and gain- and loss-of-function experiments will help conclude whether Pdx1 and Ptf1a's role in specifying pancreatic cell fate has been conserved during deuterostome evolution.

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Program/Abstract # 425
Embryonic origin of osteoblasts in scales and fins of medaka fish
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Exoskeletons, or dermal bones, in vertebrates are body covering skeletal elements that develop in the dermis through intramembranous occification. This type of bone is generally thought to be derived from the neural crest. However, while contribution of the neural crest to the cranial exoskeleton (skull, etc.) is well documented mainly in chick, its contribution to the post-cranial exoskeleton (scales and fin rays infish, etc.) is still unclear. To address this, we have developed a tissue transplantation technique for medaka embryos, and transplanted dorsal neural tubes (with neural crest cells) and somites from double transgenic donor embryos, Tg (*β-actin:DsRed, osterix:EGFP*), into unlabelled host embryos at somitogenesis stages. Surprisingly, tracking the transplanted cells revealed that the neural-crest-derived cells never differentiated into GFP-positive osteoblasts in scales, dorsal- or anal fins, whereas they were always colonized by somite-derived cells, indicating that the fish post-cranial exoskeletons are not of neural crest origin but derived from the mesoderm. From these, we propose the dual origin of the fish exoskeleton, one in the head from the neural crest and the other in the trunk region from the mesoderm.

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Program/Abstract # 426
Gcm2 enhancers specific for the skin surface have contributed to the evolution of the ionocytes rich in proton pomp in zebrafish
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In higher teleosts, ionocytes in the skin are known to maintain body fluid homeostasis, yet molecular mechanisms that control development of ionocytes during the evolution of higher teleosts remain to be investigated. We discuss a possible connection between the evolution of gcm2 enhancers and an acquisition of ionocytes rich in proton pomp (HRCs: H^+-ATPase Rich Cells) of zebrafish. The antisense morpholino of gcm2 abolished development of only HRCs in three types of ionocytes, suggesting that gcm2 is essential for their development. To examine further a role of gcm2 in development of HRCs, we analyzed enhancer elements of gcm2 in currently available vertebrate genomes and identified 8 kb and −37 kb regions of gcm2 loci that enhance gcm2 expression in HRCs of zebrafish. The similar enhancers of gcm2 in zebrafish have not been found in other vertebrates. In addition, our data show that in Polypterus, known to be one of the extant primitive bony fishes, gcm2 was expressed in the outer gills but not in the skin surface during their larval stages. All results suggest that the enhancers have evolved uniquely in zebrafish and that the acquisition of enhancers for the expression of gcm2 may have contributed to the evolution of HRCs in zebrafish.

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Program/Abstract # 427
Gata and bHLH factors form a conserved regulatory circuit for deuterostome immunocyte development
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Two major cell types carry out immunity in the purple sea urchin larva: pigment cells, which migrate to sites of infection and injury, and sub-sets of the blastocoelar cells, which phagocytose foreign particles, and express a suite of immune receptors and effectors. Specification of immunocytes occurs early in a ring of cells localized in the vegetal plate of the mesenchyme blastula. We have identified homologues of key vertebrate hematopoietic transcription factors, with expression profiles consistent with a role in sub-specification of these cells. These include Sp-Gatac, a zinc-finger transcription factor homologous to vertebrate Gata-1, -2 and -3 and a homolog of the Scl, Tal2 and Lyl1 members of the bHLH family, Sp-Scl, which play distinct roles in immunocyte precursor sub-specification in the sea urchin embryo. Sp-Gatac perturbation has a profound effect on blastocoelar cell ingression, while Sp-Scl knock-down results in a signal dependant, non-cell autonomous pigment cell defect. Other components of vertebrate hematopoietic gene regulatory networks, including Sp-E2A, homologous to vertebrate hematopoietic E-proteins E2A, HEB and ITF-2, an Id-1/2/3/4 homologue, Sp-Id, and the cofactor Sp-Lmo2, are also expressed in these cells. This suggests the existence of a conserved gene regulatory circuit for early immune cell development, involving GATA and bHLH transcription factors that are active even in the very simple developmental context of the sea urchin larva.

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Program/Abstract # 428
y* and *e* contribute to abdominal pigmentation variation in *Drosophila ananassae
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In *Drosophila* species, abdominal pigmentation is a highly variable trait with a well understood genetic and biochemical basis that makes pigmentation an excellent model for reconstructing the molecular mechanisms behind evolutionary changes. My study investigated the genetic basis for intraspecific variation between light and dark strains of *D. ananassae*. Genes *ebony* (*e*) and *yellow* (*y*) are known to contribute to color pattern variation in several *Drosophila* species. To test the hypothesis that *y* and *e* also contribute to pigmentation regulation and intraspecific variation in *D. ananassae*, I genotyped an introgression cross between light and dark strains of *D. ananassae*. I found that *y* and *e* exhibited a strong linkage with the phenotypic variation observed in *D. ananassae,* supporting my hypothesis. I am currently investigating which regions of *e* and *y* contribute to this variation. To accomplish this, DNA sequencing is in progress for *e* and *y* loci from multiple dark and light strains of *D. ananassae* originating from different geographic locations. My current results show that the upstream regions of *y* and *e* are highly differentiated between the light and dark strains of *D. ananassae.*

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