SD (n= 4; (ST6GALNAC2: p = 0.0275 (**A**); ST6GALNAC4: p = 0.0583 (**A**), p = 0.4882 (**B**); ST6GALNAC5: p = 0.0366 (**A**), p = 0.024 (**B**); ST6GALNAC6: p = 0.0339 (**A**), p = 0.1311 (**B**)).

Finally, we quantified the expression of ST8SIA 1-6. Glycation influenced more strongly the expression level of these sialyltransferases in BEN-MEN-1 cells compared to the malignant IOMM-Lee cell line. The expression of ST8SIA1 was highly increased (2.696 ± 0.627 fold change) after glycation in the benign cell line (figure 6A) and decreased (0.744 ± 0.07712 fold change) in the glycated malignant cell line (figure 6B). The expression of ST8SIA2 (3.2171 ± 0.6837 fold change) and ST8SIA5 (1.696 ± 0.3475 fold change) were both increased in BEN-MEN-1 (figure 6A). ST8SIA5 expression was not influenced by glycation in IOMM-Lee cells. The expression of ST8SIA6 was not influenced by glycation in both cell lines.



Figure 6: Relative mRNA expression of ST8SIA1-6 in BEN-MEN-1 (**A**) and IOMM- Lee (**B**). Figure 6**A**: Normalized control (**grey**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**green**). Figure 6**B**: Normalized control (**black**) and mRNA expression after 24 h treatment with 0.3 mM MGO (**red**). Statistical analysis was performed using t-test and error bars represent SD (n= 4; (ST8SIA1: p = 0.00912 (**A**), p = 0.00521 (**B**); ST8SIA2: p = 0.00558(**A**); ST8SIA5: p = 0.0202 (**A**), p = 0.4901 (**B**); ST8SIA6: p = 0.1501 (**A**), p = 0.0636 (**B**)).

MGO-treatment decreases ganglioside GM3 expression in BEN-MEN-1

To proof, that MGO-induced reduction of ST3GAL5 expression has an impact on BEN-MEN-1 cells, we quantified ganglioside GM3 by PGC nano-LC-ESI-MS/MS. Figure 7A summarizes the biosynthesis of GM3. Figure 7B shows the signal intensity of GM3 before and after glycation in comparison to the internal standard of GT1b in BEN-MEN-1 cells. The absolute quantification of GM3 is shown in figure 7C. We could show a decreased GM3 expression after glycation (p= 0.00314), which is in line with the decreasing expression of ST3GAL5 (see: figure 3A). The normalized copy number of GM3 per cell in the untreated BEN-MEN-1 cell line ($1.32x10^8 \pm 9.15x10^6$) were decreased by 235% compared to the glycated cells ($5.61x10^7 \pm 3.89x10^6$).



Figure 7: Absolute quantification of GM3 signal by PGC nano-LC-ESI-MS/MS. Figure 7**A**: Schematic representation of the GM3 biosynthesis. Cer = Ceramide; GalCer = Galactosylceramide; GlcCer = Glucosylceramide; LacCer = Lactosylceramide; GM3 = Monosialoganglioside 3. Figure 7**B**: Signal intensity of GM3 in BEN-MEN-1 Ctrl and BEN-MEN-1 0.3 mM MGO in comparison to the internal standard GT1b. Figure 7**C**: Absolute quantification of GM3 signal by PGC nano-LC-ESI-MS/MS of Ctrl (**grey**) and 0.3 mM MGO-treated BEN-MEN-1 (**green**). Statistical analysis was performed using t-test and error bars represent SD (n= 3; p = 0.00134).

Glyoxal-treatment has different effects in ST3GAL5

Finally, we analyzed whether another glycation agent than MGO has the same effect on ST3GAL5 expression as MGO. We could show by Westernblot analysis that 0.3 mM glyoxal (GO) leads to glycation in both cell lines (data not shown). Using qPCR of cDNA of BEN-MEN-1 cells (figure 8A) or IOMM-Lee (figure 8B), which were grown for 24 h in the presence of 0.3 mM GO, we could show that GO-induced glycation had the same effect on ST3GAL5 expression as MGO treatment in BEN-MEN-1 cells. However, GO did not alter the expression of ST3GAL5 in malignant IOMM-Lee cells, which is in contrast to MGO. This suggests a glycation agent-specific change of ST3GAL5 expression.



Figure 8: Relative mRNA expression of ST3GAL5 in BEN-MEN-1 (**A**) and IOMM-Lee (**B**). A shows the relative expression of ST3GAL5 in untreated (**grey**), 0.3mM MGO (green) and 0.3 mM GO (**dark green**) treated BEN-MEN-1. B shows the relative expression of ST3GAL5 in untreated (**black**), 0.3 mM MGO (**red**) and 0.3 mM GO (**dark red**) treated IOMM-Lee. Statistical analysis was performed using t-test and error bars represent SD (n= 4; ST3GAL5 GO (A) p = 0.007; (B) p = 0.415).

Discussion

Many studies demonstrated that sialylation has an impact on tumorigenesis [51–55]. Abnormal levels of different glycosyltransferases were found in different types of human cancers [56,57]. In addition, high serum levels of sialyltransferases are associated with the progression of advanced breast cancer [58].

But little is known about the influence on glycosylation by glycation, which is increased in several cancers because of the Warburg effect [59,60]. In this study, we could show, that glycation affects sialylation by modulating ST expression, which could have an impact on different ganglioside patterns and thereby on tumor development. Most of the STs were expressed in both, BEN-MEN-1 and IOMM-Lee, cell lines. Glycation of both cell lines resulted in an increasing level of STs in the benign meningioma cells and decreasing level in the malignant cells.

There are many reports of changes in ST expression in cancer. Overexpression of ST3GAL1 in ovarian cancer led to transforming growth factor (TGF)-β1-induced epithelial-mesenchymal-transition, migration, and invasion, and a knockdown resulted in the opposite [61]. Another study by Mehta et al. has revealed that ST3GAL2 and ST6GAL1 were significantly upregulated

in tumors with positive perineural invasion status [62], which we observed in the glycated benign cell line. ST3GAL3 was increased in the glycated BEN-MEN-1 cell line but decreased in glycated IOMM-Lee cells. Expression of ST3GAL3 is important for the regulation of biosynthesis of brain disialoganglioside (GD)1a and trisialoganglioside (GT)1b [57]. In several studies, the altered expression of ST3GAL3 has an impact on cell adhesion and invasion. Glycation of meningioma cell lines resulted in decreased ST3GAL5 expression in both cell lines. This sialyltransferase is also known as monosialoganglioside (GM)3 synthase [63] and suppresses the epidermal growth factor receptor (EGFR) phosphorylation, which influences the cell proliferation [64] and the cellular resistance to oxidative stress and radiation therapy through upregulation of extracellular signal-regulated kinases (ERK) [42]. The total amount of GM3 was decreased in BEN-MEN-1 cells after glycation. Yamashita and colleges reported that GM3 synthase knockout mice displayed enhanced ligand-induced insulin receptor phosphorylation. Furthermore, they could show that an increased sensitivity in glucose and insulin tolerance consequently results in an elevated insulin signaling response [65]. Other studies show that decreasing expression of GM3 leads to decreased cell motility and cell adhesion through ERK phosphorylation along with Ras upregulation. This regulates migration through mitogen-activated protein kinase (MAPK) [41,42,66,67]. The glycating agent GO has the same effect in BEN-MEN-1 cells (down-regulation of ST3GAL5) as MGO. However, in IOMM-Lee cells, we observed no effect after glycation with GO, which could be explained by higher glyoxalase 1 activity, which degradates dicarbonyls and has been described in many studies on cancer and glycation [68–70]. The expression of ST3GAL6 was reduced in both glycated meningioma cell lines, which is known to play a key role in the generation of functional Sialyl Lewis X [71]. Decreasing levels of ST3GAL6 can lead to decreasing migration and invasion in 5637 and J82 UBC cells as well as decreasing adhesion and migration in multiple myeloma cells [72,73].

Increased ST6GAL1 expression as we have shown in glycated BEN-MEN-1 cells, was also found in lung, colon, glioma, prostate, cervical, and breast cancer tissues [74–80]. The downregulation of ST6GAL1 decreased metalloproteinases (MMPs) expression and suppressed invasive potential of A549 and H1299 cells in vitro [79], whereas bladder cancer has ST6GAL1 upregulation a tumor-suppressive role [81]. The upregulation of ST6GAL2 was found in different types of cancer and was associated with breast cancer with higher expression of intracellular adhesion molecule (ICAM)-1, vascular adhesion molecule (VCAM)-1, CD24, MMP2, MMP9 and C-X-C motif chemokine receptor (CXCR)4 [82,83].

ST6GALNAC2 is known as a metastasis suppressor in breast cancer and a low expression of it, as we observed in glycated BEN-MEN-1 cells, is associated with a bad prognosis [84,85]. In Colorectal Carcinoma, Venkitachalam et al. have observed the same [86]. In contrast,

Schneider et al. could show, that a high expression of ST6GALNAC2 correlates with metastases to the lymph system [87]. The expression level may be a prognostic marker, but it seems that the mutation of the gene is more important. In our study, ST6GALNAC4 expression was elevated in glycated BEN-MEN-1. High expression of ST6GALNAC4 leads to the prevention of O-glycan chain elongation [88]. In another study of Follicular Thyroid Carcinoma (FTC)-238 cells the suppression of the ST6GALNAC4 gene led to an inhibition of invasive behavior *in vitro* and *in vivo* [89]. The lower expression of ST6GALNAC5 in both glycated meningioma cell lines in our study could be a sign of transformation, because it is restricted to the brain and synthesizes GD1alpha in the nervous tissues [90,91]. We have observed an increased expression of ST6GALNAC6 is responsible for the synthesis of sialyl Lewis (a), which is a significant inductive mechanism in cancer progression [92,93].

The increased expression of ST8SIA1 in glycated BEN-MEN-1 cells could lead to a weak prognosis for patients. In contrast, we observed decreased expression of ST8SIA1 after glycation in IOMM-Lee cells. In melanoma brain metastases, it was shown that ST8SIA1 (GD3) synthases) is upregulated and the GD3 expression is increased, which was associated with a bad prognosis [94]. In gliomas, malignancy increased by higher GD3 and GD2 expression [95]. In addition, ST8SIA1 is one of the key drivers for malignancy in glioblastoma [96]. Mennel et al. reported on different expression levels of GD3 and GD2 in meningiomas, depending on the tumor origin [97]. A study for neuroblastoma and melanoma cells demonstrated that most neuroblastoma cells had a high expression of GD2 and melanoma cells had high expression of GD3 [98]. The increased expression of ST8SIA2, as we observed in glycated BEN-MEN-1 cells, plays a role in the invasive behavior and was significantly associated with the risk of relapse in non-small cell lung carcinoma [99]. The sialyltransferase ST8Sia5, which is in BEN-MEN-1 cells, is increased glycated known to synthesize GD1c/GT1a/Tetrasialogangliotetraosyl-ceramide (GQ)1b from GM1b/GD1a/GT1b. The group of Schiopu et al. has identified thirty-four distinct glycosphingolipid components (one GM4, nine GM3, two GM2, two GD3, nine GM1, and six GD1) differing in their ceramide compositions [100].

The glycation of meningioma cell lines has opposite effects in benign or glycated malignant meningioma cells. Overall, **BEN-MEN-1** cells express more sialyltransferases than unglycated, whereas glycation of IOMM-Lee cells leads to a downregulation of the sialyltransferase expression. These observations support our recent observations that glycation of BEN-MEN-1 cells lead to increased invasive potential [30].

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Conclusion

To sum up, glycation of meningioma cell lines has cell line-specific effects. The glycated BEN-MEN-1 cell line is affected in a different expression of ST3GAL1/2/3/5/6; ST6GAL1/2; ST6GALNAC2/6 and ST8SIA1/2. These STs have a direct or indirect impact on tumor progression. The decreased expression of ST3GAL5 after glycation results in a decreasing expression of GM3 in benign meningioma cells. The expression level of some sialyltransferases (ST3GAL1/2/3; ST6GALNAC5 and ST8SIA1) of glycated IOMM-Lee cell line were inhibited which indicates less aggressive behavior.

Author Contributions

For research articles with several authors, a short paragraph specifying their individual contributions must be provided. The following statements should be used "Conceptualization, P.S.; methodology, P.S., K.B., M.W. and T.Z.; software, K.B and P.S.; validation, P.S.; formal analysis, P.S., M.W. and T.Z.; investigation, P.S.; resources, P.S., K.B. and R.H.; data curation, P.S.; writing—original draft preparation, P.S.; writing—review and editing, M.S., R.H. and P.S.; visualization, P.S., M.S.; supervision, R.H., C.S.; project administration, R-H., C.S. and M.S.; funding acquisition, R.H., M.S. and C.S. All authors have read and agreed to the published version of the manuscript."

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Conflicts of Interest

The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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Erklärungen

(1) Ich erkläre, dass ich mich an keiner anderen Hochschule einem Promotionsverfahren unterzogen bzw. eine Promotion begonnen habe.

(2) Ich erkläre, die Angaben wahrheitsgemäß gemacht und die wissenschaftliche Arbeit an keiner anderen wissenschaftlichen Einrichtung zur Erlangung eines akademischen Grades eingereicht zu haben.

(3) Ich erkläre an Eides statt, dass ich die Arbeit selbstständig und ohne fremde Hilfe verfasst habe. Alle Regeln der guten wissenschaftlichen Praxis wurden eingehalten; es wurden keine anderen als die von mir angegebenen Quellen und Hilfsmittel benutzt und die den benutzten Werken wörtlich oder inhaltlich entnommenen Stellen als solche kenntlich gemacht.

Datum, Unterschrift

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