Wilms Tumor 1 (WT1) is Required in Diaphragm and Early Lung Development

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Background

- Congenital diaphragmatic hernia (CDH) is a common and severe congenital malformation affecting 1 in 3500 live births.
- The high mortality in CDH patients is due to a combination of lung hypoplasia and pulmonary hypertension.
- Our hypothesis is that a core group of genes is responsible for both diaphragm formation and pulmonary development.
- Whole genome sequencing identified mutations in the WT1 gene in two patients with CDH.
- WT1 encodes a transcription factor that is expressed specifically in the mesothelium and required for organ development and injury recovery.



Figure 1: Whole genome sequencing in the DHREAMS study identified two CDH patients with mutations in the WT1 gene in Exon 9 (highlighted in red). Exon 9 encodes the 3rd zinc finger that is required for DNA binding and regulation of gene transcription.

Objectives

- Identify role of WT1 in diaphragm development
- Identify the role of *Wt1* in lung development

Methods: Tissue-specific conditional deletion of Wt1 in diaphragm or lung

Diaphragm and lung mesenchyme Specific Deletion

A. P0.5 Diaphragm

B. E16.5 Lung





Figure 2: *Tbx4*-rtTA; *Tet-O-Cre* induces cell specific recombination in the diaphragm mesothelium(A) and the lung mesenchyme (B). The timing of recombination induction leads to different phenotypes giving us insight to spatial and temporal requirements of Wt1.



of left diaphragm development at E12.5 (red circle) but normal right diaphragm (B). The left diaphragm in Wt1 mutants shows increased distance between the septum transversum and the pleuroperitoneal fold (PPF, D).

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