

1 Article

2 SN1 transporter regulation by Sp1 in ammonia- 3 treated mouse cortical astrocytes: role of Sp1 4 phosphorylation status

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10

11 **Abstract:** The involvement of astrocytic SN1 (SNAT3) transporter in ammonia-induced L-glutamine
12 retention was recently documented in mouse cultured astrocytes. Here we investigated the
13 involvement of specificity protein 1 (Sp1) transcription factor in SN1 regulation in ammonium
14 chloride ("ammonia")-treated astrocytes. Sp1 expression and its cellular localization were
15 determined using real-time qPCR, Western blot and confocal microscopy, respectively. Sp1 binding
16 to *Snat3* promoter was analyzed by chromatin immunoprecipitation. Ammonia-induced Sp1
17 regulatory role in SN1-mediated [³H]glutamine transport was verified using siRNA and
18 mithramycin A. The involvement of protein kinase C (PKC) isoforms in Sp1 level/phosphorylation
19 status was verified using siRNA technology. Sp1 translocation to the nuclei and its enhanced
20 binding to *Snat3* promoter, along with Sp1 dependence of system N-mediated [³H]glutamine
21 transport were observed in astrocytes upon ammonia exposure. Ammonia decreased the level of
22 phosphorylated Sp1, and the effect was reinforced by long-term incubation with PKC modulator,
23 phorbol 12-myristate 13-acetate, a treatment likely to dephosphorylate Sp1. Furthermore,
24 silencing of PKCδ isoform abolished the increase of Sp1 level by ammonia. Collectively, the results
25 demonstrate the regulatory role of Sp1 in regulation of SN1 expression and activity in ammonia-
26 treated astrocytes and implicate altered Sp1 phosphorylation status in this capacity.

27 **Keywords:** astrocytes, glutamine, SN1 (SNAT3), Sp1, protein kinase C, ammonia, transport

28

29 1. Introduction

30 L-glutamine (Gln) is the most abundant amino acid in the central nervous system (CNS) where
31 its concentration is at least one order of magnitude higher than any other amino acid [1-3]. In the
32 brain Gln is synthesized in astrocytes from L-glutamate (Glu) and ammonia in the reaction catalyzed
33 by glutamine synthetase [4]. The glutamate/glutamine cycle is known as a metabolite shuttle in which
34 Gln transported from astrocytes to adjacent neurons is converted to Glu or gamma-aminobutyric acid
35 (GABA) in enzymatic reaction catalyzed by glutaminase or glutamate decarboxylase [4-7].

36 Gln is considered to play an important role in the pathogenesis of neurological diseases
37 associated with hyperammonemia, including hepatic encephalopathy (HE) due to its excessive
38 synthesis and accumulation in astroglial cells [8-11]. Astrocytes, the main place of ammonia
39 detoxification in the brain are considered as a target of ammonia-derived Gln excess [12, 13]. *In vitro*
40 experiments documented that in astrocytes treated with pathologically relevant concentrations of
41 ammonia, as well as in cells exposed to a high concentrations of Gln [14, 15], the induction of
42 mitochondrial permeability transition accompanied the astrocytic swelling [16-18]. Accordingly,
43 astrocyte swelling is considered as a primary cause of cytotoxic component of brain edema, a frequent
44 and fatal complication of acute HE forms [19, 20]. It have been also shown that induction of mitogen-
45 activated protein kinases (MAPK) occurs in the astroglial cells exposed to the excess of Gln [21]. In

46 addition, intracellular Gln accumulation induces the osmotic stress and activates the p38 cascade [22,
47 23]. Therefore an efficient transport by specific amino acid carriers guarantying proper Gln inter-
48 cellular distribution in hyperammonemic astrogliaopathy is of importance.

49 Gln transport in astrocytes is primarily mediated by Na⁺-coupled amino acid transport system
50 N that consists of three carriers: SN1 (aliases: SLC38A3, SNAT3), SN2 (aliases: SLC38A5, SNAT5) and
51 SN7 (aliases: SLC38A7, SNAT7). SN1, the most abundant system N transporter, is responsible for the
52 release of newly synthesized Gln from astrocytes [13, 24, 25] and its expression dominates in cultured
53 mouse cortical astrocytes [13]. It was shown that Glu, GABA and glycine synthesis is enhanced by
54 the presence of SN1 [26]. The involvement and importance of SN1 in neurotransmitter recycling was
55 confirmed by the lack of SN1 immunoreactivity in oligodendrocytes where presynaptic processes are
56 absent [27]. Moreover, it was demonstrated that silencing of system N transporters causes the
57 retention of Gln in astrocytes and that ammonia-derived Gln release from astrocytes is mediated by
58 impairing of SN1-mediated Gln efflux [13, 25]. SN1 is abundant in neocortex, cerebellum and
59 olfactory bulb, therefore the functional ablation of this transporter with N-ethyl-N-nitrosourea
60 (ENU)-induced mutagenesis *in vivo* leads to ataxia in mice [26]. This, albeit indirectly, confirms the
61 important role of SN1 in sustaining proper neurotransmission. Therefore, investigation of the
62 mechanisms involved in the regulation of SN1 is an important issue for understanding the Gln
63 metabolic fates in the brain.

64 The *Snat3* gene promoter region possesses a well-conserved G-rich sequence with characteristics
65 of a GT box, a potential sequence for the DNA-binding specificity protein (Sp) factors and related GT
66 box-binding proteins [28, 29]. Sp1 is an ubiquitously expressed transcription factor responsible for
67 activation of expression of many genes due to its ability to recruit TATA-binding protein and to fix
68 the transcriptional start site at TATA-less promoters [30]. It is involved in many cellular processes
69 such as cell cycle regulation, chromatin remodeling, propagation of methylation-free islands [31],
70 apoptosis, angiogenesis or carcinogenesis [30]. Consequently, cells lacking Sp1 are severely retarded
71 and die after 10 days of development [31]. Interestingly, the Sp1 transcription factor is regulated by
72 pH changes [32]. Of note in this context, the role of SN1 in pH regulation has been investigated in
73 gliomas *in situ* in which SN1 was overexpressed [33, 34]. More recently, the literature data indicated
74 that Sp1 interacts with SN1 in mouse liver, intestine, kidney and HepG2 cell line. Balkrishna et al.
75 (2014) investigated the mechanisms underlying SN1 expression in the liver and in the brain, where
76 SN1 levels are relatively high. It has been documented that SN1 expressing tissues contain de-
77 methylated promoters and RNA polymerase complex occupies transcriptional start-sites, what
78 allows activation of transcription of SN1 by Sp1 transcription factor [28]. ENCODE database indicates
79 the enhanced activity of *Snat3* promoter in HepG2 cell line, liver, cerebellum and brain cortex [35]. It
80 was further shown that SN1 up-regulation occurs mainly due to enhanced binding of Sp1 to *Snat3*
81 promoter [28]. Moreover, it was demonstrated that SN1 expression is regulated by transcription
82 factor binding, mRNA stability and epigenetic control mechanisms. Those mechanisms mediate
83 tissue-specific, cell-specific and pH-specific changes of mRNA levels and further changes of protein
84 abundance [28]. More importantly in the context of this study, an increase of Sp1 mRNA expression
85 was previously observed in cultured rat cortical astrocytes treated for 24 h with 5 mM ammonia [36].

86 Sp1 is a subject of posttranslational modifications such as phosphorylation, glycosylation and
87 acetylation. The isoforms of protein kinase C (PKC) have been suggested to phosphorylate Sp1 as the
88 PKC modulator phorbol 12-myristate 13-acetate (PMA) upregulate Sp1 in multiple cell types [30]. In
89 turn, long-term exposure (12 hours) of oligodendrocytes to PMA, decreases the expression of Sp1
90 [37]. This classical mechanism controls intracellular distribution and activity of different membrane
91 proteins. We recently demonstrated that at the translational level SN1 transporter cells cell surface
92 expression and activity are regulated by PKC, mainly by the PKC δ isoform in ammonia-treated
93 astrocytes [25].

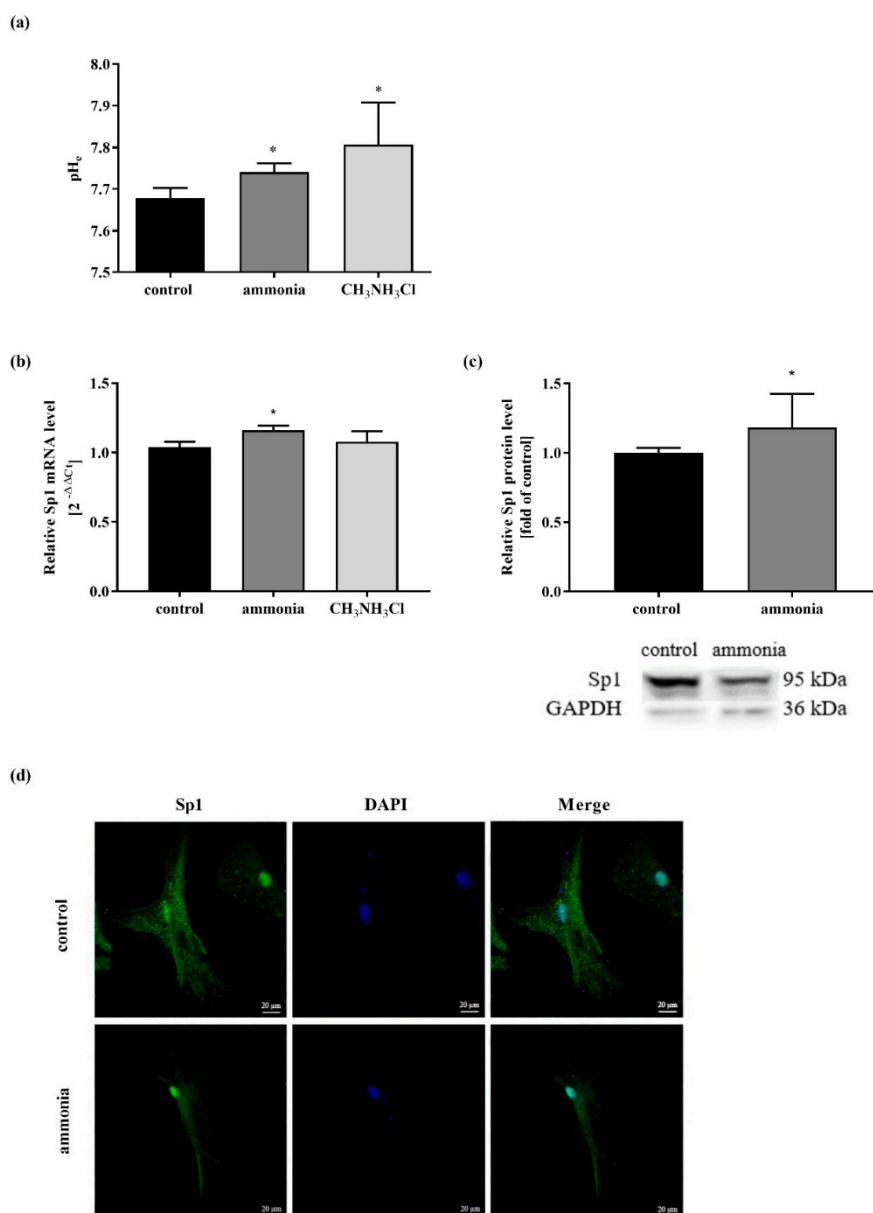
94 Based on above described information and the structure of the *Snat3* gene regulatory region we
95 aimed to analyze the possible contribution of Sp1 in the ammonia effect on the SN1 regulation. We
96 hypothesized that the mechanism by which ammonia interferes SN1 expression and Gln efflux from
97 astrocytes may be related to the activation of Sp1 and its enhanced interaction with *Snat3* promoter.

98 The study also included the analysis of the role of PKC in Sp1 phosphorylation and its role in SN1
99 mRNA level upon ammonia exposure.

100 2. Results

101 2.1. Ammonia-induced Sp1 expression increase and Sp1 translocation to the nucleus

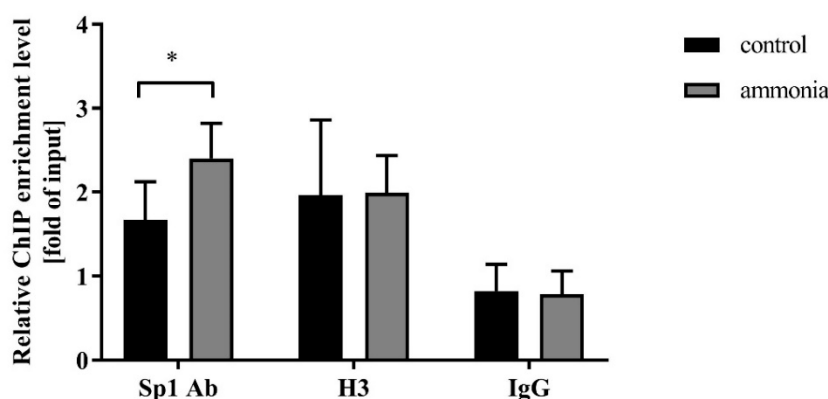
102 Sp1 mRNA expression level after 24-hour treatment with 5 mM ammonia and 5 mM $\text{CH}_3\text{NH}_3\text{Cl}$
103 was analyzed in real-time qPCR experiments. $\text{CH}_3\text{NH}_3\text{Cl}$, a metabolically inert compound that
104 induces intracellular pH changes similar to ammonia [38] was used to evaluate the effect of ammonia
105 on the Sp1 mRNA level. In our experiments the extracellular pH was increased after both treatments
106 (Figure 1a), whereas the upregulation of Sp1 transcription factor was observed only in the presence
107 of ammonia (Figure 1b, c) proving a direct role of ammonium ion (NH_4^+) in Sp1 regulation. Since our
108 results were in line with the results of Bodega et al. (2006), the extended experiments further revealed
109 cellular localization of Sp1 transcription factor, as was observed using confocal microscopy. In
110 astrocytes treated with ammonia Sp1 was observed in cell nuclei, while in control astrocytes Sp1
111 transcription factor was observed mainly in the cytoplasm (Figure 1d).



113 **Figure 1.** (a) Extracellular pH after 24-hour incubation of astrocytes with 5 mM ammonia and
 114 $\text{CH}_3\text{NH}_2\text{Cl}$. Results are mean \pm SD (n=4). (*) $p < 0.05$ vs control, One-Way ANOVA. (b) Sp1 mRNA level
 115 in mouse cortical astrocytes after 24-hour 5 mM ammonia or 5 mM $\text{CH}_3\text{NH}_2\text{Cl}$ treatment. Results are
 116 mean \pm SD (n=4). (*) $p < 0.05$ vs control; One-Way ANOVA with Dunnett post-hoc test. (c) Sp1 protein
 117 level in mouse cortical astrocytes after 24-hour 5 mM ammonia treatment. Upper panel shows
 118 densitometry analysis, lower panel shows representative immunoblot. Results are mean \pm SD (n=4).
 119 (*) $p < 0.05$ vs control, student t-test. (d) Intracellular Sp1 transcription factor localization after 24-hour
 120 5 mM ammonia treatment.

121 2.2. Ammonia enhances Sp1 binding to the *Snat3* promoter region

122 Sp1 binding activity on the *Snat3* promoter was measured by using a chromatin
 123 immunoprecipitation (ChIP) assay. We observed the enrichment for the *Snat3* promoter region in
 124 both, control and ammonia-treated mouse astrocytes versus the negative control IgG (Figure 2). The
 125 obtained results indicate higher enrichment for the *Snat3* promoter region in astrocytes after
 126 ammonia treatment (Figure 2).

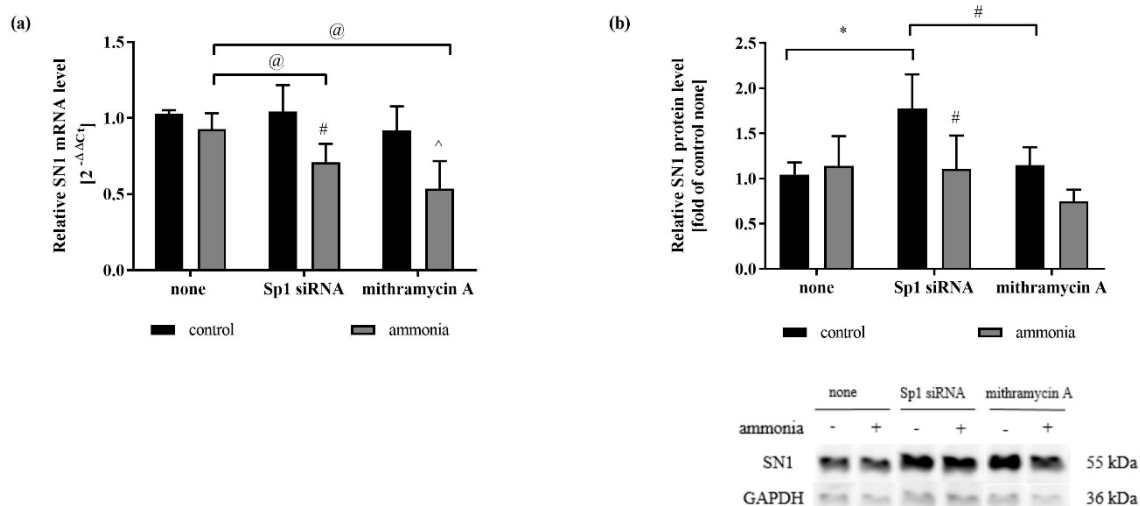


127

128 **Figure 2.** Sp1 transcription factor binding to the *Snat3* promoter region (Sp1 Ab) in mouse astrocytes
 129 treated with 5 mM ammonia for 24 hours. Histone H3 was used as a positive control, IgG was used
 130 as a negative control of Sp1 binding to the *Snat3* promoter region. Results are mean \pm SD (n=4).
 131 (*) $p < 0.05$ vs control; Two-Way ANOVA, Bonferroni post-hoc test.

132 2.3. Silencing of Sp1 transcription factor affects SN1 expression in the presence of ammonia

133 In the next set of experiments, the expression of SN1 after silencing of Sp1 in the presence or
 134 absence of ammonia was analyzed. The knock-down of Sp1 transcription factor or its
 135 pharmacological inhibition was achieved by 1) siRNA silencing technology (2 nM, 24 h), or 2)
 136 application of Sp1 inhibitor mithramycin A (10 μM , 1 h). In the absence of ammonia, Sp1 silencing
 137 did not affect the SN1 mRNA expression (Figure 3a) while Sp1 silencing increased the SN1 protein
 138 level (Figure 3b). In turn, ammonia treatment specifically decreased both mRNA (Figure 3a) and
 139 protein level (Figure 3b) of SN1 in astrocytes with Sp1 transcription factor knock-down.



140

141 **Figure 3.** The effect of Sp1 transcription factor silencing (Sp1 siRNA) or inhibition (mithramycin A) on SN1
 142 expression in mouse astrocytes treated or not with 5 mM ammonia: (a) SN1 mRNA level. (b) SN1 protein level.
 143 Results are mean \pm SD (n=4). (*)p<0.05 vs control none, (@)p<0.05 vs ammonia none, (#)p<0.05 vs control Sp1
 144 siRNA; (^)p<0.05 vs control mithramycin A; Two-Way ANOVA, Bonferroni post-hoc test.

145 2.4. The effect of Sp1 transcription factor silencing on system N activity in the presence or absence of
 146 ammonia

147 Further, the verification of Sp1 involvement in the [³H]glutamine transport via system N in
 148 astrocytes was conducted. Silencing of Sp1 by siRNA technology decreased total and system N-
 149 mediated [³H]glutamine uptake after ammonia treatment while Sp1 inhibition by mithramycin A
 150 affected only total [³H]glutamine uptake in ammonia-treated astrocytes (Table 1). Additionally, total
 151 and system N-mediated release of preloaded [³H]glutamine, expressed as the % of the total
 152 radioactivity lost, was reduced in astrocytes treated with 5 mM ammonia after silencing or
 153 pharmacological inhibition of Sp1 by used methods (Table 1). Moreover, Sp1 silencing led to the
 154 major decrease of [³H]glutamine efflux after ammonia treatment (Table 1).

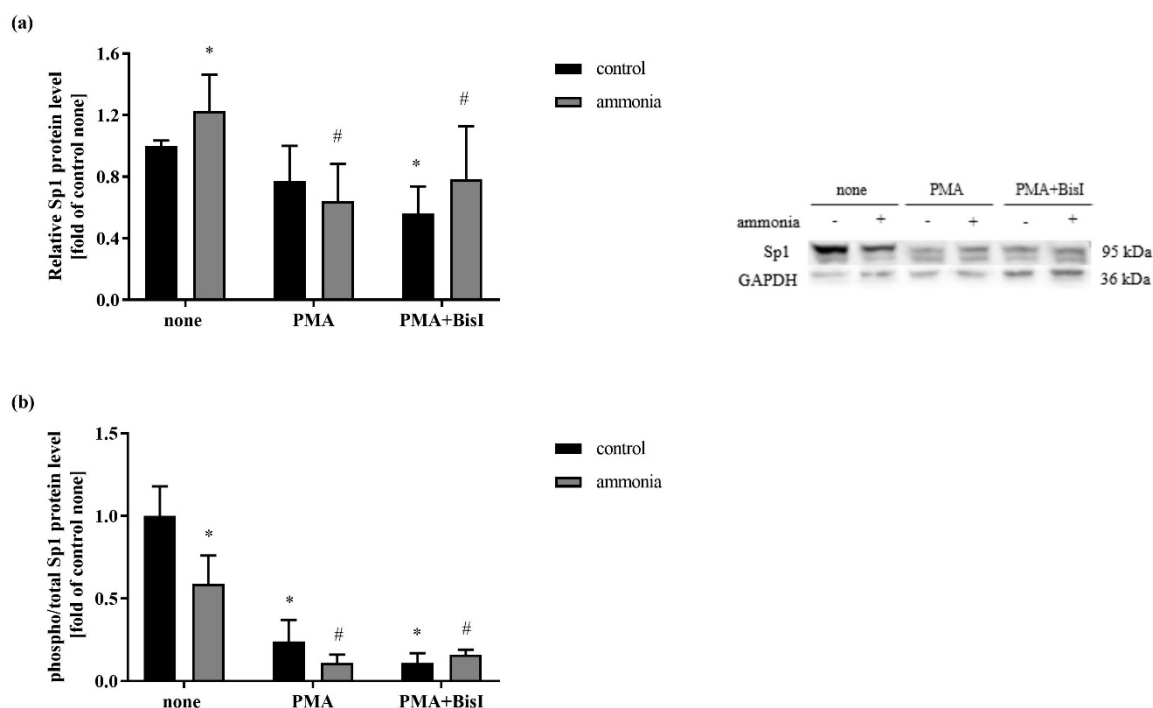
155 **Table 1.** Total and system N-mediated [³H]glutamine uptake and efflux from mouse cortical
 156 astrocytes after silencing of Sp1 transcription factor by 2 nM siRNA or 10 μ M mithramycin A and 5
 157 mM ammonia exposure. Results are mean \pm SD (n = 4). (*)p<0.05 vs control none (total), (#)p<0.05 vs
 158 control none (system N), (&)p<0.05 vs ammonia none (total), (^)p<0.05 vs control Sp1 siRNA (total),
 159 (!)p<0.05 vs ammonia Sp1 siRNA (total), (+)p<0.05 vs control Sp1 siRNA (system N), (?)p<0.05 vs
 160 ammonia none (system N), (@)p<0.05 vs control mithramycin A (total), (%)p<0.05 vs ammonia
 161 mithramycin A (total), (\$)p<0.05 vs control mithramycin A (system N), Two-Way ANOVA,
 162 Bonferroni post-hoc test.

		ammonia	Gln uptake (fold of control none)	Gln efflux (fold of control none)
none	total	-	0.98 \pm 0.09	1.02 \pm 0.06
		+	1.01 \pm 0.17	0.84 \pm 0.06*
	system N	-	0.39 \pm 0.11*	1.82 \pm 0.25*
		+	0.36 \pm 0.13&	1.43 \pm 0.25#,&
Sp1 siRNA	total	-	1.04 \pm 0.19	1.13 \pm 0.19
		+	0.73 \pm 0.12 ^{^,&}	0.87 \pm 0.09 [^]
	system N	-	0.42 \pm 0.06 [^]	2.22 \pm 0.45 ^{#,^}

mithramycin A	total	+	0.29±0.06 ^{+!}	1.64±0.30 ^{+!}
		-	1.28±0.24 [*]	1.16±0.17
	system N	+	1.10±0.14 ^{\$}	0.90±0.17 [@]
		-	0.24±0.10 [#]	2.16±0.34 ^{#,@}
		+	0.15±0.04 [?]	1.59±0.22 ^{%,}

163 2.5. Sp1 phosphorylation is decreased in astrocytes treated with ammonia

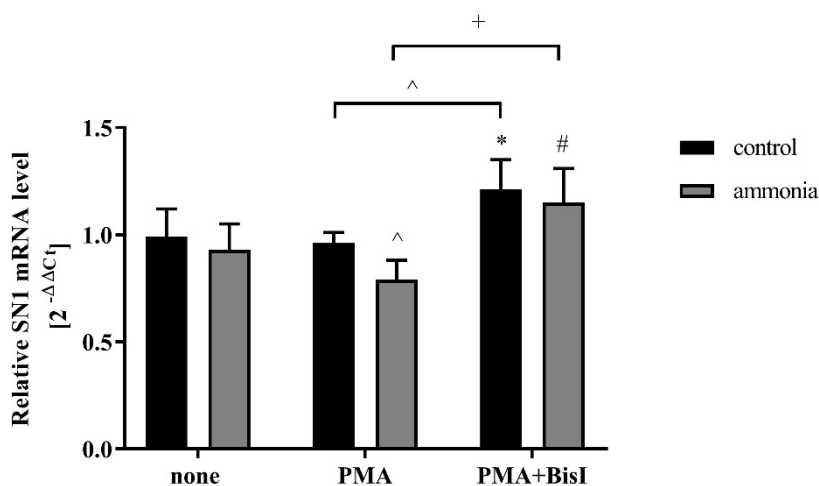
164 Sp1 can be phosphorylated by different kinases such as protein kinase C (PKC) [39], protein
 165 kinase A (PKA) [40], cyclin-dependent kinase (CDK) [41], MAPK [42]. To test the involvement of PKC
 166 in Sp1 phosphorylation, the astrocytes were exposed to 200 nM PMA, a modulator of PKC activity.
 167 To verify whether the phosphorylation of Sp1 regulates the SN1 transcription in ammonia-treated
 168 astrocytes, the phosphorylation status of Sp1 was analyzed by quantification of two Sp1 forms with
 169 different molecular weight. The level of Sp1 phosphorylation status was determined by obtaining the
 170 ratio of the higher molecular weight, phosphorylated form with the total Sp1 protein level including
 171 both forms. As shown in Figure 4b in the astrocytes treated with ammonia, Sp1 phosphorylation was
 172 lower. When the cells undergo PMA treatment the phosphorylation of Sp1 was further decreased.



173 **Figure 4.** (a) Sp1 protein level in the astrocytes treated with 5 mM ammonia for 24 hours and 200 nM
 174 PMA and/or 1 μ M BisI. Results are mean \pm SD (n=4). (*)p<0.05 vs control none; (#)p<0.05 vs ammonia
 175 none; Two-Way ANOVA, Bonferroni post-hoc test. (b) The ratio of phospho-Sp1 to the total Sp1
 176 protein level in astrocytes treated with 5 mM ammonia for 24 hours and 200 nM PMA and/or 1 μ M
 177 BisI. Results are mean \pm SD (n=4). (*)p<0.05 vs control none; (#)p<0.05 vs ammonia none; Two-Way
 178 ANOVA, Bonferroni post-hoc test.
 179

180 2.6. The effect of PKC activation on SN1 mRNA expression in the presence or absence of ammonia

181 In the presence of ammonia, PMA treatment decreased the SN1 mRNA expression (Figure 5).
 182 The effect was reversed after incubation of astrocytes with PKC inhibitor, BisI (Figure 5). Moreover,
 183 inhibition of PKC activity by BisI treatment upregulated SN1 mRNA level (Figure 5).

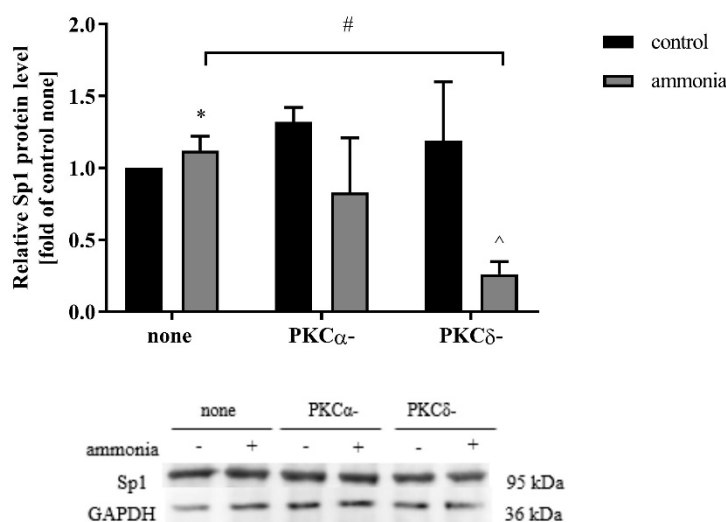


184

185 **Figure 5.** The effect of PKC activation on the SN1 mRNA level in mouse cortical astrocytes treated
 186 with 5 mM ammonia for 24 hours. Results are mean \pm SD (n=4). (*)p<0.05 vs control none; (#)p<0.05
 187 vs ammonia none; (^)p<0.05 vs PMA control; (+)p<0.05 vs PMA ammonia; Two-Way ANOVA,
 188 Bonferroni post-hoc test.

189 2.7. PKC δ isoform depletion abolishes ammonia-induced increase of Sp1

190 According to the results described above, we aimed to identify the involvement of selected PKC
 191 isoforms in the Sp1 level. Therefore we analyzed Sp1 protein content in ammonia-treated astrocytes
 192 with silenced PKC α and δ isoforms. Ammonia decreased the Sp1 protein level in astrocytes with
 193 silenced PKC δ isoform, while in astrocytes with silenced PKC α isoform the protein level remained
 194 unaltered (Figure 6).



195

196 **Figure 6.** Sp1 protein level in astrocytes treated with 5 mM ammonia for 24 hours and after silencing
 197 of PKC α (PKC α -) or PKC δ (PKC δ -) isoform. Results are mean \pm SD (n=4). (*)p<0.05 vs control none;
 198 (#)p<0.05 vs ammonia none; (^)p<0.05 vs control PKC δ -. Two-Way ANOVA, Bonferroni post-hoc test.

199 3. Discussion

200 The present study demonstrates that ammonia increases the Sp1 transcription factor level and
 201 its translocation to the astrocytic nucleus (Figure 1, 2), and implicates the above sequence of events
 202 in the regulation of SN1 transporter expression and activity in ammonia-exposed cultured cortical

203 astrocytes (Figure 3, Table 1). The present study further documents that ammonia-induced alteration
204 in the phosphorylation status of Sp1 transcription factor may influence SN1 transporter regulation.

205 It has been shown that prolonged (1, 3 or 5 days) ammonia exposure (1, 3 and 5 mM) reduced
206 Sp1 mRNA level in rat astroglial cells [36]. The ammonia-induced downregulation of Sp1 mRNA was
207 inversed to the rising ammonia concentration with the maximal effect at 1 mM ammonia.
208 Interestingly, 5 mM ammonia treatment for 1 day caused an increase of Sp1 mRNA expression [36].
209 Sp1 activation occurring by its nuclear translocation [36, 43-46] is regulated by extracellular pH
210 changes [32, 47]. In our study astrocytes treated with both ammonium chloride and
211 methylammonium chloride at 5 mM concentration induced identical changes in extracellular pH
212 value (Figure 1a), however the Sp1 mRNA expression level was affected differently (Figure 1b). The
213 lack of Sp1 mRNA changes in the presence of methylammonium chloride indicated that in our
214 experimental setting Sp1 activation is specifically induced by ammonium ion *per se*, not by ammonia-
215 induced pH changes. Of note in this context, pathophysiological levels of ammonia do not necessarily
216 affect the intra- or extracellular pH in astrocytes, but even a short- pH change may trigger cell
217 signaling. The previous study documented that the effects of acute exposure to ammonia were
218 mediated by an increase in intracellular pH, resulting in cytosolic alkalinization leading to calcium-
219 dependent Glu release from astrocytes. The observation implicated that ammonia-induced
220 deregulation of Glu release from astrocytes might be involved in dysfunction of the glutamatergic
221 neurotransmission observed in acute form of HE [48].

222 Pathophysiological concentrations of ammonia lead to the intracellular Gln accumulation in
223 astrocytes, which further cause osmotic stress and activate the family members of the mitogen-
224 activated protein (MAP) kinases [21]. Stimulation of p38MAPK triggers, as have been documented,
225 the increase of Sp1 expression [36] and its activation was further implied as a possible cause of altered
226 expression of different genes during HE [36, 43-46].

227 Sp1 transcription factor is considered to be involved in the regulation of SN1 transporter in
228 mouse kidney during ammonia-induced acidosis [28]. The mechanism of this regulation is likely to
229 rely on the different ability of Sp1 to bind to the DNA sequences of target genes in the presence and
230 absence of kidney acidosis. There were identified two Sp1 binding sites in the region 50 bp upstream
231 of the SN1 transcription start site, one important for the basal activation of the promoter, and another,
232 pH sensitive responsible for the upregulation of SN1 in the ammonia-induced acidosis [28].
233 According to the available data, in the physiological condition Sp1 binds to the consensus sequences
234 further upstream transcriptional start-site than during acidosis. Therefore, it is likely that above
235 described interaction cause the upregulation of SN1 transcription in acidosis, and Sp1 consensus
236 sequence closest to the transcriptional start-site could be a stresses-induced transcription factor
237 binding site [28]. Our observations are in line with the latter finding. In our study ammonia caused
238 the decrease of the mRNA and protein level of SN1 transporter in astrocytes with silenced Sp1
239 transcription factor (Figure 3a, b) suggesting that SN1 expression in astrocytes exposed to ammonia
240 may be dependent on the Sp1 transcription factor.

241 The ChIP analyses of the interaction between SN1 and Sp1 transcription factor showed higher
242 enrichment for the *Snat3* promoter region in the ammonia-treated astrocytes (Figure 5). Thus, the
243 results implicate a stronger occupancy of this transcription factor on the promoter region of SN1
244 transporter in ammonia-exposed mouse astrocytes. Moreover, the interaction between SN1 and
245 histone H3 remains unaltered upon ammonia exposure (Figure 2). This observation might be related
246 to the decreased level of histone H3 by ammonia [49] and its role in the induction of SN1 transcription
247 [28]. Taken together, the literature data and the observed lack of changes in the expression of SN1
248 after ammonia exposure may suggest that interaction of SN1 with histone H3 in ammonia-treated
249 astrocytes remains unchanged compared to the control cells.

250 Analysis of the inward and outward [³H]glutamine transport in mouse astrocytes fully
251 confirmed functional significance of the SN1 upon mechanism the Sp1 control. Indeed, ammonia
252 decreases total and system N-mediated [³H]glutamine uptake to astrocytes with silenced Sp1
253 transcription factor (Table 1). Moreover, ammonia potentiates the decrease of the total and system N-
254 mediated [³H]glutamine release from astrocytes with silenced Sp1 transcription factor (Table 1).

255 It has been shown that phosphorylation of Sp1 transcription factor reversibly regulates its
256 activity in the regenerated liver [50], where Sp1 dephosphorylation allows hepatocytes to accomplish
257 more proliferative cell status. In turn, Sp1 up-regulation in differentiated keratinocytes [51], caused
258 mainly by increased level of phosphorylated form of Sp1 protein was also induced by PKC [52].
259 Additionally, myelin basic protein transcription was also dependent on Sp1 phosphorylation in
260 differentiated oligodendrocytes [37]. Considering the above evidence, we hypothesized that this
261 mechanism may also contribute to the ammonia-induced Sp1-mediated changes in SN1. Towards the
262 same end, our recent study shown that ammonia reduces PKC activity in cultured mouse cortical
263 astrocytes [25]. In accordance with these presumptions, here we observed alterations in the Sp1
264 phosphorylation status in astrocytes treated with ammonia. The level of Sp1 phosphorylated form
265 was lower in astrocytes treated with ammonia and the effect was potentiated in astrocytes exposed
266 to PMA (Figure 5). However, co-treatment of astrocytes with the PKC inhibitor, bisindolylmaleimide
267 I (Bis I), turned out to be ineffective in reversing PMA-evoked Sp1 phosphorylation status decrease
268 (Figure 5). The reasons of this apparent discrepancy remains to be elucidated. One other unsolved
269 issue of our study concerns the observed decrease of Sp1 in the absence of PKC δ . So far, the
270 identification of the regulatory role of one selected PKC isoform has remained beyond the
271 experimental methodology of present study. It is worth noting that, Sp1 phosphorylation could be
272 affected not only by PKC but also by PKA [40], DNA-dependent protein kinase [53] or CDK [41].
273 Clearly, the specific involvement of other kinases in ammonia-exposed astrocytes needs further
274 evaluation.

275 The role of the Sp1 phosphate residues in the activation of *Snat3* promoter by Sp1 is obscure. It
276 is possible that Sp1 phosphorylation may change its interaction with other transcription factors. This
277 phenomenon has been reported for Pur α , which tended to associate with phosphorylated rather than
278 with dephosphorylated Sp1 [54]. Further, it has been shown in cultured rat cortical astrocytes that,
279 Nrf2 transcription factor forms complexes with the transcription factor Sp1 upon the exposure to
280 tricarbonyldichlororuthenium(II) dimer, a carbon monoxide (CO) source [55]. The complex formed,
281 after binding to ARE1 binding site, directly affects the regulation of Sp1 and Nrf2 target genes [55].

282 Our results suggest that the decrease of SN1 mRNA expression in ammonia-treated astrocytes
283 induced by PMA (Figure 6) might be mediated, at least in part, by dephosphorylation of the
284 transcription factor Sp1. The reason why in ammonia treated astrocytes, the mRNA and protein level
285 of SN1 remains unchanged despite the stronger association of Sp1 transcription factor with
286 transporter remains to be elucidated. The obtained results are in contrast to those obtained by
287 Balkrishna et al. (2014) which suggest Sp1 to be an enhancer of SN1 in kidney during ammonia-
288 induced acidosis. Importantly, the transcriptional regulation of SN1 was reported as tissue-specific
289 and predominantly controlled by various epigenetic factors [28]. In this context it is plausible that in
290 contrast to kidney, in ammonia-treated astrocytes Sp1 acts as a silencer of SN1. Worth mentioning
291 in this context is the postulated role of one other transcription factor, Nrf2. Recently it was shown that
292 Nrf2 is involved in the regulation of SN1 upon metabolic acidosis in the kidney. However, the results
293 obtained by Lister and colleagues documented that Nrf2 did not control basal expression of SN1
294 mRNA in the liver and brain, suggesting insensitivity of both organs to SN1 increase during
295 metabolic acidosis, implicating a kidney-specific mechanism of control [56]. The role of Nrf2 to in
296 SN1 regulation in ammonia-treated astrocytes has not been examined as yet.

297 In conclusion, results of this research provide substantial evidence that pathologically elevated
298 ammonium ions activate Sp1 transcription factor and enhance its binding to the *Snat3* promoter
299 region, in this way contributing to the alteration in Gln transport in cultured mouse cortical
300 astrocytes. Moreover, the Sp1-mediated SN1 control may in addition be exerted by Sp1
301 phosphorylation status. The relevance of the findings for understanding the role of Sp1 in the
302 regulation of SN1 transporter and SN1-mediated Gln transport in the brain during hyperammonemia
303 *in vivo* remains to be documented using more native systems.

304

305 4. Materials and Methods

306 4.1. Materials

307 Plastic tissue culture dishes were purchased from Corning Costar (Sigma-Aldrich, St. Louis, MO,
308 USA), culture medium from Sigma-Aldrich (St. Louis, MO, USA), fetal bovine serum (FBS) from
309 Biosera (Nuaille, France), antibiotic antimycotic from Gibco (ThermoFisher Scientific, USA) and
310 HiPerfect Transfection Reagent (Qiagen, Germany). All other chemicals of the purest grade were
311 purchased from available commercial sources.

312 4.2. Astrocyte cultures and treatment

313 Cortical astrocytes were isolated from 7-day-old C57BL6/J mice of both sexes and cultured as
314 described earlier [57]. The C57BL6/J mice were obtained from the animal colony of the Mossakowski
315 Medical Research Centre, Polish Academy of Sciences in Warsaw. All animal experiments were
316 performed according to institutional guidelines for animals, and all efforts were made to minimize
317 the number of animals used (institutional approval no. 55/2015). Briefly, cortex was passed through
318 Nitex nylon netting (80 µm pore size) into Dulbecco's modified Eagle's medium containing 20% (v/v)
319 FBS. Medium was changed 2 days after plating and subsequently twice a week gradually changing
320 to 10% FBS. In the third week of culturing, dBcAMP was added to the culture medium to promote
321 morphological differentiation. Cells were grown at 37°C in the atmosphere of 95% O₂ and 5% CO₂,
322 on 24-well, 6-well plates or on 60 mm and 100 mm dishes. Experiments were performed on 3-week-
323 old astrocytes. Mature cells were exposed to 5 mM ammonium chloride (ammonia, Sigma-Aldrich,
324 USA) or 5 mM methylammonium chloride (CH₃NH₃Cl; EMD Millipore, Bellerica, MA, USA) for 24
325 hours. In analysis of the role of PKC in the Sp1 expression, astrocytes were treated with 200 nM PMA
326 and/or 1 µM BisI for 24 hours.

327 4.3. Sp1 transcription factor and PKC isoforms silencing

328 In order to down-regulate Sp1 transcription factor, PKCα and PKCδ isoforms, astrocytes were
329 transfected with a mix of four types of siRNA duplexes consisting 21 nucleotides targeted to a
330 different gene region to obtain the most effective silencing. Sense strands for Sp1 silencing used in
331 this study were: 5'-CAGCACATTTGTCACATCCAA-3', 5'-CAGATTCTATATTATATATAT-3', 5'-
332 CCAGGTGATCATGGAAGTCAA-3', 5'-CAGGATGGTTCTGGTCAAATA-3'; for PKCα silencing:
333 5'-ATGAACTGTTTCAGTCTATAA-3', 5'-CAGGAGCAAGCACAAGTTCAA-3', 5'-
334 CAGCTGGTCATTGCTAACATA-3', 5'-AAGCATTATCTTAGTGGATGA-3' and for PKCδ silencing:
335 5'-CCGATTCAAGGTTTATAACTA-3', 5'-AGGGAAGACACTGGTACAGAA-3', 5'-
336 TTGAATGTAGTTATTGAAATA-3', 5'-CCGGGTGGACACACCACACTA-3'. Mature astrocytes
337 were washed with phosphate-buffered saline (PBS), trypsinized to detach cells from the plates and
338 then seeded at a density of 1.8x10⁵ cells per well in six-well plates in 1.5 ml of astrocytic growth
339 medium (Dulbecco's modified Eagle's medium with 10% FBS). Subsequently cells were transfected
340 with siRNA duplexes and HiPerfect Transfection Reagent (Qiagen, Hilden, Germany) according to
341 fast-forward protocol designed for adherent cells provided by manufacturer. Briefly, 4.5 µl of 2 µM
342 siRNA duplexes and 9 µl of HiPerfect Transfection Reagent were diluted in 300 µl of OptiMEM (Gibco)
343 without serum. After 30 min incubation at room temperature prepared complexes of reagent and
344 siRNA were added drop-wisely to the cells. Transfected astrocytes were cultivated under normal
345 growth conditions for 24 h and then used for monitoring gene silencing.

346 Sp1 transcription factor was also downregulated by 1 hour treatment of astrocytes with its
347 inhibitor, mithramycin A in the concentration of 10 µM.

348 4.4. Real-time qPCR analysis

349 Total RNA from astrocytes was isolated using TRI Reagent (Sigma-Aldrich, St. Louis, MO, USA).
350 RNA concentration was measured by NanoDrop1000 Spectrophotometer (ThermoFisher) and 1 µg
351 of RNA was reverse transcribed using High-Capacity cDNA Reverse Transcriptase Kit (Applied

352 Biosystems, Warrington, UK). Real-time PCR was performed in 96-well plates with The Applied
353 Biosystems 7500 Fast Real-Time PCR System using the minor groove binder (MGB) Taqman probe
354 assay. Primers and probes for SN1, Sp1 and endogenous control β -actin (Mm0120670_m1,
355 Mm00489039_m1 and Mm00607939_s1 respectively) were purchased from Applied Biosystems. Each
356 reaction contained 5 μ l TaqMan Fast Universal PCR Master Mix (Applied Biosystems) in a total
357 volume of 10 μ l, and 1.5 μ l of cDNA. The real-time PCR reactions were performed at 95°C for 20 s
358 followed by 45 cycles of 3 s at 95°C and 30 s at 60°C. The results of the analysis were calculated and
359 expressed according to an equation ($2^{-\Delta\Delta Ct}$) that gives the amount of the target, normalized to an
360 endogenous control (β -actin). Ct is a threshold cycle for target amplification⁵⁸.

361 4.5. Protein isolation and western blot

362 Astrocytes were washed with PBS, scrapped off and centrifuged at 1000g for 5 min at 4°C. Pellets
363 were homogenized in RIPA buffer containing protease (concentration 1:200, Sigma-Aldrich, St. Louis,
364 MO, USA) and phosphatase (concentration 1:100, Sigma-Aldrich, St. Louis, MO, USA) inhibitors and
365 50 mM sodium fluoride (Fluka, Sigma-Aldrich, Switzerland) by sonication and subsequently
366 centrifuged for 10 min at 10000g at 4°C. Supernatant was collected and subjected to Western blot
367 analysis. Protein concentration was measured using Pierce BCA Protein Assay Kit (Thermo Scientific,
368 Thermofischer). Cell lysates containing 30 μ g of protein were denatured by boiling in SDS-Page
369 loading buffer for 10 min at 95°C, separated on SDS polyacrylamide gel electrophoresis and
370 transferred onto nitrocellulose membrane. Membranes were blocked in 5% BSA in TBS-T buffer.
371 Incubation with antibodies against SN1 (1:800, ProteinTech, Manchester, UK), Sp1 (1:500, Abcam,
372 Cambridge, UK) was done in 1% BSA in TBS-T buffer overnight at 4°C followed by 1-hour incubation
373 with HRP-conjugated-antirabbit IgG (1:3000 for SN1 and 1:5000 for Sp1; Sigma-Aldrich, USA) for
374 detection by Clarity Western ECL Substrate (Bio-Rad Laboratories, Hercules, CA, USA). The
375 antibodies were stripped of with 0.1 M glycine, pH 2.9, and the membranes were incubated with
376 HRP-conjugated antibody against Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) for 1 h at
377 room temperature (1:7500, Proteintech, Manchester, UK). The chemiluminescent signal acquisition
378 and densitometry analysis were conducted using the G-Box system (SynGene, Cambridge, UK) and
379 GeneTools software (SynGene) respectively.

380 4.6. Gln uptake

381 Cultured astrocytes were washed twice with Krebs buffer (29.5 mM NaCl, 1.13 mM KCl, 0.3 mM
382 KH_2PO_4 , 0.3 mM MgSO_4 , 11 mM glucose, 25 mM NaHCO_3 , 2.5 mM CaCl_2) and then pre-incubated in
383 this buffer for 15 min at 37°C. incubation mixtures containing Krebs buffer with 0.1 $\mu\text{Ci}/\text{mL}$ L-[3,4-
384 $^3\text{H}(\text{N})$]-glutamine (PerkinElmer, Waltham, MA, USA; specific radioactivity 37 MBq/mL), 0.1 mM
385 unlabelled Gln. The mixtures contained also 10 mM L-Ala and 10 mM L-Leu in order to block other
386 than N, Gln transporter systems. The incubation was terminated after 4 min by adding cold Krebs
387 buffer followed by two washing cycles with 1 ml of cold Krebs buffer. 0.5 ml of 1M NaOH was added
388 to lyse the cell. The radioactivity of cell lysates was measured in a Wallac 1409 Liquid Scintillation
389 Counter (Perkin-Elmer, Finland).

390 4.7. Gln efflux

391 Cultured critical astrocytes were incubated in Krebs buffer containing 0.25 $\mu\text{Ci}/\text{mL}$ 1 mM L-[3,4-
392 $^3\text{H}(\text{N})$]-glutamine for 30 min at 37°C. The efflux was initiated by removing extracellular radioactivity
393 by washing cells twice with cold Krebs buffer. 1 ml of Krebs buffer or a mixture of Krebs buffer and
394 10 mM L-Ala and 10 mM L-Leu was added to the cells. Samples were collected from supernatant
395 after 10 min. The [^3H]-glutamine radioactivity released from the cells was measured. Cells were lysed
396 in 1 ml of 1 M NaOH and the radioactivity of cell lysates were measured in a Wallac 1409 Liquid
397 Scintillation Counter (Perkin-Elmer, Finland).

398

399 4.8. Chromatin immunoprecipitation

400 10⁷ cells were used for each experiment. Astrocytes were cross-linked in 1% formaldehyde for
401 10 min at room temperature (RT). The reaction was stopped by addition of glycine in final
402 concentration of 0.125M for 5 min. The cells were centrifuged for 3 min at 1500 rpm at 4°C and then
403 washed twice in cold PBS. The cell suspension was centrifuged for 5 min at 1500 rpm at 4°C. The
404 pellet was dissolved in sonication buffer (10 mM Tris-HCl, pH 8; 1 mM EDTA; 0.5 mM EGTA)
405 containing complete protease inhibitors (Roche, Mannheim, Germany), sonicated and then
406 centrifuged for 2 min at maximum speed at 4°C. Supernatant was diluted in ChIP dilution buffer
407 (0.01% SDS; 1.1% Triton-X-100; 1.2 mM EDTA; 17 mM Tris-HCl, pH 8.1; 167 mM NaCl) with an
408 addition of protease inhibitors. The samples were incubated with salmon sperm agarose beads
409 (Merck Millipore, Temecula, CA, USA) for 30 min at 4°C and centrifuged (30 s, 1500 rpm, 4°C). 50 µl
410 of collected supernatant was taken as an input and the rest of supernatant was treated overnight at
411 4°C either with 5 µg of Sp1 antibody (Abcam, Cambridge, UK), histone H3 (Cell Signaling, Leiden,
412 The Netherlands) or control IgG (Cell Signaling, Leiden, The Netherlands). After 1-hour incubation
413 at 4°C with salmon sperm agarose beads, the samples were centrifuged (1 min, 100 rpm, 4°C) and the
414 pellet was washed for 3 min in the following buffers: low salt (0.1% SDS; 1% Triton-X-100; 2 mM
415 EDTA; 20 mM Tris-HCl, pH 8.1; 150 mM NaCl) and high salt (0.1% SDS; 1% Triton-X-100; 2 mM
416 EDTA; 20 mM Tris-HCl, pH 8.1; 0.5 M NaCl) immune complex washing buffers, LiCl buffer (252 mM
417 LiCl; 1% Np-40; 1% deoxycholic acid; 1 mM EDTA; 10 mM Tris-HCl, pH 8.1) and twice in TE buffer
418 (10 mM Tris-HCl, pH 8; 1 mM EDTA). The samples were de-crosslinked by dissolving the washed
419 beads in the elution buffer (0.1 M NaHCO₃, 1% SDS) and addition of 5M NaCl and overnight
420 incubation at 65°C with shaking (950 rpm). The input samples were also prepared in the same way.
421 The samples were incubated for 1 hour at 45°C with the mix of 0.5 M EDTA, 1 M Tris-HCl (pH 6.5)
422 and proteinase K and then DNA from each sample was purified using
423 phenol:chloroform:isoamylalcohol solution (Sigma-Aldrich, St. Louis, MO, USA) with an addition
424 of glycogen (Roche, Mannheim, Germany). The quantitative analysis of the performed experiment
425 was checked in the real-time qPCR reactions performed using Platinum Taq DNA Polymerase kit
426 (Invitrogen, Carlsbad, CA, USA), 10 mM dNTPs (Invitrogen, Carlsbad, CA, USA) and SYBR Green
427 (solution 1:2000; Invitrogen, Eugene, OR, USA). The enrichment at *Snat3* promoter region was
428 normalized versus input as calculated and normalized versus amylase (non-binding region). The
429 primers used in this study are as follow: *Snat3* promoter region (sense strand: 5'-
430 AAACACTTGGAGGGGCTTCT-3', antisense strand: 5'-CCTCGAAATCGGTGAAGTGT-3'),
431 amylase (sense strand: 5'-CTCCTTGTACGGGTTGTT-3', antisense strand: 5'-
432 AATGATGTGCACAGCTGAA-3').

433 4.9. Immunocytochemistry

434 In order to investigate the cellular localization of Sp1 transcription factor in the astrocytes, the
435 cells were cultured on poly-L-lysine coated glass coverslips in 24-well plates. The cells were washed
436 with PBS and fixed with 4% paraformaldehyde for 20 min at RT and then permeabilized with 0.25%
437 Triton X-100 for 15 min at RT. The cells were blocked in 3% BSA and 3% NGS (normal goat serum,
438 Sigma-Aldrich, St. Louis, MO, USA) for 1 hour. Incubation with antibody against Sp1 (1:100;
439 ProteinTech, Manchester, UK) was done in 3% BSA and 3% NGS in PBS buffer overnight at 4°C and
440 followed by 1-hour incubation with goat anti-rabbit IgG Alexa Fluor 488 (1:500, Invitrogen, Waltham,
441 MA, USA), for 1 hour at RT in the dark. The cells were placed on the microscope slides using
442 VectaShield mounting medium containing DAPI stain (Vector Laboratories, Burlingame, CA, USA)
443 that labelled the cell nuclei. To obtain the detailed images of the labeled cells, a confocal laser scanning
444 microscope LSM 780 (Zeiss) was used. An argon laser (488 nm) was used for the excitation of Alexa
445 Fluor 488 and diode 405 nm for the excitation of DAPI. Following the acquisition, the images were
446 processed using the ZEN 2012 (Zeiss, Jena, Germany). Immunocytochemistry studies were
447 performed in the Laboratory of Advanced Microscopy Techniques, Mossakowski Medical Research
448 Centre, Polish Academy of Sciences.

449 4.10. Statistical analysis

450 Statistical analysis was performed using GraphPad Prism 5 software (GraphPad Software, La
 451 Jolla, CA, USA). Confirmation of normality of the data distribution was checked using Kolmogorov–
 452 Smirnow test. Statistical significance was determined by t-test, one-way analysis of variance (One-
 453 Way ANOVA) followed by Dunnet post-hoc test and two-way analysis of variance (Two-Way
 454 ANOVA) followed by Bonferroni post-hoc test. A probability value of 0.05 or less was considered
 455 statistically significant.

456

457 **Author Contributions:** M.Z. and K.D. conceived and designed the experiments; K.D. performed the experiments
 458 and analyzed the data; K.D. contributed reagents/materials/analysis tools; K.D. and M.Z. wrote the paper.

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461 **Abbreviations**

BisI	bisindolylmaleimide I
CDK	cyclin-dependent kinase
ChIP	chromatin immunoprecipitation
CH ₃ NH ₃ Cl	methylammonium chloride
CNS	central nervous system
dBcAMP	dibutyryl cyclic adenosine monophosphate
ENU	N-ethyl-N-nitrosourea
ERK	extracellular signal-regulated kinases
GABA	γ-aminobutyric acid
GAPDH	glyceraldehyde 3-phosphate dehydrogenase
Gln	L-glutamine
Glu	L-glutamate
HE	hepatic encephalopathy
MAPK	mitogen-activated protein kinases
pHe	extracellular pH
PKA	protein kinase A
PKC	protein kinase C
PKCα-	silenced expression of protein kinase C isoform α
PKCδ-	silenced expression of protein kinase C isoform δ
PMA	phorbol 12-myristate 13-acetate
SN1	SNAT3, solute carrier family 38 member 3
SN2	SNAT5, solute carrier family 38 member 5
Sp1	specificity protein 1

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