Scientific correspondence

Genetic heterogeneity for SMARCB1, H3F3A and BRAF in a malignant childhood brain tumour: genetic–pathological correlation

Intra-tumour heterogeneity is an important diagnostic, therapeutic and prognostic challenge. Its extent and mechanism in brain tumours is incompletely understood [1]. We describe a malignant tumour with unique pathological and genetic features. Most notably, the tumour contained mutations in the SMARCB1 gene (typically associated with atypical teratoid/rhabdoid tumours [2]), the H3F3A gene (typically associated with high grade glioma in children [3]) and the BRAF gene. Furthermore, there was marked heterogeneity in mutation load between different parts of the tumour. This heterogeneity has implications both for the evolution of the tumour and for its diagnosis.

A previously healthy 14-year-old girl presented with acute onset of headache, vomiting, blurred vision, olfactory and gustatory hallucinations, and flashes of past experience. Magnetic resonance imaging of the brain showed a localized heterogeneous haemorrhagic lesion in the left mesial temporal region (Figure 1). She underwent subtotal tumour resection and was then treated with cranio-spinal irradiation. However, residual tumour persisted through treatment and she had cytological evidence of CSF dissemination. She died 3 months after presentation.

The tumour (Figure 2) was of high cellularity and consisted of large cells with eosinophilic cytoplasm and large vesicular nuclei. Some cells had prominent nucleoli. There were frequent mitotic figures and apoptotic bodies, and moderate to severe nuclear pleomorphism. Some areas resembled a glioblastoma by virtue of areas of pseudopalisading necrosis. There was no microvascular proliferation, no Rosenthal fibres and no eosinophilic granular bodies. In some areas, there was a myxoid stroma, vascular reaction and tumour reticulin deposition. Immunostaining was positive for vimentin and showed patchy reactivity for desmin, EMA, synaptophysin, CD34, but was negative for SMA, neurofilament and cytokeratin. There were a few foci of GFAP-positive tumour cells throughout the tumour, but most tumour cells were negative. The Ki67 labelling index was very high. There was a mixture of parts of the tumour where many of the tumour cells retained INI-1 immunoreactivity (‘region 1’) and other parts of the tumour where most of the tumour cells showed loss of INI-1 immunoreactivity (‘region 2’).

Genetic heterogeneity was demonstrated by sequencing of the coding regions of SMARCB1 gene, exon 15 of the BRAF gene and exon 1 of the HIST1H3B and H3F3A genes from the two regions of the tumour. SMARCB1 gene copy number was demonstrated using multiplex ligation-dependent probe amplification (MLPA).

A 2 bp duplication was detected in exon 5 of the SMARCB1 gene, leading to a frameshift mutation c.560_561dupCC (Figure 3). This results in a predicted truncated protein p.Ile189Profs*21. We examined the mutation in two regions of the tumour: one of which showed residual INI-1 staining with only focal loss (‘region 1’) and in one of which most cells were negative for INI-1 (‘region 2’). The mutation was detected reproducibly at high levels in region 2 but only at low levels in region 1. MLPA using SMARCB1 Kit P258 (MRC Holland, Amsterdam, the Netherlands) demonstrated loss of heterozygosity (LOH) for the entire SMARCB1 gene and several additional genes within the 22q11 region only in region 1 but not region 2. However, it should be noted that the limit of detection with MLPA is high which may have masked the extent of LOH in these heterogeneous samples.

A c.1799T>A mutation was detected in exon 15 of the BRAF gene in both areas, resulting in the amino acid change p.Val600Glu. The mutation load in region 1 was greater than that observed in region 2 (Figure 3). Histones 3.1 (HIST1H3B) and 3.3 (H3F3A) were analysed by Sanger sequencing. The region encompassing codons Lys28 and Gly35, commonly mutated in paediatric high-grade gliomas, was assessed using the current Reference Sequences, NP_003528.1 (HIST1H3B) and NP_002098.1 (H3F3A). Historically, these codons have often been referred to as Lys27 and Gly34 in the literature. A c.83A>T missense mutation was detected in the H3F3A gene in region 1, resulting in the protein change p.Lys28Met (Figure 3). This mutation was not detected in region 2 allowing for the limit of detection of Sanger sequencing of approximately 20%. Region 1 showed the
presence of two variants in the \textit{HIST1H3B} gene, c.174G > A and c.267G > A. These variants are predicted to result in synonymous polymorphisms p.(Ser58Ser) and p.(Ala89Ala) respectively. These two variants were not detected in the DNA extracted from region 2. The p.Ala89Ala variant has been reported in a small number of healthy individuals in the dbSNP database, rs139461801 (NCBI). The other variant, p.Ser58Ser, has not been reported in any of the online databases. The presence of this polymorphism in region 1 but not region 2 may either represent LOH in region 2 or somatic variants in region 1.

We have described an unusual malignant brain tumour with areas that had histopathological features consistent with both glioblastoma and atypical teratoid rhabdoid tumour (ATRT). This morphological variability was reflected in striking genetic heterogeneity (summarized in Table 1). Uniquely, this tumour has a combination of mutations in \textit{SMARCB1}, \textit{H3F3A} and \textit{BRAF}. We detected the \textit{SMARCB1} mutation at the highest levels in the parts of the tumour that showed histological features of an ATRT (i.e. INI-1 loss by immunohistochemistry). In contrast, we only found mutations in the \textit{H3F3A} gene in the parts that showed retained INI-1 staining. The V600E \textit{BRAF} mutation was present in both regions examined but was present at a higher level in the INI1-retained region. The mutation in \textit{SMARCB1} is novel and is predicted to generate a truncated protein.

To the best of our knowledge, this pattern of morphology with matched genetic heterogeneity has not been previously described. It raises a number of diagnostic possibilities. The first is that this is a rhabdoid glioblastoma (R-GBM). R-GBM is a rare subtype of GBM, which may be morphologically indistinguishable from ATRT. INI-1 staining is usually retained, but can be focal, or the level of expression can be low in the rhabdoid cells [4], but mutations in the \textit{SMARCB1} gene have not been seen [5].

The second possibility is that this is an example of an ATRT arising from a pre-existing tumour. The development of ATRT-like tumours has been rarely described in the context of other, often low grade, tumours [6–8]. Finally, our findings suggest the alternative explanation that the two components of this tumour have evolved out of a single precursor lesion, which lacked mutations in \textit{SMARCB1} or \textit{H3F3A}, but may have had a mutation in \textit{BRAF}. Out of that precursor lesion, one component developed a mutation in \textit{SMARCB1} and one component developed a mutation in \textit{H3F3A}. This heterogeneity has important implications for the mechanism of tumour evolution. In addition, it has implications for diagnosis, as sequencing of single regions may not identify the spectrum of mutations in the tumour.

\section*{Conflict of interest}

The authors have no conflict of interest to declare.

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Figure 2. Histological images of the tumour including areas resembling a high-grade astrocytoma (region 1) with pseudo-palisading necrosis (A) with retained INI-1 staining (C) and areas containing rhabdoid cells (B) with loss of INI-1 staining (D) (region 2). A few small collections of tumour cells in both regions express GFAP but most tumour cells were negative (E-region 1, F-region 2). Scale bars: 50 μm.
Figure 3. Sequencing of SMARCB1 (A), BRAF (B) and H3F3A (C). The top panels show region 1, the middle panels region 2 and the lower panel shows a wild type control. A SMARCB1 mutation is present in region 2 and at low levels in region 1. The BRAF mutation is present in both samples but is at a higher level in region 1. The H3F3A mutation is present only in region 1. The arrows show the site of the mutations.

Table 1. A summary of the main genetic findings in the two regions of the tumour

<table>
<thead>
<tr>
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<th>Region 1</th>
<th>Region 2</th>
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<tbody>
<tr>
<td>INI1 immunohistochemistry</td>
<td>Mostly retained</td>
<td>Mostly lost</td>
</tr>
<tr>
<td>SMARCB1 insertion</td>
<td>Present at very low levels</td>
<td>Present at high levels</td>
</tr>
<tr>
<td>SMARCB1 LOH</td>
<td>Present</td>
<td>Absent</td>
</tr>
<tr>
<td>V600E BRAF mutation</td>
<td>Present</td>
<td>Present (at lower levels than region 1)</td>
</tr>
<tr>
<td>H3F3A mutation</td>
<td>Present</td>
<td>Absent</td>
</tr>
<tr>
<td>HIST1H3B polymorphisms</td>
<td>Present</td>
<td>Absent</td>
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Author contributions

All the authors contributed to writing the manuscript and reviewed the final version. JC, NA and SH did the genetic analysis and SMLP and TSJ the pathology studies. KM, JC, NA, SH and TSJ provided the figures for the paper.

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