LM-KnB - the knowledge base on molecular genetics mechanisms controlling human lipid metabolism.

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Lipid metabolism (LM) implies biosynthetic pathways, transport, intracellular utilization, degradation, and excretion of lipids including such very physiologically important ones as triglycerides and cholesterol. These processes are controlled by numerous proteins and genes. An interest for the LM system is extremely high due to the facts that the lipid abnormalities are associated with an increased risk for vascular disease, and especially heart attacks and strokes. To support experimental investigation of genetic factors predisposing to high blood cholesterol level, the knowledge base on molecular genetics mechanisms controlling human lipid metabolism (LM-KnB) was developed. At present LM-KnB includes several types of data.

1) The data from the GeneNet database [1] concerning molecular genetics mechanisms, which control the intracellular cholesterol level: cholesterol biosynthesis, cholesterol uptake by cells and reverse cholesterol transport. The data is presented in the form of diagram which includes objects (proteins, genes, metabolites, etc.), biochemical reactions and regulatory processes. The key regulators are transcription factors of the SREBP family which function as a part of cholesterol sensor and control expression of genes encoding enzymes of cholesterol biosynthesis, uptake and efflux [2,3].

2) The compilation of human loci and genetic variants effecting plasma concentrations of lipids (total cholesterol, high- or low-density lipoprotein cholesterol, triglycerides), revealed by genome-wide association analysis or large-scale gene-centric meta-analysis.

3) The data on SNP or mutations in the promoter regions of genes associated with lipid disorders or abnormalities. Data were extracted from scientific publications and public databases. In some cases (if known) the effect of nucleotide substitution on promoter or

transcription binding site functional activity is also characterized.

In future, we plan further development of the LM-KnB. New data will be added to the current sections. Also some novel modules will be included into the LM-KnB: i) Knowledge on potential transcription factor binding sites disrupted or created by SNP; ii) the lists of genes which were identified as SREBP-targets by genome-wide ChIP-seq.

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