plays a conserved role as a homeotic regulator, during vertebrate development.

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Program/Abstract # 417
Integrative imaging of the developing opossum cochlea
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The short-tailed opossum (*Monodelphis domestica*) is a marsupial mammal that gives birth to highly underdeveloped young that complete much of their sensory development outside the womb while fused to the mother's teat. While suckling, the primary organ of hearing, the cochlea, undergoes an extraordinary morphological transition from a cylinder to a coiled cochlea with 1.9 turns. Because this transition occurs *ex utero*, opossum cochlear development can be experimentally manipulated *in vivo*, making the opossum an ideal model for inner ear development. This is important, as the genetic underpinnings of cochlear morphogenesis are largely unknown. This study utilizes the opossum as a novel mammalian model for cochlear development, with the aim of synthesizing developmental morphogenetic and molecular signaling data to pinpoint mechanisms shaping mammalian cochlear development. High resolution computed tomography (CT) and magnetic resonance imaging (MRI) technologies allowed visualization of cochlear outgrowth and coiling. Comparisons with histological sections and cleared and stained pups indicated that MRI scans more accurately differentiated soft tissue boundaries, and these data were used to reconstruct a 3D model of opossum cochlear development. Central toward understanding cochlear outgrowth is pinpointing regions of cell proliferation and apoptosis. Apoptosis assays indicated that cell death occurred along the base of the developing cochlear coils, while proliferation (phosphohistone-H3) preferentially occurred along their lateral margins. Taken together, these results lay the foundation for future utilization of the opossum as a novel model for mammalian inner ear morphogenesis.

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Program/Abstract # 418
A new model for the evolution of the vertebrate jaw
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The appearance of jaws was a turning point in vertebrate evolution because it allowed primitive vertebrates to capture and process large, motile prey. The vertebrate jaw consists of separate dorsal and ventral skeletal elements connected by a joint. How this structure evolved from the unjointed gill bars of a jawless ancestor is an unresolved question in vertebrate evolution. To understand the developmental bases of this evolutionary transition, we examined the expression of 12 genes involved in vertebrate pharyngeal patterning in the jawless fish, lamprey. Contrary to previous reports, we find nested expression of *Dlx* genes, and combinatorial expression of *Msx*, *Hand* and *Gsc* genes along the dorso-ventral (DV) axis of the lamprey pharynx, indicating gnathostome-type pharyngeal patterning evolved before the appearance of the jaw. In addition, we find that Bapx and Gdf5, key regulators of joint formation in gnathostomes, are not expressed in the lamprey first arch, while Barx, which is absent from the intermediate first arch in gnathostomes, marks this domain in lamprey. Taken together, these data support a new scenario for jaw evolution in which recruitment of Bapx and Gdf5 into a pre-existing DV patterning program drove the evolution of the jaw by altering the identity of intermediate first arch chondrocytes. We present this "Pre-pattern/Cooption" model as an alternative to current models linking the evolution of the jaw to the evolution of novel pharyngeal DV pattern.

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Program/Abstract # 419
The role of neural crest progenitor population specification and proliferation dynamics in establishing species-specific differences in jaw size
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The diversification and adaptive success of vertebrates owes a great deal to their specialized feeding apparatuses. The jaw skeleton derives from the cranial neural crest (CNC), a population of cells unique to vertebrates. Despite its basic developmental conservation, the adult jaw varies tremendously in both size and shape. Recently, the orchestration of developmental programs regulating jaw size and shape has been shown to be under the control of CNC cells. Yet, underlying molecular and cellular mechanisms driving species-specific changes in jaw size remain unknown. To test the hypothesis that CNC progenitor population number and proliferation rates contribute to species-specific differences in jaw size, we compare CNC development in two morphologically distinct birds, duck and quail. We analyze expression of genes involved in neural tube regionalization including *Otx2*, *Foxg1*, *Fgf8*, and *Krox20*, and genes involved in the induction and maintenance of CNC such as *Pax7*, *FoxD3*, and *Sox10*, in duck and quail embryos at Hamburger and Hamilton (HH) stages 4–12. These stages span the period of time when CNC become specified and emigrate from the rostral neural tube. We also compare proliferation rates in duck and quail premigratory CNC and postmigratory mandibular mesenchyme, which show that duck CNC proliferate more slowly than those of quail. Our results indicate that molecular and cellular differences emerge early on during duck and quail development, which likely contribute to species-specific variation in jaw size.

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Program/Abstract # 420
Evolution of vertebrate skeletal myogenesis: Insights from the cyclostome lamprey
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Skeletal muscles of gnathostomes (jawed vertebrates) are categorized into epaxial and hypaxial groups morphologically separated at the level of the notochord. During development, portions of the hypaxial dermomyotome undergo delamination to provide migratory myoblasts that give rise to the tongue muscles, the tranpezius (cucullaris) muscles, and the limb muscles. These muscles require activation of specific developmental genes, such as MRFs, Pax3 and Lbx1, at the ventral (hypaxial) side of the dermomyotome. To gain

evolutionary insights on the establishment of complex and diverse morphology of skeletal muscles, we examined the expression and molecular interaction of the muscle-related genes in the cyclostome lamprey, which lacks all the migratory hypaxial muscles.

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Program/Abstract # 421
Evolutionary conservation of the role of Sox6 in terminal differentiation of skeletal muscle
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Recent findings in mice and zebrafish (Hagiwara et al. Dev Dyn 236: 2062–; von Hofsten et al. EMBO Rep 9: 683–) suggest that the role of Sox6 in skeletal muscle development is conserved in vertebrates. In mice, it has been shown that Sox6 null skeletal muscle sustains expression of slow fiber specific genes in the fetal and early postnatal stages. Based on this observation, we have proposed that Sox6 functions as a suppressor of slow fiber specific genes in developing muscle. In zebrafish, Sox6 has also been shown to function as a suppressor of slow fiber specific genes. These results suggest, although body patterns and temporal emergence of slow and fast fibers differ, the role of Sox6 in muscle development is evolutionarily conserved. Here, we report our recent data concerning the role of Sox6 in vertebrate skeletal muscle development. First, using Sox6 conditional knockout mice, we show that the slow fiber phenotype is maintained, and even more exaggerated, in adult Sox6 null skeletal muscle. Second, to examine the conserved nature of Sox6 function, the role of Sox6 in *Xenopus* muscle is being investigated. We report, in *Xenopus*: 1) Sox6 mRNA expression in embryonic muscle corresponds to the developing fast fibers, and 2) Sox6 overexpression by the Sox6 transgene has a negative effect on myoblast fusion. These new findings indicate that: A) Sox6 likely determines the fiber type specific gene expression pattern at the very beginning of the muscle fiber type differentiation, B) Sox6 may also play a role in myoblast fusion, and C) Sox6 function as a suppressor of slow fiber specific genes is conserved in vertebrate skeletal muscle development.

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Program/Abstract # 422
Lrp4 and the mammalian neuromuscular junction
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Regional specialization of the pre- and postsynaptic membrane is a common feature of all synapses. At vertebrate neuromuscular synapses, neural Agrin binds to Lrp4 in muscle, which in turn activates MuSK, a receptor tyrosine kinase. Activation of MuSK leads to pre- and postsynaptic differentiation. By mutating the intracellular domain of Lrp4, I demonstrate that the extracellular domain of Lrp4 is sufficient to mediate postsynaptic differentiation in cultured myotubes. To address the function of Lrp4 in synaptogenesis *in vivo*, I have generated mice carrying transgenes that confer muscle-specific expression of wild-type and mutant forms of Lrp4. I am currently crossing these transgenes into $lrp4^{-/-}$ mutant mice to assess the contribution of muscle-derived Lrp4 in synapse formation and the role of the intracellular domain of Lrp4 in presynaptic differentiation in vivo.

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Program/Abstract # 423
Evidence for a rudimentary colon in the elasmobranch, *Leucoraja erinacea*
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The emergence of aquatic animals onto land 370 mya required development of a water-absorbing colon in the digestive tract to prevent desiccation. The elasmobranch, *Leucoraja erinacea* provides a system in which to investigate how morphological changes occur in the vertebrate digestive tract during evolution. The cartilaginous fish are nearly isotonic with their ocean environment and thus do not actively drink seawater to maintain osmotic consistency. Despite this, we have histological, immunohistochemical and physiological evidence that a region of the spiral intestine in marine elasmobranches can absorb water. High concentrations of acid mucins and the water specific channel protein AQP4 are expressed in the distal-most region of the skate spiral intestine. In addition, we found water absorption in the spiral intestine occurs at higher rates than the stomach in *L. erinacea*. Water absorption is unaffected by increases in lumen pressure, suggesting that water transport across the membrane is not due to changes in osmotic pressure, but is the result of facilitated diffusion likely through aquaporins. Furthermore, *Hoxa13* and *Hoxd13* are expressed in the developing skate gut, suggesting conserved roles for *Hox* genes in patterning the early colon. Evidence of a colon in *L. erinacea* is surprising, since the formation of a colon was considered to be an adaptation to the evolution of terrestrial life and not a marine novelty. Our finding that the *L. erinacea* spiral intestine absorbs water is a novel function for the intestine of cartilaginous fish and suggests several models for colon development in the vertebrate lineage.

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Program/Abstract # 424
Evolution of pancreatic endo- and exocrine cells in deuterostomes
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The pancreas is a vertebrate endocrine/digestive organ that develops from foregut endoderm and plays an important role in metabolic regulation. Within the pancreas are the hormone-secreting islet cells (endocrine) and digestive enzyme-secreting acinar (exocrine) cells. The transcription factors Pdx1 and Ptf1a are necessary for endo- and exocrine tissue development in vertebrates. Together they are sufficient to induce ectopic pancreatic tissue in naïve vertebrate gut endoderm, suggesting they play a key role in the initial activation of the pancreatic developmental plan. Invertebrate deuterostomes and some fish lack more specialized gut organs, such as the pancreas. In these organisms, pancreatic function is instead accomplished by endo- and exocrine cells scattered throughout the lining of the gut. How did this change in the organization of pancreatic cells, from dispersed to localized to a single gland, occur during deuterostome evolution? To address this we are currently studying the expression and function of Pdx1, Ptf1a, and Insulin in the hemichordate marine acorn worm, *Saccoglossus kowalevskii*. These basal deuterostomes show a remarkable similarity in early body plan organization to vertebrates but lack a pancreas, making *Saccoglossus* an attractive model for studying the evolution of deuterostome pancreatic development. Our results indicate that Pdx1 and Ptf1a are fairly well conserved within the *Saccoglossus* genome and along with Insulin, are expressed in the gut during development. Co-expression studies