



Identification of Genes Involved in Foam Cell Formation and Atherosclerosis by DNA Microarray Technology

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Project Description: The overall aim of this project is to identify genes and mechanisms not previously known to be involved in the development of atherosclerosis. We have previously studied the effect of pro-atherosclerotic stimuli (oxidized LDL and copper) on macrophage gene expression by DNA microarray analysis. However, these studies do not directly address the question why some people are more susceptible to the development of atherosclerosis than others. To address this question, expression profiling of macrophages derived from 20 subjects with active atherosclerosis and 20 healthy controls will be performed. Patients are selected on the criteria of having progressing atherosclerosis and having a family history of cardiovascular disease. The macrophages will be investigated both at baseline and after oxidized LDL treatment. The RNA from treated and untreated macrophages is analyzed using DNA microarray. The combination of published data from genome-wide scans with DNA microarray data will be used for identification of novel disease genes and mechanisms. Genes that differ in expression between patients and controls, suggesting defects in regulatory regions, and are located in regions of the genome that has been linked to atherosclerosis will be selected for further investigation. The identified genes and mechanisms will be followed up by genetic and functional studies to verify their role in the development of atherosclerosis.

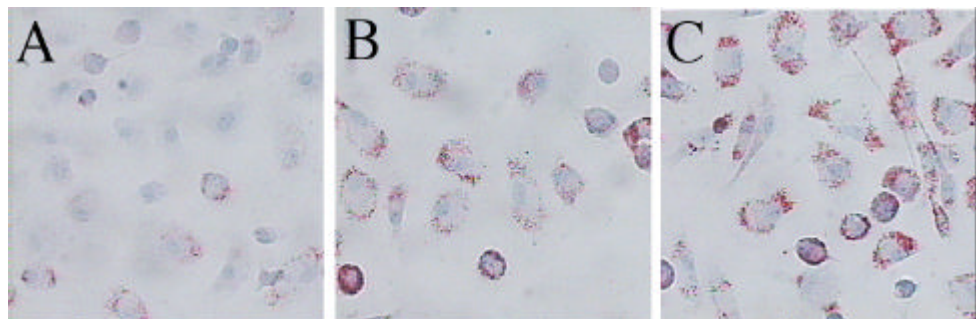


Figure. Lipid accumulation in human macrophages exposed to oxLDL as assessed by Oil Red O-staining. Macrophages were exposed to oxLDL (50 μ g/ml) for 0 h (A), 6 h (B) and 24 h (C).