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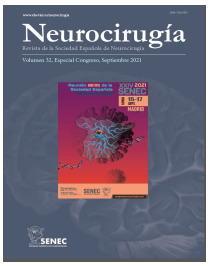

C-0116 - GLIOBLASTOMA RESPONSE TO BEVACIZUMAB IS PREDICTED BY VEGFA EXPRESSION LEVEL IN SERUM

R. Prat Acín, N. García Romero, I. Galeano Senabre, A. Roca Barber and Á. Ayuso Sacido

Neurocirugía, Hospital Universitario y Politécnico La Fe, Valencia, Spain. Faculty of Experimental Sciences, Universidad Francisco de Vitoria, Madrid, Spain. Brain tumour laboratory, Fundación Vithas, Grupo Hospitales Vithas, Madrid, Spain.

Resumen

Objectives: In glioblastoma (GBM) patients, bevacizumab demonstrated an increase in progression-free survival, but not in overall survival. However, clinical assays suffered from lack of strategies to identify subpopulation of patients that may benefit from the bevacizumab treatment.

Methods: Cancer stem cells were isolated from 77 GBM surgical samples and cultured. Cells were grown for 72 hours, and levels of VEGFA basal secretion were calculated by Enzyme-linked immunosorbent assay (ELISA). Then, the increased amount of bevacizumab needed to neutralize the VEGFA secretion was calculated in each case and angiogenic pattern and postreatment tumoral cell volume and growth addressed. Statistical analysis was performed using a 2-tailed Student t test and log rank test. Data are presented as means ± standard deviation and were calculated using the software package GraphPad Prism v. 5.0. Statistical values of $p > 0.05$ were not considered significant.

Results: Tumors volume and growth were suppressed by bevacizumab in high angiogenic cell lines. However, bevacizumab treatment did not affect tumoral activity in the models formed by the low VEGF-expressed cell lines After using increasing dosage of bevacizumab, we demonstrated a strong significant positive correlation between decreased VEGFA expression in tumor tissue and serum ($p < 0.05$). However, no correlation was observed between tissue and plasma VEGFA levels ($p = 0.153$).

Conclusions: Our data suggest that VEGFA levels in serum, might be useful to stratify glioma patients as well as to guide the recommended dosage when bevacizumab is administered. To measure the amount of VEGF in serum and not plasma can be proposed to enhance treatment efficacy.