Investigating Associations Between Smoking History and Gene Expression in Cultured Cells

Joo, Siyeon (School: Episcopal School of Acadiana)

Preliminary data shows that cigarette smoke is associated with gene expression changes in whole blood and skin. However, little is known about the epigenetic and genetic response to smoking in cells that are isolated from tissues and cultured, as smoking may induce epigenetic alterations in vivo that persist even in cell culture. Therefore, we conducted a gene expression analysis to assess the impact of cigarette smoking history on gene expression using RNA-sequencing (RNA-seq) data from immortalized skin fibroblasts and peripheral blood lymphocytes that were isolated from skin and whole blood samples respectively, harvested from postmortem donors participating in the Genotype-Tissue Expression (GTEx) project. Based on observed associations between cigarette smoke and gene expression in tissues harboring these cells, we hypothesize that smoking could also impact gene expression in cultured fibroblasts and lymphocytes. Associations between smoking and gene expression in each cell type might suggest that the epigenetic memory related to the smoking response was preserved during the transformation and/or culturing processes. Our results show no association between cigarette smoke exposure and gene expression in fibroblasts or lymphocytes. The current regression model was utilized to assess the impact of cigarette smoke on gene expression in tissues. Therefore, next steps involve adjusting the regression model to better suit gene expression analyses in cells. Future studies could examine the effects of cigarette smoke on gene expression in other main cell types or analyze how the effects of cigarette smoke differ between different subject cohorts.

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