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The CpG island methylator phenotype (CIMP) in colorectal cancer is associated with energy metabolism alterations

M. Fedorova[1]*, E. Lukyanova[1], A. Snezhkina[1], G. Krasnov[1], S. Kharitonov[1], A. Dmitriev[1], N. Melnikova[1], E. Pudova[1], M. Kiseleva[2], M. Chernichenko[2], D. Sidorov[2], A. Kudryavtseva[1]

[1] *Engelhardt Institute of Molecular Biology RAS, Moscow, Russia*

[2] *National Medical Research Radiological Center, Ministry of Health of the Russian Federation, Moscow, Russia*

** e-mail: fedorowams@yandex.ru*

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Motivation and Aim: The accurate cause of dense aberrant DNA methylation in CIMP tumors remains incompletely clear [1]. However, several factors that may be associated with this process were found, including metabolic alterations such as glycolysis activation [2]. Therefore mRNA expression for genes involved in energy metabolism in CIMP+ and non-CIMP colorectal tumors (CRC) was compared.

Methods and Algorithms: Methylation profiling and gene expression data from The Cancer Genome Atlas were analyzed using R package DESeq2. mRNA level of the glycolytic genes was estimated for Russian population with qPCR (20 CIMP+ and 20 non-CIMP CRC samples).

Results: Bioinformatics analysis revealed increased expression level (1.5–3 folds) of many glycolytic genes in CIMP+ tumors compared to non-CIMP. Increased expression level was demonstrated for genes *ENO2* (3-fold), *PFKP*, *HK*3 and *PKM* (2-fold). Expression of genes involved in the Krebs cycle in CIMP+ tumors was slightly altered. Although decreased expression of the *OGDHL* (8-fold) was demonstrated. Expression of *PKLR* gene, a participant of gluconeogenesis, was 20-fold decreased. These results were verified with qPCR analysis. Frequent increase of *ENO2* mRNA level in CIMP+ CRC samples as well as 7 and 4-fold decrease of *OGDHL* and *PKLR* genes were evaluated [3].

Conclusion: Association between CIMP+ phenotype and activation of glycolytic genes was demonstrated in CRC samples. Both characteristics commonly correlated with aggressiveness of tumors and unfavorable prognosis [4].

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