Title

TRAF7 somatic mosaicism in a patient with bilateral optic nerve sheath meningiomas: illustrative case

Journal

Journal of Neurosurgery Case Lessons, 3(23)

ISSN

2694-1902

Authors

Kaidonis, Georgia
Pekmezci, Melike
Van Ziffle, Jessica
et al.

Publication Date

2022-06-01

DOI

10.3171/case2247

Peer reviewed

JOURNAL OF NEUROSURGERY:
Case Lessons

J Neurosurg Case Lessons 3(23): CASE2247, 2022
DOI: 10.3171/CASE2247

TRAF7 somatic mosaicism in a patient with bilateral optic nerve sheath meningiomas: illustrative case

Georgia Kaidonis, MBBS, PhD,[1] Melike Pekmezci, MD,[1,2] Jessica Van Ziffle, PhD,[2] Kurtis I. Auguste, MD,[3] and Jonathan C. Horton, MD, PhD[1]

Departments of [1]Ophthalmology, [2]Pathology, and [3]Neurosurgery, University of California, San Francisco, San Francisco, California

BACKGROUND In the past decade, next-generation sequencing has spurred significant progress in the understanding of cytogenetic alterations that occur in meningiomas. Eighty percent of adult meningiomas harbor pathogenic somatic variants involving *NF2*, *TRAF7*, *SMARCB1*, *KLF4*, *PI3K*, or *POLR2A*. Somatic variants in *TRAF7* associated with meningiomas usually localize to the gene's WD40 domains but are mutually exclusive to germline mutations, which cause a distinctive autosomal dominant syndrome.

OBSERVATIONS This case involved a 15-year-old girl with bilateral optic nerve sheath meningiomas, diffuse meningiomatosis, and syndromic features, including craniosynostosis, brain anomalies, syndactyly, brachydactyly, epicanthus, and patent ductus arteriosus. Genetic testing of the meningioma specimen 7 years after biopsy showed a pathogenic p.R641C variant within the WD40 domain of the *TRAF7* gene. Additional testing of unaffected tissues identified the same variant at lower allele frequencies, consistent with postzygotic somatic mosaicism.

LESSONS The authors report postzygotic somatic mosaicism for a p.R641C variant in the *TRAF7* gene in a patient with bilateral optic nerve sheath meningiomas, diffuse meningiomatosis and a constellation of systemic findings previously recognized in patients with germline mutations of this gene. This is the first report of optic nerve sheath meningioma in a patient with mutation in the *TRAF7* gene.

https://thejns.org/doi/abs/10.3171/CASE2247

KEYWORDS WD40 domain; p.R641C; meningiomatosis; craniosynostosis; *TRAF7* syndrome; mosaicism

Cytogenetic alterations in meningioma specimens were first discovered more than 50 years ago.[1] Loss of the long arm of chromosome 22 was identified as a pathogenic somatic alteration in meningioma tissue.[2,3] Subsequently, the neurofibromatosis type 2 (NF2) tumor suppressor gene was discovered on chromosome 22q.[4] Approximately 50% of patients with autosomal dominant NF2 develop meningioma.[5] Somatic *NF2* gene mutation or loss (or both) contributes to 50% to 60% of sporadic adult meningiomas.[6–10] Other genetic conditions carrying an increased risk of meningioma have also been identified, including Gorlin syndrome, Rubenstein-Taybi syndrome, nevoid basal cell carcinoma syndrome, multiple endocrine neoplasia 1, Cowden syndrome, and Werner syndrome.[11,12]

The advent of next-generation sequencing has led to the detection of new pathogenic somatic mutations in meningioma. In a survey of 300 tumors, genomic analysis identified mutations in four genes: tumor necrosis factor receptor-associated factor 7 (*TRAF7*), Krupple-like factor 4 (*KLF4*), v-akt murine thymoma viral oncogene homolog 1 (*AKT1*), and smoothened, frizzled family receptor (*SMO*).[8] Subsequent studies have identified other somatic mutations causing meningioma.[6–10] Apart from NF2, mosaicism is believed to be rare in patients with meningioma who harbor these mutations.[13]

ABBREVIATIONS *AKT1* = v-akt murine thymoma viral oncogene homolog 1; *CHEK2* = checkpoint kinase 2; *FGFR* = fibroblast growth factor receptor; *FUBP1* = far upstream element protein 1; IDO = indoleamine 2,3-dioxygenase; *KLF4* = Krupple-like factor 4; MEKK3 = mitogen-activated kinase kinase kinase 3; MRI = magnetic resonance imaging; NF2 = neurofibromatosis type 2; PD-L1 = programmed death-ligand 1; *pTERT* = telomerase reverse transcriptase; *SMAD* = some mothers again decapentaplegic; *SMO* = smoothened, frizzled family receptor; TDO2 = tryptophan 2,3-dioxygenase; *TRAF7* = tumor necrosis factor receptor-associated factor 7; TWIST1 = Twist Family BHLH Transcription Factor 1.

INCLUDE WHEN CITING Published June 6, 2022; DOI: 10.3171/CASE2247.
SUBMITTED January 28, 2022. **ACCEPTED** March 29, 2022.

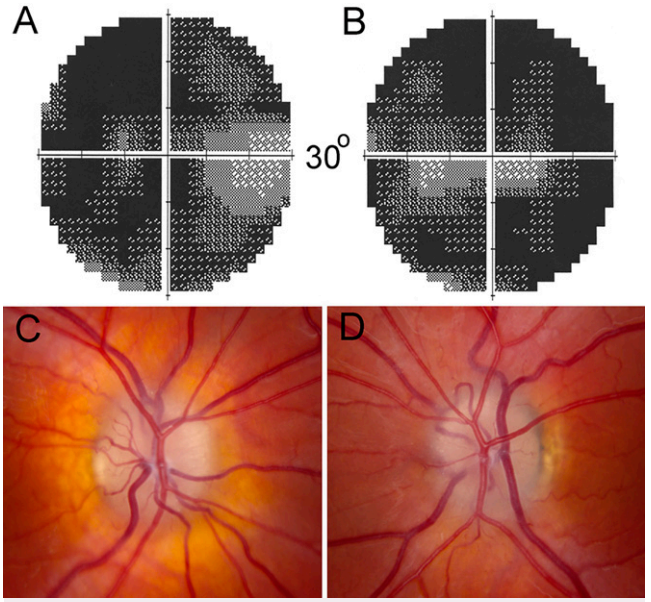


FIG. 1. Humphrey visual field tests and fundus photography at presentation. **A and B:** Thirty-degree threshold visual field tests showing severe depression in both eyes. **C and D:** Fundus photographs showing bilateral optic disc swelling with pallor and pseudodrusen.

Here we report a child with diffuse meningiomatosis leading to development of bilateral optic nerve sheath meningiomas. Next-generation sequencing of tumor tissue showed a pathogenic mutation in *TRAF7*. No prior study has found any gene, other than *NF2*, mutated in bilateral optic nerve sheath meningiomas. Analysis of other tissues revealed the presence of the same mutant allele at a low frequency. Review of the patient's history uncovered systemic features heretofore only described in germline *TRAF7* syndrome.

Illustrative Case

A 15-year-old girl was referred to the neuroophthalmology clinic by an optometrist who had observed bilateral optic disc swelling. The patient reported a recent history of declining vision and new onset of headache. The child's parents were of European ancestry. The patient had second–third toe syndactyly and first–fourth/fifth toe brachydactyly. Facial features were significant for epicanthal folds and a low hairline. There was a history of postnatal surgical repair of a patent ductus arteriosus.

On examination, visual acuity was 20/40 in the right eye and 20/100 in the left eye. The pupillary reflexes were normal. No Marcus Gunn pupil was present. Extraocular eye movements were full. Humphrey threshold visual field tests revealed severe depression in both eyes (Fig. 1A and B). Slit-lamp examination was unremarkable, and intraocular pressure was normal. Dilated fundus examination revealed bilateral optic disc swelling (Fig. 1C and D). Certain features suggested chronicity, such as pallor and pseudodrusen. Cranial examination was notable for scaphocephaly with frontal bossing. Neurological examination, including the cranial nerves, was otherwise unremarkable. The patient was a high school student with average scholastic ability.

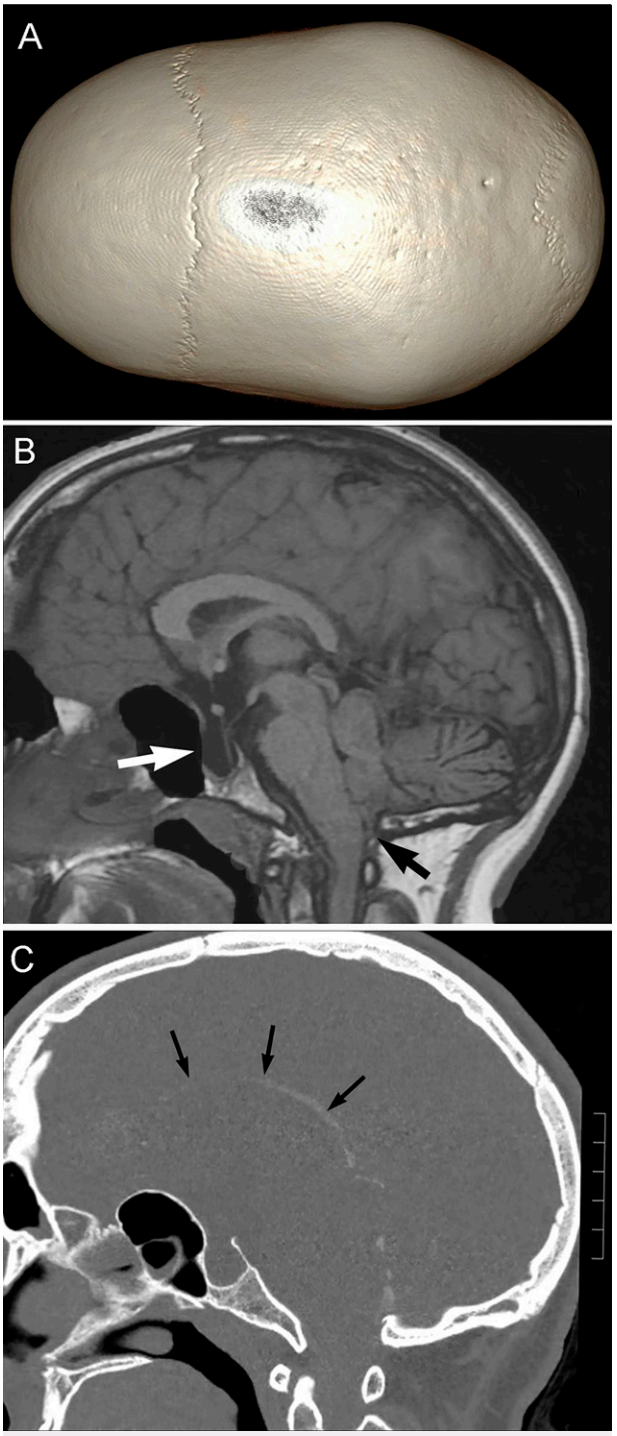


FIG. 2. Head and brain anomalies. **A:** Three-dimensional reconstruction computed tomography (CT) demonstrating absence of the sagittal suture with scaphocephaly. **B:** Noncontrast sagittal MRI showing small posterior fossa, platybasia, cerebellar tonsillar herniation (*black arrow*), narrow foramen magnum, hypoplasia of the posterior corpus callosum, and pronounced enlargement of the sella turcica (*white arrow*) with an elongated pituitary stalk and partially empty appearance. **C:** Noncontrast sagittal CT showing calcification along the inferior border of the falx cerebri (*arrows*) and at its junction with the tentorium.

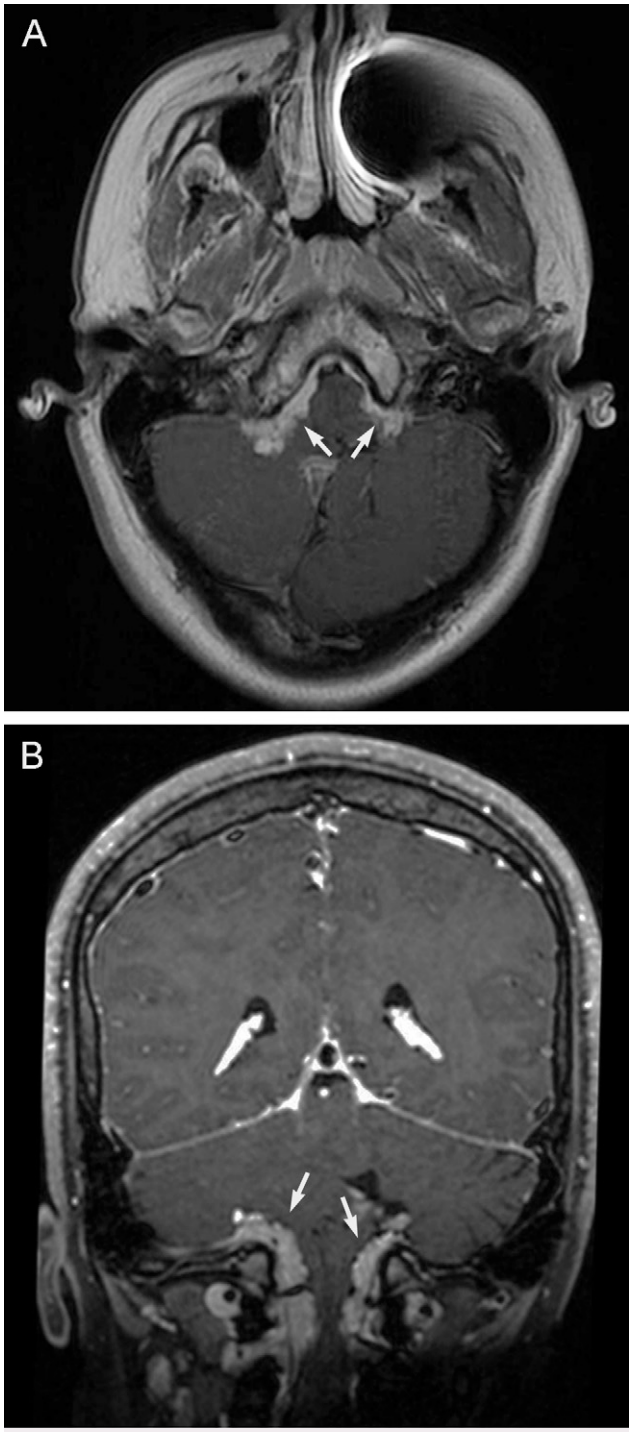


FIG. 3. Meningiomatosis of the skull base. **A:** Postgadolinium axial MRI showing diffuse nodular thickening of the leptomeninges (*arrows*) extending bilaterally from the cerebellopontine angles. **B:** Postgadolinium coronal MRI showing the thickened leptomeningeal mass extending down through the foramen magnum and encasing the brainstem (*arrows*).

Neuroimaging revealed extensive, previously undiagnosed developmental anomalies. There was absence of the sagittal suture with resulting scaphocephaly on three-dimensional reconstruction computed tomography (Fig. 2A). Noncontrast magnetic resonance imaging (MRI) showed a constellation of abnormalities, including a small posterior fossa, platybasia, cerebellar tonsillar herniation, narrow foramen magnum, hypoplasia of the posterior corpus callosum, and pronounced enlargement of the sella turcica with an elongated pituitary stalk and partially empty appearance (Fig. 2B). Calcification was present along the inferior border of the falx cerebri and at its junction with the tentorium (Fig. 2C).

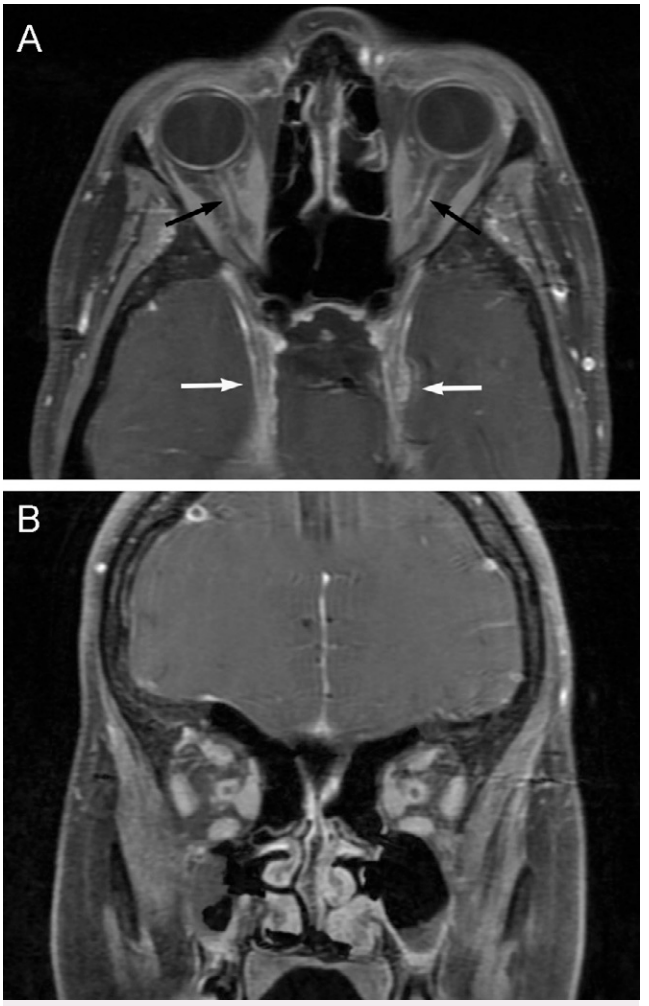
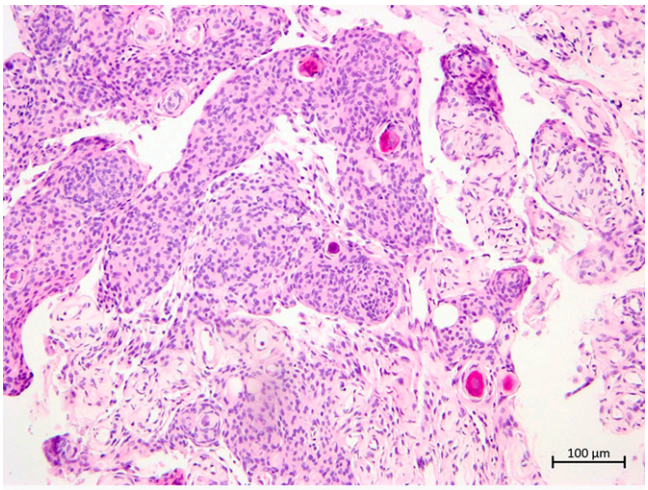


FIG. 4. Bilateral optic nerve sheath meningiomas. **A:** T1-weighted, fat-saturated, gadolinium-enhanced axial image showing a tram track sign (*black arrows*) signifying optic nerve sheath meningioma in each orbit. The tumors were contiguous with intracranial meningiomatosis (*white arrows*). **B:** Coronal image showing an enhancing ring of tumor encasing each optic nerve.

Postgadolinium MRI disclosed diffuse nodular thickening of the leptomeninges extending bilaterally from the cerebellopontine angles down through the foramen magnum (Fig. 3). The contrast-enhancing mass encased the brainstem. There was thickening and enhancement of the petroclival ligaments, caverno-apical triangles, and tuberculum sellae. The abnormal dural enhancement extended through the optic canals to involve both optic nerve sheaths. There was a classic "tram track" sign, associated with optic nerve sheath meningioma (Fig. 4A). Coronal images showed a typical appearance for optic nerve sheath meningiomas (Fig. 4B).



Specimen Source	Meningioma 1	Meningioma 2	Skull tissue	Buccal cells	Saliva	Blood
TRAF7 Variant	p.R641C	p.R641C	p.R641C	p.R641C	p.R641C	p.R641C
Number of mutant/total reads by NGS	16/218	22/97	22/160	9/1205	7/197	1/1061
Variant allele frequency	7.3%	22.7%	13.7%	0.7%	3.6%	0.1%

FIG. 5. Meningioma biopsy specimen and *TRAF7* p.R641C mutation. Numerous small whorls of meningothelial cells are seen without significant nuclear atypia, consistent with a World Health Organization grade I meningothelial meningioma. Scattered psammoma bodies are also present. Chart shows *TRAF7* p.R641C variant allele encountered in formalin-fixed pathology specimens (meningioma, skull) and in fresh samples (buccal mucosa, saliva, blood). H&E stain, original magnification $\times$100.

The appearance of these lesions on MRI was concerning for neoplastic disease. A diffuse pachymeningeal process such as diffuse meningiomatosis was suspected, given the extent of dural calcification that correlated with enhancing lesions on MRI.

Blood tests and cerebrospinal fluid analysis were negative for an infectious, inflammatory, or neoplastic process. A suboccipital decompression was performed with biopsy of the enhancing dural-based lesion at the craniocervical junction. Histopathological examination of the specimen showed meningothelial cells arranged in whorls associated with psammomatous calcifications, consistent with World Health Organization grade I meningothelial meningioma (Fig. 5).

Chromosomal analysis revealed a normal female karyotype. Array comparative genomic hybridization did not reveal significant chromosomal gains or losses (including on chromosome 22). Genetic screening for craniosynostosis syndromes (including Crouzon, Pfieffer 2–3, Apert, Beare-Stevenson, and Jackson-Weiss) was negative. DNA sequencing of exon 10 of the *FGFR1* gene, exons 8 and 10 of the *FGFR2* gene, exons 7 and 10 of the *FGFR3* gene, and the *TWIST1* gene revealed no disease-causing mutation.

Given the patient's profound vision loss, she was treated with 54 Gy in 30 fractions over 6 weeks using an intensity-modulated radiation therapy technique. Despite treatment, her visual function in both eyes continued to slowly deteriorate.

After 7 years of follow-up, visual function had declined to a level of 20/800 in each eye. Fundus examination showed severe, bilateral optic nerve pallor with no swelling. The patient obtained an associate degree from a community college and is employed as a physical therapy assistant. She agreed to pursue further genetic testing given the availability of next-generation sequencing for tumor gene testing.

Seven years after her biopsy was performed, two formalin-fixed, paraffin-embedded meningioma specimens were retrieved from storage and analyzed via the UCSF500 Cancer Gene Test. It uses capture-based next-generation sequencing to target and analyze the coding regions of 479 cancer genes and select introns of 47 genes (Supplementary Table 1).[14] Sequencing revealed a hotspot missense mutation c.1921C $>$ T (p.R641C) in the *TRAF7* gene localizing to the WD40 domain near the C-terminus of the protein. The two meningioma specimens showed mutant allele frequencies of 7.3% and 22.7% (Fig. 5). No additional pathogenic mutations, rearrangements, amplifications, or deletions were identified in any of the other genes analyzed, including *TERT*, *SMO*, *NF2*, *AKT1*, *PIK3CA*, *PIK3R1*, *KLF4*, *SUFU*, *ARID1A*, *CDKN2A*, *SMARCB1*, and *BAP1*, which have been previously associated with meningioma.[6,7] Copy number analysis showed a balanced genome without large-scale chromosomal gains or losses. Paired normal testing was also performed via the UCSF500 test on peripheral blood, buccal swab, and uninvolved skull bone, showing the same *TRAF7* variant at mutant allele frequencies of 0.1%, 0.7%, and 13.7%, respectively (Fig. 5). Additionally, whole exome sequencing performed on a saliva sample showed the same variant at an allele frequency of 3.6%. These findings reflect a postzygotic somatic mosaicism of the *TRAF7* variant, and could explain the patient's dural meningiomatosis, craniosynostosis, syndactyly, brachydactyly, and patent ductus arteriosus.

Discussion

Observations

This 15-year-old girl had diffuse meningiomatosis accompanied by bilateral optic nerve sheath meningiomas. She was found to have other abnormalities, including craniosynostosis, brain deformities, syndactyly, brachydactyly, history of patent ductus arteriosus, and abnormal facies.

At the time of her diagnosis, testing for craniosynostosis syndromes and copy number variations was negative. More sophisticated genetic testing was not available to explain her disparate findings. Seven years later, molecular analysis of her meningioma biopsy specimen showed a pathogenic mutation within the WD40 domain of the *TRAF7* gene. Mutations in this gene have been reported in a subset of adults with meningioma[8–10,15] but have not been previously reported in a child with meningioma or in a patient of any age with bilateral optic nerve sheath meningioma. Testing of normal skull, saliva, buccal mucosa, and blood later identified the same variant at lower allele frequencies, indicative of postzygotic somatic mosaicism.

TRAF7 Function in Tumor Development

Overexpression of the TRAF family of proteins is a common feature in certain human cancers.[16] For *TRAF7*, somatic mutations are associated with mesothelioma and meningioma.[7,16,17] TRAF7 is composed of an N-terminal RING finger domain, a zinc-finger domain and a coiled-coil domain, features common to all TRAF proteins. It differs at its C-terminal, where a sequence of 40 amino acids followed by a tryptophan (W) aspartic acid (D) dipeptide is repeated 7 times (WD40).[18] The WD40 repeats allow TRAF7 to interact with a number of proteins as well as with DNA to mediate

tumor necrosis factor signaling, immune response pathways, cellular differentiation, and apoptosis.[16,18] *TRAF7* mutations associated with meningioma are localized to the WD40 domains, suggesting that molecular interactions with this region of the protein play an important role in tumorigenesis.[6,16] TRAF7 is involved in p53, MEKK3, nuclear factor-κB and ubiquitination pathways, which are key regulators of tumor development.[16,18] In addition, meningiomas with *TRAF7* mutations overexpress the checkpoint inhibitors programmed death-ligand 1 (PD-L1), indoleamine 2,3-dioxygenase (IDO), and tryptophan 2,3-dioxygenase (TDO2), impeding the ability of immune cells to migrate into a tumor site.[19]

TRAF7 Syndrome

Nearly a decade after the role of *TRAF7* somatic mutation was identified in meningioma formation, a distinct germline TRAF7 syndrome was recognized. It is characterized by abnormal facies, skeletal and cardiac defects, and developmental delay.[20,21] Most reported cases involve missense mutations within the WD40 domains of *TRAF7*.[21] Three *TRAF7* variants involving the coiled-coil domain (rather than WD40 repeats) have also been identified; however, patients with these variants did not always present with the same characteristic facies.[21] In nearly all cases, the germline variant arises de novo.[7,18]

Only a single prior case of postzygotic somatic mosaicism of a pathogenic *TRAF7* mutation has been described.[20] The patient (subject #7) harbored a mutation in the coiled-coil domain. The mosaic phenotype in this patient was just as severe as that found in other patients with germline mutations.

Our patient had multiple congenital anomalies described in TRAF7 syndrome, including patent ductus arteriosus, brain anomalies, craniosynostosis, abnormal facies, and digital anomalies. However, she did not have intellectual disability, a feature that is present in all other reported cases of TRAF7 syndrome.[20,21] Testing excluded a germline *TRAF7* mutation. However, multiple uninvolved tissues (saliva, buccal swab, skull, blood) tested at different times identified a p.R641C variant located in the WD40 domain of *TRAF7*. This particular variant has not previously been reported in patients with germline or mosaic mutations in *TRAF7*.

Curiously, the variants reported to cause germline TRAF7 syndrome have so far been mutually exclusive from the somatic mutations that occur in meningioma.[21] Moreover, meningioma has been reported in only a single patient with germline TRAF7 syndrome.[20] The distinct phenotypes seen in germline versus somatic mutations may reflect differences in the activity of the mutant TRAF7 protein with respect to its downstream roles in tumorigenesis and signal transduction. Most meningiomas with mutations in *TRAF7* also harbor a second pathogenic variant,[6] which implies that there are limited loci that can independently promote tumor formation. Little is known about the direct role of the TRAF7 protein in the various developmental anomalies seen in TRAF7 syndrome, although downstream MEKK3 pathways are thought to be important in cardiac and craniofacial development.[22] Further study of TRAF7 pathways and their role in normal development and disease is required to better understand the effects of alterations at the specific loci associated with both meningioma and TRAF7 syndrome.

TRAF7 Variants in Meningiomas

Recent studies have uncovered the genetic landscape of adult meningioma.[6–10] A somatic *TRAF7* mutation is present in 20% of adult meningiomas.[6] Approximately 75% of these cases manifest an additional mutation in *KLF4*, *AKT1*, or *PIK3CA* genes.[6] Interestingly, it is rare to find concomitant mutations in *TRAF7* and *NF2*.[6–10] Our patient was negative for any other gene mutation reported in meningioma. Her mutation at the R641C locus has been reported in 4% of meningiomas with *TRAF7* gene mutations.[6]

For pediatric meningioma, the molecular pathogenesis has been less well established. Battu et al. evaluated specimens from 36 children with sporadic meningioma and found 72% of cases positive for 22q deletion, 16% with combined 1p and 14q deletion, and 8% with isolated 1p deletion.[23] They identified no cases with a mutation in *AKT*, *SMO*, *KLF4*, *TRAF7*, or *pTERT*, which are present in adult meningiomas.[23] A second study cataloged genetic abnormalities in 38 pediatric meningiomas and reported 68% showing somatic loss-of-function mutations in *NF2* or chromosome 22 loss.[24] This study identified pathogenic variants in four cases, including *SMARCB1*, *FUBP1*, *BRAF*, *pTERT*, *CHEK2*, *SMAD*, and *GATA3*. No cases of *TRAF7* mutation were reported.[24] These two studies suggest that genetic findings in adult and pediatric meningioma differ. Although prior to our case no *TRAF7* mutation had been reported in a pediatric patient with meningioma, it is difficult to evaluate this finding given the limited data published about meningioma within the postpubertal age group. It is possible that the molecular pathogenesis of meningiomas arising in adolescent patients is more concordant with that seen in adult patients.

Optic Nerve Sheath Meningiomas

There is only a single case previously reported of bilateral optic nerve sheath meningioma in a child.[25] Patients with optic nerve sheath meningiomas rarely undergo resection or incisional biopsy because the diagnosis can usually be made via neuroimaging and surgery carries a high risk of vision loss.[26] Consequently, there are limited data regarding the molecular pathogenesis of isolated optic nerve sheath meningiomas. A notable study showed chromosome 22q loss in 10/14 patients with orbital meningioma but only 1/5 with optic nerve sheath meningioma.[27] Another molecular change included copy number alterations involving chromosome 2.[27] There have been no prior reports of a gene mutation in *TRAF7* in a primary optic nerve sheath meningioma specimen. It must be noted that the specimens collected in our patient were from meningioma at the craniocervical junction, not the optic nerve sheaths. However, the tumor extended continuously from the biopsy site up the skull base and through the optic canals into the orbits. The detection of a somatic variant known to cause meningioma supports the inference that it was also present in the patient's optic nerve sheath meningiomas.

Lessons

We report a case of postzygotic somatic mosaicism of the *TRAF7* p.R641C variant in a patient with bilateral optic nerve sheath meningioma, diffuse meningiomatosis, and some features of TRAF7 syndrome. *TRAF7* germline mutations cause an autosomal dominant syndrome with mutations frequently localizing to the WD40 domains but mutually exclusive to WD40 somatic variants found in meningiomas. The mosaic p.R641C variant identified in this case has not been reported previously in a patient with a germline or mosaic mutation in *TRAF7.*

Acknowledgments

This work was supported by grants EY029703 and EY02162 (Vision Core Grant) from the National Eye Institute and by an unrestricted grant from Research to Prevent Blindness (grant EY029703 awarded to J.C.H. and the other two grants awarded to the Department of Ophthalmology).

References

1. Zang KD, Singer H. Chromosomal constitution of meningiomas. *Nature.* 1967;216(5110):84–85.
2. Zankl H, Zang KD. Correlations between clinical and cytogenetical data in 180 human meningiomas. *Cancer Genet Cytogenet.* 1980;1(4):351–356.
3. Dumanski JP, Rouleau GA, Nordenskjöld M, Collins VP. Molecular genetic analysis of chromosome 22 in 81 cases of meningioma. *Cancer Res.* 1990;50(18):5863–5867.
4. Rouleau GA, Merel P, Lutchman M, et al. Alteration in a new gene encoding a putative membrane-organizing protein causes neurofibromatosis type 2. *Nature.* 1993;363(6429):515–521.
5. Goutagny S, Kalamarides M. Meningiomas and neurofibromatosis. *J Neurooncol.* 2010;99(3):341–347.
6. Yuzawa S, Nishihara H, Tanaka S. Genetic landscape of meningioma. *Brain Tumor Pathol.* 2016;33(4):237–247.
7. Youngblood MW, Duran D, Montejo JD, et al. Correlations between genomic subgroup and clinical features in a cohort of more than 3000 meningiomas. *J Neurosurg.* Published online October 25, 2019. doi:10.3171/2019.8.JNS191266.
8. 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(6123):1077–1080.
9. 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(5):649–655.
10. Yuzawa S, Nishihara H, Yamaguchi S, et al. Clinical impact of targeted amplicon sequencing for meningioma as a practical clinical-sequencing system. *Mod Pathol.* 2016;29(7):708–716.
11. Kerr K, Qualmann K, Esquenazi Y, Hagan J, Kim DH. Familial syndromes involving meningiomas provide mechanistic insight into sporadic disease. *Neurosurgery.* 2018;83(6):1107–1118.
12. Lyons CJ, Wilson CB, Horton JC. Association between meningioma and Cowden's disease. *Neurology.* 1993;43(7):1436–1437.
13. Ruggieri M, Huson SM. The clinical and diagnostic implications of mosaicism in the neurofibromatoses. *Neurology.* 2001; 56(11):1433–1443.
14. Kline CN, Joseph NM, Grenert JP, et al. Targeted next-generation sequencing of pediatric neuro-oncology patients improves diagnosis, identifies pathogenic germline mutations, and directs targeted therapy. *Neuro Oncol.* 2017;19(5):699–709.
15. Youngblood MW, Miyagishima DF, Jin L, et al. Associations of meningioma molecular subgroup and tumor recurrence. *Neuro Oncol.* 2021;23(5):783–794.
16. Zotti T, Scudiero I, Vito P, Stilo R. The emerging role of TRAF7 in tumor development. *J Cell Physiol.* 2017;232(6):1233–1238.
17. Bueno R, Stawiski EW, Goldstein LD, et al. Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. *Nat Genet.* 2016;48(4):407–416.
18. Zotti T, Vito P, Stilo R. The seventh ring: exploring TRAF7 functions. *J Cell Physiol.* 2012;227(3):1280–1284.
19. Hao S, Huang G, Feng J, et al. Non-NF2 mutations have a key effect on inhibitory immune checkpoints and tumor pathogenesis in skull base meningiomas. *J Neurooncol.* 2019;144(1):11–20.
20. Tokita MJ, Chen CA, Chitayat D, et al. De novo missense variants in TRAF7 cause developmental delay, congenital anomalies, and dysmorphic features. *Am J Hum Genet.* 2018;103(1): 154–162.
21. Castilla-Vallmanya L, Selmer KK, Dimartino C, et al. Phenotypic spectrum and transcriptomic profile associated with germline variants in TRAF7. *Genet Med.* 2020;22(7):1215–1226.
22. Newbern J, Zhong J, Wickramasinghe RS, et al. Mouse and human phenotypes indicate a critical conserved role for ERK2 signaling in neural crest development. *Proc Natl Acad Sci U S A.* 2008;105(44): 17115–17120.
23. Battu S, Kumar A, Pathak P, et al. Clinicopathological and molecular characteristics of pediatric meningiomas. *Neuropathology.* 2018;38(1):22–33.
24. Toland A, McNulty SN, Pekmezci M, et al. Pediatric meningioma: a clinicopathologic and molecular study with potential grading implications. *Brain Pathol.* 2020;30(6):1134–1143.
25. Nickel M, Löbel U, Holst B, et al. Unexplained loss of vision in a child: consider bilateral primary optic nerve sheath meningioma. *Neuropediatrics.* 2014;45(5):321–324.
26. Parker RT, Ovens CA, Fraser CL, Samarawickrama C. Optic nerve sheath meningiomas: prevalence, impact, and management strategies. *Eye Brain.* 2018;10:85–99.
27. Ho CY, Mosier S, Safneck J, et al. Genetic profiling by single-nucleotide polymorphism-based array analysis defines three distinct subtypes of orbital meningioma. *Brain Pathol.* 2015; 25(2):193–201.

Disclosures

The authors report no conflict of interest concerning the materials or methods used in this study or the findings specified in this paper.

Author Contributions

Conception and design: Horton, Kaidonis, Van Ziffle. Acquisition of data: all authors. Analysis and interpretation of data: Horton, Kaidonis, Pekmezci, Van Ziffle. Drafting the article: Horton, Kaidonis, Van Ziffle. Critically revising the article: Horton, Kaidonis, Pekmezci, Van Ziffle. Reviewed submitted version of manuscript: Horton, Kaidonis, Pekmezci, Auguste. Approved the final version of the manuscript on behalf of all authors: Horton. Statistical analysis: Kaidonis. Administrative/technical/material support: Horton, Kaidonis, Pekmezci. Study supervision: Horton.

Supplemental Information

Online-Only Content

Supplemental material is available with the online version of the article.
Supplementary Table 1. https://thejns.org/doi/suppl/10.3171/CASE2247.

Correspondence

Jonathan C. Horton: University of California, San Francisco, CA. jonathan.horton@ucsf.edu.