

## **Preliminary assessment of differential expression of candidate genes associated with atherosclerosis**

### **ABSTRACT**

Identifying susceptible genes associated with the pathogenesis of atherosclerosis (ATH) may contribute toward better management of this condition. This preliminary study was aimed at assessing the expression levels of 11 candidate genes, namely tumor protein (TP53), transforming growth factor, beta receptor II (TGFBR2), cysthathionenine-beta-synthase (CBS), insulin receptor substrate 1 (IRS1), lipoprotein lipase (LPL), methylenetetrahydrofolate reductase (MTHFR), thrombomodulin (THBD), lecithin-cholesterol acyltransferase (LCAT), matrix metalloproteinase 9 (MMP9), low density lipoprotein receptor (LDLR), and arachidonate 5-lipoxygenase-activating protein (ALOX5AP) genes associated with ATH. Twelve human coronary artery tissues (HCATs) were obtained from deceased subjects who underwent post-mortem procedures. Six atherosclerotic coronary artery tissue (ACAT) samples representing the cases and non-atherosclerotic coronary artery tissue (NCAT) samples as controls were gathered based on predetermined inclusion and exclusion criteria. Gene expression levels were assessed using the GenomeLab Genetic Analysis System (GeXP). The results showed that LDLR, TP53, and MMP9 expression levels were significantly increased in ACAT compared to NCAT samples ( $p < 0.05$ ). Thus, LDLR, TP53, and MMP9 genes may play important roles in the development of ATH in a Malaysian study population.

**Keyword:** Atherosclerosis; Candidate genes; Differential gene expression; Genomelab genetic analysis system