Making it easier to study personalized genomic biomarkers of lung disease

In the past few years, there has been significant progress in understanding how lung disease develops and predict who will respond to certain targeted therapies by obtaining lung tissue from research participants and studying changes in mechanistic genomic markers of DNA and RNA of the lungs in people with and without lung disease. However, a significant barrier to progress is the ability to obtain lung tissue, as doing so involves risks to the patient, such as a bronchoscopy (scope into the lungs), and biopsy (sample from the lung), which is invasive, requires a specialist with extensive training, and involves sedation and even general anesthesia in kids. This would not be practical in a clinical setting and problematic to ethically implement in a research setting in children. A huge barrier to moving these types of genomic findings to patients is figuring out how to obtain tissue in a noninvasive way.

Studies have recently shown that cells in the nose behave very similar to those in the lungs. However, traditional methods of obtaining cells from the nose requires special equipment and extensive training. In this study, we recruited 12 adults and compared whether obtaining cells from the front of the nose (anterior nares) using a special qtip would provide results equivalent to the traditional methods, which involves using a nasal speculum, headlamp, and a nasal brush to obtain cells deeper in the nose (inferior turbinate).

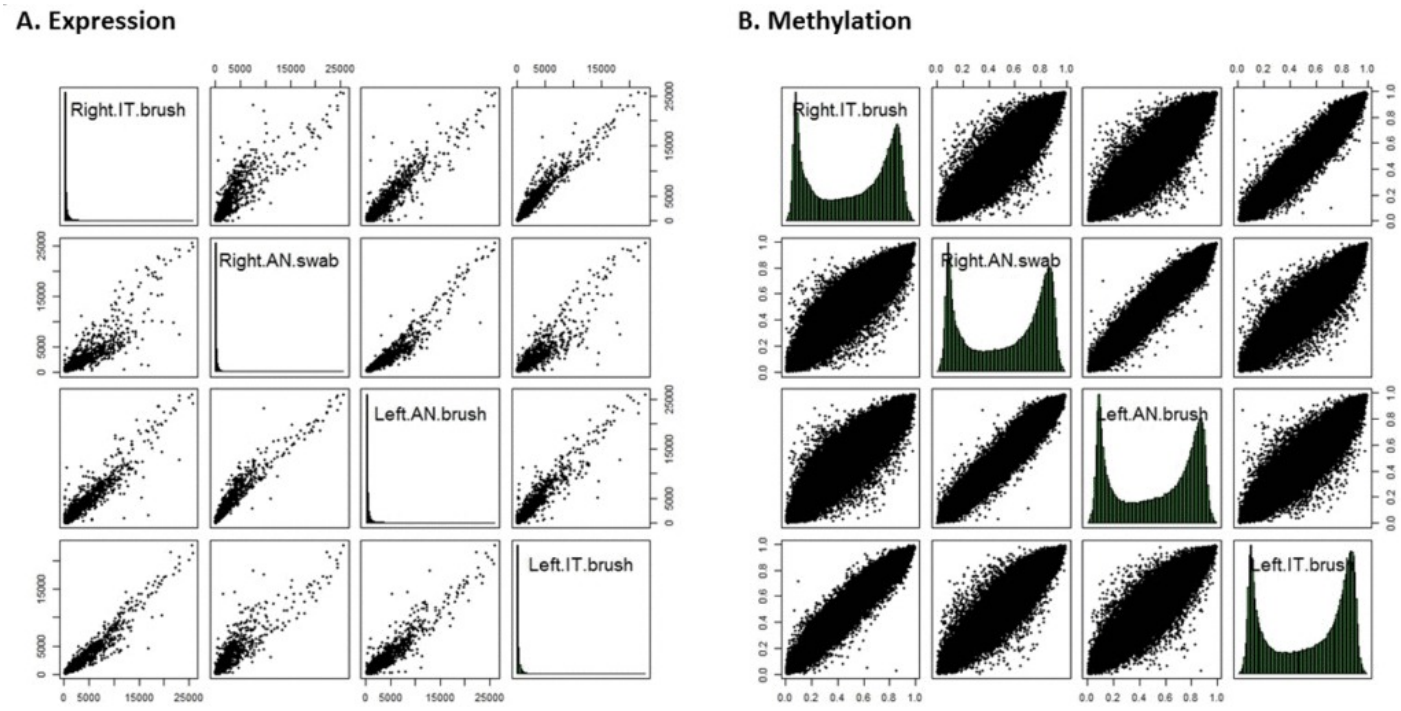

Fig. 1. Comparing patterns in RNA (gene expression) and DNA (methylation) using the qtip method vs. the traditional method of obtaining cells from the nose.

1A. Scatterplot of gene-level expression intensities from Illumina HumanHT-12 v4 Expression BeadChip array. Nasal samples obtained using the traditional method (cells from the inferior turbinate (IT)) and the qtip method (cells from the anterior nares (AN)). Histogram of expression intensities for each sample plotted on the diagonal. 1B. Scatterplot of all varying methylation sites from Illumina Beadchip Infinium HD array. All samples obtained from subject 10. Note that the qtip samples (cells from anterior nares) and traditional method (cells from inferior turbinate) samples are highly correlated for both gene expression and methylation. However, RNA from the qtip samples was significantly degraded.

We found that the qtip method was more comfortable than the traditional method. Importantly, we found that changes in DNA was comparable between the qtip method and the traditional methods. RNA from the qtip method was degraded compared to the traditional method but otherwise showed similar results to the traditional method (Fig. 1).

Studies like this are important in moving findings in research to useful tests in clinics or hospitals. The qtip method is already widely used in clinical settings and is familiar to most people, including children. If researchers can identify certain patterns of DNA change that will predict how a patient with lung disease will responsd to interventions, studies like this can help translate these finding into useful tests that clinicians can perform to manage a patient's lung disease. Further study and refinement of these methods are needed.

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