Genomic Profiling of Primary Diffuse Large B-Cell Lymphoma of the Central Nervous System Suggests Novel Potential Therapeutic Targets

Genomic profiling of CNS-DLBC suggests novel potential therapeutic targets.

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ABSTRACT

Primary diffuse large B-cell lymphoma of the CNS (CNS-DLBCL) is an aggressive disease, with dismal prognosis despite the use of high dose methotrexate (MTX)-based polychemotherapy. Our study aimed to expand the biologic profiles of CNS-DLBCL and to correlate them with clinical/imaging findings to gain diagnostic insight and possibly identify new therapeutic targets. We selected 61 CNS-DLBCL whose FFPE samples at first diagnosis were available. These were investigated by immunohistochemistry, cMYC rearrangements were explored by fluorescence in situ hybridization and CNS-DLBCL mutated genes were evaluated by Next Generation Sequencing. CD10, BCL6 and IRF4 were observed in 16%, 83.6% and 93% of cases respectively. As typical of CNS-lymphoma 10/61 (16.4%) cases were classified as germinal center (GCB) and type and 51/61 (83.6%) as non-germinal center (non-GCB) type according to the Hans algorithm. Double expression (DE) status for BCL2 and cMYC was detected in 36/61 (59%) cases while 25/61 (41%) were non DE. Rearrangement of the *cMYC* gene was detected in 2 cases, associated with *BCL6* translocation only 1 case. *MYD88, PIM1*, *CD79B* and *TP53* were mutated in 54.5%, *53.5%*, 30.2% and 18.4% cases respectively. Novel mutations not previously reported in CNS-DLBCL were found: *AIP* in 23,1%, *PI3KCA* in 15%, *NOTCH1 in* 11,4%, *GNAS* 8.1%, *CASP8 in* 7.9%, *EGFR* in 6.4% *PTEN* in 5.1 and *KRAS* in 2.6%. Survival was significantly longer for patients with mutated *MYD88* (8.7 months vs. 1.7 months; log-rank test = 5.43; p = 0.020) and for patients with mutated *CD79B* (10.8 months vs. 2.5 months; log-rank test = 4.64; p = 0.031).*MYD88* and *CD79B* predicted a longer survival in patients affected by CNS-DLBCL. Notably, we identified novel mutations that enrich mutational landscape of CNS-DLBCL, suggest a role of PTEN-PI3K-AKT and RTK-RAS-MAPK signalling in a subset of CNS-DLBCL and provide new potential therapeutic targets.

Introduction

Diffuse large B cell lymphoma of the primary central nervous system (CNS-DLBCL) accounts for <3% of brain tumor with a peak incidence between the 5th and 6th decade[1]. The most frequent (60%) localization is the supra-tentorial frontal region. Ocular lesions develop concurrently in 20% of patients,[1,2] while extra-neural dissemination is rare.[1,3] CNS-DLBCL lesions may be single or multiple, with distinct margins or poorly defined with diffuse parenchyma infiltration .[1] The neoplastic population consists of medium/large proliferating blasts, with a mature B phenotype.[1] Most CNS-DLBCL are $BCL6^+/IRF4^+$ and[1,4] approximately 80% of CNS-DLBCL are $BCL2^+/cMYC^+$ (double expressors), a protein profile that confers poor clinical prognosis; double-hit or triple-hit high grade B-cell lymphomas, with MYC and BCL2 and/or BCL6 rearrangements, are rare.[5,6] Despite high-dose polychemotherapy and methotrexate (MTX), the prognosis remains poor, with a median overall survival (OS) of about 3 years and a median progression free survival (PFS) of 12 months.[7] At the bio-pathological level, proliferation and survival of the neoplastic clones are supported by the constitutive activation of the B-cell receptor (BCR), Toll-like receptor (TLR) and NF-kB signaling pathways caused by mutations of *MYD88* and/or *CD79B*.[1] Recently, the landscape of recurrent genetic drivers in DLBCL has been expanded by Schmitz G et al and Chapuy B et al. that uncovered genetic subtypes of DLBCL with distinct clinical characteristics, providing a potential nosology for precision-medicine strategies in DLBCL.[8,9] These subtypes showed distinct outcomes after immunochemotherapy with the potential to affect the selection of targeted therapies owing to their distinct oncogenic abnormalities. Wright et al revealed a high prevalence of the sub-type termed MCD (based on the co-occurrence of *MYD88* p.L265P and *CD79B* mutations) in primary CNS-DLBCL, defined by gene aberrations involving *MYD88*, *CD79B* and *PIM1*.[10] Their combined genetic, phenotypic, functional, and clinical data suggest that MCD-subtype may be sensitive to BTK, PI3K, BET, BCL2, and JAK inhibitors.[11]

Despite all attempts, the prognosis of CNS-DLBCL remains poor and new therapeutic approaches are needed to improve patient survival. With this background, our aim was to characterize and

105 correlate the biologic profiles CNS-DLBCL to clinical findings and explore new potential
106 therapeutic targets.

107 **Methods**

108 *Patients' selection and tumour samples collection.* From the review of the medical records of the
109 Department of Neurosurgery of IRCCS Istituto Delle Scienze Neurologiche, Bologna, we identified
110 107 pathologically confirmed cases of CNS-DLBCL diagnosed between 2005 and 2020. Of those,
111 sixty-one cases with formalin fixed paraffin embedded (FFPE) adequate material were included in
112 the study. The study was approved by local ethics committee (620/2020/OSS/AUSLBO) and it was
113 performed in accordance with the Declaration of Helsinki. Thirty patients (49.2%) were male and
114 31 females (50.8%), with an age range between 32 and 82 years and a median age of 66 years (IQR:
115 57–72).

116 *Immunohistochemistry.* Paraffin-embedded sections were deparaffinized in HistoClear and
117 dehydrated through graded ethanol. The antigen retrieval was performed in the PT-Link (Agilent
118 Dako, Santa Clara, CA, USA, code PT100/ PT 101), for 5 min at 92°C in EnVision Flex Target
119 retrieval solution High pH (Agilent Dako, code K 8004). Then, tissue samples were incubated at RT
120 for 30 minutes with the following antibodies: CD20 (Agilent Dako 1:300, clone L26, code M0755),
121 CD10 (Leica NewCastle, UK, 1:30, clone 56C6 code CD10-270-L), BCL2 (Abcam, Cambridge ,
122 UK, 1:100, clone E17, code Ab32124), BCL6 (kindly provided by Prof. Falini, indiluted, clone PG-
123 B6p), cMYC (Epitomics, Burlingame, CA 1:80, clone Y69, code 1472-1,), IRF4 (kindly provided
124 by Prof. Falini, 1:3, clone IRF4). Immunostaining has been completed using the Alkaline REAL
125 Detection System Alkaline Phosphatase/RED Rabbit/Mouse (Agilent Dako, code K5005) and
126 chromogen (Fast red), provided with the kit. Finally, slides were counterstained with Hematoxylin,
127 mounted in Glycerine and observed and analysed by Olympus microscope. Slides were observed by
128 2 expert pathologists (CA, SA). Results were recorded as percentage of positive cells and graded as
129 follows: + if >30% positive neoplastic cells, for CD10/BCL6/IRF4 according to Hans' algorithm.

130 [11] A case was defined as cMyc or BCL2 positive if ≥40% and ≥50% cells were stained
131 respectively.[6]
132 *Genetic analysis.*
133 *Fluorescence in situ hybridization (FISH).* Paraffin embedded tissue were deparaffinized and then
134 pre-treated with two different antigen retrievals. The slides were before incubated in 1mM EDTA
135 buffer (pH 8) in a pressure cooker (9 minutes) and after in Pepsin solution (Sigma Aldrich code
136 P7012) for 14 minutes at 38°C [12]. The probes and the samples were denatured at 80 °C for 22 min
137 and then hybridizated at 38°C for 22 hours in a hybridizer (Agilent Dako, Santa Clara, CA USA).
138 The experiments were conducted using the probes LSI MYC Dual Color Break Apart
139 Rearrangement (Vysis, Abbott, Downers Grove, Illinois, USA, code 01N63-020, cut-off 3,8%), LSI
140 BCL2 Dual Color Break Apart Rearrangement (Vysis Abbott, code 05N51-020, cut-off 4,7%) and
141 LSI BCL6 dual color Break apart Rearrangement t(3q27) (Vysis Abbott, code 01N23-020, cut off
142 5,5%). Following a stringency washes (0,4XSSC/0,03%NP-40 pH 7,4 solutions at 73°C for 2 min
143 and with 2XSSC/0,1% NP-40 pH 7 solutions at room temperature for 1 min), the slides were
144 mounted and counterstained with DAPI I (Vysis Abbott, code 06J49-001). Microscopical analysis
145 were carried out with an Olympus BX61 microscope and images were recorded using the Cell^F
146 program. *BCL6* and *BCL2* rearrangements were investigated only in cases with translocation of the
147 *cMYC* gene.
148 *Next Generation Sequencing*. DNA from FFPE PCNSL tissue samples was purified by Quick
149 Extract FFPE DNA Extraction Kit (Epicentre, Madison, WI) with some modifications described by
150 Ricci C et al.[13] DNA mutations were detected using the protocol described previously[14] analysing
151 the following gene panel: *MYD88, CD79B, PIM1, GNAS, NOTCH1, KRAS, PIK3CA, EGFR,*
152 *CASP8, AIP, PTEN*. In brief, after target enrichment by multiplex PCR, libraries with tagged
153 primers were generated using Nextera adapters. Each run on MiSEQ platform (Illumina, Palo Alto,
154 CA) was designed to allocate at least 2K reads/region aimed to have a depth of coverage of at least
155 2000×. FASTQ files were filtered with PHRED quality score > Q30 and length > 100 bp, and reads

156 were mapped in a Galaxy Project environment to the hg38 human reference genome with BWA-
157 MEM, GATK local realignment, HaplotypeCaller and Picard MarkDuplicates.[15] The BAM files
158 were visualized using the Integrative Genomic Viewer (IGV) to identify mutations with Variant
159 Allele Frequency (VAF) of at least 10%; only bidirectional variant calls with more than 10 reads
160 were reported. [15] Next generation sequencing analysis was available in 46 cases, as fifteen FFPE
161 specimens were over-fixed and not amplifiable. Protein sequence and functional information were
162 obtained by Uniprot database.

163 *Statistical analysis.* Demographic and clinical features were described using absolute frequencies
164 and percentages for categorical variables, mean and standard deviation for quantitative symmetrical
165 variables or median and interquartile range (IQR) for quantitative asymmetrical variables. The
166 associations between immunohistochemistry and radiology, between immunohistochemistry and
167 mutated genes, and between radiology and mutated genes were investigated using the $\chi 2$ test, or
168 Exact Fisher's test when expected cell count is less than 5. The Kaplan–Meier product limit was
169 used to estimate the overall survival (OS) curve. Differences in survival between subgroups were
170 assessed with the log-rank test. Statistical analysis was performed with IBM SPSS version 25.0 and
171 Stata 13. The significance level was set at $p<0.05$.

172 **Results**

173 *Phenotypic profile.* By immunohistochemistry, diffuse and strong expression of CD20 characterized
174 all 61 (100%) samples. CD10, BCL6 and IRF4 were observed in 10 (16%), 51 (83.6%) and 57
175 (93%) of 61 cases respectively. As typical of CNS-lymphoma 10 of 61 (16.4%) cases were
176 classified as GCB type and 51/61 (83.6%) as non-GCB type according to the Hans algorithm.
177 BCL2 and cMYC proteins were expressed in 51 (83.6%) and 41 (67.2%) of 61 samples
178 respectively. Double expression (DE) status for BCL2 and cMYC was detected in 36 (59%) cases
179 while 25 (41%) were non DE. The immunohistochemical data is summarized in Table 1.

180 *Fish analysis.* FISH analysis was successful in 59 of 61 (96.7%) samples; *cMYC* rearrangements
181 were present in 2 (3.4%) of 59 cases and in one was associated to *BCL6* translocation. This latter
182 harboured *MYD88* mutated (p.L265P).
183 Next generation sequencing showed *MYD88* mutations in 24 (54.5%) of 44, all carrying p.L265P
184 except one case with p.A260T. Both mutations are located in the Toll/Il-1 Receptor (TIR) domain
185 of the protein.
186 Twenty-three cases carried a mutation in proto-oncogene with serine/threonine kinase *PIM1 (23/43,*
187 *53.5%)*, with a great variety of different mutations, mostly missense mutations, occurring at protein
188 kinase domain, of which the p.E135K was the most common involving four cases. In 9 samples 2 or
189 3 different *PIM1* mutations were simultaneously present. *CD79B* missense mutations were found in
190 13 cases (of 43, 30.2%), located within immunoreceptor tyrosine-based activation motif (ITAM), 5
191 of which had p.Y196H, 2 cases p.Y196N, 2 p.Y196S, 2 p.Y196C, 1 p.Y196D, and one the rare
192 p.E198G. Concurrent mutations were found: *MYD88*, *PIM1* and *CD79B* in 4 cases, *MYD88* and
193 *PIM1* in 13 cases, *MYD88* and *CD79B* in 9 cases, and *CD79B* and *PIM1* in 8.
194 Seven cases carried missense mutations in *TP53* gene (7 of 38, 18.4%). Additional mutations were
195 found: *NOTCH1 in* 4 of 35 (11,4%), *AIP in* 9 of 39 (23,1%), *GNAS in* 3 of 37 (8.1%) and *CASP8*
196 *in* 3 of 38 (7.9%).
197 *PI3KCA* missense mutations were found in 6 of 40 (15%); in 5 cases they produced an amino acid
198 substitution in the catalytic domain (p.A1046V, p.D1045N, p.G1049S and p.G1049D in two cases).
199 *PTEN and EGFR* genes mutations were found in 2 of 39 (5.1%) and 2 of 31 (6.4%) cases
200 respectively, while p.G12D and in CIS p.G13D mutations of *KRAS* gene co-occurred in a single
201 patient (1/39). Table 2 summarizes all these sequencing data.
202 *Clinical findings.* The disease presented with a single lesion in 25 of 61 (41%) of patients and with
203 multiple lesions in 36 of 61 (59%). On MRI, most patients showed deeply located lesions with
204 homogeneous contrast-enhancement (36 of 50, 72%). Multiple enhancing was seen in 53%. Only
205 one of 34 patients with DWI performed showed a high ADC value, all others presented

206 hyperintense diffusion signal. Perfusion T2-w studies was available in 24 patients, 54% with 2 to 7
207 times higher value of rCBV. No significant statistical correlations were observed between
208 biological and clinical parameters and neuroradiological features.
209 Gross total resection was achieved in 13 of 61 (21%), subtotal resection in 21 (35%) and biopsy in
210 27 (44%). Twenty-four patients, whose treatment was known, had undergone the matrix protocol
211 MTX + cytarabine or MATRix regimen. Of the 61 patients included in the study, 57 died during the
212 follow-up, with a median follow-up time of 3.3 months (95% CI: [2.1 - 5.0]). The longest follow-up
213 was 69.2 months. Figure 1 shows the Kaplan-Meier survival curve. One-month, 3-month, 6-month
214 overall survival rates were 88.5% (95% CI: [77.4% - 94.4%]), 52.5% (95% CI: [39.3% - 64.1%]),
215 and 37.7% (95% CI: [25.7% - 49.6%]), respectively.
216 No statistically significant correlation was found between cell of origin GCB/non-GCB, BCL2 and
217 cMYC expression and survival nor between DE or non-DE status and prognosis. Survival was
218 significantly longer for patients with mutated *MYD88* (8.7 months vs. 1.7 months; log-rank test =
219 5.43; p = 0.020) compared to those without *MYD88* mutation, and for patients with mutated *CD79B*
220 (10.8 months vs. 2.5 months; log-rank test = 4.64; p = 0.031) compared to those without *CD79B*
221 mutation.

222 **Discussion**

223 CNS-DLBCL, together with vitreoretinal and testicular DLBCL, is now grouped in a new category
224 called large B-cell lymphoma of the immune-privileged sites.[16] The prognosis of CNS-DLBCL
225 remains poor and new therapeutic approaches are needed to improve patient survival. OS is lower in
226 our series than prior studies, this could be due to patient selection bias, which in our study had a
227 median older age (56 vs 64) and a much higher frequency of multiple lesions (59% vs 30%).[1]
228 Similar to previously reported, based on our data, single and double hit rearrangements of MYC
229 gene were rare .[1,6] Differently from a recent report by Asano et al and Kim et al DE status for BCL2
230 and cMYC expression did not impact on prognosis in our cohort of patients.[5,17]

231 Genomic studies suggest that cell proliferation and survival in CNS-DLBCL are driven by
232 deregulated TLR and BCR signaling pathways inducing constitutive NFκB activation, with a high
233 frequency of somatic non-synonymous mutations in *MYD88* and *CD79B* genes.[18-24] Therefore
234 inhibitors of TLR/BCR signaling such as ibrutinib, blocking Bruton's tyrosine kinase (BTK), was
235 proposed as alternative therapeutic target and seem to be effective in CNS-DLBCL.[25-28] We found
236 *MYD88* mutations in 54.5% of the cases resulting the most frequently mutated gene in our series;
237 *CD79B* mutations considered one of the hallmark of CNS-DLBCL mutational signature, were
238 demonstrated in 30.2% of the cases. This gene encodes the Ig-beta protein of BCR multimeric
239 complex and its activating mutations reinforce BCR signalling contributing to sensitivity to
240 Ibrutinib. Interestingly, survival was significantly longer for patients with mutated *MYD88* and
241 *CD79B* compared to those with wild type genes. Our findings confirm data reported by Curran et al
242 and Zhou et al respectively, and are in contrast with two studies reporting a poor prognosis
243 associated with the MYD88 mutation. [29-32] These conflicting results might reflect a selection bias
244 among small study populations, given the rarity of CNS-DLBCL.
245 *PIM1* was found to be the second most frequently mutated gene (53.5%), with a great variety of
246 different mutations. PIM1 protein belongs to the Ser/Thr protein kinase family which is
247 overexpressed in hematopoietic malignancies and in prostate and breast cancers where it was
248 proposed as new therapeutic target.[33-35] Although *PIM1* mutation status was reported to impact the
249 outcome, we did not find any correlation with prognosis.[32]
250 *TP53* alterations seem to play a minor role in CNS-DLBCL. Zorofchian et al (26.7%) and other
251 authors have suggested that disruption of the p53-pathway may be associated with poor PFS.[37,38]
252 In our series *TP53* mutations were not significantly related to prognosis.
253 Notably, we detected for the first time *AIP* mutations in CNS-DLBCL (23,1% of the cases). Aryl
254 hydrocarbon receptor-interacting protein (*AIP*) is a co-chaperone to heat shock proteins and nuclear
255 receptors which behaves as tumor suppressor gene. In colorectal, pancreatic and gastric cancer high
256 expression of AIP is associated with tumour development and more aggressive disease and

257 inhibiting aryl hydrocarbon receptor was proposed as potential therapeutic target.[39-41] Recently *AIP*
258 was found to be a positive regulator of BCL6 expression in germinal centers cells, protecting BCL6
259 from ubiquitin-mediated proteasomal degradation, and deletion of *AIP* in B cells decrease BCL6
260 expression, reducing germinal center B cells and diminishing adaptive immune responses.[42]
261 Furthermore AIP was required for optimal AKT signaling in response to BCR stimulation and
262 seems to be highly expressed in primary DLBCL compared to healthy tissue with implications for
263 the pathobiology of this disease.[42]
264 The NOTCH signalling pathway is widely involved in cellular proliferation, differentiation, and
265 apoptosis.[43] We *NOTCH1* mutations in 11,4% of the samples: *NOTCH1* mutations are distinctive
266 drivers of systemic DLBCL and were not previously described in CNS-DLBCL.[8]
267 *GNAS* and *CASP8* were mutated in 8.1% and 7.9% of the cases, respectively. *GNAS* is the most
268 frequently mutated G-protein in human cancers and activating mutations in the gene GNAS have
269 been found in pituitary, thyroid, pancreatic, biliary tract and intestine tumors as well as in Burkitt
270 lymphoma, systemic DLBCL and Hodgkin lymphoma.[44-47] Zhou et al reported *GNA13* mutations to
271 be associated with a shorter PFS and overall survival in primary central nervous system lymphoma
272 patients, however we did not find any correlation with prognosis.[48] We also identified somatic
273 mutations *CASP8* for which a functional role has not been previously suspected in CNS-DLBCL,
274 although p.R472* nonsense mutation detected in one of our samples was previously reported in
275 systemic DLBCL.[49] *CASP8* encodes a member of the cysteine-aspartic acid protease (caspase)
276 family and sequential activation of caspases plays a central role in the execution-phase of cell
277 apoptosis. In addition, caspase-8 participates in maintenance of genomic integrity and loss of
278 caspase-8 in B lymphocytes leads to B-cell malignancies; moreover, *CASP8* mutations were found
279 in mantle cell lymphoma.[50]

280 *PI3KCA* missense mutations, previously described in several types of carcinomas,[1] were found in 6
281 of 40 (15%), while *PTEN* mutations were detected in 2 of 39 samples (5.1%). The
282 PI3K/AKT/mTOR is an important pro-survival pathway which plays a pivotal role in the
283 development of malignant tumours being often aberrantly activated in different types of cancer also
284 including lymphomas. Zang et al recently showed that PI3K/AKT/mTOR signaling is aberrantly
285 activated in CNS-DLBCL and correlated with a poor prognosis.[51] They found that p-mTOR
286 expression was an independent risk factor in terms of PFS in patients with CNS-DLBCL.
287 Moreover, Takashima et al found that copy number losses in the PTEN-PI3K-AKT proapoptotic
288 pathway are associated with poor prognosis in CNS-DLBCL patients while PTEN mutation was
289 related to shorter OS in the study of Todorovic et al.[52,53] PI3K/mTOR inhibitors has also become a
290 potential therapeutic target in CNS-DLBCL. A phase II trial of 37 relapsed/refractory CNS-DLBCL
291 patients demonstrated that temsirolimus had a positive effect with 54% overall response rate, while
292 lower response rate of 25% was seen in a clinical trial targeting using the pan-PI3K inhibitor
293 buparlisib.[54,55] The use of dual pan-PI3K/mTOR inhibitor bimiralisib (PQR309) in a multicenter
294 phase I/II trial (NCT02669511) as well as BAY80-6946 (copanlisib) in a phase Ib/II clinical trial
295 (NCT03581942) are still under investigation in relapsed/refractory CNS-DLBCL. Moreover,
296 Inhibition of the PI3K isoforms p110α/p110δ or mTOR synergized with ibrutinib to induce cell
297 death in CD79B-mutant CNS-DLBCL cells suggesting that combined inhibition of BTK and
298 PI3K/mTOR could overcome the resistance of lymphoma cells to ibrutinib.[56] So far, no PI3K
299 mutations were described in CNS-DLBCL and our data provide a strong rational for a clinical
300 application of inhibitors targeting the PI3K/ AKT/mTOR signalling pathway at least in a subset of
301 patients.
302 Finally, mutations in the *EGFR* and *KRAS* genes were found in in 6.4% and 2.6% of the cases
303 respectively that could be promising therapeutic targets. Although copy number alterations with

amplifications in RTK-RAS-MAPK signalling has been correlated to a poorer prognosis in CNS-DLBCL we didn't find any association with survival. [52]

Conclusion

MYD88 and *CD79B* predict a longer survival in patients affected by CNS-DLBCL. The *rearrangements* of the *MYC* gene are rare as well as double hit events involving BCL6 and/or BCL2 genes in the present series of CNS-DLBCL. COO and DE status does not affect the prognosis of the 61 CNS-DLBCL cases. Notably, we identified novel mutations that enrich the mutational landscape of CNS-DLBCL, suggests a role of PTEN-PI3K-AKT and RTK-RAS-MAPK signalling in a subset of CNS-DLBCL and that provides new potential therapeutic targets.

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