



A Poorly Differentiated Non-keratinizing Sinonasal Squamous Cell Carcinoma with a Novel *ETV6-TNFRSF8* Fusion Gene

Justin Bubola^{1,2} · Christina M. MacMillan^{1,3} · Ilan Weinreb⁴ · Ian Witterick⁵ · David Swanson¹ · Lei Zhang⁶ · Cristina R. Antonescu⁶ · Brendan C. Dickson^{1,3,7}

Received: 19 October 2020 / Revised: 5 November 2020 / Accepted: 6 November 2020 / Published online: 4 January 2021
© Springer Science+Business Media, LLC, part of Springer Nature 2021

Abstract

Squamous cell carcinoma of the sinonasal tract is relatively rare and morphologically and genetically heterogeneous. We report the case of an adult male with a left sphenoid sinus mass. A biopsy revealed an undifferentiated carcinoma composed of sheets of epithelioid cells lacking keratinization and glandular formation. The tumor was associated with a prominent lymphoplasmacytic inflammatory infiltrate. Immunohistochemical staining demonstrated diffuse expression of pankeratin and p63; it was negative for p16. In addition, EBER was also negative. Morphologically the findings raised the possibility of non-keratinizing squamous cell carcinoma. RNA sequencing was undertaken to exclude the possibility of NUT carcinoma; interestingly, this revealed a novel *ETV6-TNFRSF8* fusion transcript, which was independently confirmed by fluorescence in situ hybridization. The current case is illustrative because it broadens our understanding of the molecular pathogenesis of non-keratinizing squamous cell carcinoma and adds to the diversity of *ETV6*-rearranged malignancies.

Keywords Sinonasal carcinoma · *ETV6* · *TNFRSF8*

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s12105-020-01249-6>) contains supplementary material, which is available to authorized users.

✉ Brendan C. Dickson
Brendan.Dickson@sinahealth.ca

- ¹ Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, ON, Canada
- ² Faculty of Dentistry, University of Toronto, Toronto, ON, Canada
- ³ Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario, Canada
- ⁴ Department of Pathology, University Health Network, Toronto, ON, Canada
- ⁵ Department of Otolaryngology Head and Neck Surgery, Department of Surgical Oncology, University Health Network, Toronto, ON, Canada
- ⁶ Department of Pathology, Memorial Sloan Kettering Cancer Center, New York, NY, USA
- ⁷ Pathology & Laboratory Medicine, Mount Sinai Hospital, 600 University Ave, Suite 6.500.12.5, Toronto, ON M5G 1X5, Canada

Introduction

Squamous cell carcinoma arising within the sinonasal tract is relatively uncommon and is currently divided by the World Health Organization into: keratinizing, non-keratinizing, spindle cell (sarcomatoid), and lymphoepithelial subtypes [1]. Risk factors vary from environmental exposures to infectious aetiologies (i.e., human papillomavirus and Epstein-Barr virus). The underlying molecular attributes tend to overlap with tumors at other anatomic sites, which mostly exhibit complex karyotypes and aneuploidy with frequent loss of *TP53* and *CDKN2A/B* tumor suppressor genes [2–6]. In contrast to salivary gland neoplasms, chromosomal translocations are relatively uncommon in squamous cell carcinoma. Herein we report the case of an adult male with a poorly differentiated carcinoma of the sphenoid sinus harboring a novel *ETV6-TNFRSF8* gene fusion.

Case Report

A 66-year-old male presented with diplopia and mild proptosis with no sinonasal symptoms. CT and MRI imaging showed an infiltrative mass in the base of skull centered

along the left sphenoid sinus and extending into the left cavernous sinus and sella, which prompted an endoscopic sphenoidotomy and biopsy. Microscopic examination revealed a neoplasm composed of sheets of epithelioid cells with a vague fascicular-storiform pattern (Fig. 1a–c). The cytoplasm was abundant and eosinophilic and lacked overt keratinization. The nuclei were ovoid with mild-moderate pleomorphism and prominent small nucleoli; mitotic activity was conspicuous (Fig. 1d). There was a brisk lymphoplasmacytic inflammatory infiltrate and occasional neutrophils (Fig. 1c, d). Immunohistochemical staining demonstrated the tumor was diffusely positive for keratin (AE1/AE3), p40 and p63; it was negative for p16, CD30, CD45, CD56, and S100; INI-1 was intact (Fig. 2). In situ hybridization was negative for Epstein-Barr virus-encoded small RNAs (EBER) (not shown). Based on the findings, the differential diagnosis included non-keratinizing squamous cell carcinoma, NUT carcinoma, adamantinoma-like Ewing sarcoma, and adenoid cystic carcinoma. Targeted RNA sequencing was performed which excluded the presence of *NUTM1*, *EWSR1*, *FUS*, *MYB*, *MYBL1* and *NFIB* rearrangement, amongst others (Illumina TruSight RNA fusion panel; San Diego, CA). Surprisingly, it revealed a novel *ETV6-TNFRSF8* fusion product involving *ETV6* (exon 5 of 8; NCBI Reference Sequence: NM_001987.4) and *TNFRSF8* (exon 13 of 15; NM_001243.4). Independent validation of this event by

fluorescence in situ hybridization (FISH)—using custom probes from bacterial artificial chromosomes (Supplementary Table 1)—confirmed the presence of *ETV6* rearrangement (Fig. 3). The molecular findings therefore suggest a novel form of non-keratinizing squamous cell carcinoma.

Staging revealed T4N2M0 disease. The patient received induction chemotherapy followed by concurrent chemoradiotherapy with high-dose cisplatin. There was no evidence of recurrence at the 1-year follow-up.

Discussion

In contrast to salivary gland neoplasms, oncogenic fusion genes are relatively uncommon in squamous carcinoma of the head and neck. A notable exception includes NUT carcinoma—characterized by *NUTM1*-rearrangement—which may represent an aggressive subtype of squamous cell carcinoma [6]. More recently, squamous cell carcinomas with other gene fusions have been reported in the literature. For example, the *DEK-AFF2* fusion gene in a subset of non-keratinizing squamous cell carcinoma of the middle ear and temporal bone [7, 8]. These neoplasms can be morphologically undifferentiated, necessitating immunohistochemistry to highlight evidence of squamous differentiation. Herein

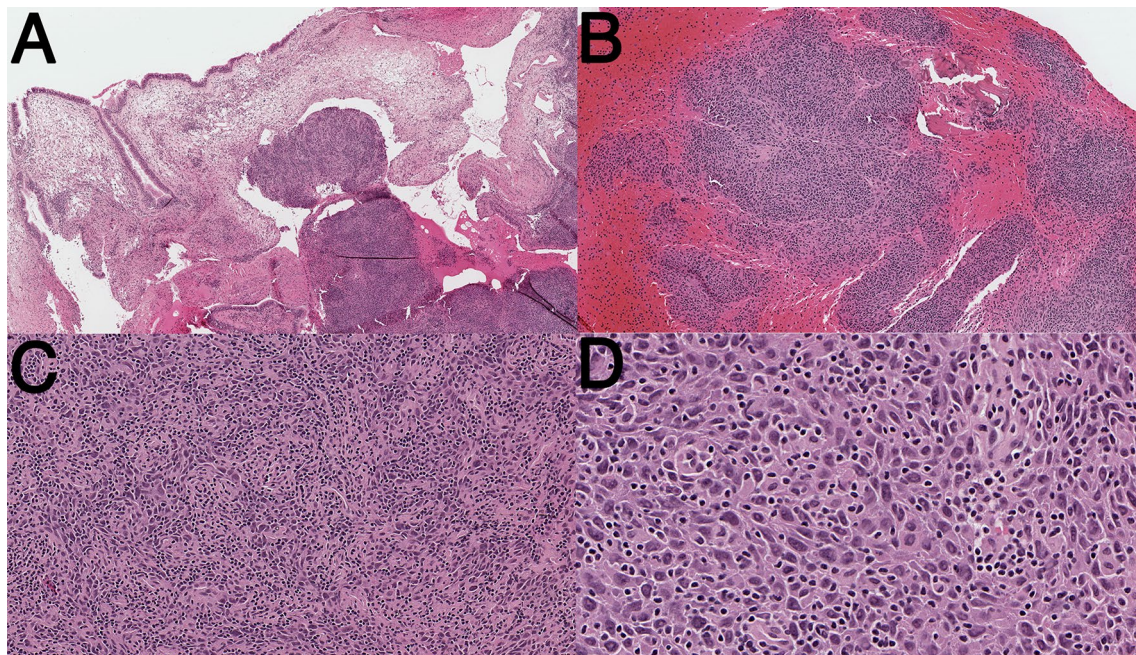


Fig. 1 Representative photomicrographs of *ETV6-TNFRSF8* associated carcinoma (Hematoxylin and Eosin). **a** Low-power magnification showing respiratory-type mucosa overlying neoplasm. **b** Intermediate power magnification demonstrating infiltration of bone. **c** Intermediate magnification showing sheets of epithelioid to spindle

cells with a prominent lymphoplasmacytic inflammatory infiltrate. **d** High power magnification highlighting moderate nuclear atypia and numerous mitotic figures. There is no evidence of overt keratinization, or glandular formation

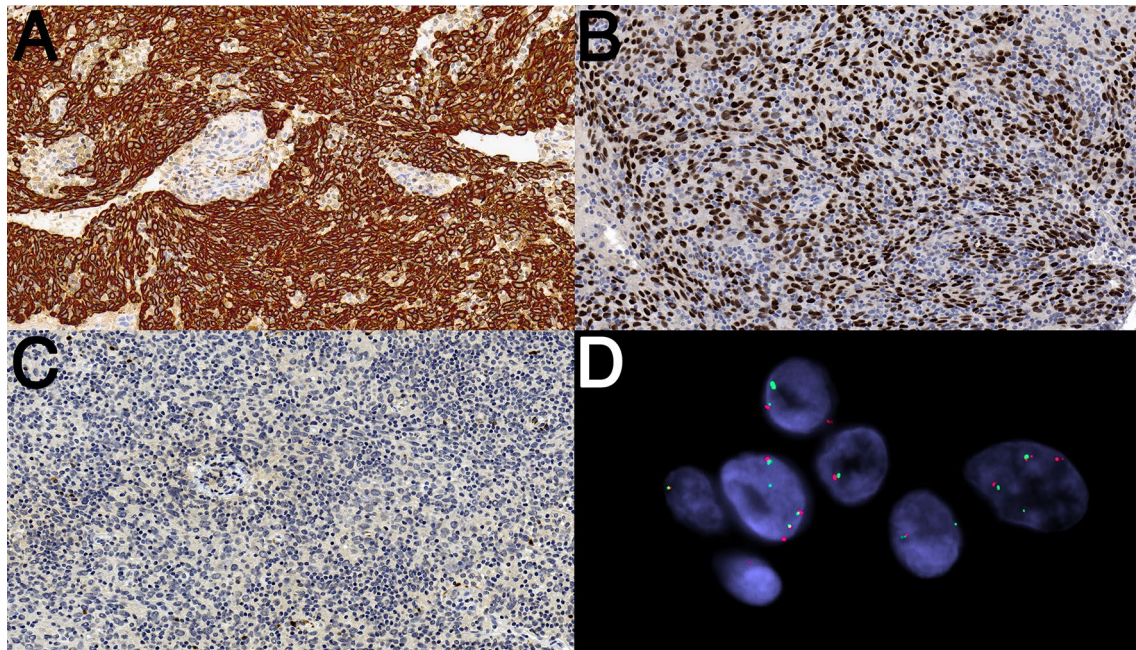


Fig. 2 Immunohistochemical staining and fluorescence in situ hybridization of *ETV6-TNFRSF8* associated carcinoma. **a** Diffuse cytoplasmic immunostaining for pan-cytokeratin. **b** Diffuse nuclear immunostaining for p63. **c** The tumor is negative for p16. **d** Fluorescence

in situ hybridization showing unbalanced *ETV6* gene rearrangement with deletion of the centromeric signal (red), in cells with 2n, 3n, and 4n copies (polysomic) of *ETV6* (red, centromeric; green, telomeric)

ETV6

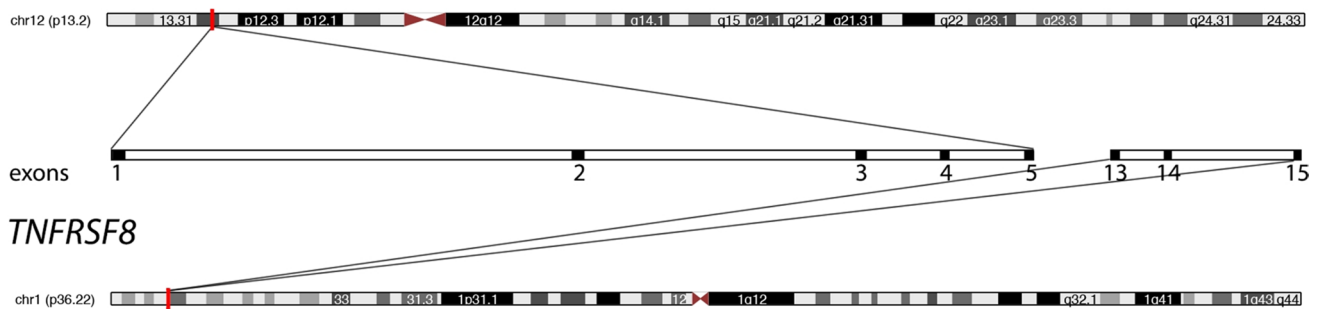


Fig. 3 Diagrammatic representation of *ETV6-TNFRSF8* fusion transcript. The gene location is highlighted by red band on each chromosome (<http://genome.ucsc.edu>) [31]. The expanded view in the center of the image depicts the spatial relationship of the exons for each gene

we describe another carcinoma, arising at the base of skull, which harbored a novel *ETV6-TNFRSF8* fusion product.

ETV6 encodes ETS variant transcription factor 6, which is normally involved in hematopoiesis through the regulation of stem cells and maintenance of vascular networks [9]. *ETV6* fusions with various partner genes are well-documented in hematologic malignancies; however, *ETV6* rearrangements in solid tumors are increasingly recognized [9]. The *ETV6-NTRK3* fusion gene has been demonstrated in secretory carcinoma of the breast [10], salivary gland [11], thyroid gland [12, 13] and skin [14] as well as

in low-grade sinonasal adenocarcinoma [15, 16], infantile fibrosarcoma [17], congenital mesoblastic nephroma [18], ALK-negative inflammatory myofibroblastic tumor [19], gastrointestinal stromal tumor [20], radiation-associated papillary thyroid carcinoma [21], pediatric high grade glioma [22] and melanocytic neoplasms such as Spitz tumors [23]. Alternate *ETV6* fusion partners have also been described. These include *ALK* in epithelioid fibrous histiocytoma [24] as well as *RET*, *MET* and *MAML3* in secretory carcinoma of the salivary glands [25, 26]. To the

best of our knowledge, *TNFRSF8* has not previously been reported as an *ETV6* fusion partner.

The *TNFRSF8* gene is a member of the tumor necrosis factor receptor superfamily. It encodes for CD30 protein, a well-known marker of Hodgkin and anaplastic large cell lymphoma [27]. CD30 interacts with its ligand, CD30L, to activate NF- κ B, MAP kinase, and Akt signaling pathways [27, 28]. Depending on the specific cell type and costimulatory signals involved, signal transduction can either promote cell proliferation and survival or promote apoptosis and cell cycle arrest [28, 29]. Rare cases of lung adenocarcinoma and breast carcinoma harboring *TNFRSF8- PLEKHG5* and *TNFRSF8-STAR13* fusions, respectively, have been reported in the literature [30].

The tumor in our patient was morphologically undifferentiated and characterized by sheets of epithelioid cells lacking keratinization. Immunohistochemical stains revealed squamous differentiation. Interestingly, the tumor contained a brisk lymphoplasmacytic infiltrate, raising the possibility of lymphoepithelial carcinoma; however, EBER was negative. Targeted RNA sequencing was performed to exclude the possibility of NUT carcinoma, amongst other considerations; surprisingly, it revealed a novel *ETV6-TNFRSF8* fusion gene. While the presence of *ETV6*-rearrangement in a tumor at this location raises the possibility of secretory carcinoma or a low-grade sinonasal adenocarcinoma with *ETV6* rearrangement, these tumors can be readily differentiated based on their distinctive morphologies and immunophenotypes. Based on its undifferentiated morphology and immunohistochemical evidence supporting squamous differentiation, this tumor is believed to be best classified as an undifferentiated carcinoma given the information available to date. This fusion product is potentially diagnostically relevant; however, at present, it does not appear to have direct therapeutic relevance.

In summary, we report an undifferentiated carcinoma arising in the sphenoid sinus that harbored a novel *ETV6-TNFRSF8* fusion gene. This finding expands the spectrum of neoplasms characterized by *ETV6*-rearrangement. Further studies are necessary to determine the prevalence of this finding, and ascertain whether this is restricted to carcinoma of the sinonasal tract.

Funding Panov 2 Research Fund.

Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

References

1. El-Naggar A, Chan J, Grandis J, Takata T, Sliotweg P. WHO Classification of head and neck tumours. 4th ed. Lyon: International Agency for Research on Cancer; 2017.
2. Chung CH, Guthrie VB, Masica DL, et al. Genomic alterations in head and neck squamous cell carcinoma determined by cancer gene-targeted sequencing. *Ann Oncol*. 2015;26(6):1216–23.
3. Stransky N, Egloff AM, Tward AD, et al. The mutational landscape of head and neck squamous cell carcinoma. *Science*. 2011;333(6046):1157–60.
4. Seiwert TY, Zuo Z, Keck MK, et al. Integrative and comparative genomic analysis of HPV-positive and HPV-negative head and neck squamous cell carcinomas. *Clin Cancer Res*. 2015;21(3):632–41.
5. Network CGA. Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*. 2015;517(7536):576–82.
6. French CA. Pathogenesis of NUT midline carcinoma. *Annu Rev Pathol*. 2012;7:247–65.
7. Todorovic E, Truong T, Eskander A, et al. Middle ear and temporal bone nonkeratinizing squamous cell carcinomas with DEK-AFF2 fusion: an emerging entity. *Am J Surg Pathol*. 2020;44(9):1244–50.
8. Yang W, Lee KW, Srivastava RM, et al. Immunogenic neoantigens derived from gene fusions stimulate T cell responses. *Nat Med*. 2019;25(5):767–75.
9. Biswas A, Rajesh Y, Mitra P, Mandal M. *ETV6* gene aberrations in non-haematological malignancies: a review highlighting *ETV6* associated fusion genes in solid tumors. *Biochim Biophys Acta Rev Cancer*. 2020;1874:188389.
10. Tognon C, Knezevich SR, Huntsman D, et al. Expression of the *ETV6-NTRK3* gene fusion as a primary event in human secretory breast carcinoma. *Cancer Cell*. 2002;2(5):367–76.
11. Skálová A, Vanecek T, Sima R, et al. Mammary analogue secretory carcinoma of salivary glands, containing the *ETV6-NTRK3* fusion gene: a hitherto undescribed salivary gland tumor entity. *Am J Surg Pathol*. 2010;34(5):599–608.
12. Dogan S, Wang L, Ptashkin RN, et al. Mammary analog secretory carcinoma of the thyroid gland: a primary thyroid adenocarcinoma harboring *ETV6-NTRK3* fusion. *Mod Pathol*. 2016;29(9):985–95.
13. Dettloff J, Seethala RR, Stevens TM, et al. Mammary analog secretory carcinoma (MASC) involving the thyroid gland: a report of the first 3 cases. *Head Neck Pathol*. 2017;11(2):124–30.
14. Amin SM, Beattie A, Ling X, Jennings LJ, Guitart J. Primary cutaneous mammary analog secretory carcinoma with *ETV6-NTRK3* translocation. *Am J Dermatopathol*. 2016;38(11):842–5.
15. Andreasen S, Skálová A, Agaimy A, et al. *ETV6* gene rearrangements characterize a morphologically distinct subset of sinonasal low-grade non-intestinal-type adenocarcinoma: a novel translocation-associated carcinoma restricted to the sinonasal tract. *Am J Surg Pathol*. 2017;41(11):1552–60.
16. Andreasen S, Kiss K, Melchior LC, Laco J. The *ETV6-RET* gene fusion is found in *ETV6*-rearranged low-grade sinonasal adenocarcinoma without *NTRK3* involvement. *Am J Surg Pathol*. 2018;42(7):985–8.
17. Knezevich SR, McFadden DE, Tao W, Lim JF, Sorensen PH. A novel *ETV6-NTRK3* gene fusion in congenital fibrosarcoma. *Nat Genet*. 1998;18(2):184–7.
18. Anderson J, Gibson S, Sebire NJ. Expression of *ETV6-NTRK3* in classical, cellular and mixed subtypes of congenital mesoblastic nephroma. *Histopathology*. 2006;48(6):748–53.
19. Allassiri AH, Ali RH, Shen Y, et al. *ETV6-NTRK3* is expressed in a subset of ALK-negative inflammatory myofibroblastic tumors. *Am J Surg Pathol*. 2016;40(8):1051–61.

20. Brenca M, Rossi S, Polano M, et al. Transcriptome sequencing identifies ETV6-NTRK3 as a gene fusion involved in GIST. *J Pathol.* 2016;238(4):543–9.
21. Leeman-Neill RJ, Kelly LM, Liu P, et al. ETV6-NTRK3 is a common chromosomal rearrangement in radiation-associated thyroid cancer. *Cancer.* 2014;120(6):799–807.
22. Xu T, Wang H, Huang X, et al. Gene fusion in malignant glioma: an emerging target for next-generation personalized treatment. *Transl Oncol.* 2018;11(3):609–18.
23. Yeh I, Tee MK, Botton T, et al. NTRK3 kinase fusions in Spitz tumours. *J Pathol.* 2016;240(3):282–90.
24. Dickson BC, Swanson D, Charames GS, Fletcher CD, Hornick JL. Epithelioid fibrous histiocytoma: molecular characterization of ALK fusion partners in 23 cases. *Mod Pathol.* 2018;31(5):753–62.
25. Skalova A, Vanecek T, Martinek P, et al. Molecular profiling of mammary analog secretory carcinoma revealed a subset of tumors harboring a novel ETV6-RET translocation: report of 10 cases. *Am J Surg Pathol.* 2018;42(2):234–46.
26. Guilmette J, Dias-Santagata D, Nosé V, Lennerz JK, Sadow PM. Novel gene fusions in secretory carcinoma of the salivary glands: enlarging the ETV6 family. *Hum Pathol.* 2019;83:50–8.
27. So T, Ishii N. The TNF-TNFR family of co-signal molecules. *Adv Exp Med Biol.* 2019;1189:53–84.
28. Ward-Kavanagh LK, Lin WW, Šedý JR, Ware CF. The TNF receptor superfamily in co-stimulating and co-inhibitory responses. *Immunity.* 2016;44(5):1005–19.
29. Oflazoglu E, Grewal IS, Gerber H. Targeting CD30/CD30L in oncology and autoimmune and inflammatory diseases. *Adv Exp Med Biol.* 2009;647:174–85.
30. Yoshihara K, Wang Q, Torres-Garcia W, et al. The landscape and therapeutic relevance of cancer-associated transcript fusions. *Oncogene.* 2015;34(37):4845–54.
31. Kent WJ, Sugnet CW, Furey TS, et al. The human genome browser at UCSC. *Genome Res.* 2002;12(6):996–1006.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.