

Case Reports [Neuropathology](#). 2023 Nov 2. doi: 10.1111/neup.12948. Online ahead of print.

SEGA-like circumscribed astrocytoma in a non-NF1 patient, harboring molecular profile of GBM. A case report

Seiji Yamada ^{1 2}, Motoki Tanikawa ¹, Yuko Matsushita ³, Ryota Fujinami ¹, Hiroshi Yamada ¹, Kaishi Sakomi ⁴, Tomohiro Sakata ¹, Hidehito Inagaki ⁵, Hideaki Yokoo ⁶, Koichi Ichimura ³, Mitsuhiro Mase ¹

Affiliations

PMID: 37919875 DOI: [10.1111/neup.12948](https://doi.org/10.1111/neup.12948)

Abstract

Subependymal giant cell astrocytoma (SEGA) is a low-grade periventricular tumor that is closely associated with tuberous sclerosis complex (TSC). SEGA typically arises during the first two decades of life and rarely arises after the age of 20-25 years. Nevertheless, it has also been reported that glioma histologically resembling SEGA, so-called SEGA-like astrocytoma, can arise in neurofibromatosis type 1 (NF1) patients, even in the elderly. Herein, we report a case of SEGA-like circumscribed astrocytoma arising in the lateral ventricle of a 75-year-old woman. Whole-exome sequencing revealed a somatic variant of NF1. Methylation array analysis led to a diagnosis of "methylation class glioblastoma, IDH-wildtype, mesenchymal-type (GBM, MES)" with a high calibrated score (0.99). EGFR amplification, CDKN2A/B homozygous deletion, chromosomal +7/-10 alterations, and TERT promoter mutation, typical molecular abnormalities usually found in GBM, were also observed. While most reported cases of SEGA-like astrocytoma have arisen in NF1 patients, the patient was neither TSC nor NF1. Near total removal was accomplished with endoscopic cylinder surgery. At the 36-month follow-up, there was no tumor recurrence without adjuvant therapies. This clinical behavior did not match GBM. SEGA-like astrocytoma of the elderly is rare, and this is the oldest case reported so far. In addition, high-grade molecular features found in circumscribed tumor remain unclear. Further investigations among larger series are needed for clarifying the underlying molecular mechanisms.

Keywords: DNA methylation array; NF1; SEGA; TSC; whole-exome sequencing.

© 2023 Japanese Society of Neuropathology.

[PubMed Disclaimer](#)