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Differential effects of glucose deprivation on the survival of fetal versus adult neural stem cells-derived oligodendrocyte precursor cells

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(Article begins on next page)

1 **Differential effects of glucose deprivation on the survival of fetal versus adult neural**
2 **stem cells-derived oligodendrocyte precursor cells.**

3

4 **Running title: OPCs metabolism drives OGD vulnerability**

5

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21

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32 Main points:

33 - fetal OPCs are selectively vulnerable to hypoxia/ischemia

34 - fetal NSCs-derived mixed cultures are glycolytic, while adult mainly use OXPHOS

35 - fetal and adult OPCs show different vulnerability to metabolic challenges in mixed cultures

36 containing astrocytes

37

38

39 **Abstract**

40

41 Impaired myelination is a key feature in neonatal hypoxia/ischemia (HI), the most common
42 perinatal/neonatal cause of death and permanent disabilities, which is triggered by the
43 establishment of an inflammatory and hypoxic environment during the most critical period of
44 myelin development. This process is dependent on oligodendrocyte precursor cells (OPCs)
45 and their capability to differentiate into mature oligodendrocytes.

46 In this study, we investigated the vulnerability of fetal and adult OPCs derived from neural
47 stem cells (NSCs) to inflammatory and HI insults. The resulting OPCs/astrocytes cultures
48 were exposed to cytokines to mimic inflammation, or to oxygen-glucose deprivation (OGD)
49 to mimic an HI condition. The differentiation of both fetal and adult OPCs is completely
50 abolished following exposure to inflammatory cytokines, while only fetal-derived OPCs
51 degenerate when exposed to OGD.

52 We then investigated possible mechanisms involved in OGD-mediated toxicity: i) T3-
53 mediated maturation induction; ii) glutamate excitotoxicity; iii) glucose metabolism. We
54 found that while no substantial differences were observed in T3 intracellular content
55 regulation and glutamate-mediated toxicity, glucose deprivation lead to selective OPC cell
56 death and impaired differentiation in fetal cultures only.

57 These results indicate that the biological response of OPCs to inflammation and
58 demyelination is different in fetal and adult cells, and that the glucose metabolism
59 perturbation in fetal central nervous system (CNS) may significantly contribute to neonatal
60 pathologies. An understanding of the underlying molecular mechanism will contribute greatly
61 to differentiating myelination enhancing and neuroprotective therapies for neonatal and adult
62 CNS white matter lesions.

63

64 **Keywords**

65 oligodendrocyte precursor cells, inflammation, hypoxia/ischemia, oxygen-glucose
66 deprivation, white matter lesion

67

68

69 **1. Introduction**

70
71 Myelin depletion is a major pathological event in inflammatory diseases, vascular and
72 traumatic lesions of the central nervous system (CNS), and a major cause of consequent
73 neurodegeneration and chronic disabilities in both infants and adults (Verden & Macklin,
74 2016). Oligodendrocyte precursors (OPCs) are the cells responsible for myelin formation
75 during development, and for myelin turnover and repair during the adult life, thanks to their
76 ability to differentiate into myelinating oligodendrocytes (OLs) (Alizadeh, Dyck, & Karimi-
77 Abdolrezaee, 2015). During gestational development, OPCs progenitors migrate in three
78 regionally and temporally distinct waves to populate the white and grey matters, partially
79 differentiating into myelinating OLs which guarantee proper white matter formation, and
80 partially remaining at undifferentiated stage (resident OPCs) (Michalski & Kothary, 2015).
81 During adult life, and under appropriate conditions, resident and newly generated OPCs from
82 neural stem cells (NSCs) of the subventricular zone (SVZ) can proliferate, migrate to the nude
83 axons, and differentiate into mature oligodendrocytes (OLs) to provide myelin turnover and
84 repair following lesion (Crawford, Chambers, & Franklin, 2013; Trotter, Karram, &
85 Nishiyama, 2010).

86
87 Both OPCs and mature OLs are highly vulnerable to inflammation and hypoxia/ischemia
88 (HI), the main pathogenic mechanisms determining demyelination through a number of
89 downstream cellular and molecular mechanisms (Calzà et al., 2018). In particular, neonatal HI
90 is the most common cause of death, as well as of motor, sensory and cognitive disability,
91 during the perinatal/neonatal period (Millar, Shi, Hoerder-Suabedissen, & Molnár, 2017).
92 Clinical conditions leading to neonatal HI generally occur in the time window when OPCs
93 should switch to myelinating OLs to guarantee proper myelination, i.e. from late embryonic
94 gestation throughout early post-natal life (Fancy, Chan, Baranzini, Franklin, & Rowitch,
95 2011). HI and associated inflammation induces OPC proliferation through Cdk2 pathway
96 activation, but also delayed/impaired maturation and apoptosis (Back et al., 2002; Jablonska
97 et al., 2012; Janowska and Sypecka, 2014), finally resulting in an impairment of myelination
98 (Rocha-Ferreira & Hristova, 2016). The overproduction of cytokines/chemokines itself also
99 promotes OPCs proliferation and inhibits their differentiation into myelinating OLs (Patel &
100 Klein, 2011; Tognatta & Miller, 2016).

101 As well as in neonatal injuries, the OPC differentiation block is considered a major cause of
102 myelin repair impairment during adult life, as demonstrated in multiple sclerosis (MS), spinal

103 cord injury and related animal models (Irvine & Blakemore, 2008; Mekhail, Almazan, &
104 Tabrizian, 2012; van Tilborg et al., 2018). In these conditions, OPCs proliferate (Picard-Riera
105 et al., 2002), and part of them differentiate into astrocytes, while the remaining cells are
106 mainly blocked in an OL progenitor phenotype (Picard-Riera et al., 2002; Sozmen et al.,
107 2016). Moreover, both inflammation and HI interfere with the thyroid hormone- (T3)
108 dependent mechanism of OPC cell cycle arrest (Billon, Jolicoeur, Tokumoto, Vennström, &
109 Raff, 2002) and differentiation induction (Fernández, Baldassarro, Sivilia, Giardino, & Calzà,
110 2016).

111

112 Since OPCs are the cells responsible for both developmental myelination and myelin turnover
113 and repair during adult life, it has been suggested that remyelination in adulthood resembles
114 the developmental myelination mechanism (Franklin & Hinks, 1999), and this hypothesis has
115 driven research for remyelination enhancing therapies. However, various studies indicate a
116 number of differences in mechanisms responsible for myelin formation during development
117 and myelin repair during adulthood, leading to the view that this process is differentially
118 regulated depending on age (Baldassarro, Marchesini, Giardino, & Calzà, 2017; Miron,
119 Kuhlmann, & Antel, 2011).

120

121 To investigate the vulnerability of fetal and adult OPCs to inflammation and HI in terms of
122 cell death and differentiation, we analyzed the *in vitro* response of OPCs derived from both
123 the fetal and the adult brain to stimuli responsible for myelin loss *in vivo*. To explore the
124 impact of these challenges on maturation, from stem cells to myelinating OLs, we
125 differentiated OPCs from NSCs obtained from the fetal forebrain and the SVZ of adult mice.
126 We preferred this model respect to primary OPCs, because we intended generate a
127 spontaneous mixed culture also containing astrocytes, to better mimic the *in vivo*
128 environment. In order to dissect the mixed cell population, we monitored the GFAP-positive
129 cells (astrocytes) in all the tested conditions.

130 In the first part of the study, we exposed these cell systems to experimental conditions
131 mimicking *in vitro* inflammation (a cytokine cocktail composed of TGF- β 1, TNF- α , IL-1 β ,
132 IL-6, IL-17 and IFN- γ) or to an HI model (oxygen-glucose deprivation, OGD). All the
133 noxious stimuli were applied to target the precursor phase of the OLs, when cells actively
134 proliferate, to mimic the inflammatory/HI challenge during developmental myelination. We
135 demonstrated that T3-induced differentiation is blocked by the cytokine cocktail in both fetal
136 and adult OPCs. In contrast, OGD impairs differentiation and induces cell death in fetal but

137 not adult OPCs. We then explored possible mechanisms underlying vulnerability in fetal
138 OPCs, focusing on glutamate toxicity, apoptosis, and metabolic profile, finally finding a
139 different basal and induced metabolism between fetal and adult mixed cultures responsible for
140 driving the differing vulnerability to OGD. Results from this study may have important
141 implications for developing myelin-enhancing therapies and neuroprotection strategies in
142 adult and fetal demyelination diseases and CNS lesions.

143

144 **2. Materials and methods**

145

146 *2.1 Cell preparation and cultures*

147

148 All animal protocols described herein were carried out according to European Community
149 Council Directives (86/609/EEC) and comply with the guidelines published in the *NIH Guide*
150 *for the Care and Use of Laboratory Animals*.

151 Fetal and adult NSCs were isolated from E.13.5 fetal forebrain or 2.5 month old adult sub-
152 ventricular zone (SVZ), following the Ahlenius and Kokaia protocol (Ahlenius & Kokaia,
153 2010). Oligodendrocyte differentiation was performed following the Chen protocol (Chen et
154 al., 2007) with some modifications. Tissues were enzymatically dissociated using trypsin
155 (Sigma-Aldrich, Saint Louis, MO, USA), hyaluronidase (Sigma-Aldrich) and DNase (Sigma-
156 Aldrich), then mechanically dissociated by pipetting. The solution was filtered, centrifuged
157 and the resulting pellet was washed twice in HBSS. Following 7 minutes centrifugation at 400
158 \times g, the cellular pellet was resuspended in serum-free medium (DMEM/F12 GlutaMAX 1 x; 8
159 mmol/L HEPES; 100 U/100 μ g Penicillin/Streptomycin; 0.1 x B27; 1 x N-2; 20 ng/mL bFGF;
160 20 ng/mL EGF; Thermo Fisher Scientific, Waltham, MA, USA), and following cell count,
161 cells were plated in suspension at a density of 10 cells/ μ l in a final volume of 3 mL in low-
162 attachment 6-well plates (Nunc, Roskilde, DK). The half medium was changed every three
163 days, centrifuging the cell suspension at 300 \times g for 5 minutes and gently resuspending the
164 cellular pellet in fresh medium. Neurospheres were allowed to proliferate until they attained a
165 diameter of about 100 μ m.

166 To obtain oligospheres, primary neurospheres were centrifuged at 300 x g for 5 minutes. The
167 pellet was mechanically dissociated by pipetting and cells were counted and plated again at a
168 density of 10 cells/ μ l in a final volume of 3 mL of OPC medium (DMEM/F12 GlutaMAX 1
169 x; 8 mmol/L HEPES; 100 U/100 μ g Penicillin/Streptomycin; 0.1 \times B27; 1 \times N-2; 20 ng/mL
170 bFGF; 20 ng/mL PDGF; Thermo Fisher Scientific) in low-attachment 6-well plates (Nunc).

171 Oligospheres were centrifuged and the pellet was mechanically dissociated to obtain a single
172 cell suspension. Following cell count, cells were plated at a density of 3000 cells/cm² on poly-
173 D,L-ornithine (50µg/ml)/laminin (5µg/ml; Sigma-Aldrich) coating, in OPC medium.
174 To induce oligodendrocyte differentiation and maturation, the OPC medium was replaced
175 with the oligodendrocyte differentiation medium (DMEM/F12 GlutaMAX 1 x; 8 mmol/L
176 HEPES; 100 U/100 µg Penicillin/Streptomycin; 0.1 x B27; 1 x N-2; 50 nM T3; 10 ng/ml
177 CNTF; 1x *N*-acetyl-L-cysteine – NAC; Thermo Fisher Scientific) following 3 DIVs.

178

179 *2.2 Cytokine exposure*

180

181 Following primary neurosphere splitting, fetal and adult cultures were divided in two groups:
182 one treated with a mix of six different cytokines (TGF-β1, TNF-α, IL-1β, IL-6, IL-17 and
183 IFN-γ; 20 ng/mL each; Thermo Fisher Scientific), the other treated with vehicle (0.04% of the
184 cytokine solvent: 10% glycerol/100 nM glycine/25 nM Tris, pH 7.3). Following oligosphere
185 expansion, the medium was changed to the standard medium, without cytokines, in both
186 groups.

187

188 *2.3 Oxygen-glucose deprivation exposure*

189

190 OGD was performed using an air-tight hypoxia chamber (Billups-Rothenberg Inc., Del Mar.,
191 CA) saturated with 95% N₂ and 5% CO₂ (Goldberg & Choi, 1993). Glucose deprivation was
192 achieved using a glucose-free complete medium (Thermo Fisher Scientific). Oxygen was
193 removed by flushing the hypoxia chamber with N₂-CO₂ mixture for 6-8 min at 25 l/min. The
194 flushing was repeated after half of the incubation time. The OGD condition was maintained
195 for 3 h, after which plates were re-oxygenated in the old glucose-containing medium in the
196 incubator.

197

198 *2.4 Iopanoic acid treatments*

199

200 To study the role of deiodinase 3 (D3) activation following OGD-exposure, the effect of
201 deiodinase inhibition was analyzed in fetal cultures. Iopanoic acid (IOP, 10 µM) treatment
202 was performed starting from 24 hours prior to OGD exposure (-1 DIV) and continuing
203 throughout the entire differentiation phase (12 DIV; Figure 4 A). The percentage of D3-
204 positive cells was quantified both at 0 and 12 DIVs. Moreover, at the end of the

205 differentiation phase (12 DIV), the mature/myelinating OLs (CNPase/MBP-positive cells)
206 were quantified.

207

208 *2.5 Glutamate/NMDA treatments*

209

210 To study the role of glutamate excitotoxicity in fetal OGD-induced cell death, another set of
211 experiments was set up.

212 Cells were exposed in parallel to normoxia or OGD, or treated with Glutamate or NMDA (1
213 mM) (Matute, 2009). Moreover, to inhibit the glutamate action, all groups were treated with
214 vehicle, MK801 or NBQX in a concentration (10 μ M) already proven to rescue primary
215 neurons from excitotoxicity (Baldassarro et al., 2018) from 1h prior to the challenge exposure
216 throughout the entire differentiation phase (12 DIV).

217 At the end of the differentiation phase, cell number and cell death were analyzed in all groups
218 using cell-based HCS.

219

220 *2.6 Glucose deprivation exposure, 2-DG and Oligomycin treatments*

221

222 To study the role of glucose metabolism perturbation in fetal OGD-induced cell death, in
223 another set of experiments, cells were exposed to 24 or 3 hours of glucose deprivation, 2-
224 deoxy-D-glucose (2-DG; 50 mM; Cayman Chemical, Ann Arbor, MI, USA) or oligomycin (1
225 μ M; Cayman Chemical) treatment, 24 hours prior to T3-mediated differentiation induction.

226 Cells exposed for 24 hours were analyzed for lactate production, while cells exposed for 3
227 hours, were analyzed for caspase activation (0 DIV) and cell death and differentiation (0 and
228 6 DIV) by using specific markers for OPCs (PDGF α R-positive cells), mature OLs (CNPase-
229 positive cells) and myelinating OLs (MBP-positive cells).

230

231 *2.7 Lactate quantification*

232

233 Lactate production was quantified in fetal and adult cultures 24 hours following GD exposure,
234 2-DG or oligomycin treatments, using the colorimetric glycolysis cell-based assay kit
235 (Cayman Chemical) and normalizing the absorbance on the control group (standard culture
236 conditions treated with vehicle).

237

238 *2.8 Immunocytochemistry*

239

240 Indirect immunofluorescence was used to identify OPCs (NG2 or PDGF α R-positive cells),
241 mature (CNPase-positive cells) and myelinating (MBP-positive cells) oligodendrocytes,
242 neurons (β -III-tubulin-positive cells), astrocytes (GFAP-positive cells) and deiodinase 3
243 expressing cells (D3). The following primary antisera were used: mouse anti- β -III-tubulin
244 (R&D system, Trento, IT) 1:3000; rabbit anti-GFAP (Glial Fibrillary Acidic Protein, Dako,
245 Santa Clara, CA, USA) 1:1000; rabbit anti-NG2 (chondroitin sulphate proteoglycan,
246 neural/glial antigen 2, Millipore, Merck S.p.a., Milan, IT) 1:350; mouse anti-CNPase (2', 3'-
247 cyclic nucleotide 3'-phosphodiesterase, Millipore) 1:500; rabbit anti-MBP (Myelin Basic
248 Protein, Dako) 1:500; goat anti-D3 (deiodinase type 3, Santa Cruz Biotechnology, Dallas, TX,
249 USA) 1:100; rabbit anti-cleaved caspase 3 (BD Pharmingen, San Jose, CA, USA) 1:200 and
250 rabbit anti-PDGF α R (Platelet derived growth factor alpha receptor; Santa Cruz
251 Biotechnologies) 1:300. Donkey Alexa 488-conjugated anti mouse IgG donkey Alexa 568-
252 conjugated anti-rabbit IgG, 1:500 (Invitrogen, Carlsbad, CA, USA) and DyLight488-
253 conjugated affinity-pure donkey anti-Goat IgG (Jackson ImmunoResearch, Cambridge, UK)
254 1:100 were used as secondary antisera. Following immunofluorescence staining, cells were
255 incubated with the nuclear dye Hoechst 33258 (1 μ g/mL in PBS, 0.3% Triton-X 100) for 20
256 min at RT. Finally, cells were washed in PBS and mounted in glycerol and PBS (3:1, v/v)
257 containing 0.1% paraphenyldiamine.

258

259 *2.9 Fluorescence microscopy*

260

261 Fluorescence microscopy was used to quantify the percentage of D3-expressing cells and
262 cleaved-caspase 3 – positive cells in fetal cultures 24 hours following OGD or GD
263 exposure.

264 Images were captured using a Nikon Eclipse E600 microscope equipped with a digital
265 CCD camera Q Imaging Retiga-2000RV (Q Imaging, Surrey, BC, CA). Measurements
266 were performed using Nis-Elements AR 3.2 software.

267 Five random fields per glass (duplicate per group) were analyzed. Marker-positive cell
268 percentage was calculated on the total number of cells per field, identified by the nuclear
269 staining.

270

271 *2.10 High Content Screening*

272

273 For HCS analysis, cells were grown in 96 flat-bottom well HCS plates (Nunc). Analysis of
274 condensed nuclei, cell number and lineage/differentiation markers were performed with Cell
275 Insight™ CX5 High Content Screening (HCS; Thermo Fisher Scientific), using the
276 *Compartmental analysis* BioApplication. Based on nuclear staining, the software is able to
277 recognize the nuclei and calculate the percentage of high intensity/small-sized condensed
278 nuclei. Moreover, based on the identification of the nuclei, the software is able to detect the
279 presence of the marker-specific staining in the cell body, calculating the percentage of
280 immunoreactive cells. Lineage/differentiation marker analysis was performed only on cells
281 showing intact nuclei, excluding condensed nuclei from the percentage calculation. The HCS
282 system permits analysis of the whole culture, avoiding the bias in choosing random fields. A
283 mean of 10000 cells/wells was included in this analysis.

284

285 2.11 *RNA extraction, reverse transcription and PCR arrays*

286

287 The RNeasy Micro Kit (Qiagen, Venlo, NL) was used for total RNA extraction, and 500 ng
288 was retrotranscribed using the RT² First Strand Kit (Qiagen) following the manufacturer's
289 instructions. Cells were lysed 24 hours following normoxia or OGD exposure, and three
290 samples from independent experiments were used in the analysis. For the study of glucose-
291 related gene expression, PCR array for mouse glucose metabolism (Table S1; PAMM-
292 006ZA; Qiagen) was used in combination with the RT² SYBR Green qPCR Mastermix
293 (Qiagen).

294

295 2.12 *Study design and statistical analysis*

296

297 Experiments were performed in triplicate (three independent experiments) for cell number
298 and viability, and in duplicate for cell marker analysis. Data is reported as mean ± SEM.
299 Prism software (GraphPad Software, San Diego, CA, USA) was used for statistical analyses
300 and graph generation. Student's t-test or one-way ANOVA were used to analyze data. Results
301 were considered significant when the probability of their occurrence as a result of chance
302 alone was less than 5% ($p < 0.05$).

303

304 **3. Results**

305

306 3.1 *The cell systems*

307
308 OPCs were obtained by driving NSCs differentiation using specific factors (Figure 1 A).
309 Primary neurospheres were obtained in the presence of EGF and bFGF. Following
310 neurosphere splitting, EGF was replaced by PDGF in the culture medium, starting the OPC
311 differentiation (oligospheres). To obtain the OPCs, oligospheres were seeded as single cell,
312 and the bFGF/PDGF medium replaced with T3 containing medium after 3 days, allowing the
313 OLs to mature for 12 DIVs.

314 NSCs-derived cultures are mixed cultures composed of OPCs, OLs and astrocytes, with a
315 small percentage of neurons (Baldassarro et al., 2017). Lineage progression from NG2-
316 positive OPCs (DIV0) through CNPase-positive, mature OLs as far as myelinating
317 CNPase/MBP-positive OL is illustrated in Fig. 1 B-D (representative images). The culture
318 composition changes during the 12 DIV differentiation period, starting from 0 DIV, where the
319 majority of cells are NG2 positive (NG2-positive cells 80%; CNPase-positive cells 5%),
320 passing thorough DIV 6, where CNPase cells are growing in number (NG2-positive cells
321 60%; CNPase-positive cells 30%), reaching the end of the differentiation with CNPase/MBP
322 positive cells representing the majority of cells (CNPase-positive cells; 70% in fetal and 45%
323 in adult cultures; MBP-positive cells, 40% in fetal and 30% in adult cultures). Both cultures
324 show around 40% of GFAP-positive cells at 12 DIVs, and a small percentage (6-8%) of beta-
325 III-tubulin positive cells (neurons).

326 The experimental design used in all experiments aims to expose the cell system to the
327 challenge during the T3-mediated cell cycle arrest and maturation induction of OPCs (Billon
328 et al., 2002), keeping a mixed environment also containing astrocytes.

329

330 *3.2 Inflammatory cytokines block OPC differentiation in both fetal and adult OPCs*

331

332 In a first set of experiments, we tested fetal and adult OPCs in the presence of inflammatory
333 stimuli. Fetal and adult NSCs-derived OPCs were exposed to an inflammatory cytokine mix
334 composed of TGF- β 1, TNF- α , IL-1 β , IL-6, IL-17 and IFN- γ . This cocktail blocks adult OPC
335 differentiation when applied in the proliferation phase of the culture, while exposure during
336 the differentiation phase results in cytotoxic effects (Fernández et al., 2016). Thus, the
337 cytokine mix was applied to the oligosphere phase, during replication, and in the absence of
338 differentiating stimuli (Figure 2A). Three days after the OPC cell seeding, cells were
339 triggered to differentiate into OPCs by T3. At the end of the differentiation phase (12 DIV),
340 cell number, cell death and differentiation were analyzed using HCS technology.

341 Fetal cultures treated with the cytokine mix show an increase in total cell number (Student's t-
342 test: $p < 0.0001$) and a reduction in the percentage of condensed nuclei ($p = 0.0007$; Figure 2
343 B). Adult cells also show an increase in cell number ($p = 0.0009$), while no changes in cell
344 death was detected (Figure 2 C).

345 At the end of the differentiation period, cytokine-treated cells show a different cell
346 composition compared to vehicle-treated cells. Fetal cultures show no changes in the
347 percentage of precursors (NG2-positive cells), but a drastic decrease in mature/myelinating
348 OLs (Student's t-test: CNPase, $p < 0.0001$; MBP, $p < 0.0001$). Moreover, a reduction in
349 astrocyte population was also observed (GFAP-positive cells, $p = 0.0030$; Figure 2 D).

350 As already described (Fernández et al., 2016), cytokine treatment in adult cultures causes an
351 increase in the percentage of NG2-positive cells (Student's t-test, $p = 0.0025$). Moreover, as
352 per the fetal cultures, adult cell differentiation/maturation is drastically reduced in the
353 cytokine- compared to the vehicle-treated cells (Student's t-test, CNPase, $p = 0.0273$; MBP, p
354 $= 0.0036$). As well as in fetal cultures, astrocyte differentiation is also impaired in cytokine
355 treated cells ($p = 0.0001$; Figure 2 E). As already described for adult cultures (Fernández et
356 al., 2016), this perturbation during differentiation/maturation maintains cells at
357 undifferentiated state, as indicated by negativity to all tested lineage-specific markers
358 Representative images of CNPase and MPB-immunofluorescence staining in fetal and adult
359 cultures treated and untreated with the cytokines mix are included in Figure 2 (F-M).

360

361 3.3 Fetal but not adult OPCs are vulnerable to OGD-

362

363 In these experiments, we tested fetal and adult OPC vulnerability to OGD, the most widely
364 used *in vitro* model for HI. OGD was applied for 3 hours, followed by 24 hours of
365 reperfusion/reoxygenation during the proliferation phase of seeded OPCs. T3-induced
366 differentiation was triggered immediately following the reperfusion/reoxygenation phase
367 (Figure 3 A). We decided to use this OGD schema, which has been widely used on neuronal
368 cultures, where it causes 50 % and 20 % cell death in pure and mixed neonatal fetal cortical
369 neurons respectively (Baldassarro et al., 2018). Here we analyzed OPCs survival and lineage
370 specification and maturation at the end of the differentiation phase (12 DIV) by HCS
371 technology.

372 OGD induces a reduction in cell number (Student's t-test, $p < 0.0001$) and an increase in cell
373 death ($p < 0.0001$; Figure 3 B) at the end of the differentiation phase in fetal cultures. In

374 contrast, adult cultures exposed to OGD show an increase in cell number ($p < 0.0001$) without
375 affecting cell death ($p = 0.1247$; Figure 3 C).

376 As already indicated, the preparation of OPCs derived from NSCs also contains astrocytes,
377 and few neurons. To establish the cell population affected by OGD, we used Cell Insight™
378 CX5 HCS. This software identifies nuclear size and morphology (normal nucleus for living
379 cells; condensed nuclei for dead cells), and the associated cytoplasm immunostaining for
380 astrocytes (GFAP), neurons (b-III-tubulin), OPCs (NG2), mature OLs (CNPase) and
381 myelinating OLs (MBP), thus allowing the identification of degenerating cell types.

382 We first quantified the percentage of the different cell-specific markers in cells showing
383 normal nuclear morphology, considered live cells. In fetal cultures, OPCs and
384 mature/myelinating OL populations are affected by OGD exposure, as shown by the decrease
385 in NG2- ($p = 0.0158$), CNPase- ($p < 0.0001$) and MBP- ($p = 0.0002$) positive cells, while no
386 effects are present in astrocyte (GFAP, $p = 0.3137$) or neuron (b-III-tubulin, $p = 0.2998$)
387 populations (Figure 3 D). In contrast, adult cultures show an increase in NG2-positive cells (p
388 $= 0.0025$), while no effects on all the other analyzed markers are observed (CNPase, $p =$
389 0.6283 ; MBP, $p = 0.3606$; GFAP, $p = 0.1530$; b-III-tubulin, $p = 0.9914$; Figure 3 E). The
390 specificity of OGD-induced cell death in fetal OPCs/OLs was also confirmed by the analysis
391 of the cells showing condensed nuclei. Fetal-derived cultures show an increase in cell death in
392 NG2, CNPase and MBP-positive cells (Student's t-test, NG2, $p = 0.0002$; CNPase, $p =$
393 0.0028 ; MBP, $p = 0.0095$), without affecting astrocytes and the small percentage of neurons
394 (GFAP, $p = 0.0880$; beta-III-tubulin, $p = 0.1272$; Figure 3 F). Adult-derived cultures, as
395 expected from the analysis of the whole culture, do not show cell death in any population
396 (NG2, $p = 0.4690$; CNPase, $p = 0.2321$; MBP, $p = 0.3568$; GFAP, $p = 0.8302$; beta-III-
397 tubulin, $p = 0.4015$, Figure 3 G). Representative images of the OGD-exposed cultures are
398 included in the figure (Figure 3 H-O).

399

400 To investigate the mechanisms underlying the OGD-induced cell death and impaired
401 differentiation of surviving cells observed in fetal but not adult cells, we examined the three
402 main players in the process: i) the T3-dependent differentiation; ii) glutamate excitotoxicity
403 and iii) glucose metabolism.

404

405 *3.4 Deiodinase inhibition is not effective in rescuing OGD-induced cell death or the*
406 *differentiation impairment of OPCs derived from fetal NSCs.*

407

408 We have already demonstrated that under cytokine exposure, and coupled with the OPC
409 differentiation block, the expression of the T3-inactivating enzyme (D3) increases in the
410 cytoplasm of OPCs, while its inhibition by IOP (10 μ M) restores proper OPC differentiation
411 (Fernandez et al., 2016). We then explored whether this mechanism also supports OPC
412 differentiation block in fetal preparations exposed to OGD. First, we demonstrated that
413 following the reperfusion/reoxygenation phase of the OGD model (0 DIV, Figure 4 A), fetal-
414 derived cultures show an increase in D3-positive cell percentage (Student's t-test, $p = 0.0009$;
415 Figure 5 B-D). However, the treatment with IOP is not able to rescue the decrease in
416 mature/myelinating OLs in the culture induced by OGD exposure (Figure 4 E). In fact, the
417 IOP treatment is able to decrease D3-positive cells in OGD-exposed cultures at the end of the
418 differentiation phase (one-way ANOVA, $F(3, 17) = 0.7360$, $p = 0.0337$; Tukey post-test $p =$
419 0.0213) and, as expected, is also able to increase the percentage of myelinating MBP-positive
420 OLs in normoxia-exposed control cultures (Dunnett's post-test, $p = 0.0162$). Following OGD
421 exposure, however, the composition of the culture shows a decrease in mature/myelinating
422 OPCs in both vehicle and IOP-treated cells after 12 DIVs (one-way ANOVA, CNPase, $F(2,$
423 $28) = 1.099$, $p < 0.0001$, Dunnett's post-test, vehicle, $p < 0.0001$, IOP $p < 0.0001$; MBP, $F(3,$
424 $32) = 1.438$, $p < 0.0001$, Dunnett's post-test, vehicle $p < 0.0001$, IOP $p < 0.0001$).

425

426 *3.5 Glutamate excitotoxicity is not involved in the OGD-induced cell death of OPCs derived*
427 *from fetal NSCs*

428

429 Glutamate-triggered cell death is a mechanism proposed in several *in vitro* and *in vivo*
430 conditions, including HI characterized by OL and OPC cell death (Káradóttir & Attwell,
431 2007); (Simonishvili, Jain, Li, Levison, & Wood, 2013); (Deng, Rosenberg, Volpe, & Jensen,
432 2003). To study the possible role of glutamate excitotoxicity in OGD-induced cell death in
433 fetal NSCs-derived OPCs, we compared different treatment schemas with glutamate and
434 glutamate receptor antagonists in normoxia and OGD conditions. In particular, we exposed
435 fetal cultures to normoxia, or OGD and glutamate or NMDA (1mM) to confirm glutamate
436 excitotoxicity in our experimental conditions. Moreover, to test a protective treatment by
437 glutamate receptor antagonists, cells were treated with vehicle, MK801 (NMDA-inhibitor) or
438 NBQX (AMPA-inhibitor), starting one hour prior to the exposures and continuing throughout
439 the entire differentiation phase (Fig. 5 A).

440 We first examined the effect of glutamate in our cell system in normoxia. At the end of the
441 differentiation phase (12 DIV), glutamate-treated cultures showed a reduction in cell number,

442 while glutamate and NMDA treatment had no effects on the percentage of condensed nuclei.
443 The treatment with the two glutamate antagonists was also ineffective in normoxia (Fig. 5 B,
444 one-way ANOVA, $F(10, 75) = 0.4191$, $p < 0.0001$; Sydak's post-test, glut, $p < 0.0198$; glut-
445 MK801, $p = 0.0054$; glut-NBQX, $p = 0.0033$).

446 We then tested the effect of glutamate receptor antagonists in OGD. As described above, in
447 the OGD exposed cultures, we observed a decrease in cell number (Sydak's post-test, OGD, p
448 $= 0.0375$) and an increase in condensed nuclei (one-way ANOVA, $F(10, 77) = 13.37$, $p <$
449 0.0001 ; Sydak's post-test, $p < 0.0001$), while the exposure to the two glutamate antagonists
450 was ineffective in both cell number (Sydak's post-test, MK801, $p = 0.0133$; NBQX, $p =$
451 0.0002) and cell death (Sydak's post-test, MK801, $p < 0.0001$; NBQX, $p < 0.0001$) rescues.

452

453 *3.6 Glucose metabolism perturbation is responsible for the OGD-induced cell death of OPCs*
454 *derived from fetal NSCs*

455

456 Finally, we investigated the contribution of glucose metabolism to OGD-induced cell death in
457 OPCs derived from fetal NSCs. We first attempted to establish the glucose metabolic state in
458 both fetal and adult cells, by using tools able to differentiate glycolysis and oxidative
459 phosphorylation (OXPHOS). We exposed cultures to glucose deprivation-only (GD), and to
460 metabolic path interfering agents (2-DG and oligomycin), before measuring glycolytic
461 activity by lactate production following 24 hours of exposure (0 DIV; Figure 6 A, red arrow).
462 2-DG contains the 2-hydroxyl group replaced by hydrogen, thus blocking glycolysis at early
463 stages, resulting as toxic to highly glycolytic cells (Coleman et al., 2008); oligomycin
464 inhibits ATP synthase, blocks the proton channel and consequently OXPHOS, resulting in a
465 compensatory increase in glycolysis activity (Bertina, Steenstra, & Slater, 1974).

466 Fetal and adult NSCs-derived OPCs/astrocytes mixed cultures show a different metabolic
467 state in basal conditions. In particular, fetal cultures metabolism resulted as being completely
468 dependent on glycolysis (Figure 6 B). In fact, the relative quantification of lactate production
469 showed a decrease in this parameter following 24 hours of GD exposure or 2-DG treatment
470 compared to the standard condition (100%) (one-way ANOVA, $F(3, 11) = 40.14$, $p < 0.0001$;
471 Dunnett's post-test, GD, $p < 0.0001$; 2-DG, $p < 0.0001$), but oligomycin treatment showed no
472 changes in lactate levels, proving that the entire metabolism of these cells is based on
473 glycolysis.

474 On the other hand, adult cell metabolism is not strictly glycolytic (Figure 6 C). In fact, even
475 when lactate production breaks down during GD or 2-DG exposure, these cultures show a

476 compensatory activation of glycolysis, as indicated by increased lactate production, when
477 exposed to oligomycin (one-way ANOVA, $F(3, 8) = 97.57$, $p < 0.0001$; Dunnett's post-test,
478 GD, $p = 0.0029$; 2-DG, $p = 0.0030$; oligomycin, $p < 0.0001$)

479 The absence of a compensatory overproduction of lactate in oligomycin treated fetal cultures
480 suggests that no compensatory glycolytic activity is needed when OXPHOS is blocked,
481 meaning that the entire metabolism of these cells is based on glycolysis in standard
482 conditions. By contrast, adult cells need to compensate when treated with oligomycin, with
483 increasing glycolytic activity, indicating that their metabolism in basal conditions
484 contemplates OXPHOS.

485

486 To investigate the role of glucose metabolism block as a component of OGD action and
487 downstream effects (cell death and differentiation), we used the same tools of the OGD
488 experiments (3 hours followed by 24 hours of reperfusion). The effect of the different
489 treatments on cell metabolism was analyzed at intermediate stages of the
490 differentiation/maturation process, i.e. after the reperfusion phase (0 DIV; Figure 6 A, red
491 arrow) or in the middle of the differentiation phase (6 DIV; Figure 6 A, black arrow). Glucose
492 metabolism perturbation induced a reduction of cell number and an increase of cell death in
493 fetal cultures only. In particular, cell number was reduced at both time points in fetal cultures
494 (Figure 6 D; one-way ANOVA, 0 DIV, $F(3, 8) = 109.4$, $p < 0.0001$; 6 DIV, $F(3, 8) = 54.05$,
495 $p < 0.0001$) in cells exposed to GD (Sidak's post-test, 0 and 6 DIV, $p < 0.0001$) and 2-GD (0
496 and 6 DIV, $p < 0.0001$), while no effect was detected in fetal cultures treated with oligomycin
497 and in adult cultures in all the tested conditions (Figure 6 E).

498 Moreover, we detected cell death, expressed as percentage of condensed nuclei, in fetal
499 cultures only, at both time points (Figure 6 F; one-way ANOVA, 0 DIV, $F(2, 14) = 6.718$, p
500 $= 0.0005$; 6 DIV, $F(2, 14) = 0.3273$, $p = 0.0003$), but at 0 DIV only 2-DG treatment (i.e. the
501 glycolysis block) resulted in an increase in cell death (Sidak's post-test, $p = 0.0004$), while at
502 a late stage, both GD exposure and 2-DG treatment showed strong cell death induction
503 (Sidak's post-test, GD $p = 0.0107$, 2-DG $p = 0.0001$). As expected, treatments had no effect
504 on adult cultures (Figure 6 G).

505

506 To explore the down-stream effects of glucose metabolism perturbation in fetal cultures, we
507 analyzed apoptosis activation and OPC differentiation (Figure 7 A).

508 First, we analyzed the effect of GD on apoptosis by quantifying the percentage of cells
509 positive for cleaved caspase-3 following reperfusion (0 DIV). Cultures show an increase in

510 the percentage of cleaved-caspase 3 positive cells (Student's t-test, $p < 0.0001$; Figure 6 C-E),
511 proving that the absence of glucose induces apoptosis as soon as 24 hours later.

512

513 Keeping the focus on the mixed composition of the NSCs-derived OPCs cultures, we already
514 showed that only OPCs/OLs lineages are vulnerable to OGD insult. Thus, we quantified the
515 lineage-specific cell death also in GD, 2-DG and oligomycin exposed fetal cultures, showing
516 that at an intermediate time point in the differentiation phase (6 DIV) only OPCs are
517 vulnerable to glucose metabolism perturbation (Figure 7 E). In particular, only PDGF α R-
518 positive cells show vulnerability at 6 DIV (one-way ANOVA, $F(9, 32) = 52.87$, $p < 0.0001$)
519 only after GD and 2-DG exposure (Sidak's post-test, GD, $p < 0.0001$; 2-DG, $p < 0.0001$).

520 Finally, we analyzed the composition of the culture in the middle of the differentiation phase
521 (6 DIV; Figure 7 F-O) for OPCs (PDGF α R-positive cells), mature OLs (CNPase-positive
522 cells) and myelinating OLs (MBP-positive cells), in both GD-exposed and 2-DG treated
523 cultures. A decrease in the three cell populations (one-way ANOVA, PDGF α R, $F(2, 6)$, $p <$
524 0.0001 ; CNPase, $F(2, 6) = 0.4218$, $p = 0.0003$; MBP, $F(2, 6) = 4.602$, $p = 0.0021$) was
525 observed. In particular, the exposure to both challengers strongly decreases the PDGF α R
526 population (Sidak's post-test, GD, $p < 0.0001$; 2-DG, $p < 0.0001$; Figure 6 G-I), but also the
527 CNPase-positive (Sidak's post-test, GD, $p = 0.0237$; 2-DG, $p = 0.0002$; Figure 6 J-L) and
528 myelinating MBP-positive OL populations (Sidak's post-test; GD, $p = 0.0262$; 2-DG, $p =$
529 0.0015 ; Figure 6 M-O).

530

531 *3.7 OPCs derived from fetal NSCs are not able to react to OGD*

532

533 Once we had established that the different response to glucose metabolism perturbation of
534 mixed OPCs/astrocytes cultures may drive the selective vulnerability of fetal OPCs to OGD,
535 we investigated how fetal and adult cells respond to this challenge in terms of metabolic re-
536 adaptation. To do so, we used a PCR array® to analyze the main genes involved in glucose
537 metabolism in basal conditions and 24 hours after OGD exposure (0 DIV; Figure 8 A). In
538 particular, the array allows the analysis of 86 genes involved in different glucose-related
539 processes: glycolysis, gluconeogenesis, glucose metabolism regulation, the tricarboxylic acid
540 (TCA) cycle, the pentose phosphate pathway (PPP), glycogen synthesis, glycogen
541 degradation, and glycogen metabolism regulation (the full list of genes is reported in the
542 supplementary data, Table S1).

543 Following OGD and reperfusion/reoxygenation, the gene expression of fetal cells does not
544 change (Figure 8 B). On the other hand, adult cultures respond to OGD, increasing the
545 expression of 37 genes (Figure 8 C) related to glucose metabolism (Table 1).

546

547 **4. Discussion**

548

549 White matter injury is recognized as a major determinant in long-term outcome following
550 traumatic CNS and vascular lesions in both infancy and adulthood, impacting on axonal
551 integrity, function, and retrograde neuronal degeneration (Fern, Matute, & Stys, 2014),
552 making hypomyelinating and demyelinating white matter pathology a recognized target for
553 pharmacological intervention (Chew & DeBoy, 2016). OPCs, when differentiating into
554 mature/myelinating OLs in a T3-driven, synchronized process (Raff, Lillien, Richardson,
555 Burne, & Noble, 1988), are the cells responsible for both developmental myelination and
556 myelin turnover and repair during adulthood, leading to the hypothesis that myelin repair
557 “recapitulates” developmental myelination (Fancy et al., 2011).

558 The ability of OPCs to correctly establish or repair the myelin sheaths is severely impaired
559 during pathological conditions characterized by HI and severe inflammation both in
560 development and adulthood, OPCs and OLs being the most vulnerable cells in the CNS
561 (Bradl & Lassmann, 2010; Y. Lee et al., 2012). Moreover, oligodendroglial lineage
562 susceptibility to adverse stimuli is also dependent on developmental and maturation stage,
563 from early precursors to mature OLs (Amaral, Hadera, Tavares, Kotter, & Sonnewald, 2016),
564 and drug development strategy should be undertaken accordingly.

565 To investigate the vulnerability of fetal and adult OPCs to inflammation and HI, and the
566 effects of these challenges on cell survival, maturation and developmental myelination and/or
567 myelin repair, in this study we exposed fetal and adult OPCs to *in vitro* models of
568 inflammation and HI. To shed light on the entire differentiation/maturation window of these
569 cells, from multipotent NSCs through precursor (OPCs) to mature and myelinating OLs, we
570 differentiate OPCs from fetal and adult NSCs. This system allows the establishment of a
571 mixed cellular environment enriched in OPCs/OLs but keeping astrocytes (30-40%)
572 throughout the whole differentiation period, thus avoiding the bias of isolated OPCs.
573 Moreover, we monitored the effect of the tested stimuli also in the astrocytes.

574

575 We first demonstrated that no substantial differences are observed in vulnerability to cytokine
576 exposure in fetal and adult NSCs-derived OPCs. In particular, cytokine exposure during the

577 proliferative phase leads to an increased proliferation and a differentiation block in both fetal
578 and adult OPCs, as indicated by lineage progression marker analysis. Numerous *in vitro* and
579 *in vivo* studies have indicated that inflammatory cytokines promote OPC proliferation,
580 involving, among others, the VEGFR2 (Choi et al., 2018) and Notch pathways (Wang et al.,
581 2017). Inflammatory cytokines are also proved to be involved specifically in the
582 differentiation block of OPCs derived from the adult brain, affecting cell cycle exit and the
583 expression of genes encoding for proteins that regulate and determine remyelination (Chew,
584 King, Kennedy, & Gallo, 2005; Falahati et al., 2013; Kang et al., 2013; Su et al., 2011;
585 Tanner, Cherry, & Mayer-Pröschel, 2011). The most investigated example of the role of
586 inflammation in remyelination failure is MS, the most diffuse inflammatory/demyelinating
587 disease in humans (Goodin, 2014). In the acute focal phase of the disease, remyelination is
588 efficient (Rodgers, Robinson, & Miller, 2013), however this process fails progressively
589 (Boyd, Zhang, & Williams, 2013; Lassmann, van Horssen, & Mahad, 2012). The most
590 accredited hypothesis for remyelination failure is the block of OPC differentiation and
591 maturation into myelinating OLs (Kuhlmann et al., 2008; Miller & Mi, 2007), leading to
592 inefficient myelin repair (Zhang, Luo, Wu, & Xu, 2015). We have previously demonstrated
593 that a complex dysregulation of TH tissue signaling is present in experimental CNS
594 inflammation/demyelination models (experimental allergic encephalomyelitis in rodents and
595 non-human primates) (D'Intino et al., 2011; Dell'Acqua et al., 2012; Fernández et al., 2016),
596 which correlates with the rise of inflammatory cytokines released by peripheral cells and
597 resident microglia (Borjini, Fernández, Giardino, & Calzà, 2016). This pathological feature is
598 causally linked to an increase in D3-positive cells and D3 expression both *in vivo* and *in vitro*,
599 causing the inactivation of T3 and subsequent OPC differentiation block. This hypothesis has
600 been confirmed by *in vitro* studies of our group, in which we demonstrated that the inhibition
601 of D3 restores OPC differentiation during exposure to the inflammatory cytokine cocktail
602 (Fernández et al., 2016). An increase in D3 activity and mRNA expression level has been also
603 described in other neurological conditions characterized by inflammation and demyelination,
604 e.g. ischemia-induced hypoxic brain damage (Jo et al., 2012) and nerve lesion (Li et al.,
605 2001).

606

607 While inflammation evokes the same cellular outcome in both fetal and adult OPCs, blocking
608 the differentiation process, here we demonstrated that fetal and adult OPCs substantially
609 differ in vulnerability to OGD. In adult cultures, 3 hours of OGD applied 24 hours prior to the
610 T3-mediated differentiation does not affect the cell death (nuclear condensation) or

611 differentiation process. In contrast, in fetal cultures we observed an increase in cell death, a
612 reduction in cell number, and impaired differentiation of surviving cells. Notably, OGD-
613 induced cell death is selective for OPC/OL lineage, not affecting the astrocyte population.
614 The effect of OGD on OPC maturation seems to be stage-dependent, PreOLs (late OPCs)
615 being the most susceptible cells, followed by early OPCs and mature OLs. This *in vitro* result
616 corresponds to *in vivo* studies, where the death of PreOLs and the OPC differentiation block
617 in the pre-myelinating and immature state are indicated as responsible for the subsequent
618 failure of myelination in neonatal encephalopathy and related animal models (Back et al.,
619 2002).

620 Notably, in both inflammation and OGD-induced differentiation block, the whole lineage is
621 perturbed, as indicated by the presence of cells that are negative to all the tested lineage
622 markers, and cells that co-express OPCs/OLs markers. This is probably due to the fact that
623 OLs-specific markers identification is not a black-or-white system, but lineage antigens
624 expression and disappearance overlaps in the maturation steps (Silbereis, Huang, Back, &
625 Rowitch, 2010).

626

627 Having described the fetal-selective vulnerability of OPCs to OGD, we then investigated the
628 main components that may be implicated in this selective cell death and differentiation
629 impairment.

630 First, since OPC differentiation is a T3-driven process, we investigated intracellular T3
631 metabolism. In fact, as already described for inflammation mediated-differentiation block, an
632 appropriate T3 intracellular concentration and signaling in OPCs is mandatory for proper
633 OPC differentiation into myelinating OLs (Calzà et al., 2018; J. Y. Lee & Petratos, 2016).
634 The most remarkable demonstration of this is observed in Allan-Herndon-Dudley syndrome,
635 due to a mutation of the TH cell membrane transporter MCT8, characterized by impaired OL
636 maturation, hypo/dis-myelination and mental retardation (La Piana, Vanasse, Brais, &
637 Bernard, 2015). The causal role of the inappropriate intracellular T3 content on OPC
638 differentiation block has been also demonstrated by the *in vitro* manipulation of the MCT8
639 transporter in human embryonic stem cell-derived OLs (J. Y. Lee et al., 2017). In this study,
640 we demonstrated that as well as inflammatory cytokine exposure, OGD also generates an
641 increase in the percentage of D3-positive cells, suggesting a perturbation of T3-mediated OPC
642 differentiation. As expected, the pharmacological inhibition of D3 by IOP favors OPC
643 maturation in normoxia, as indicated by the increased percentage of MBP-positive cells, but is

644 unable to restore OL differentiation following OGD, in contrast to the positive results
645 obtained in adult OPCs exposed to cytokines (Fernández et al., 2016).

646 These results indicated that, even if a perturbation of T3-mediated differentiation may occur
647 in OPCs exposed to OGD, the restoration of a suitable T3 level by D3 inhibition is not
648 enough to rescue OPC differentiation. However, we cannot exclude that a long-lasting TR
649 perturbation also occurs in the experimental conditions used in this study.

650

651 We then explored alternative mechanisms to explain the selective sensitivity of fetal OPCs to
652 OGD. Extensive literature points to the role of glutamate receptor overactivation in HI-
653 induced cell death. In particular, AMPA/kainite, but not NMDA receptors, have been
654 considered the mediator of glutamate excitotoxicity in glial cells (Tekkök & Goldberg, 2001),
655 in particular in the glutamate-mediated cell death of preOLs during HI (Deng, Yue,
656 Rosenberg, Volpe, & Jensen, 2006).

657 We then tested glutamate and NMDA treatment in fetal OPCs in normoxia. The cell system
658 resulted as being partially sensitive to glutamate, which reduces cell number without inducing
659 cell death. On the contrary, exposure to NMDA is ineffective. We then used specific NMDA
660 and AMPA inhibitor (MK801 and NBQX respectively) treatments to interfere with potential
661 glutamate excitotoxicity during OGD, showing that OGD-mediated cell death is not rescued
662 by MK801 and NBQX treatments. This data suggests that in a complex system, consisting of
663 OPCs and astrocytes, OGD is able to evoke oligodendroglial specific cell death, which is not
664 mediated by glutamate release and excitotoxicity. A different expression of NMDA receptors
665 during the differentiation process may explain the different sensitivity to glutamate at
666 different stages. In particular, OPCs show a high expression of the AMPA/kainite receptor
667 mGluR, while postmitotic OLs have high NMDA receptor expression (Butts, Houde, &
668 Mehmet, 2008). Therefore, we cannot exclude that a different exposure scheme targeting
669 OPCs at a different maturation stage might result in a different sensitivity to glutamate
670 excitotoxicity.

671

672 Finally, we hypothesized that a different metabolic profile might drive the different
673 vulnerability to OGD of fetal compared to adult OPCs/astrocytes mixed cultures. In fact,
674 previous studies from other groups have described that OLs at late differentiation stages
675 avidly metabolize glucose and pyruvate derived from glucose, also demonstrating a high
676 degree of cellular independence (Amaral et al., 2016). We decided to perform also these
677 experiments using OPCs/astrocytes mixed cultures, and not isolated OPCs and astrocytes,

678 because of the importance of the metabolic cross-talk between OPCs and astrocytes (Kıray,
679 Lindsay, Hosseinzadeh, & Barnett, 2016). In the balance between losing the cell-specificity of
680 the metabolism information, and the bias derived from isolating a single cell type which
681 implies the risk of producing inconsistent results because of the metabolic modifications
682 induced by the procedure itself, we considered that mixed cultures derived from neurospheres
683 were more appropriate for the aim of the study.

684 Here we first demonstrated that fetal and adult NSC-derived OPCs/astrocytes mixed cultures
685 differ in their metabolism in basal conditions. In particular, glycolysis within fetal mixed
686 OPC-astrocyte preparations is crucial to ensure OPC survival, which is not the case in adult
687 cultures. In fact, even if we cannot discern the cell type producing or not lactate in the mixed
688 cultures, fetal cells do not increase lactate levels when exposed to OXPHOS block, showing
689 that both fetal OPCs and astrocytes are at the maximum level of glycolysis activity. This may
690 explain the death of fetal OPCs during glucose depletion, while adult OPCs are not sensitive
691 to this insult. A limitation of this result is that we cannot identify if the fetal OPCs death is
692 directly linked to glucose deprivation, or indirectly related to the astrocytes metabolism
693 perturbation. However, the goal of the study is to investigate the vulnerability of the OPC/OL
694 lineage cells, always taking into account the astrocytic component of the culture. In fact,
695 using the cell-based HCS, and as already described for OGD experiments, we are able to
696 discriminate the lineage-specific cell death and differentiation. As we described in long term
697 cultures (12 DIV) after OGD exposure, both OPCs and OLs are sensitive to the noxious
698 stimulus, as indicated by increased cell death. In the middle term cultures (6 DIV) cell death
699 is restricted to OPCs after glucose metabolism perturbation, probably for the low percentage
700 of mature OLs at this time point.

701 Interestingly the astrocytic component of the culture is sensitive to cytokine mix in term of
702 differentiation, while OGD or glucose metabolism are ineffective neither in cell survival nor
703 differentiation. Due to the complex metabolic crosstalk between astrocytes, OPCs and OLs
704 (Kıray et al., 2016) future studies are needed to discern the respective roles during metabolic
705 disturbance.

706 Moreover, glucose metabolism perturbation in the OPCs/astrocytes mixed cultures, when
707 cells are still precursors, results in impaired differentiation of fetal OPCs, something which
708 could potentially lead to long-term effects. Even if in our model we cannot selectively study
709 the OPCs metabolism, the fundamental role of glycolysis has been already observed in human
710 primary OPCs/OLs, with a higher susceptibility of precursors to glucose metabolism
711 perturbation (Rone et al., 2016). Not only energy metabolism, but also the significant

712 reduction in lactate production itself, by OPCs and/or astrocytes, observed following GD or in
713 response to 2-DG, may underlie the vulnerability of OPCs, particularly in terms of
714 differentiation. In fact, lactate itself induces the cell cycle, differentiation/myelination,
715 reduces cell death in OPCs (Ichihara et al., 2017), and has been described as fundamental for
716 developmental myelination (Rinholm et al., 2011). More generally, it is well-known that low
717 oxygen tension, by shifting the cell metabolism towards anaerobic glycolysis, enhances
718 pluripotency-related gene expression, including Wnt (De Miguel, Alcaina, de la Maza, &
719 Lopez-Iglesias, 2015), which arrests OPC differentiation (Yuen et al., 2014).

720

721 All these experiments from other groups contribute to indicating a primary role of glucose
722 metabolism in fetal-derived OPCs, pointing to this intrinsic characteristic as the main culprit
723 behind the selective OGD-induced noxious effect. Given that the different basal metabolism
724 of the mixed system may result in the different vulnerability to OGD of OPCs, finally we
725 analyzed the expression of the main genes related to glucose metabolism in fetal and adult
726 OPCs/astrocytes mixed cultures in normoxia or following OGD. Notably, OGD alters the
727 gene expression profile in adult cultures only, increasing the expression level of genes
728 involved in glycolysis, the regulation of glucose metabolism, the TCA cycle, PPP, glycogen
729 synthesis, glycogen degradation, and glycogen metabolism. This gene expression regulation
730 indicates that adult OPCs/astrocytes mixed cultures exposed to OGDs are able to regulate
731 glycolysis, as was expected, but that they also fuel production from alternative substrates,
732 such as glycogen, necessary for OPC survival and differentiation (Ichihara et al., 2017).

733

734 In conclusion, we demonstrated that OPCs derived from NSCs from the fetal forebrain and
735 from the adult SVZ are differentially vulnerable to challenges mimicking pathogenic
736 mechanisms in inflammatory and vascular diseases, thus supporting the view that drug
737 development strategies for myelination/remyelination enhancing therapies must be selectively
738 designed for neonatal and adult demyelinating diseases and lesions.

739

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747

748 **Conflict of interests**

749

750 All the authors have no conflict of interest to declare in respect of the manuscript contents.

751

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1000
1001

1002 **Legend to table and figures.**

1003

1004 *Table 1. Mouse Glucose Metabolism PCR array analysis*

1005

1006 The table shows the Gene Bank code, gene symbols, gene names and fold of increase in OGD

1007 vs normoxia of all modified genes in adult OPC cultures.

1008

1009 *Figure 1. Experimental design*

1010

1011 (A) Following NSC isolation and neurosphere expansion, in the presence of bFGF and EGF,

1012 oligospheres were generated by spheroid disaggregation and bFGF/PDGF exposure.

1013 Oligospheres were then dissociated and single cell cultures seeded in the same medium. After

1014 3 DIVs, the medium was changed and the cells were exposed to T3 for 12 DIVs to induce

1015 differentiation.

1016 (B-D) Representative images of culture progress from OPCs (NG2-positive cells, 0 DIV, B),

1017 through mature OLs (CNPase-positive cells, 6 DIV, C) to mature/myelinating OLs

1018 (CNPase/MBP-positive cells, 12 DIV, D).

1019 *Abbreviations: CNPase, 2',3'-cyclic nucleotide 3'-phosphodiesterase; MBP, myelin basic*

1020 *protein; NG2, chondroitin sulphate proteoglycan, neural/glia antigen 2.*

1021

1022 *Figure 2. The effect of cytokine exposure effect on viability and differentiation in fetal and*

1023 *adult NSCs-derived OPCs.*

1024

1025 (A) Experimental design. Cells were exposed to cytokine mix during the oligosphere

1026 proliferation phase. Three days after cell seeding, differentiation was induced by T3 exposure.

1027 Cells were analyzed at the end of the differentiation phase (black arrow, 12 DIV).

1028 (B) Graph shows the cell number (total cell number per well) and cell death (percentage of

1029 cells showing condensed nuclei on total number of cells per well) measured at the end of the

1030 differentiation phase (12 DIV), in fetal cultures exposed to vehicle or cytokine mix.

1031 (C) Graph shows the cell number (total cell number per well) and cell death (percentage of

1032 cells showing condensed nuclei on total number of cells per well) measured at the end of the

1033 differentiation phase (12 DIV), in adult cultures exposed to vehicle or cytokine mix.

1034 (D) Graph shows the percentage of lineage-specific positive cells at the end of the
1035 differentiation phase (12 DIV) in fetal cultures, exposed to vehicle or cytokine mix. The
1036 percentage of OPCs (NG2-positive cells), mature OLs (CNPase-positive cells), myelinating
1037 OLs (MBP-positive cells), and astrocytes (GFAP-positive cells) was calculated on the total
1038 cell number per well, showing a normal nuclear morphology.

1039 (E) Graph shows the percentage of lineage-specific positive cells at the end of the
1040 differentiation phase (12 DIV) in adult cultures, exposed to vehicle or cytokine mix. The
1041 percentage of OPCs (NG2-positive cells), mature OLs (CNPase-positive cells), myelinating
1042 OLs (MBP-positive cells), and astrocytes (GFAP-positive cells) was calculated on the total
1043 cell number per well, showing a normal nuclear morphology.

1044 (F-M) Images show CNPase-positive (F, J, H, L) and MBP-positive cells (G, K, I, M)
1045 detected in fetal (F, G, J, K) and adult (H, I, L, M) cultures exposed to vehicle (F-I) or
1046 cytokine mix (J-M). White bar in image L: 50 μ m.

1047 Bars represent mean value + SEM. Statistical analysis: Student's t-test; * $p < 0.05$, ** $p <$
1048 0.01 , *** $p < 0.001$, **** $p < 0.0001$.

1049 *Abbreviations: CNPase, 2',3'-cyclic nucleotide 3'-phosphodiesterase; GFAP, Glial fibrillary*
1050 *acidic protein; MBP, myelin basic protein; NG2, chondroitin sulphate proteoglycan,*
1051 *neural/glial antigen 2.*

1052

1053 *Figure 3. OGD effect on viability of fetal and adult NSCs-derived OPCs*

1054

1055 (A) Experimental design. Cells were exposed to 3 hours OGD, followed by 24 hours of
1056 reoxygenation, one day prior to T3-mediated differentiation induction.

1057 (B) Graph shows the cell number (total cell number per well) and cell death (percentage of
1058 cells showing condensed nuclei on total number of cells per well) measured at the end of the
1059 differentiation phase (12 DIV), in fetal cultures exposed to normoxia or OGD.

1060 (C) Graph shows the cell number (total cell number per well) and cell death (percentage of
1061 cells showing condensed nuclei on total number of cells per well) measured at the end of the
1062 differentiation phase (12 DIV), in adult cultures exposed to normoxia or OGD.

1063 (D) Graph shows the percentage of lineage specific positive cells at the end of the
1064 differentiation phase (12 DIV), in fetal cultures exposed to normoxia or OGD. The percentage
1065 of OPCs (NG2-positive cells), mature OLs (CNPase-positive cells), myelinating OLs (MBP-
1066 positive cells), astrocytes (GFAP-positive cells) and neurons (beta-III-tubulin), was calculated
1067 on the total cell number per well, showing a normal nuclear morphology.

1068 (E) Graph shows the percentage of lineage-specific positive cells at the end of the
1069 differentiation phase (12 DIV), in adult cultures exposed to normoxia or OGD. The
1070 percentage of OPCs (NG2-positive cells), mature OLs (CNPase-positive cells), myelinating
1071 OLs (MBP-positive cells), astrocytes (GFAP-positive cells) and neurons (beta-III-tubulin),
1072 was calculated on the total cell number per well, showing a normal nuclear morphology.

1073 (F) Graph shows the percentage of lineage-specific positive cells which also show condensed
1074 nuclei, at the end of the differentiation phase (12 DIV), in fetal cultures exposed to normoxia
1075 or OGD. The percentage of OPCs (NG2-positive cells), mature OLs (CNPase-positive cells),
1076 myelinating OLs (MBP-positive cells), astrocytes (GFAP-positive cells) and neurons (beta-
1077 III-tubulin), was calculated on the total cell number per well, showing a normal nuclear
1078 morphology.

1079 (G) Graph shows the percentage of lineage-specific positive cells which also show condensed
1080 nuclei, at the end of the differentiation phase (12 DIV), in adult cultures exposed to normoxia
1081 or OGD. The percentage of OPCs (NG2-positive cells), mature OLs (CNPase-positive cells),
1082 myelinating OLs (MBP-positive cells), astrocytes (GFAP-positive cells) and neurons (beta-
1083 III-tubulin), was calculated on the total cell number per well, showing a normal nuclear
1084 morphology.

1085 (H-O) Images show NG2-positive (H, L, J, N) and CNPase/MBP-positive cells (I, M, K, O)
1086 detected in fetal (H, I, L, M) and adult (J, K, N, O) cultures exposed to normoxia (H-K) or
1087 OGD (L-O). White bar in image J: 50 μ m.

1088 Bars represent mean value + SEM. Statistical analysis: Student's t-test; ** $p < 0.01$; *** $p <$
1089 0.001 , **** $p < 0.0001$.

1090 *Abbreviations: CNPase, 2',3'-cyclic nucleotide 3'-phosphodiesterase; GFAP, Glial fibrillary*
1091 *acidic protein; MBP, myelin basic protein; NG2, chondroitin sulphate proteoglycan,*
1092 *neural/glia antigen 2; OGD, oxygen-glucose deprivation.*

1093

1094 *Figure 4. Role of D3 induction in OGD-mediated differentiation impairment in fetal NSC-*
1095 *derived OPCs*

1096

1097 (A) Experimental design. Fetal cultures were exposed to 3 hours OGD, followed by 24 hours
1098 of reoxygenation, one day prior to T3-mediated differentiation induction. During OGD
1099 exposure and the entire differentiation phase, cells were exposed to vehicle or IOP.

1100 (B) Graph shows the percentage of D3-positive cells following OGD/reoxygenation exposure
1101 (DIV 0).

1102 (C-D) Images show D3-positive cells following normoxia (C) or OGD/reoxygenation (D)
1103 exposure (DIV 0). White bar in image H: 50µm.

1104 (E) Graph shows the percentage of D3, CNPase and MBP-positive cells at the end of the
1105 differentiation phase (12 DIV).

1106 Bars represent mean value + SEM. Statistical analysis: One-way ANOVA followed by
1107 Tukey's post-test * $p < 0.05$; **** $p < 0.0001$.

1108 *Abbreviations: CNPase, 2',3'-cyclic nucleotide 3'-phosphodiesterase; D3, deiodinases 3;*
1109 *MBP, myelin basic protein; OGD, oxygen-glucose deprivation.*

1110

1111 *Figure 5. Role of glutamate excitotoxicity in OGD-mediated cell death in fetal NSCs-derived*
1112 *OPCs*

1113

1114 (A) Experimental design. Fetal cultures were exposed to 3 hours OGD, followed by 24 hours
1115 of reoxygenation or to 3 hours of glutamate (1mM) or NMDA (1mM), prior to T3-mediated
1116 differentiation induction. During OGD, glutamate or NMDA exposure and the entire
1117 differentiation phase, cells were exposed to vehicle, MK801 or NBQX.

1118 (B) Graph shows the cell number at the end of the differentiation phase (12 DIV), in cells
1119 exposed to normoxia, OGD, glutamate and NMDA and treated or not with MK801 or NBQX.
1120 Bars represent the total cell number per well.

1121 (C) Graph shows the cell death at the end of the differentiation phase (12 DIV), in cells
1122 exposed to normoxia, OGD, glutamate and NMDA, and treated or untreated with MK801 or
1123 NBQX. Bars represent the percentage of cells showing condensed nuclei, on the total number
1124 of cells per well.

1125 Bars represent mean value + SEM. Statistical analysis: One-way ANOVA followed by
1126 Tukey's post-test * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

1127 *Abbreviations: Glut, glutamate; OGD, oxygen-glucose deprivation.*

1128

1129 *Figure 6. Effect of glucose metabolism perturbation in fetal and adult NSC-derived OPCs*

1130

1131 (A) Experimental design. Fetal and adult cultures were exposed to 24 hours of GD, 2-DG or
1132 oligomycin treatment to analyze lactate production. In another set of experiments, cells were
1133 exposed to 3 hours GD, 2-DG or oligomycin treatment, followed by 24 hours of reperfusion,
1134 prior to T3-mediated differentiation induction.

1135 (B-C) Graph shows the relative quantification of lactate production following 24 hours of
1136 GD, 2-DG or oligomycin treatment, compared to standard culture conditions (100%) in fetal
1137 (B) and adult (C) cultures.

1138 (D-E) Graph shows the cell number at the beginning (0 DIV) and the middle (6 DIV) of the
1139 differentiation phase, in fetal (D) and adult € cultures exposed to standard conditions, GD, 2-
1140 DG or oligomycin treatment.

1141 (F-G) Graph shows the cell death at the beginning (0 DIV) and the middle (6 DIV) of the
1142 differentiation phase, in fetal (F) and adult (G) cultures exposed to standard conditions, GD,
1143 2-DG or oligomycin treatment. Bars represent the percentage of cells showing condensed
1144 nuclei, on the total number of cells per well.

1145 Bars represent mean value + SEM. Statistical analysis: One-way ANOVA followed by
1146 Dunnet's post-test * $p < 0.05$; *** $p < 0.001$; **** $p < 0.0001$.

1147 *Abbreviations: 2-DG, 2-deoxy-D-glucose; GD, glucose deprivation; olig, oligomycin.*

1148

1149

1150 *Figure 7. Effect of glucose metabolism perturbation in fetal NSC-derived OPC differentiation*

1151

1152 (A) Experimental design. Fetal cultures were exposed to 3 hours GD or 2-DG treatment,
1153 followed by 24 hours of reperfusion, prior to T3-mediated differentiation induction.

1154 (B) Graph shows the percentage of cleaved-caspase 3 positive cells following GD exposure (0
1155 DIV).

1156 (C-D) Images show cleaved-caspase 3 staining in cultures exposed to standard conditions
1157 (Ctrl; C) or GD (D). White bar in image E: 50µm.

1158 (E) Graph shows the percentage of lineage-specific positive cells which also show condensed
1159 nuclei, at the middle of the differentiation phase (6 DIV), in fetal cultures exposed to standard
1160 condition, GD, 2-DG or oligomycin treatment. The percentage of OPCs (PDGFαR-positive
1161 cells), mature OLs (CNPase-positive cells), myelinating OLs (MBP-positive cells) and
1162 astrocytes (GFAP-positive cells), was calculated on the total cell number per well showing a
1163 normal nuclear morphology.

1164 (F) Graph shows the percentage of lineage-specific positive cells in the middle of the
1165 differentiation phase (6 DIV) in cultures exposed to standard conditions, GD or 2-DG
1166 treatment. The percentage of OPCs (PDGFαR-positive cells), mature OLs (CNPase-positive
1167 cells) and myelinating OLs (MBP-positive cells) was calculated on the total cell number per
1168 well, showing a normal nuclear morphology.

1169 (G-O) Images show PDGF α R (G-I), CNPase (J-L) and MBP-positive (M-O) cells detected in
1170 fetal cultures exposed to standard conditions (Ctrl; G, J, M), GD (H, K, N) or 2-DG treatment
1171 (I, L, O). White bar in image J: 50 μ m.

1172 Bars represent mean value + SEM. Statistical analysis: Student t-test (B) or one-way ANOVA
1173 followed by Sidak's post-test (E, F) * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

1174 *Abbreviations: 2-DG, 2-deoxy-D-glucose; CNPase, 2',3'-cyclic nucleotide 3'-*
1175 *phosphodiesterase; GD, glucose deprivation; MBP, myelin basic protein; PDGF α R, platelet*
1176 *derived growth factor alpha receptor.*

1177

1178 *Figure 8. Effect of OGD on glucose metabolism-related gene expression in fetal and adult*
1179 *NSC-derived OPCs.*

1180

1181 (A) Experimental design. Cells were exposed to 3 hours OGD, followed by 24 hours of
1182 reperfusion/reoxygenation, one day prior to T3-mediated differentiation induction.

1183 (B-C) Representation of gene expression changes in fetal (B) and adult (C) OPC cultures.

1184 Graphs represent the fold of change of expression of all the analyzed genes in OGD vs.
1185 normoxia groups.

1186 *Abbreviations: OGD, oxygen-glucose deprivation.*