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## **The Role of Prrx Transcription Factors In Salivary Gland Development**

**Objectives:** Mouse models containing combinatorial deletions of the homeobox transcription factors Prrx1 and Prrx2 develop craniofacial malformations. These defects are due to abnormal epithelial-mesenchymal interactions and abnormal neural crest contribution. Our objective was to assess the role of Prrx1 and Prrx2 in salivary gland development, a process also dependent on epithelial-mesenchymal interactions and neural crest.

**Methods:** Wild type (WT) (Prrx1<sup>+/+</sup> Prrx2<sup>+/+</sup>) and double knockout (Prrx1<sup>-/-</sup>Prrx2<sup>-/-</sup>) embryos were harvested and analyzed by H&E and PAS-Mucin stains to look at the morphology and differentiation of submandibular glands (SMG). Three-dimensional reconstructions were generated from histological sections of SMG. Immunohistochemistry was used to determine the location of Prrx expression, along with a possible downstream target: Platelet Derived Growth Factor Receptor-Beta (PDGFR $\beta$ ). Transient co-transfection assays with a PDGFR $\beta$  promoter reporter construct were used to assess the direct regulation of this promoter by the Prrx transcription factors.

**Results:** The SMG in Prrx double knockout embryos are hypoplastic, undifferentiated, and malpositioned compared to WT embryos. In WT embryos Prrx1 expression increases from E13.5 to E16.5, while PDGFR $\beta$  decreases. In Prrx mutants PDGFR $\beta$  is not down-regulated as observed in WT embryos.

**Conclusion:** Prrx transcription factors are instrumental in proper salivary gland development, and may regulate SMG morphogenesis via the PDGF signaling pathway.