Biomarker for secondary glioblastoma

Mansouri et al. in 2017 provided an overview of our latest understanding of the molecular diversity of Glioblastoma, specifically as it pertains to primary and secondary Glioblastomas, and how it influences prognostication and therapeutic decision-making [1].

PTPRZ1-MET fusion transcript: Protein tyrosine phosphatase receptor type Z1 (PTPRZ1)-MET proto-oncogene receptor tyrosine kinase (MET) (ZM) fusion has been identified as a biomarker for secondary glioblastoma (sGlioblastoma) that is involved in glioma progression, but the mechanism of gliomagenesis and pathology of ZM-negative sGlioblastoma has remained to be fully elucidated. A whole-transcriptome signature is thus required to improve the outcome prediction for patients with sGlioblastoma without ZM fusion.

In a study, whole-transcriptome sequencing on 42 sGlioblastoma samples with or without ZM fusion from the Chinese Glioma Genome Atlas database identified mRNAs with differential expression between patients with and without ZM fusion and the most significant survival-associated genes were identified. A 6-gene signature was identified as a novel prognostic model reflecting survival probability in patients with ZM-negative sGlioblastoma. Clinical characteristics in patients with a high or low risk score value were analyzed with the Kaplan-Meier method and a two-sided log-rank test. In addition, ZM-negative sGlioblastoma patients with a high risk score exhibited an increase in immune cells, NF-κB-induced pathway activation and a decrease in endothelial cells compared with those with a low risk score. The present study demonstrated the potential use of a next-generation sequencing-based cancer gene signature in patients with ZM-negative sGlioblastoma, indicating possible clinical therapeutic strategies for further treatment of such patients [2].

[1]

Mansouri A, Karamchandani J, Das S. Molecular Genetics of Secondary Glioblastoma. In: De Vleeschouwer S, editor. Glioblastoma [Internet]. Brisbane (AU): Codon Publications; 2017 Sep 27. Chapter 2. Available from http://www.ncbi.nlm.nih.gov/books/NBK469981/ PubMed PMID: 29251857.

[2]

Chen BS, Wang KY, Yu SQ, Zhang CB, Li GZ, Wang ZL, Bao ZS. Whole-transcriptome sequencing profiling identifies functional and prognostic signatures in patients with PTPRZ1-MET fusion-negative secondary glioblastoma multiforme. Oncol Lett. 2020 Nov;20(5):187. doi: 10.3892/ol.2020.12049. Epub 2020 Sep 3. PMID: 32952656; PMCID: PMC7479526.