Biomarkers associated to treatment response and prognosis in Glioblastoma Multiforme


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BACKGROUND:
Gliomas represents more of 80% of malignant tumors of central nervous system. Glioblastoma Multiforme is the most aggressive glioma with an average overall survival (OS) of 12 months, and the most prevalent, about 60-70% of all gliomas. Chromosomal, genetic and epigenetic mutations in GBM are under investigation to determine their role in clinical practice.

PURPOSE:
Determine the main biomarkers evaluated for possible clinical utility in GBM

MATERIAL AND METHODS:
Bibliographic review focused on biomarkers associated to treatment response/prognosis in GBM published in 2009 or later in a third or upper quartile in its category.

RESULTS:
42 Articles reviewed

The main biomarkers identified

- Mutations involving isocitrate dehydrogenase
- 1p/19q deletion status
- O-6-methylguanine-DNA methyltransferase (MGMT) promoter methylation status

MGMT status is the most acknowledged, being considered as predictive factor to chemotherapy response. MGMT gene encodes an enzyme that repairs the damage induced by O(6)-alkylating agents, as temozolomide.

About 50% of patients show this promoter methylated in tumoral cells, resulting in low expression of this enzyme.

Several studies show higher OS and free survival progression (FSP) in patients with methylated promoter.

The most accepted method to determine promoter status is polymerase chain reaction after extraction of DNA and sodium bisulphite conversion.

CONCLUSION:
MGMT promoter methylation status could help therapeutic managing of GBM patients. Although the role of this biomarker in GBM response to temozolomide is well known, it is not yet implemented in clinical routine for decision making.