

ABSTRACT CITATION ID: NOAE144.110  
P02.07.B FIBROBLAST ACTIVATION PROTEIN EXPRESSING  
MESENCHYMAL CELLS INFLUENCE T CELL ABUNDANCE AND  
FUNCTION IN GLIOBLASTOMA

N. Ternerova<sup>1</sup>, M. Houdova Megova<sup>1</sup>, T. Buna<sup>1</sup>, T. Svablova<sup>1</sup>,  
B. Vymolova<sup>1</sup>, E. Balaziova<sup>1</sup>, Z. Vanickova<sup>1</sup>, E. Krepela<sup>1</sup>, P. Hrabal<sup>2</sup>,  
R. Tomas<sup>3</sup>, D. Netuka<sup>4</sup>, P. Busek<sup>1</sup>, A. Sedo<sup>1</sup>; <sup>1</sup>Laboratory of Cancer Cell  
Biology, Institute of Biochemistry and Experimental Oncology, First Faculty

## Abstracts

of Medicine Charles University, Prague, Czech Republic, <sup>2</sup>Department of Pathology, Military University Hospital, Prague, Czech Republic, <sup>3</sup>Department of Neurosurgery, Na Homolce Hospital, Prague, Czech Republic, <sup>4</sup>Department of Neurosurgery and Neurooncology, First Faculty of Medicine, Charles University and Military University Hospital, Prague, Czech Republic.

**BACKGROUND:** Glioblastomas (GBMs) are aggressive brain tumors with strong immunosuppressive properties. In epithelial cancers, mesenchymal cells expressing fibroblast activation protein (FAP) play an important role in modulating the T cell response. We have recently shown that FAP<sup>+</sup> mesenchymal cells are present in human GBMs. The aim of this study was to determine their effect on T cell abundance and function. **MATERIAL AND METHODS:** GBM tumors (16 samples) were mechanically and enzymatically dissociated and analyzed for immune cell subpopulations by flow cytometry. Expression of T cell related genes was analyzed by qRT-PCR in GBMs selected based on FAP protein concentration determined by ELISA (14 FAP high [upper tercile], 16 FAP low [lower tercile]). Immunohistochemistry (IHC) was used to compare the number of CD3<sup>+</sup>, CD4<sup>+</sup>, and CD8<sup>+</sup> T cells in GBMs with high (upper tercile, n=21) and low abundance of FAP<sup>+</sup> stroma (lower tercile, n=20). Co-localization of FAP<sup>+</sup> mesenchymal cells and CD3, PD-L1 and PD-L2 was evaluated by immunofluorescence in frozen sections. 8 FAP<sup>+</sup> mesenchymal and 3 glioblastoma stem-like cell cultures were derived from human GBMs and PD-L1 and PD-L2 expression was determined using ELISA. Peripheral blood mononuclear cells were isolated from healthy donors' buffy coats. Proliferation of stimulated T cells in conditioned media from FAP<sup>+</sup> mesenchymal cells was analyzed by flow cytometry. **RESULTS:** The percentage of T cells in CD45<sup>+</sup> cells from GBMs positively correlated with FAP expression. Expression of the T cell inhibitory molecule PD-L2 was higher in FAP high GBMs. Immunohistochemistry revealed that the numbers of CD3<sup>+</sup> and CD8<sup>+</sup> T cells were higher in GMBs with a high abundance of FAP<sup>+</sup> stroma and T cells were frequently in close proximity to FAP<sup>+</sup> mesenchymal cells, which were often PD-L2 positive. *In vitro*, FAP<sup>+</sup> mesenchymal cells expressed more PD-L2 than glioblastoma stem-like cells. T cell proliferation was decreased after exposure to conditioned media from FAP<sup>+</sup> mesenchymal cells. **CONCLUSION:** FAP<sup>+</sup> mesenchymal cells influence T cell abundance in GBMs and may affect T cell functions by limiting their proliferation via soluble factors or cell-cell contact. Acknowledgment: This work was supported by the National Institute for Cancer Research (LX22NPO5102), the Center for Tumor Ecology (CZ.02.1.01/0.0/0.0/16\_019/0000785), Charles University project GAUK 365022 and Cooperatio Program Oncology and Haematology“.