doi:10.1093/jnci/djv377 First published online December 13, 2015 Brief Communication



OXFORD

TERT Promoter Mutations and Risk of Recurrence in Meningioma

Felix Sahm^{*}, Daniel Schrimpf^{*}, Adriana Olar^{*}, Christian Koelsche, David Reuss, Juliane Bissel, Annekathrin Kratz, David Capper, Sebastian Schefzyk, Thomas Hielscher, Qianghu Wang, Erik P. Sulman, Sebastian Adeberg, Arend Koch, Ali Fuat Okuducu, Stefanie Brehmer, Jens Schittenhelm, Albert Becker, Benjamin Brokinkel, Melissa Schmidt, Theresa Ull, Konstantinos Gousias, Almuth Friederike Kessler, Katrin Lamszus, Jürgen Debus, Christian Mawrin, Yoo-Jin Kim, Matthias Simon, Ralf Ketter, Werner Paulus, Kenneth D. Aldape, Christel Herold-Mende, Andreas von Deimling

Affiliations of authors: Department of Neuropathology, Institute of Pathology, Ruprecht-Karls-University Heidelberg, Heidelberg, Germany (FS, DS, CK, DR, JB, AK, DC, SS, AvD); Clinical Cooperation Unit Neuropathology, German Consortium for Translational Cancer Research (DKTK), German Cancer Research Center (DKFZ), Heidelberg, Germany (FS, DS, CK, DR, AK, DC, AvD); Department of Pathology (AO), Department of Genomic Medicine (QW), Department of Radiation Oncology (QW, EFS), and Department of Bioinformatics and Computational Biology (QW), The University of Texas MD Anderson Cancer Center, Houston, TX; Department of Radiation Oncology (SA, JD) and Department of Neurosurgery (MSc, TU, CHM), University Hospital Heidelberg, Heidelberg, Germany; Department of Neuropathology, Charité Medical University, Berlin, Germany (AK); Department of Pathology, University Hospital Nürnberg, Nürnberg, Germany (AFO): Department of Neurosurgery, Medical Faculty of the Ruprecht-Karls-University of Heidelberg, Mannheim, Germany (SB); Department of Neuropathology, Institute of Pathology (WP), University Hospital Münster, Germany (BB); Department of Neurosurgery, University Hospital Nürnberg, Neurosurgery, University Hospital Nürnster, Münster, Germany (BB); Department of Neurosurgery, University Hospital Bonn, Bonn, Germany (KC), SG; UP), University Hospital Würzburg, Würzburg, Germany (AFK); Department of Neurosurgery, University Hospital Hamburg, Hamburg, Germany (KL); Department of Neuropathology, Otto von Guericke University Magdeburg, Magdeburg, Germany (CM); Institute of Pathology, Saarland University, Homburg, Saarland, Germany (YJK); Department of Neurosurgery, Saarland University, Homburg, Germany (KK); MacFeeters-Hamilton Brain Tumour Centre, Princess Margaret Cancer Center, Toronto, Ontario, Canada (KDA); Division of Biostatistics, German Cancer Research Center (DKFZ), Heidelberg, Germany (TH).

*Authors contributed equally to this work.

Correspondence to: Felix Sahm, MD, Department of Neuropathology, Institute of Pathology, Ruprecht-Karls-University Heidelberg, and Clinical Cooperation Unit Neuropathology, German Consortium for Translational Cancer Research (DKTK), German Cancer Research Center (DKFZ), Im Neuenheimer Feld 224, 69120 Heidelberg, Germany (e-mail: felix.sahm@med.uni-heidelberg.de) or Andreas von Deimling, MD, Department of Neuropathology, Institute of Pathology, Ruprecht-Karls-University Heidelberg, and Clinical Cooperation Unit Neuropathology, German Consortium for Translational Cancer Research (DKTK), German Cancer Research Center (DKFZ), Im Neuenheimer Feld 224, 69120 Heidelberg, Germany (e-mail: andreas.vondeimling@med.uni-heidelberg.de).

Abstract

COMMUNICATION

The World Health Organization (WHO) classification and grading system attempts to predict the clinical course of meningiomas based on morphological parameters. However, because of high interobserver variation of some criteria, more reliable prognostic markers are required. Here, we assessed the TERT promoter for mutations in the hotspot regions C228T and C250T in meningioma samples from 252 patients. Mutations were detected in 16 samples (6.4% across the cohort, 1.7%, 5.7%, and 20.0% of WHO grade I, II, and III cases, respectively). Data were analyzed by t test, Fisher's exact test, log-rank test, and Cox proportional hazard model. All statistical tests were two-sided. Within a mean follow-up time in surviving patients of 68.1 months, TERT promoter mutations were statistically significantly associated with shorter time to progression

(P < .001). Median time to progression among mutant cases was 10.1 months compared with 179.0 months among wild-type cases. Our results indicate that the inclusion of molecular data (ie, analysis of TERT promoter status) into a histologically and genetically integrated classification and grading system for meningiomas increases prognostic power. Consequently, we propose to incorporate the assessment of TERT promoter status in upcoming grading schemes for meningioma.

Meningiomas are the most common primary central nervous system tumors, accounting for a third of all intracranial and spinal neoplasms. While 80% of meningioma patients can be cured by surgery alone, the tumors recur in up to 20% of patients. To identify patients at risk for recurrence, surgical specimens are subjected to histopathological evaluation and grading according to the World Health Organization (WHO) classification (1). However, some of the current grading criteria are vaguely defined and prone to a high interobserver bias (2–4). In consequence, a fraction of patients requiring adjuvant therapy are not identified while others may receive dispensable radiation therapy. Thus, meningioma classification and grading needs more powerful markers to identify the risk of recurrence, and, similar to other brain tumors, molecular parameters may contribute to this aim.

A potential biomarker for meningioma is TERT promoter mutation. The protein encoded by the TERT gene, telomerase reverse transcriptase, contributes essentially to the immortalization of cancer cells by extending their telomeres. Mutations in the promoter region at hotspots chr5:1,295,228 (C228T) or chr5:1,295,250 (C250T), result in new binding sites for members of the E-twenty-six (ETS) transcription factor family. Increased ETS-binding drives upregulation of TERT expression and consecutively maintains telomere length of the proliferating cancer cells (5-7). Interestingly, increased Ets-1 expression appears associated with aggressive courses of meningioma (8). After initial detection of TERT promoter mutations in melanoma (5,6), we have recently reported on the presence of such mutations in meningiomas, predominantly of higher grade (9). Others subsequently have described six meningioma cases with TERT mutations, five of which associated with recurrence (10).

Despite the reported associations with higher grade and recurrence in a few cases, no data is available on the prognostic power of TERT promoter mutations in meningiomas. Thus, we set out to identify its potential role and investigated the TERT promoter status in a cohort of 252 meningioma patients with clinical follow-up data and compared the prediction power of TERT status to that of the current WHO classification.

Tissue (119 meningioma WHO grade I, 88 WHO grade II, and 45 WHO grade III, mean observation time = 68.08 months, median = 66.87 months) was obtained from the Institutes and Departments of Neuropathology or Neurosurgery at the University Hospitals Berlin, Bonn, Hamburg, Heidelberg, Homburg, Magdeburg, Münster, Würzburg, Tübingen (all Germany), and the MD Anderson Cancer Center, Houston, TX, in accordance with local ethical requirements, based on respective institutional review board approval and informed consent by the patients for scientific use of tissue and data. Simpson grade was assessed by the neurosurgeon intra-operatively; grading was based on the WHO classification for brain tumors of 2007 (1).

Sanger Sequencing was performed as previously described (9). MD Anderson cases underwent targeted next-generation sequencing (Supplementary Methods, available online).

Fisher's exact test (two-tailed) was used for nominal variables, adjusted with Bonferroni correction. Univariate survival analysis was performed with the Kaplan-Meier estimator and log-rank test (for multivariable analysis and conditional tree, see Supplementary Methods, available online). Prediction power was assessed with a modified Brier score; the calculation was done with the R package pec (split method "Boot632plus" with 1000 iterations, R version 3.2). All statistical tests were two-sided, and a P value of less than .05 was considered statistically significant.

Of 252 meningiomas, 16 carried a TERT promoter mutation (6.4%) (Table 1). Of 119 WHO grade I tumors, two harbored the mutation (1.7%, both C228T). Of 88 WHO grade II tumors, five carried the mutations (5.7%, thereof 2 with C228T and three with C250T variant), and of 45 WHO grade III tumors, nine presented with TERT promoter mutations (20.0%, thereof 5 with C228T and 4 with C250T variant). Mutational variants were not associated with sex, localization, or distinct outcome, nor was TERT mutation associated with certain localizations (8 tumors were located at the skull base and 8 at the convexity). WHO grade, time to progression (TTP), age at diagnosis, sex, localization, and mutational variant are given in Supplementary Table 1 (available online).

Among grade I tumors, TERT promoter mutation was statistically significantly associated with morphologically progressive recurrence, ie, recurrence presenting as tumor of higher WHO grade (Fisher's exact test P = .01). Among grade II and grade III tumors, TERT promoter mutations were also associated with recurrence (P = .02 and P = .009, respectively) (Table 1). Importantly, TERT promoter mutation was a prognostic marker of unfavorable TTP over the entire cohort (Figure 1), with a mean observation time of 68.1 months. And here, TERT mutated meningiomas WHO grade III recurred statistically significantly earlier than those without mutation (P < .001, median = TTP 10.1 months compared with 179.0 months among wild-type cases). This observation also holds true when analyzing only cases with at least 60 (P < .001) or 96 (P < .004) months of follow-up (80% of patients with relapse developed recurrence in 60 months, 90% in 96 months). In line with the literature, WHO grade (P = .005, Student's t test) and sex (P < .001, Student's t test, unfavorable for male patients) were associated with recurrence across our cohort. We also found strong association between recurrence and TERT promoter mutation (P < .01, Student's t test). Distribution of age, sex, Simpson grade, recurrent cases, and TERT mutation among WHO grades are given in Supplementary Table 2 (available online), hazard

Table 1. TERT promoter status in WHO grade I-III meningioma and recurrence status $\!\!\!^*$

WHO Grade	All (mut/n)	Recurred (mut/n)	Higher grade at recurrence (mut/n)
I	2/119	2/32	2/4
II	5/88	5/39	2/11
III	9/45	8/26	NA
All grades	16/252	15/97	4/15

* Occurrence of TERT promoter mutations among meningioma of WHO grades I, II, and III ("all"), stratification for TERT promoter mutations among cases that resulted in recurrence ("recurred") and cases that recurred with histologically higher grade ("higher grade at recurrence"). mut = mutant; WHO = World Health Organization.

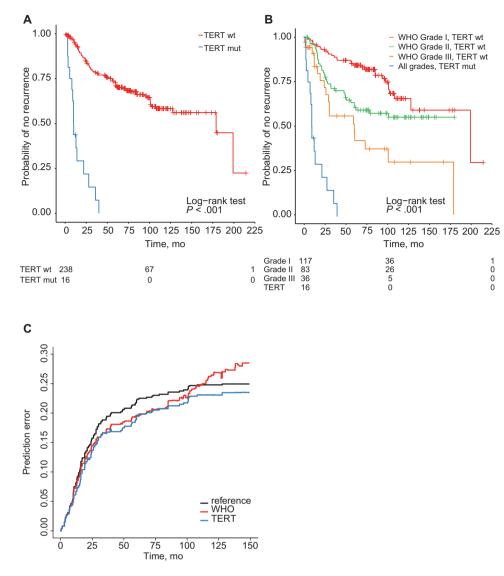


Figure 1. Kaplan-Meier plots of time to progression in TERT promoter mutant vs wild-type samples (A) and World Health Organization (WHO) grade I-III vs TERT mutant (B). Tables below plots indicate patients at risk at time points 0, 100, and 225 months. All statistical tests were two-sided Brier prediction plot of WHO grading vs TERT status. The reference group is the marginal Kaplan-Meier prediction model (C). mut = mutant; WHO = World Health Organization; wt = wild-type.

ratios and P values for Cox univariate and multivariable analyses in Supplementary Tables 3 and 4 (available online). Of note, the majority of TERT mutant cases were male (10/16), with 4% of all female and 11% of all male patients in the cohort harboring TERT mutations. Mean age at diagnosis was 63 years (SD = 10 years) for mutant and 56 years (SD = 14 years) for wild-type cases.

Thus, the prediction power of TERT promoter status essentially supports current WHO grading in identifying patients at risk for early recurrence. In a conditional inference tree model with the five predictors Simpson grade, age at diagnosis, sex, TERT status, and WHO grade, TERT status was the dominant criterion for TTP prediction (P < .001) (data not shown). In line, TERT status was superior to WHO grade in predicting TTP in a modified prediction error model (P < .001) (Figure 1C).

Thus, TERT promoter status proved to be a valuable tool in identification of a subset with shorter TTP compared with meningiomas with TERT wild-type status. Of note, mutant TERT promoter status also identified cases with early recurrence among samples histologically attributed to WHO grades I or II.

Previous studies striving for more reliable predictors of meningioma progression focused on cytogenetics and expression profiles (2,3,7,8,11,12). However, none of the proposals have been implemented in diagnostic routine. The data here paradigmatically demonstrate that genes recently found mutated in meningiomas such as TERT, KLF4, AKT1, TRAF7, and SMO (9,13-16) may be translated into novel markers of prognostic power. Application of such markers will assist in overcoming the current limitations of histological classification. Applying molecular genetics for tumor stratification is in line with the recommendations of the "ISN-Haarlem" guidelines proposed by the International Society of Neuropathology as basis for an updated WHO classification of brain tumors (17). Based on this concept, meningioma diagnostics may also soon be "layered" as proposed for parenchymal brain tumors (18), taking into account histological classification (eg, meningothelial meningioma), histological WHO grade (eg, grade I), and molecular information (eg, TERT promoter mutant). Information on TERT promoter mutation will also allow the clinician to identify cases that are even more aggressive than other meningiomas with anaplastic

grade III histology. However, consideration of assigning grade IV to this subgroup would require comparison of overall survival with other entities with grade IV variants. Lack of those overall survival data is a limitation of this study, along with the lack of external validation data and functional characterizations. Further, the number of mutant cases (n = 16) does not allow for robust biological conclusions on the effect of sex and age among TERT mutant cases, although statistically significant in this dataset (Supplementary Tables 3 and 4, available online).

In conclusion, TERT promoter mutations are associated with higher meningioma grades and with early recurrence and may be a useful tool assisting in the grading of meningioma.

Funding

This study was supported by grant 110670 of the German Cancer Aid to FS, RK, and AvD, grant 110983 of the German Cancer Aid to AvD and FS, and by the Forschungsgruppe Aggressive Meningeome (FORAMEN) initiative within the German Neurosurgical Society (DGNC), National Institutes of Health Cancer Center Support Grant CA016672 (to the Sequencing and Microarray Facility, UT MD Anderson Cancer Center). AO was supported by the National Institutes of Health/National Cancer Institute (Training Grant No. 5T32CA163185). FS is a fellow of the Medical Faculty Heidelberg Post Doc Program.

Notes

The study funders had no role in the design of the study; the collection, analysis, or interpretation of the data; the writing of the manuscript; or the decision to submit the manuscript for publication.

References

 Louis DN, Ohgaki H, Wiestler OD, et al. The 2007 WHO classification of tumours of the central nervous system. Acta Neuropathol. 2007;114(2):97–109.

- Domingues PH, Sousa P, Otero A, et al. Proposal for a new risk stratification classification for meningioma based on patient age, WHO tumor grade, size, localization, and karyotype. Neuro Oncol. 2014;16(5):735–747.
- 3. DeAngelis LM. Brain tumors. N Engl J Med. 2001;344(2):114–123.
- Olar A, Wani KM, Sulman EP, et al. Mitotic Index is an Independent Predictor of Recurrence-Free Survival in Meningioma. Brain Pathol. 2015;25(3):266–275.
- Huang FW, Hodis E, Xu MJ, et al. Highly recurrent TERT promoter mutations in human melanoma. *Science*. 2013;339(6122):957–959.
 Horn S, Figl A, Rachakonda PS, et al. TERT promoter mutations in familial
- norm 5, rigit A, Rachakonda PS, et al. 1EK1 promoter mutations in familial and sporadic melanoma. Science. 2013;339(6122):959–961.
 Maillo A. Orfao. A. Saurapico BA et al. New chariferentiae echarge for the science of the
- Maillo A, Orfao A, Sayagues JM, et al. New classification scheme for the prognostic stratification of meningioma on the basis of chromosome 14 abnormalities, patient age, and tumor histopathology. J Clin Oncol. 2003;21(17):3285–3295.
- Okuducu AF, Zils U, Michaelis SA, et al. Increased expression of avian erythroblastosis virus E26 oncogene homolog 1 in World Health Organization grade 1 meningiomas is associated with an elevated risk of recurrence and is correlated with the expression of its target genes matrix metalloproteinase-2 and MMP-9. Cancer. 2006;107(6):1365–1372.
- Koelsche C, Sahm F, Capper D, et al. Distribution of TERT promoter mutations in pediatric and adult tumors of the nervous system. Acta Neuropathol. 2013;126(6):907–915.
- Goutagny S, Nault JC, Mallet M, et al. High incidence of activating TERT promoter mutations in meningiomas undergoing malignant progression. Brain Pathol. 2014;24(2):184–189.
- Mawrin C, Perry A. Pathological classification and molecular genetics of meningiomas. J Neurooncol. 2010;99(3):379–391.
- Riemenschneider MJ, Perry A, Reifenberger G. Histological classification and molecular genetics of meningiomas. *Lancet Neurol.* 2006;5(12):1045–1054.
- Sahm F, Bissel J, Koelsche C, et al. AKT1E17K mutations cluster with meningothelial and transitional meningiomas and can be detected by SFRP1 immunohistochemistry. Acta Neuropathol. 2013;126(5):757–762.
- Reuss DE, Piro RM, Jones DT, et al. Secretory meningiomas are defined by combined KLF4 K409Q and TRAF7 mutations. Acta Neuropathol. 2013;125(3):351– 358.
- 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.
- Brastianos PK, Horowitz PM, Santagata S, et al. Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. Nat Genet. 2013;45(3):285–289.
- Louis DN, Perry A, Burger P, et al. International Society Of Neuropathology-Haarlem consensus guidelines for nervous system tumor classification and grading. Brain Pathol. 2014;24(5):429–435.
- Reuss DE, Sahm F, Schrimpf D, et al. ATRX and IDH1-R132H immunohistochemistry with subsequent copy number analysis and IDH sequencing as a basis for an "integrated" diagnostic approach for adult astrocytoma, oligodendroglioma and glioblastoma. Acta Neuropathol. 2015;129(1):133–146.