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SMARCE1 mutation screening in classification of clear cell meningiomas

Miriam J Smith,[1,*] Soomin Ahn,[2,*] Jung-Il Lee,[3] Michael Bulman,[1] Daniel du Plessis[4] & Yeon-Lim Suh[5]

[1]*Manchester Centre for Genomic Medicine, Manchester Academic Health Sciences Centre (MAHSC), St Mary's Hospital, University of Manchester, Manchester, UK,* [2]*Department of Pathology, Ewha Womans University School of Medicine,* [3]*Department of Neurosurgery, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea,* [4]*Department of Cellular Pathology and Greater Manchester Neurosciences Centre, Salford Royal Hospitals NHS Foundation Trust, Salford, UK, and* [5]*Department of Pathology and Translational Genomics, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea*

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Aims: Clear cell meningioma (CCM) is a rare subtype of meningioma and shows not only unusual histology, but also unique clinical features. Recently, *SMARCE1* mutations have been shown to cause spinal and cranial CCMs. We present 12 cases which were diagnosed with CCM in a single institution between 1997 and 2014, and investigate their *SMARCE1* mutation status.

Methods and results: To investigate the *SMARCE1* mutation status of these tumours, we used a combination of Sanger sequencing and multiplex ligation-dependent probe amplification analysis and also performed SMARCE1 immunohistochemical staining. We found both *SMARCE1* mutational hits, including novel *SMARCE1* mutations, in six of eight tested patients. Immunohistochemical analysis showed loss of SMARCE1 protein staining in all but two cases. Two individuals who were diagnosed originally with CCM were negative for *SMARCE1* mutations, but tested positive for *NF2* mutations. As a result, these two tumours were re-analysed and eventually reclassified, as a microcystic and a mixed pattern of meningothelial meningioma with focal clear cell areas, respectively.

Conclusions: These results expand the spectrum of pathogenic variants in *SMARCE1* and show that mutation screening can help to facilitate meningioma classification. This may have implications for prognosis and future clinical management of patients, as CCMs are classed as grade II tumours, while microcystic and meningothelial meningiomas are classed as grade I.

Keywords: *SMARCE1*, meningioma, clear cell

Introduction

Meningiomas are the most common form of primary neoplasm in the adult central nervous system (CNS).[1,2] Meningiomas account for 1.0–4.6% of childhood brain tumours.[3] While most meningiomas have a good prognosis, high recurrence rates have been observed for World Health Organization (WHO) grades II and III meningiomas.[4] Among grades II and III meningiomas, clear cell meningioma (CCM) is rare, consisting of only 0.2–0.81% of all meningiomas.[5] Histologically, CCMs are characterized by patternless distribution of polygonal cells with a clear, glycogen-rich cytoplasm and blocky, perivascular and interstitial collagen. CCMs show not only unusual histology, but also unique clinical features. They tend

Address for correspondence: Y-L Suh, Department of Pathology and Translational Genomics, Samsung Medical Center, Sungkyunkwan University School of Medicine, 81 Irwon-ro, Gangnam-gu, Seoul, 06351, Korea. e-mail: ylsuh76@skku.edu
*These authors contributed equally to this work.

to occur in young patients, and are more likely to recur or metastasize than other common subtypes.[6] Recurrence and CNS metastasis occurred in 37.8 and 8.1% of the cases reported in the literature, respectively.[6]

Although the molecular genetic alterations occurring in meningiomas have not yet been elucidated fully,[5,7] meningiomas exhibit a wide spectrum of molecular alterations. *NF2* mutations are the most common somatic genetic alteration found in sporadic meningiomas, and germline mutation of the *NF2* gene is known to predispose to multiple meningiomas as part of the neurofibromatosis type 2 (NF2) phenotype.[8] Genomic sequencing of a subset of meningiomas lacking *NF2* alteration elucidated recurrent *SMO* and *AKT1* mutations, which have the potential to guide new therapeutic strategies.[9] Furthermore, genomic changes are associated with histological subtype and genomic data of various subtypes are expected to facilitate more accurate histological grading and subtyping.[10–13] In case of CCM, germline loss-of-function mutations in the *SMARCE1* chromatin remodelling factor were identified as a cause of both spinal and cranial CCM.[8,14] To date, 12 families with *SMARCE1*-associated CCM have been reported (Table 1).[14–18] *SMARCE1*

Table 1. Clinical and genetic data on reported *SMARCE1* mutated clear cell meningioma

Study	Patient	Sex	Age of onset (years)	Location	Germline mutation	Predicted protein alteration	Tumour mutations
Smith *et al.* 2013[14]	1	Female	27	Spinal	c.715C>T	p.Arg239*	NA
	2	Female	30	Spinal	c.237+2T>C	p.Lys79_Val80ins3* p.Ala53_Lys79del	NA
	3	Male	26	Spinal	c.311G>A	p.Trp104*	Tumour 1: c.311G>A heterozygous Tumour 2: c.311G>A + LOH
	4	Female	17	Spinal	c.572insC	p.Thr191Thrfs*14	c.572insC heterozygous
Smith *et al.* 2014[16]	5	Male	7	Spinal	Not tested	Not tested	Hit 1: c.624_627delTGAG, p.(Ser208Argfs*26) Hit 2: LOH
	6	Female	22	Cranial	Not tested	Not tested	Hit 1: c.357C>G, p.(Tyr119*) Hit 2: LOH
	7	Male	10	Cranial	Not tested	Not tested	Hit 1: c.688C>T, p.(Gln230*) Hit 2: LOH
	8	Male	8	Spinal	Not tested	Not tested	Hit 1: Del promoter-E5/6 Hit 2: LOH
	9*	Male	2	Spinal	c.275_276insA	p.Leu93Valfs*17	Hit 1: c.275_276insA, p.(Leu93Valfs*17) Hit 2: LOH
	10†	Female	14	Cranial	c.374_395inv22	p.(Glu125_Ala132delinsGly LeuHisArgPhelleValLeu)	Hit 1: c.374_395inv22, p.(Glu125_Ala132delinsGly LeuHisArgPhelleValLeu) Hit 2: c.267delT, p.(Asp90Thrfs*2)
	11	Female	17	Spinal	Del promoter-E5/6	No protein product	Hit 1: del promoter to E5/6 Hit 2: c.757C>T, p.(Gln253*)
Gerkes *et al.* 2016[18]	12	Male	10	Cranial	c.814delA	p.Arg272Glyfs*5	Hit 1: c.814delA, p.(Arg272Glyfs*5) Hit 2: LOH

NA, Not available; LOH, Loss of heterozygosity.
*Discussed in more detail in Evans *et al.* 2015.[17]
†Discussed in more detail in Raffalli-Ebezant *et al.* 2015.[15]

mutations appear to be specific for the clear cell histological subtype, rather than tumour location or syndromic presentation.[8] Previously, intracranial CCM has also been reported in one child diagnosed with NF2 disease on clinical grounds[19] and one adult, also on clinical grounds,[16] while most meningiomas that occur in NF2 show a fibroblastic or transitional histology.[20] In this study, we report 12 cases which were diagnosed as a CCM in a single institute in Korea during an 18-year period. We investigated the involvement of *SMARCE1* mutation in these tumours.

Materials and methods

PATIENT POPULATION AND DATA COLLECTION

A retrospective search of the pathology database at the Samsung Medical Center, using the term 'CCM', identified a total of 14 samples from 12 patients. All patients underwent surgery at the neurosurgery unit of the Samsung Medical Center, Seoul, South Korea, between 1997 and 2014. For patient 5, who underwent a two-staged operation, two surgical specimens (5-1 and 5-2) were included. Patient 6 underwent an initial operation at an outside hospital. The sample used in this study was a recurrent tumour with a 9-year interval. The primary tumour sample for this patient was not available. For patient 11, who showed progression of disease, the initial tumour (11-1) and progressed tumour (11-2), with a 3-month interval, were analysed. A blood sample was also acquired from this patient. All patients were followed-up until October 2015, with a median follow-up time of 59 months. Formalin-fixed paraffin-embedded (FFPE) tissue was obtained from a retrospectively collected archive. Clinical information including age, tumour site, local and adjuvant therapy, recurrence and survival data were evaluated by reviewing the medical records. The study was approved by the institutional review board (IRB) at the Samsung Medical Center.

DNA EXTRACTION

Genomic DNA was extracted using a Qiagen DNA FFPE tissue kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. After extraction, concentration, 260/280 and 260/230 nm ratio were measured by spectrophotometer (ND1000; Nanodrop Technologies, Thermo-Fisher Scientific, Waltham, MA, USA).

SANGER SEQUENCING

SMARCE1 exons were amplified from tumour DNA, using GoTaq G2 Green Master Mix (Promega, Southampton, UK). The products were purified using AxyPrep Mag polymerase chain reaction (PCR) clean-up beads (Appleton Woods, Birmingham, UK). Sequencing PCR was performed using the BigDye® Terminator version 3.1 Cycle Sequencing Kit (ABI; Life Technologies, Paisley, UK). The products were purified using AxyPrep Mag DyeClean beads (Appleton Woods) and analysed on an ABI 3730*xl* DNA Analyzer (ABI; Life Technologies).

MULTIPLEX LIGATION-DEPENDENT PROBE AMPLIFICATION (MLPA)

MLPA was carried out using SALSA MLPA kits, X072-X1 and P043-NF2 (MRC-Holland, Amsterdam, the Netherlands), according to the manufacturer's instructions. Briefly, 100 ng DNA were used for hybridization, ligation and amplification of exon probes for control and test samples and the products were analysed on an ABI 3100 sequencer (Applied Biosystems, Warrington, UK).

IMMUNOHISTOCHEMISTRY

Paraffin-embedded meningioma sections were immunostained for SMARCE1 protein, as described previously.[14] Briefly, 1:100 anti-SMARCE1 HPA003916 antibody (Sigma-Aldrich, St Louis, MO, USA) was used to stain sections, using an indirect peroxidase method on the Roche Ultra IHC autostainer. This antibody is polyclonal and has been raised against the C-terminal end of SMARCE1 (amino acids 301–408).

Results

CLINICOPATHOLOGICAL FEATURES OF 12 PATIENTS DIAGNOSED WITH CCM

The clinicopathological information of the patients is summarized in Table 2. There were five spinal tumours and seven cranial tumours. The tumour sites were as follows: spinal cord, frontal lobe, cerebellomedullary cistern, cerebellopontine angle, and falx cerebelli and low cranial nerve. The sample from patient 6 was a recurrent tumour (9-year interval) and patient 11 showed disease progression (3-month interval). However, to date, none of the patients have died due to tumour recurrence or progression. All

patients reported no familial history or past history of brain or spinal tumour.

SMARCE1 STATUS

Immunohistochemical analysis of paraffin-embedded tissue from each tumour showed loss of SMARCE1 protein staining in 12 of 14 tumours (Figure 1, Table 2).

To investigate the *SMARCE1* mutation status of these tumours, we used a combination of Sanger sequencing and MLPA analysis (Table 2). Four tumours were excluded from genetic analysis due to poor DNA quality. We found two *SMARCE1* mutational hits in each of six out of eight tested patients. We identified two splice-site mutations, three nonsense mutations, three frameshift mutations and one indel. These included three novel mutations located in exons 3 [c.23delC, p.(Pro9Hisfs*62)] and 10 [(c.831delA, p.(Lys277Lys*1) and (c.957delC, p.(Pro320Leufs*122)]. The *SMARCE1* exon 9 mutation, c.715C>T, p.(R239*), identified in one patient, has been seen previously in another cohort.[14] In the current study this mutation was associated with a recurrent tumour.

For patient 11, showing tumour progression, an identical mutation, c.331G>T, p.(E111*), was found in both the original and progressed tumour samples (11-1 and 11-2). A blood sample was available for analysis and we were able to confirm the presence of this mutation in the germline. Two surgical specimens for the tumour from patient 5 (5-1 and 5-2) also showed identical mutations.

Tumours from three individuals contained two point mutations, rather than one point mutation and loss of heterozygosity (LOH). These included an exon 6 splice-site mutation and an exon 10 frameshift in the cranial CCM of a 16-year-old male; two frameshift mutations involving exons 3 and 8 were identified in the spinal CCM of a 19-year-old female. Finally, a nonsense mutation in exon 6 and a frameshift alteration in exon 10 were detected in the spinal CCM of a 10-year-old female.

For the two tumours in which no *SMARCE1* mutations were found (from patients 8 and 9), we analysed the *NF2* gene and identified bi-allelic inactivating mutations in both tumours. The first contained a frameshift mutation, c.579delA, p.(Ala194Alafs*15) in exon 6, with LOH. The second tumour contained the missense mutation, c.755C>T, p.(Pro252Leu), in exon 8, also with LOH. The variant p.(Pro252Leu) is non-truncating, but was not found on ESP6500SI-V2 or ExAC and was predicted to be damaging by Polyhphen2, SIFT, Mutation Taster and Align GVGD, suggesting that it is pathogenic.

HISTOLOGICAL RECLASSIFICATION

As we identified two *NF2* alterations in each of these last two tumours, SMARCE1 protein staining was positive, and as we could not find *SMARCE1* mutations in either of these tumours, the tissue was reassessed (by SA, YS and DdP). It was determined that the major histology for the tumour from patient 8 was, in fact, microcystic (Figure 2). For patient 9, the tumour contained a focal clear cell component; however, the tumour was heterogeneous in composition, also containing meningothelial and small cell constituents (Figure 2).

After removing these two males without conventional CCM morphology, the male-to-female ratio was 6:4 and cranial-to-spinal tumour ratio was equal (5:5). In this cohort, the mean and median ages at diagnosis of meningioma were not significantly different between males (27 and 24 years, respectively) and females (23 and 24.5 years, respectively).

Discussion

Meningiomas consist of various histological subtypes which appear to be determined by distinct genetic alterations. Recently, several large-scale genomic studies of meningioma extended our knowledge of somatic molecular alteration in various types of meningioma.[9,10,13,21,22] These data can be used to fine-tune diagnostic accuracy, both subtyping and potentially grading.[11–13,21] In CCM, germline loss-of-function mutations in the *SMARCE1* chromatin remodelling factor were identified as a cause of both spinal and cranial CCM.[14,16] To date, including the current study, pathogenic *SMARCE1* mutations have been associated with CCM in individuals from 20 separate families. The majority of identified *SMARCE1* mutations are nonsense or frameshift variants, predicted to lead to protein inactivation and complete loss of the protein product. Previous studies have shown two unrelated families to have a large multi-exon deletion, while one family has an intra-exonic inversion mutation and two families have a small exonic indel (Table 1). To date, missense mutations have not been associated with CCM. The majority of *SMARCE1* nonsense and frameshift mutations have been found in exon 6. The functional significance of this region is highlighted further by three splice-site mutations that have been found in exons 5 and 6, with the potential to generate

Table 2. Clinical and genetic information of 12 patients diagnosed with a clear cell meningioma

Sample no.	Age (years)	Sex	Location	Treatment	Recur	Death	FU period (month)	SMARCE1 protein staining	*SMARCE1* mutation 1	*SMARCE1* mutation 2	*NF2* mutation 1	*NF2* mutation 2
1	22	M	Spinal cord (L4-S2)	GTR	No recur	Alive	106	Negative	ND	ND	ND	ND
2	39	M	CPA	STR and RT	No recur	Alive	157	Negative	ND	ND	ND	ND
3	16	M	CMC	STR and RT	No recur	Alive	18	Negative	Exon 6 c.238-1G>A, p.(?)	Exon 10 c.957delC, p.(Pro320Leufs*122)	Not tested	Not tested
4	26	M	CPA	GTR	No recur	Alive	51	Negative	ND	ND	ND	ND
5-1	11	M	CPA	STR	No recur	Alive	100	Negative	Exon6 c.369+1G>C, p.(?)	LOH	Not tested	Not tested
5-2				GTR				Negative	Same as no.5-1	Same as no.5-1	Not tested	Not tested
6*	33	F	Spinal cord (L5-S2)	GTR	Recurrent	Alive	83	Negative	Exon 9 c.715C>T, p.(R239*)	LOH	Not tested	Not tested
7	48	M	Spinal cord (L5-S2)	GTR	No recur	Alive	59	Negative	ND	ND	ND	ND
8†	58	M	Falx cerebelli	STR and RT	No recur	Alive	58	Positive	Negative	Negative	NF2 Exon 6 c.579delA, p.(Ala194Alafs*15)	LOH
9†	31	M	Frontal lobe	STR and RT	No recur	Alive	59	Positive	Negative	Negative	NF2 Exon 8 c.755C>T, p.(Pro252Leu)	LOH
10	19	F	Spinal cord (T12)	GTR	No recur	Alive	25	Negative	Exon 3 c.23delC, p.(Pro9Hisfs*62)	Exon 8 c.689_698delinsCCAGT, p.(Gln230Profs*13)	Not tested	Not tested
11-1‡	30	F	Low cranial nerve	STR and RT	Progressive	Alive	30	Negative	Exon 6 c.331G>T, p.(E111*)	LOH	Negative	Negative
11-2‡				STR and RT				Negative	Same as no.11-1	Same as no.11-1	Negative	Negative
12	10	F	Spinal cord (L1-2)	GTR	No recur	Alive	16	Negative	Exon 6 c.313C>T, p.(R105*)	Exon 10c.831delA, (p.Lys277Lys*1)	Not tested	Not tested

CPA, Cerebellopontine angle; CMC, Cerebellomedullary cistern; GTR, Gross total resection; STR, Subtotal resection; RT, Radiotherapy; ND, Not determined due to poor DNA quality; FU, Follow-up; LOH, Loss of heterozygosity.

*This case was studied on the recurrent tumour after previous operation at an outside hospital.

†tumours were reclassified as microcystic meningioma (tumour 8) and mixed pattern of meningothelial meningioma with focal clear cell component (tumour 9).

‡germline mutation was identified in the blood sample.

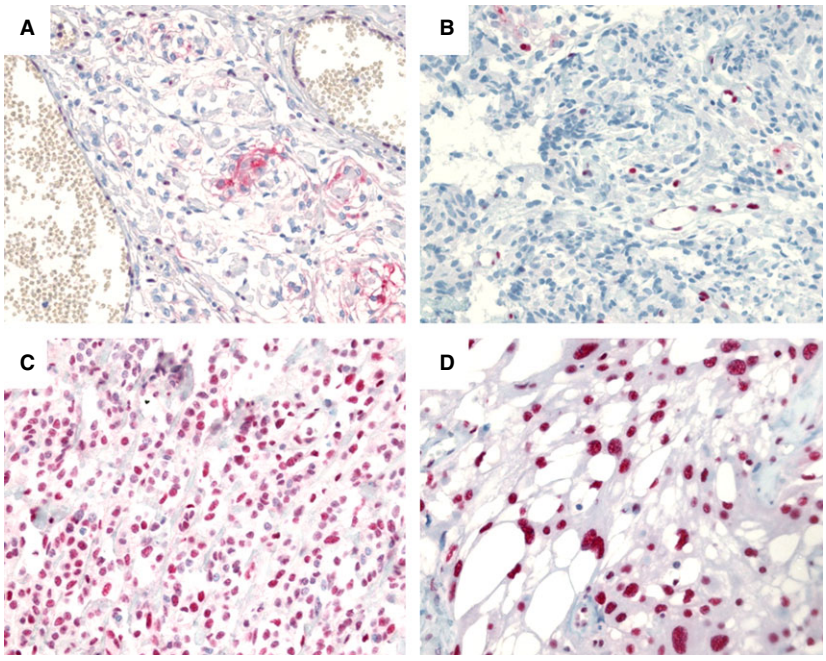

Figure 1. Representative images of immunohistochemical staining of meningiomas for SMARCE1. **A**, Cases 1 and **B**, 11 show typical loss of nuclear staining with positive staining restricted to endothelial and leucocytic nuclei plus mucoid/glycogen content of tumour cells. **C**, Cases 8 and **D**, 9 show retained SMARCE1 staining.

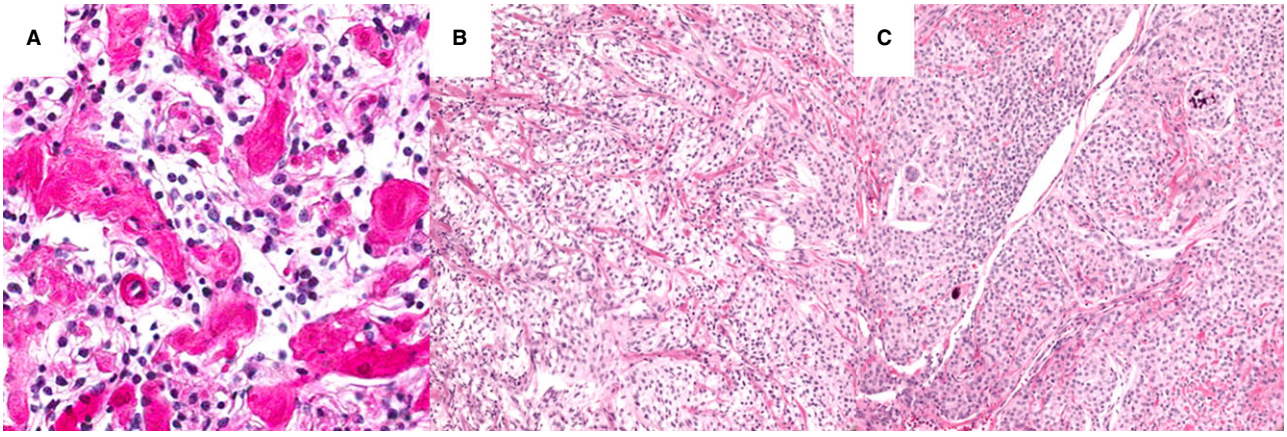

Figure 2. **A**, Haematoxylin and eosin (H&E)-stained section for case 5-1 showing a patternless growth of clear cells and prominent perivascular and interstitial collagen, typical of clear cell meningioma (CCM). **B**, H&E-stained section for case 9 (region 1), showing a heterogeneous histology with focal CCM features. **C**, H&E-stained section for case 9 (region 2), indicating a meningothelial growth pattern.

aberrantly spliced transcripts and therefore to perturb protein structure and function. However, immunohistochemical analysis of available tissue has shown loss of SMARCE1 protein in all *SMARCE1* mutation-positive tumours, suggesting that if any alternatively spliced products are generated, they are unstable.

Mutational analysis in the current cohort identified two *SMARCE1* mutations in eight tumours from six people. No *SMARCE1* mutations were identified in two remaining tumours, but two mutational hits were identified in *NF2* (a point mutation and LOH) in each tumour. Each of these *NF2*-mutated tumours showed an unconventional morphology for CCM, and subsequent re-analysis of their histology established one to be a microcystic meningioma (patient 8) and the other to have a mixed histology (patient 9). Microcystic meningiomas are known to be problematic to distinguish from CCMs. The tumour from patient 9 contained a focal clear cell component; however, the tumour was heterogeneous in composition, also containing meningothelial and small cell constituents (Figure 2).

CCMs are classed as grade II meningiomas and show unique clinical features. They tend to occur in young patients, and are more likely to recur or metastasize than other common subtypes.[6] In this cohort the mean

and median ages at diagnosis of meningioma were not significantly different between males (27 and 24 years, respectively) and females (23 and 24.5 years, respectively). This is in contrast to previous studies, indicating an earlier onset in males versus females. The reason for this is unknown. However, as the mutation status in tumours from four adult males is unknown and no lymphocyte DNA was available for any of these patients to test germline status, it is possible that these are sporadic tumours occurring at a later age, while the younger male patients have a germline predisposition. The limitations of this study are that the follow-up period was relatively short for some patients and germline DNA was only available for one patient, limiting our ability to determine which cases were due to germline mutation and which were sporadic.

This study adds to the known spectrum of meningioma-associated variants in *SMARCE1* and the natural history of CCMs. To our knowledge, this is the first study examining *SMARCE1* mutation status in Asian patients with CCM. It also demonstrates the utility of genetic screening in accurate classification of meningiomas. This may have implications for future clinical management of patients, as CCMs are classed as grade II tumours, while microcystic are classed as grade I. The study findings also raise the prospect that meningiomas with focal clear cell components do not share the same genotype as conventional, 'pure' CCM and may not, by implication, carry the same adverse prognosis. This, however, requires validation, requiring the genotyping of larger numbers of mixed meningiomas with focal clear cell areas.

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Conflicts of interest

The authors declare no conflicts of interest.

References

1. Riemenschneider MJ, Perry A, Reifenberger G. Histological classification and molecular genetics of meningiomas. *Lancet Neurol.* 2006; **5**; 1045–1054.
2. Ostrom QT, Gittleman H, Liao P *et al.* CBTRUS statistical report: primary brain and central nervous system tumors diagnosed in the United States in 2007–2011. *Neuro Oncol.* 2014; **16** (Suppl. 4); iv1–iv63.
3. Caroli E, Russillo M, Ferrante L. Intracranial meningiomas in children: report of 27 new cases and critical analysis of 440 cases reported in the literature. *J. Child Neurol.* 2006; **21**; 31–36.
4. Louis DN, Ohgaki H, Wiestler OD *et al.* The 2007 WHO classification of tumours of the central nervous system. *Acta Neuropathol.* 2007; **114**; 97–109.
5. Mawrin C, Perry A. Pathological classification and molecular genetics of meningiomas. *J. Neuro-oncol.* 2010; **99**; 379–391.
6. Ohba S, Sasaki H, Kimura T, Ikeda E, Kawase T. Clear cell meningiomas: three case reports with genetic characterization and review of the literature. *Neurosurgery* 2010; **67**; E870–E871; discussion E871.
7. Perez-Magan E, Campos-Martin Y, Mur P *et al.* Genetic alterations associated with progression and recurrence in meningiomas. *J. Neuropathol. Exp. Neurol.* 2012; **71**; 882–893.
8. Smith MJ. Germline and somatic mutations in meningiomas. *Cancer Genet.* 2015; **208**; 107–114.
9. Brastianos PK, Horowitz PM, Santagata S *et al.* Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. *Nat. Genet.* 2013; **45**; 285–289.
10. Clark VE, Erson-Omay EZ, Serin A *et al.* Genomic analysis of non-NF2 meningiomas reveals mutations in TRAF7, KLF4, AKT1, and SMO. *Science* 2013; **339**; 1077–1080.
11. Sahm F, Schrimpf D, Olar A *et al.* TERT promoter mutations and risk of recurrence in meningioma. *J. Natl. Cancer Inst.* 2016; **108**; djv377.
12. Aizer AA, Abedalthagafi M, Bi WL *et al.* A prognostic cytogenetic scoring system to guide the adjuvant management of patients with atypical meningioma. *Neuro Oncol.* 2016; **18**; 269–274.
13. Abedalthagafi MS, Merrill PH, Bi WL *et al.* Angiomatous meningiomas have a distinct genetic profile with multiple chromosomal polysomies including polysomy of chromosome 5. *Oncotarget* 2014; **5**; 10596–10606.
14. Smith MJ, O'Sullivan J, Bhaskar SS *et al.* Loss-of-function mutations in SMARCE1 cause an inherited disorder of multiple spinal meningiomas. *Nat. Genet.* 2013; **45**; 295–298.
15. Raffalli-Ebezant H, Rutherford SA, Stivaros S *et al.* Pediatric intracranial clear cell meningioma associated with a germline mutation of SMARCE1: a novel case. *Childs Nerv. Syst.* 2015; **31**; 441–447.
16. Smith MJ, Wallace AJ, Bennett C *et al.* Germline SMARCE1 mutations predispose to both spinal and cranial clear cell meningiomas. *J. Pathol.* 2014; **234**; 436–440.
17. Evans LT, Van Hoff J, Hickey WF *et al.* SMARCE1 mutations in pediatric clear cell meningioma: case report. *J. Neurosurg. Pediatr.* 2015; **16**; 296–300.
18. Gerkes EH, Fock JM, den Dunnen WF *et al.* A heritable form of SMARCE1-related meningiomas with important implications for follow-up and family screening. *Neurogenetics* 2016; **17**; 83–89.
19. Jain D, Sharma MC, Sarkar C *et al.* Clear cell meningioma, an uncommon variant of meningioma: a clinicopathologic study of nine cases. *J. Neuro-oncol.* 2007; **81**; 315–321.
20. Wellenreuther R, Kraus JA, Lenartz D *et al.* Analysis of the neurofibromatosis 2 gene reveals molecular variants of meningioma. *Am. J. Pathol.* 1995; **146**; 827–832.
21. Gunel M. 218 Meningioma driver mutations determine their anatomical site of origin. *Neurosurgery* 2016; **63**(Suppl. 1); 185.
22. Abedalthagafi M, Bi WL, Aizer AA *et al.* Oncogenic PI3K mutations are as common as AKT1 and SMO mutations in meningioma. *Neuro Oncol.* 2016; **18**; 649–655.