Spatial transcriptomics for respiratory research and medicine

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Shareable abstract (@ERSpublications)
In combination with scRNA-seq, spatial transcriptomics have the potential to lead to an unprecedented view of lung architecture at the single cell level, providing original information on lung physiology and physiopathology https://bit.ly/3uDYir0

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Recent developments in single-cell technologies, and particularly single cell RNA sequencing (scRNA-seq), have provided invaluable tools to decipher complex biological systems like the lung. In the respiratory system, scRNA-seq analyses have led to the discovery of new cell types, such as ionocytes, as well as to a refined classification of the cells composing the lung [1–4]. Profiling of more than 300 000 cells from patients suffering lung pathologies, such as idiopathic pulmonary fibrosis (IPF), has allowed to identify new sub-populations of aberrant basal and endothelial cells that are specific to IPF [5]. Furthermore, collective efforts such as the Human Cell Atlas, aiming at characterising all cells in the human body at the molecular and spatial levels, have flagged the lung as a priority organ [6]. Ongoing efforts are now directed towards the development of spatial transcriptomic techniques allowing identification of cell localisation and description of prevailing cell–cell interactions in the organ in order to define a physiological cell atlas. Although technologies able to sequence *in situ* the transcriptome of individual cells are rapidly emerging, they still lack the resolution required to depict the extreme cell heterogeneity that characterises the anatomy of the lung. This article will present an overview of the different spatial transcriptomic methodologies that could be applied to the lung, as well as their potential impact for respiratory research and medicine.