c-MET

c-Met, also called tyrosine-protein kinase Met or hepatocyte growth factor receptor (HGFR), is a protein that in humans is encoded by the MET gene.

C-MET inhibitor.

Dismal glioblastoma outcome (Glioblastoma) prompts for the identification of response predictors and therapeutic resistance mechanisms of current therapies. Carvalho et al. investigated the impact of c-Met, HGF, VEGFR2 expression and microvessel density (MVD) in Glioblastoma patients submitted to second-line chemotherapy with bevacizumab. Immunohistochemical expression of c-Met, HGF, VEGFR2, and MVD was assessed in tumor specimens of Glioblastoma patients treated with bevacizumab, after progression under temozolomide. Survival analysis was evaluated according to the expression of the aforementioned biomarkers. c-Met overexpression was associated with a time-to-progression (TTP) after bevacizumab of 3 months (95% CI, 1.5-4.5) compared with a TTP of 7 months (95% CI, 4.6-9.4) in patients with low or no expression of c-Met ($p = 0.05$). VEGFR2 expression was associated with a TTP after bevacizumab of 3 months (95% CI, 1.8-4.2) compared with a TTP of 7 months (95% CI, 5.7-8.3) in patients with no tumoral expression of VEGFR2 ($p = 0.009$). Concomitant c-Met/VEGFR2 overexpression was associated with worse overall survival (13 months) compared with concomitant c-Met/VEGFR2 negative expression (19 months; $p = 0.025$). This data support the hypothesis that c-Met and VEGFR2 overexpression have a role in the development of glioblastoma early resistance and might predict poorer responses to anti-angiogenic therapies. [1].

1)
Carvalho B, Lopes JM, Silva R, Peixoto J, Leitão D, Soares P, Fernandes AC, Linhares P, Vaz R, Lima J. The role of c-Met and VEGFR2 in glioblastoma resistance to bevacizumab. Sci Rep. 2021 Mar 16;11(1):6067. doi: 10.1038/s41598-021-85385-1. PMID: 33727583.