MOLECULAR CHARACTERIZATION OF AN AGGRESSIVE PRIMARY CULTURE OF Glioblastoma

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Introduction and objectives: Glioblastomas are the most frequent and deadly brain tumors. Genomic alterations, as well as its high heterogeneity, are important features of these tumors. Despite the advances in the biology of these tumors, it is essential to develop models, such as primary tumor cell cultures, that better mimic their genomic diversity and therapeutic behavior. We aimed to characterize the molecular profile of HCB151, a glioblastoma primary culture. Material and methods: The HCB151 was established from a glioblastoma sample cultured with DMEM+10%BFS+1%PS. The cells were molecularly characterized, using arrayCGH, next generation sequencing (Ion Torrent) using a glioblastoma-specific panel and Sanger sequencing, miRNA expression and CNV using NanoString platform. The tumorigenic capacity was determined in vivo by the chicken chorioallantoic membrane (CAM) assay, and its response to temozolomide-based chemotherapy was done by MTS. Results: The HCB151 was characterized by gains of chromosomes 7, 9, 12, 17q, 18 and X and losses of chromosomes 1q, 8p, 13, 14, 17p, 20 and 22. It exhibited mutations in the TP53, PTEN, LZTR1 and TERT genes, and an unique miRNA profile. The CAM assay showed that HCB151 was able to form high vascularized tumors. In addition, HCB151 showed resistance to TMZ (IC₅₀=783µM) when compared to commercial glioblastomas cell lines (23-441µM). Conclusions: The present findings showed that the primary glioblastoma cell line (HCB151) showed classic genomic features of glioblastomas and exhibited a similar biological behavior, suggesting that this cell line is a good model for glioblastoma preclinical studies.

Keywords: glioblastoma primary cell culture, chromosomal alterations, mutations.

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