INVESTIGATING THE ONSET AND PROGRESSION OF CORONARY ATHEROSCLEROSIS USING SYSTEMS ANALYSIS, SINGLE NUCLEOTIDE POLYMORPHISMS AND BIOCHEMICAL PATHWAYS

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ABSTRACT

Coronary artery diseases (CAD) are known to be one of the most detrimental causes of morbidity and death in the developed countries, and also happens to be the cause for long term disability in survivors. Coronary Atherosclerosis (CA) is one of the major CAD that leads to ischemia or stroke. CA is a multifactorial disease with its development and progression extending its limbs into various metabolical, demographic, lifestyle related and genetic causes. In the current study, we focus primarily on the association of various mutations, their associated Single nucleotide polymorphisms (SNPs) and transcriptomic data to identify pathways and mechanisms by which CA can be assessed further genetically. We carried out functional validation of 680 SNPs as we designed an integrated systems analysis pathway using GEO database, to help gain further insights in to the progression of the disease, or in other words Atherogenesis. The datasets that were data mined from existing literature, were further analyzed using ClueGo, and the genes were categorically synced into their respective metabolic pathways. Our analysis of the genes involved showed elevated levels of Calcium synthesis, LDL catabolism, Folate and Vitamin B12 enrichment, Triglyceride metabolism, Oleic acid synthesis, and blood coagulation pathways to be the major associated with the Disease.

KEYWORDS: Coronary Atherosclerosis, Systems Biology, Transcriptomics, Metabolic pathways, Single Nucleotide Polymorphisms, Gene Expression Omnibus