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Mapping the Fate of *Hoxa-5* Expressing Cells in a Mouse Model

The axial skeleton consists of the vertebral column and the ribs. As for other most other tissues, development of the axial skeleton is regulated in part by *Hox* genes, which regulate the anterior-posterior identity of each segment. However, the cellular processes that *Hox* genes regulate in order to confer specific morphologies are mostly unknown. Our research focuses on *Hoxa-5*, which patterns vertebrae surrounding the cervical-thoracic transition of the axial skeleton. To better understand how *Hoxa-5* patterns this region, we are using genetic lineage mapping to permanently label Hoxa-5 expressing cells and their descendants, and then characterize their behaviors and fates throughout development. We implemented a technique called Cre-Lox recombination. To initiate lineage mapping, we first crossbred mice to generate a line of heterozygous *Hoxa-5* mutant mice. In these heterozygotes, a Cre coding sequence was inserted into the *Hoxa-5* gene by homologous recombination, allowing Cre to be expressed in *Hoxa-5* expressing cells. The final cross between a male mouse that contained the *Hoxa-5Cre* transgene and a homozygous *Rosa26-Tomato* female mouse, a mouse genetically containing a red fluorescence reporter permanently activated by Cre, was the next step in the lineage map. Preliminary data indicate that embryos generated from this cross show expression of Cre in areas in which *Hoxa-5* is expressed, which is essential for accurate lineage mapping. Ultimately, these methods will allow us to identify parts of the axial skeleton that have cells which have a history of expressing *Hoxa-5*.