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Cystic Fibrosis Research News

Title:
Expression of cystic fibrosis lung disease modifier genes in human airway models

Lay Title:
Human airway cell models to study genes contributing to CF lung disease

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What was your research question?
Cells from the nose and from the lungs have been used to investigate new therapies that target the gene that causes cystic fibrosis (CF), i.e., CFTR. But other genes in addition to CFTR contribute to variation in CF lung disease and response to therapies. Our study aimed to determine whether these genes have similar properties in the two cell models.

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Why is this important?

Repeated cycles of infection and inflammation contribute to progressive lung disease in persons with CF. Cells collected from the human lungs have been used as the gold-standard model to develop CF therapies that improve CF lung function. However, collecting cells from human lungs is highly invasive, which limits its accessibility especially in young children. Cells from the human nose, which can be collected by a none-invasive nasal brush, are a more accessible alternative to lung cells and can be obtained from any individual to study their personalized response to different therapies.

What did you do?

We compared the occurrence (expression profile) of genes that are known to contribute to CF lung disease across cells in the nose and cells in the lungs. The expression level of a gene corresponds to its degree of contribution in the tissue being investigated. Therefore, a similar expression profile across the cells in the nose and lungs would suggest the biological processes that relate to CF are the same among the two cell types. We implemented a novel statistical method to demonstrate the similar gene expression profile with a focus on genes related to CF lung disease.

What did you find?

Among all human genes that were expressed in cells in the lungs and nose, over 90% showed similar expression level in the two cell types, including the genes that relate to CF lung disease. Notable, these genes also showed similar with each other in the two cell types. Together, we showed the genes related to CF lung disease have similar expression properties between the two cell sources.

What does this mean and reasons for caution?

The similar expression levels of genes related to CF lung disease between the two cell sources suggest the biological processes corresponding to CF lung disease are likely to be the same in the two cell types, supporting the use of nasal cells as an alternative to lung cells in studies of CF therapies and enabling personalized approaches to understanding efficacy of therapies.

What's next?

Further laboratory experiments will be conducted to understand not just the expression across cells but also the function of the cells from the nose and lungs upon treatment with different CF drugs.

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