Temporal gene expression of mesenchymal cells in the pediatric lung

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**Temporal Gene Expression of Mesenchymal Cells in the Pediatric Lung**

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**INTRODUCTION:**

The newborn lung undergoes vast biochemical and physiological changes during adaptation from the intrauterine to the extrauterine environment. Lung morphogenesis continues from approximately 10 weeks of gestation until the completion of the respiratory system at birth. Major developmental events include the establishment of lung units, initiation of blood vessel development, and growth of airways and alveoli. These processes are under the control of a complex network of transcription factors, growth factors, and cellular interactions that are essential for proper lung development.

**OBSERVATION:**

Recent advances in single-cell RNA sequencing have provided new opportunities to study cell-type diversity and molecular mechanisms in the pediatric lung. The neonatal lung is a particularly rich source of cellular heterogeneity, making it a valuable model for understanding the diversity of pulmonary cell types and pathophysiologic mechanisms associated with pediatric lung diseases.

**METHODS:**

Single-cell RNA sequencing was performed using the Illumina NovaSeq5000 at the University of Rochester Genomics Research Center, and results were analyzed using the TopoCell Algorithm. Reads were further normalized using counts per million (CPM) and variance mean calculated with R, implemented in DESeq2. Gene expression data was filtered to remove genes not expressed in at least 3 of the 8 samples, and then normalized to TotalRNAseq. Gene lists were generated using Ingenuity Pathway Analysis (IPA). Temporal mRNA expression profiles were determined using the Limma package for differential gene expression analysis.

**RESULTS I:**

Temporal analysis of genomics data utilizes samples across multiple time points and requires tailored statistical methods. In this study, we investigated the temporal gene expression profiles of mesenchymal cells in the pediatric lung using single-cell RNA sequencing.

**RESULTS II:**

Our results provide new insights into the dynamic changes in gene expression during lung development and reveal potential therapeutic targets for the treatment of pediatric lung diseases.

**CONCLUSIONS:**

This study highlights the importance of understanding the dynamic gene expression profiles of mesenchymal cells in the pediatric lung, which may provide new avenues for the development of targeted therapies for pediatric lung diseases.

**ACKNOWLEDGEMENTS & REFERENCES:**

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**METHODS:**

1. Temporal gene expression analysis was performed using single-cell RNA sequencing of human lung tissues from newborns and children. RNA sequencing was performed using the Illumina NovaSeq5000 at the University of Rochester Genomics Research Center, and results were analyzed using the TopoCell Algorithm. Reads were further normalized using counts per million (CPM) and variance mean calculated with R, implemented in DESeq2. Gene expression data was filtered to remove genes not expressed in at least 3 of the 8 samples, and then normalized to TotalRNAseq. Gene lists were generated using Ingenuity Pathway Analysis (IPA). Temporal mRNA expression profiles were determined using the Limma package for differential gene expression analysis.

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**SUMMARY:**

Analysis of dynamic gene expression in mesenchymal cells across a time series demonstrates the unique heterogeneity of pulmonary mesenchymal cells throughout adolescence. Identification of gene expression associated with immune signatures during pediatric lung development was noted. Further validation of results using this technique may advance understanding of the diversity of pulmonary cell types and pathophysiology of pediatric lung disease.