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Comprehensive analysis of global gene expression and microRNA profile in coronary artery disease

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Studying the global gene expression and microRNA (miRNA) profile can provide a better understanding on the genetic basis of Coronary artery disease (CAD). The present study was to perform global transcriptome profiling to identify novel genes / pathways for CAD, supported by miRNA profiling to understand epigenetic regulation of candidate gene expression. Blood whole transcriptome profiling was undertaken in 10 CAD patients and 10 asymptomatic controls while miRNA profile was analyzed in 14 cases and 10 controls, respectively, using the Agilent microarray platform. The study participants were selected from the ongoing Indian atherosclerosis research study (IARS). Validation of microarray findings was done in 100 cases and 100 matched controls for 10 putative candidate genes. Gene expression and miRNA data were analyzed with 'R' program and Gene Spring software respectively. 494 genes were significantly differentially expressed between cases and controls (Fold change >2 , $p<0.05$). These genes were primarily belonged to inflammation and immune response and cell regulation. Candidate gene expression showed higher expression of CXCL1, EGR3, IL8, PTGS2 and CD69 and lower expression of IFNG and FASLG in cases ($p\leq0.05$). Three miRNAs, miR-144*, miR-96 and miR-1260, were significantly up regulated while miR-185* was found to be down regulated in the cases as compared to the controls. Of note, the expression levels of ADAMTS18 and KCTD16, which are predicted gene targets of miR-96, were lower in CAD patients in the microarray dataset. Combining global gene expression and miRNA data can improve our understanding on the underlying molecular pathogenesis of atherosclerosis.

Biography

Prathima Arvind is pursuing her Ph.D. at thrombosis research Institute, India (TRI). Since 2005 she is working in TRI and involving in various projects in functional genomics unit. She has published 9 papers in reputed journals.

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