Abstract

DNA methylation is an epigenetic mechanism that affects the level of gene expression. Methylation is a physiological for imprinted genes, when is required to express a gene derived only from a particular parent. If a fault occurs in the DNA methylation of these genes, various diseases may develop.

The object of this work was to determine the level of methylation of *H19* and *KCNQ1OT1* genes, located on the short arm of chromosome 11 in 15.5 region. The aim of this study was to investigate the changes in methylation of these genes in nephroblastomas, pheochromocytomas and paragangliomas, determine what changes of target genes are present in the samples, examined and divided samples into groups according to the detected changes.

File of nephroblastomas is divided into 3 groups according to the methylation changes in genes and compared with a similar study by Scott et al. 2012. File of pheochromocytomas and paragangliomas are found according to changes in the methylation of genes divided into 4 groups entirety. Found changes are aligned with the research Margetts et al. 2005.

Key words

DNA methylation, *H19*, *KCNQ1OT1*, nephroblastoma, pheochromocytoma, paraganglioma