Title: A Comprehensive Anatomical Ontology for the Developing Lung

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Rationale: We currently lack a thorough understanding of perinatal lung development, a critical stage in the formation of the distal gas-exchange region of the lung. This process has significant clinical relevance for managing neonatal lung disease related to prematurity and abnormal lung growth, as well as for repair and regeneration of the lung after injury. The NHLBI Molecular Atlas of Lung Development Program (LungMAP) is a cooperative research project tasked with building an integrated open-access database that will characterize the molecular anatomy of the later stages of lung development, from E16 to P28 in the mouse and from 22-24 weeks of gestation to early childhood in the human. To provide a framework for this atlas, we created a detailed ontology of the anatomical structures, tissues, and cells in the developing mouse and human lung.

Methods and Results: Existing ontologies for the lung were reviewed to develop a framework that could be integrated with other ontologies. The LungMAP anatomical ontology is designed as a partonomic ("X is a part of Y" and/or "X arises from Y"), text-based hierarchy. It represents a significant expansion of existing mouse, human and cell ontologies, including the addition of both common and unique ontological terms for the developing lung. Synonyms commonly used in the literature and other ontologies are included to improve query searching. The LungMAP anatomical ontology is organized along the proximal-distal axis of the lung, from the proximal conducting airways to the distal gas-exchange regions of the lung. It includes terms for 1) well-characterized structural and functional components, 2) distinct tissue compartments, and 3) both generic and specific cell types with subpopulation designations. This ontology can be used at varying levels of resolution (e.g., whole mount or sectioned material, or isolated tissues and cells) to annotate the dynamic temporal-spatial patterns of gene and protein expression in the developing lung. The current working version is open-ended so that newly defined structures and molecularly distinct cell types can be incorporated.

Conclusion: The LungMAP anatomical ontology provides a common language and framework for annotating the molecular signatures of tissues and cells in the developing lung. This ontology will be used for the integration of both existing and new data sets, detailing molecular processes associated with normal lung development and maturation. The LungMAP anatomic ontology will serve as a unique reference resource for the larger research community.

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