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Single-cell RNA-seq profiling identified molecular signatures and transcriptional networks regulating lung maturation

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Lung formation and function are orchestrated by a diversity of cell signaling and transcriptional interactions among progenitor cells that are accomplished at the level of individual cells that are integrated by paracrine interactions among the many cells that comprise the lung. In the present study, we used massive parallel DNA sequencing coupled with an unbiased analytic approach to identify molecular mRNA signatures in single cells isolated from the entire embryonic mouse lung at the sacular phase (E16.5) of morphogenesis. Through integrative bioinformatics and systems biology analysis of single-cell RNA-seq data, we identified major cell types in the fetal mouse lung. A diversity of epithelial, endothelial, smooth muscle, bone marrow derived, and fibroblastic cell types were classified by their RNA expression similarity within cell type groups. Unique cell-specific gene signatures, key regulators, bioprocesses and functional profiles associated with each cell type and across cell types, via paracrine signaling, were identified. Single-cell mRNA-Seq analysis revealed the spectrum of transcriptional heterogeneity present within closely related pulmonary progenitor cells. We developed a bioinformatics pipeline to analyze the complex and extensive single-cell RNA data. The data provide a rich information base facilitating the understanding of lung maturation at high resolution and identifying the genetic framework that regulates cell fates during lung maturation.

Biography

Yan Xu is presently an Associate Professor at Cincinnati Children's Hospital Medical Center and the Bioinformatics Core Director of the Perinatal Institute. She graduated from Shanghai Medical University in 1986. She completed her PhD from University of South Alabama in 1997 and Postdoctoral training from University of Colorado in 2000. Her research is focused on the identification of gene signatures, regulatory networks, and biological pathways controlling lung maturation and disease. She has published 57 peer reviewed papers and served as reviewer and editor for a number of reputed scientific journals.

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