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# Single cell analysis to understand the diversity of immune cell types that drive disease pathogenesis

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## Abstract

Single-cell next-generation sequencing assays are powerful tools to understand the nature of immune cells that drive disease pathogenesis. In this brief review, we explain the value of performing assays at single-cell resolution to better understand the pathogenesis of allergy, asthma and other lung diseases. We explain the challenges in performing single-cell studies of airways and lung samples from patients with lung diseases. A major limitation comes from the amount of diseased tissue that can be utilized for research purposes. Finally, we discuss which sequencing strategies can be utilized for successfully investigate airway and lung diseases at single-cell resolution.

### Keywords

Single-cell RNA-seq; airway disease; smart-seq2

Genetic variants associated with risk of many lung diseases affect gene expression in a context-dependent manner in a specific subset of immune cell types in the human body[1-7]. The immune system contains diverse cell types required to defend from infectious agents. At the same time, immune cells can over-respond, resulting in allergy, asthma, autoimmune and inflammatory diseases. There is probably no other organ system that has a broader influence on human health. However, a complete understanding of the diversity of immune cell types and their properties that help drive disease pathogenesis is still lacking.

Next-generation sequencing (NGS) is one of the newest and most powerful tools to understand biological processes in health and disease. The study of genomes, epigenomes and transcriptomes provide unbiased information on how genetic variations and environmental signals perturb gene expression and chromatin structure in specific cell types to drive disease pathogenesis[5, 8-14]. Genomic assays like RNA-seq and microarrays are routinely performed on a population of cells under the assumption that cells of a particular

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type are highly similar. However, recent evidences from studies of single cells reveals that this assumption is incorrect; individual cells within the same population may differ dramatically, and these differences may have important consequences for the function of the entire cell population[15-22]. The application of NGS to the analysis of single-cell transcriptomes and epigenomes has enabled biologists to collect an unprecedented amount of information from each and every cell present in healthy and diseased tissues. The study of individual immune cells in blood, airways and lung samples from patients with lung diseases (*e.g.* allergy, asthma, COPD, pulmonary fibrosis, tuberculosis, bronchiectasis Figure 1) will lead to a better definition of the immune cell types driving disease pathogenesis, and also help understand the extent of cellular heterogeneity and molecular plasticity in a "hypothesis free" manner [12, 17, 18, 20, 21, 23-27]. These approaches can address significant challenges that currently exist with regard to systematically describing the "molecular status" of pathological or protective cell populations.

Is dysregulate immune response in disease associated with the development of new cell subset with pathogenic properties or a preferential expansion/contraction of pre-existing subsets of immune cells, already physiologically present in blood/lung tissue (Figure 2)? Several studies of chronic diseases in humans and in model organisms have reported the existence of immune cells that acquire a mixed phenotypes. For instance, in patients with latent tuberculosis, T cells responding specifically to *mycobacterium tuberculosis* antigens display both $T_H1$ and $T_H17$ features[8, 28]. Similarly, $T_H2$ cells with pathogenic properties have been identified from patients with allergy and asthma [29-33]. However, only studies performed at single-cell resolution will enable scientists to determine if those "disease-specific" functional features are the result of an expansion of a pre-existing population of cells or the result of differentiation in response to environmental signals[34, 35].

The power of single-cell omics analysis as a discovery tool has been well illustrated in the setting of cancer immunology. Just in the past 2 years, many studies have reported on single-cell omics analysis of the tumor microenvironment in several human cancer types. These studies have led to the identification of new immune cell subsets, new immune evasion and effector mechanisms, and potentially important molecular targets for cancer immunotherapy[24, 36-44]. For example, our recent single-cell study in lung cancer has led to the identification of a highly functional subset of tissue-resident memory T cells, which is likely to be the key cellular target of anti-PD1 therapy. Furthermore, it has defined a number of novel molecules that are likely to be important for modulating the function of this subset to achieve better anti-tumor immune responses[45, 46]. Single-cell analysis of tumor samples before and after anti-PD1 treatment have yielded insights into potential mechanisms and biomarkers that can distinguish responders from non-responders to immunotherapy[45, 47]. The studies in the cancer field highlight that single-cell analyses of diseased tissue samples can provide information relating to key pathogenic mechanisms driving disease as well as help understand mechanisms of action of novel interventions.

The relatively easy access to excess tumor tissue samples from standard diagnostic or therapeutic procedures has enabled researches to rapidly conduct these single-cell studies in large numbers of cells and patient samples. However, for lung diseases such as asthma and COPD it is not routine clinical practice to obtain airway tissue samples. This issue coupled

with the limited amount of tissue that can be obtained for research purposes may explain the relative paucity of single-cell studies in lung diseases. One way to address this limitation is to study lung diseases in model organisms. For instance, single-cell analysis of the development of tracheal epithelial cells *in vivo* has led to the identification of new cell types and a better understanding of cell lineages in the context of pulmonary fibrosis[48]. More recently, in a mouse model of asthma driven by house dust mite allergen exposure, Tibitt *et al.* showed that the repertoire of T helper cell in the inflamed lung tissue is much more heterogeneous than usually accepted[49]. However, airway and lung disease are long-lasting diseases and mouse models are, by definition, only capturing part of the complex human biology. Thus, human studies are likely to provide deeper insights into disease pathology.

An important technical limitation for studying human tissue samples with low cell numbers is that the most commonly used high-throughput platforms for single-cell analysis requires several thousand cells as input material. Sample with just tens to hundreds of cells would require a different approach that relies on single-cell sorting by flow-cytometry into 96-well plate following by single-cell library preparation (Figure 1, upper panel). By far the most successful method is the optimized single-cell RNA-seq library preparation adapted from the Smart-seq2 protocol [50-53] (also commercially developed by Takara, ICell8). When combined with index-sorting, high-dimensional protein expression data also can be obtained in parallel[54]. This method, although laborious when prepared manually, allows researchers to review the complete surface phenotype of every single cell sorted into a plate and associate that event with its transcriptome. The other method is the new generation of droplet-based single-cell RNA-seq assay[55, 56], commercialized by 10X Genomics. As shown by a comparative study[57], Drop-seq assays generate lower resolution dataset, making computational analysis difficult, especially when analyzing highly similar cell subsets such as T cell subsets, as opposed to more diverse cell types such as peripheral blood mononuclear cells (Figure 1, lower panel). Our analysis showed that smart-Seq2 assay detected twice the number of genes compared to commercial Drop-Seq assay (10X Genomics)[58]. At the level of individual genes, the sensitivity of both assays was similar for highly-expressed genes such as *B2M*. However, for several genes of interest, only 30-40% of the cells showed expression using 10X Genomics whereas 85-95% of the cells showed expression when using Smart-seq2 assay[58]. This contrast is more important when working with resting immune cells, such as T cells, that contain a much lesser amount of RNA. In early 2019, 10X Genomics has released a newer version with a higher rate of mRNA capture (resolution). This assay when coupled with sample multiplexing using DNA oligo-barcoded-antibodies[59] or DNA oligo-barcoded-lipid anchoring in cell membrane[60] will enable the study of airway and lung samples at much higher resolution in a cost-effective manner.

Recently, NGS assays that profile the epigenetic state of cells are also available for studying clinical samples with limited cell numbers. Such single-cell epigenetic methods include, histone modification profiling by immunoprecipitation followed by sequencing (sc-ChIP-seq)[61, 62] or the more accessible and cost-effective profiling of Transposase Accessible Chromatin with high-throughput sequencing (sc-ATAC-seq)[63]. These assays will complete the arsenal of tools required for understanding cellular heterogeneity and the mechanisms of cellular differentiation or activation in response to pathogenic perturbations[64].

In summary, single-cell high-dimensional immune-phenotyping, RNA-sequencing, and chromatin accessibility profiling analyses of immune cells isolated from blood, airway and lung tissue samples from patients with lung diseases will provide insights into the molecular and cellular mechanisms that are driving health and diseased states. These approaches are likely to constitute the cardinal measures for the future development of diagnostic tools, novel biomarkers and therapeutic interventions in the emerging field of precision genomic medicine.

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## List of abbreviations:

| | |
|---|---|
| **NGS** | next-generation sequencing |
| **COPD** | chronic obstructive pulmonary disease |
| **RNA-seq** | RNA sequencing |
| **ATAC-seq** | assay for transposase-accessible chromatin using sequencing |
| **ChIP-seq** | chromatin immunoprecipitation followed by sequencing |

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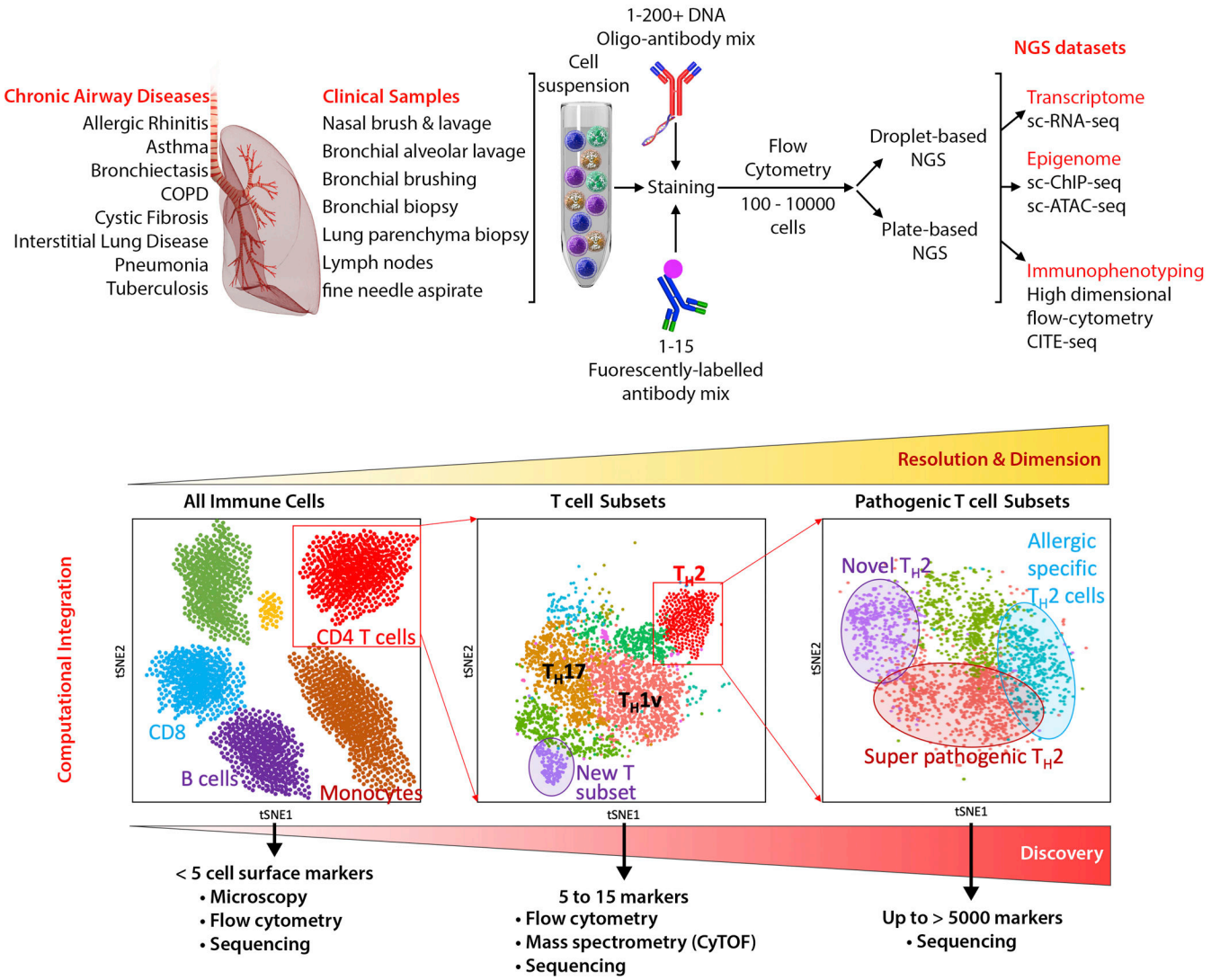


**Figure 1. Single-cell next-generation sequencing in airway and lung diseases.**

Top panel provides an overview of the processes the clinical samples can go through. Patient samples will be processed by isolating cells and staining with both a mix of antibodies recognizing cell surface markers conjugated with fluorochrome (for flow cytometry analysis) and/or with DNA-barcoded-oligos (for immunophenotyping analysis by sequencing). Depending on the number of cells and output dataset requested, stained cells will be sorted and processed through two single-cell sequencing platforms: the PCR plate-based sorted cells with Smart-seq2 library preparations or the droplet-based 10X platform. The lower panel shows the importance to select the single-cell sequencing methodology that provides the highest resolution. If working with a limited number of cells, higher is the number of genes detected per cell, higher will be clustering resolution and the possibility to separate cells with new molecular features.

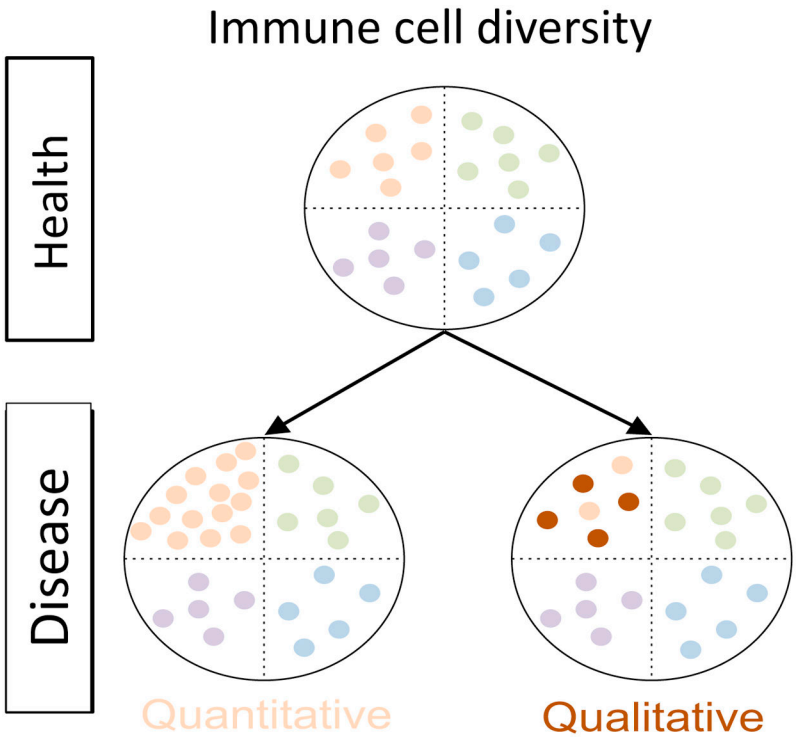


**Figure 2. Schematic representation of the information provided by single-cell analysis.**

Top panel shows the distribution of four immune cell subsets in a healthy individual. The bottom panel illustrates the possibilities that can happen in diseased states: either the relative proportion of one cell subset is increased without changes in their molecular program (quantitative change) and/or cells in one subset change their molecular program (qualitative change); such differences can be captured by single-cell analyses.