**The role of signal transduction driver genes in developing an altered energy metabolism in cancer cells**

Normal cells start glycolysis in anaerobe conditions only. Warburg observed in 1930 the same process in tumorous cell at aerobe conditions as well - this so-called „aerobe-glycolysis” makes it possible for the cancerous cells to have large macromolecules necessary for rapid cell division readily at hand. The same process was also observe in normal, rapidly dividing embryonic cells. Driver genes behind this process are GLUT1, which enables the uptake of the glucose necessary for the process and the HIF1 alpha and HIF2 alpha transcription factors responsible for the initiation of the glycolysis by triggering the expression of multiple target genes. At the same time, the altered energy metabolism is in close connection to the six hallmarks of cancer (activation of oncogenes, loss of tumor suppressors, replicative immortality, evasion of apoptosis, induction of neoangiogenesis and of metastases). This suggests, that the former one is not an independent feature, but rather a process controlled by these key hallmarks. In our research our conceptual idea is that we assume that the driver mutations will also influence alterations in glycolysis and citrate cycle in the energy metabolism of the cells. In our project we aim to evaluate expression of genes involved in metabolic cycles within sub-cohorts designated by mutation state of key driver genes. In other words, the main topic of our study are not glycolysis / mitochondrial oxidation or mutation, but the combination of the two. Besides evaluation in cell culture models, our goal is also to assessment clinical relevance in samples with known follow-up.

Investigation of enzyme activity

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