Differential expression of glycolysis pathway genes in renal, lung and breast cancer

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Glycolysis is one of the most highly conserved and ancient pathways. This is the major pathway of glucose catabolism accompanied by a synthesis of ATP. However, various tumors are characterized by frequently activated glycolysis even in aerobic conditions. Several glycolytic genes are highly expressed in all tissues and thus considered as housekeeping genes (such as *GAPDH*). At the same time, genes encoding other glycolytic enzymes are differentially expressed in a variety of normal and pathological cells. We have studied the transcriptomic data of human renal, lung and breast cancers and estimated the tissue and cancer specific glycolytic expression patterns. We have shown that in all studied neoplasms even the "core" glycolytic genes were differentially expressed in comparison to normal tissues. Among these genes we describe the overexpression of *PKFP*, *ALDOA* and *GAPDH* in renal cancer, significant upregulation of *HK2* in breast cancer and *GPI* in squamous cell lung cancer. Several genes, such as *ALDOA, ENO1, GAPDH, PGK1,* were characterized by an unstable expression level with high variation in both normal and tumor samples. We have selected the subgroups of the probable housekeeping (reference) glycolytic genes for these cancers: *HK1, ADPGK, GPI, PGK1, PKM2* for renal cancer; *ADPGK, ALDOA, GAPDH, PGK1, BPGM, ENO1, PKM2* for squamous cell lung cancer and *ADPGK, BPGM, ENO2, GPI, PKFM* for breast cancer. The cases of decrease of glycolytic enzyme's mRNA level were rare. These data were validated using real-time PCR. Therefore, we have detected dysregulation of glycolysis in all studied cancers.

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