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Expression profile of immuno-oncology related genes and associations with response to temozolomide therapy in patients with glioblastoma

Abstract

Glioblastoma (GBM) is the most common and aggressive central nervous system malignant tumour. This tumour is associated with high mortality and 5-year survival rates and is only 9.8%. Currently, the standard treatment for GBM consists of surgical resection, radiotherapy and administration of temozolomide (TMZ).

In addition to histology, molecular characteristics such as the presence of IDH mutations and MGMT methylation are related to the prognosis and prediction of response to TMZ treatment. Despite extensive studies in recent years, the survival of patients with GBM remains very low and the disease is invariably lethal.

A multitude of molecular pathways used in the progress and immunological evasion of GBM, making chemotherapy treatment difficult. In addition, rapid infiltrative growth precludes complete surgical resection and, consequently, patients recur within a few months. It has recently been reported that the immunologically distinct GBM microenvironment has infiltrated immune cells that secrete substances that favour tumour progression and infiltration. Immunological checkpoints are also often unregulated and also contribute to the immune resistance of tumour cells. The study of these factors involved in the complex interaction between tumours, microenvironment and immune response to cancer may contribute to a better understanding of tumour biology and to improve patient care.

The objectives of the present study are to evaluate the transcriptional profile of 770 genes associated with immuno-oncology and tumour microenvironment (Pan-Cancer Immune-Profiling Panel - NanoString) in 100 glioblastoma (GBM) samples from Barretos Cancer Hospital and correlated with patient's response to TMZ treatment, survival, clinical, molecular characteristics (such as MGMT methylation and IDH mutations).

The results of this study may contribute to understanding the GBM immunological microenvironment, for the identification of new biomarkers and for the development of new drugs and therapeutic compounds involved in immuno-oncology.