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Utilizing functional genomics and systems biology to understand perinatal lung maturation and associated diseases

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Abstract

Prenatal maturation of the respiratory system is fundamentally important for the transition to air breathing at birth. Lung immaturity is a major cause of morbidity and mortality in newborn infants and underlies the pathogenesis of acute respiratory failure (termed "respiratory distress syndrome" or RDS) and chronic respiratory dysfunction (bronchopulmonary dysplasia or BPD), associated with preterm birth. Lung maturation includes diverse structural, cellular, and biochemical changes in lung architecture and function that are precisely coordinated by genetic and environmental factors that synchronize the length of gestation with the process of lung maturation. We have developed a pipeline utilizing functional genomics and systems biology approaches to integrate large-scale lung gene expression data from lung specific gene deletion and mutation mouse models, with array independent genomic information to reveal transcriptional regulatory networks controlling lung maturation and surfactant homeostasis, permits the identification of new genes, pathways and transcriptional networks controlling surfactant lipid homeostasis and lung maturation. The signaling and transcriptional mechanisms that influence lung growth and maturation needed to support the abrupt adaptation to air breathing at birth are of considerable interest, and will provide a rational basis for the design of new treatment strategies for neonatal pulmonary disease.

Biography

Dr. Xu was graduated from Shanghai Medical University in 1986. She completed her Ph.D from University of South Alabama in 1997 and postdoctoral training from University of Colorado in 2000. She has leaded a Microarray-Bioinformatics Core since 2002 and has set up the infrastructure and analytic pipelines for various Bioinformatics application. Her main research interest is to apply bioinformatics and systems biology approaches to biological and clinical data to gain better understanding of molecular mechanisms underlying lung development and pathogenesis. She has published 53 peer reviewed papers and served as an editorial board member of PLosOne.