OTX2 and CRX Rescue Overlapping and Photoreceptor-Specific Functions in the Drosophila Eye
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- Human OTX factors — OTX1, OTX2 and CRX — perform overlapping, yet distinct subsets of Otd-dependent functions during Drosophila eye development, providing a system to study subfunctionalization of a family of related transcription factors.
- Human OTX factors rescue the morphogenesis of rhabdomeric photoreceptors, suggesting that ciliary and rhabdomeric photoreceptors arose from a common ancestor requiring an Otd-related factor for its development.
- Different CRX alleles associated with similar retinal degenerations can be functionally distinguished using the fly eye as a model system.

Published online 7 December 2011

Highlights in DD
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“Highlights” calls attention to exciting advances in developmental biology that have recently been reported in Developmental Dynamics. Development is a broad field encompassing many important areas. To reflect this fact, the section spotlights significant discoveries that occur across the entire spectrum of developmental events and problems: from new experimental approaches, to novel interpretations of results, to noteworthy findings utilizing different developmental organisms.

Go with the flow (Stepwise Arteriovenous Fate Acquisition During Mammalian Vasculogenesis by Diana C. Chong, Yeon Koo, Ke Xu, Stephen Fu, and Ondine Cleaver, Dev Dyn 240:2153–2165) Despite the fact that the circulatory system is essential for survival, there has only been a trickle of information regarding the timing and mechanisms of arterial and venous cell fate specification in mammals. Here, Chong and colleagues remedy this oversight, and show that vasculogenesis occurs in a stepwise manner. Angioblasts aggregate into lumenless cords, extend, form tubes, and differentiate, with arteries acquiring their fates before veins. Furthermore, markers for both arterial and venous fates are initially expressed in vessel primordia, and resolve to a classic pattern of fate specific markers (arterial or venous) over time. To test whether cell extrinsic mechanisms are required for vessel fate specification, marker expression was examined in Rasp1/−/− embryos, whose vessels have no lumens, and in cultured embryos with severed circulatory systems. In both cases, one arterial marker diminished while another was maintained, leading the authors to conclude that, while cell fate is specified at the molecular level, maintenance and/or full-fledged differentiation is under the control of hemodynamic flow. The work opens the floodgates: offering a new set of tools with which to study the multitude of existing mouse mutants with vascular remodeling defects.

Facing change (Epigenetic Integration of the Developing Brain and Face by Trish E. Parsons, Eric J. Schmidt, Julia C. Boughner, Heather A. Jamniczky, Ralph S. Marcucio, and Benedikt Hallgrimsen, Dev Dyn 240:2233–2244) As the size of the brain increased in our hominid ancestors, so did facial shape, steering toward a relatively short, broad face. Such observations caused Trish Parsons and others in the Hallgrimsen and Marcucio labs to wonder, is there a relationship between brain and face development? They approached the question by quantifying morphological characteristics of the forebrain and facial prominences in four strains of mice at gestational day (GD) 10–10.5, the time of embryonic facial formation. Statistical analysis reveals that within mice in which forebrain and facial shapes deviate most significantly from the norm, there is a strong correlation in their morphologies. For example, in one strain a longer and taller forebrain covaries with a larger, anterior-projecting maxillary process (upper jaw) and a longer frontonasal mass (nose). These findings lend evidence for direct developmental interactions between the brain and face in a background where genetic, allometric, and environmental variations are carefully controlled. The evolutionary implications are two-fold. The integration of brain and face contributes to morphological variation. Paradoxically, brain and face integration also constrains variation. This is something that our ancestors certainly could not comprehend but that we, thanks to our enlarged brain, can.

Imagine this (MicroCT for Molecular Imaging: Quantitative Visualization of Complete Three-Dimensional Distributions of Gene Products in Embryonic Limbs by Brian D. Metscher and Gerd B. Müller, Dev Dyn 240:2301–2308) In an episode of the animated sitcom The Simpsons (“Homer3”, 1995), an ordinarily two-dimensional Homer Simpson discovers that life is very different in a world with three dimensions. Here, Metscher and Müller delve into the world of 3D expression patterns, a worthy endeavor considering that embryos are, after all, three-dimensional. Compared with current 3D expression techniques based on reconstruction of stained tissue sections, which can be distorted during processing, the authors’ X-ray tomography (microCT)-based technique directly images whole-mount samples. To obtain X-ray contrast of in situ hybridization or immunostaining patterns, the researcher uses commercially available kits to render enzyme-mediated silver deposition at sites of bound secondary antibody conjugate. Analyzing the resulting high-resolution images with imaging software enables quantifiable results, such as spatial measurements and relative intensity values, that are invaluable for a sophisticated understanding of related developmental mechanisms. Plus, the eye-popping, seemingly tangible microCT images make those obtained from traditional techniques seem, well, cartoonish.