

Abstract

Cardiovascular diseases are one of the leading causes of death in the Czech population. Up to 80 % of deaths are caused by myocardial infarction, a multigene affected disease. Knowledge of the genetic etiology of multifactorial diseases is continuously expanding. Our aim was due to whole - genome expression chip characterize clinically important genes for these cardiovascular diseases. On the basis of knowledge of these genes we could predict high-risk group of patients, determine appropriate treatment procedures and contribute to the suggestion of appropriate medication.

In this work were analyzed 174 whole blood samples. Out of them 24 were stroke patients, 92 patients with myocardial infarction and 56 controls. The samples were collected at the metropolitan Hospital in Čáslav. Samples taken at acute phase of myocardial infarction were compared with control blood collections of these patients after six months from the hearth attack. To these couples of samples were matched samples from control individuals according to several criteria. Samples of stroke patients were compared only with matched controls.

Clinically and statistically significant differential expression of genes was ascertained using Bioconductor version 2.3 with package limma in language R version 2.8.1. The statistical analysis identified a group of five genes whose expression was significantly different in patients who died within 6 months after hearth attack compared with patients who didn't die.

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Keywords: cardiovascular disease, myocardial infarction, stroke, gene expression, microarray analysis