patient's tumor tissue, providing a valuable platform for studies of GB therapeutic response and resistance.

**P02.08.A. THE RELATIONS OF FOCAL AND TOTAL DNA METHYLATION IN GLIOMAS**
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**BACKGROUND:** The role of epigenetic events in gliomagenesis is undoubted. However, the role of specific pathological events is not so clear. It was shown that loss in total DNA methylation correlates with higher tumor malignancy and oxidative DNA damage. But promoter methylation of many genes was reported to be significant for glioma malignancy and predictive for the treatment outcome. In carcinogenesis in general global DNA hypomethylation and focal hypermethylation coexist. The aim of our project was to evaluate the correlation between total DNA methylation and promoter methylation of selected genes.

**MATERIAL AND METHODS:** We analyzed glioma tissues from 60 patients. For total DNA methylation analysis we used the radiolabelling method with TLC separation of nucleotides and content estimation with phosphoimager. For promoter methylation analysis we have chosen MGMT (O-6-Methylguanine-DNA Methyltransferase), MPG (DNA-3-methyladenine glycosylase), GJA1 (Gap junction alpha-1 protein / connexin 43). The promoter methylation level was evaluated with the help of sensitive-high resolution melting (MS-HRM) method. **RESULTS:** Total DNA methylation was reversely correlated with brain tumor grade, confirming that 5-methylcytosine loss is important step in gliomagenesis. From 3 genes only MPG promoter methylation showed clear correlation with tumor grade. Methylation of GJA1 were better correlated with IDH status than in MGMT. **CONCLUSION:** There is a clear correlation between total DNA methylation and tumor malignancy. Gene promoter methylation is not highly correlated with total DNA methylation and shows low significance in selected cases. Results of our study showed clear correlation with tumor grade and MPG case. That suggests diverse mechanisms steering DNA methylation in general and local changes. It also shows that total DNA methylation is best predictor of tumor grade.

**P02.09.B. VALPROIC ACID CHANGES TOTAL DNA METHYLATION LEVEL AND INFLUENCES TEMOZOLOMIDE EFFECT IN GLIOBLASTOMA CELL LINES**
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**BACKGROUND:** Valproic acid (VPA) is a first-line antiepileptic drug for glioblastoma (GBM) patients. There is also some evidence it improves therapeutic response and resistance.

**RESULTS:** We adjusted the VPA doses to the ones achieved in the clinical treatment. We report that the deletion of SRR2 in GB cells leads to a reduction of SOX2 expression, which was accompanied with an impairment of cell growth and proliferation as well as with a reduction of self-renewal capacity in vitro. These data reveal that SRR2 is required for SOX2 expression and that its deletion results in impaired tumorigenic capacity of GBM cells.

**CONCLUSION:** Our data confirm that the SRR2 regulatory region is important for SOX2 expression and reveal that SRR2 deletion reduces SOX2 levels and halts malignant activity driven by SOX2 in GB.